

Vol. 37 No. 1 2024

Print ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

**An International Journal for
Conservation and Use of Plant Diversity**



**Indian Society of Plant Genetic Resources
New Delhi, India**

INDIAN SOCIETY OF PLANT GENETIC RESOURCES

(Registration No. S/18336)

The Society was founded in 1987 with the following objectives:

- To serve and promote the scientific cause and to advance academic interest in the field of plant genetic resources.
- To disseminate knowledge relating to various aspects on plant genetic resources.
- To provide a forum for organizing symposia/conferences with a view to develop close relationship among the scientists engaged and interested in plant genetic resources activities.

Indian Journal of Plant Genetic Resources, the official publication of the Society, is published thrice in a year. The contribution to the journal, except for invited papers, is open to the members of the society only.

Membership to the society is open to all the individuals/institutions interested in various aspects of plant genetic resources. The membership fee is as follows:

Membership*	Inland	Foreign
Annual Member	Rs. 1,500.00	US\$ 120.00
Life Member	Rs. 6,000.00	US\$ 1,800.00
Institutional (Annual)	Rs. 30,000.00	US\$ 1,500.00
Institutional (5 years)	Rs. 2,00,000.00	US\$ 5,000.00
Institutional (10 years)	Rs. 4,00,000.00	US\$ 10,000.00

Issues of the journal published earlier are also available.

Limited space is available for advertisement of interest to botanists/geneticists/plant breeders and all those concerned with plant genetic resources.

CORRESPONDENCE relating to membership, advertisement and other related matters should be addressed to the General Secretary, Indian Society of Plant Genetic Resources, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012, India (E-mail: ispgr2015@gmail.com).

COMMUNICATIONS regarding the publication of research papers should be addressed to Editor-in-Chief, Indian Journal of Plant Genetic Resources, Indian Society of Plant Genetic Resources, C/o ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012, India (E-mail: ispgr2015@gmail.com).

ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

Vol. 37 No. 1 2024

Editor-in-Chief RK Tyagi

Editors (Foreign) Michael Halewood, Andriana Alercia, Ronnie Vernooy, Ehsan Dulloo

Editors (Indian) K Joseph John, M Pitchaimuthu, V Celia Chalam, Aditya Pratap, N Sivaraj, Vandana Tyagi, RK Salgotra, Kavita Gupta, Rakesh Singh, Sheikh M Sultan, Lalit Arya, Manjusha Verma, K Pradheep, Amit Singh, Sherry Rachel Jacob, CS Mohanty, S Rajkumar, Rakesh Bhardwaj, Kuldeep Tripathi, Rajiv Kumar and Somnath Roy



INDIAN SOCIETY OF PLANT GENETIC RESOURCES

NBPGR CAMPUS, NEW DELHI-110012, INDIA

Web: ispgr.nbpgr.ernet.in

INDIAN SOCIETY OF PLANT GENETIC RESOURCES

Patrons MS Swaminathan, RS Paroda, Mangala Rai

Honorary Fellows MS Swaminathan, GS Khush, S Rajaram, RS Paroda, Mangala Rai, Emile Frison, RB Singh, SK Datta, HY Mohan Ram, KS Gill, SK Vasal, Kamal Bawa, PL Gautam, BS Dhillon

EXECUTIVE COUNCIL (2022-24)

President RS Paroda (New Delhi)

Vice Presidents RK Tyagi (New Delhi); Jai Chand Rana (New Delhi)

General Secretary Anuradha Agrawal (New Delhi)

Joint Secretary Manjusha Verma (New Delhi)

Treasurer Kuldeep Tripathi

Ex Officio Member GP Singh, Director, ICAR-NBPGR

Councillors	North Zone:	Monika Singh (New Delhi)	Kuldeep Tripathi (New Delhi)
	East Zone:	Mohan Lal (Jorhat)	Veerendra Kumar Verma (Umiam)
	West Zone:	Sandip K. Bera (Junagadh)	Anil Patidar (Jaisalmer)
	South Zone:	N. Sivaraj (Hyderabad)	Rose Mary Francies (Thrissur)
	Central Zone:	Shailesh Tiwari (Varanasi)	Surendra Kumar Barpete (Madhya Pradesh)

EDITORIAL BOARD

Editor-in-Chief:

RK TYAGI

Indian Society of Plant Genetic Resources (ISPGR)
editor.pgr@gmail.com

Foreign Editors

Michael HALEWOOD

Head of Policy Unit
Bioversity International Rome, Italy
m.halewood@cgiar.org

Adriana ALERCIA

Germplasm Documentation Specialist ITPGRFA,
FAO Rome, Italy
adriana.alercia@fao.org

Ronnie VERNOOY

Genetic Resources Policy Specialist
Centre for Development Innovation Wageningen University
and Research, Netherlands
r.vernooy@cgiar.org

Ehsan DULLOO

Team Leader, Integrated Conservation Strategies
Bioversity International
Mauritius
e.dulloo@cgiar.org

Indian Editors

K. Joseph JOHN

Principal Scientist
ICAR-NBPGR Regional Station – Thrissur
Thrissur-680 656, Kerala
joseph.k@icar.gov.in; nbpgtrsr@gmail.com

Pitchaimuthu M.

Principal Scientist
Division of Vegetable Crops
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bengaluru-560 089
m.pitchaimuthu@icar.gov.in

V. Celia CHALAM

Principal Scientist
Division of Plant Quarantine
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
celia.chalam@icar.gov.in

Aditya PRATAP

Principal Scientist
ICAR-Indian Institute of Pulses Research
Kanpur-208 024, Uttar Pradesh
Aditya.Pratap@icar.gov.in

N. SIVARAJ

Principal Scientist
ICAR-NBPGR Regional Station – Hyderabad
ARI Campus, Rajendra Nagar
Hyderabad-500 030, Andhra Pradesh
n.sivaraj@icar.gov.in

Vandana TYAGI

Principal Scientist
Germplasm Exchange Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
vandana.tyagi@icar.gov.in

R.K. SALGOTRA

Professor & Coordinator
School of Biotechnology
Sher-e-Kashmir University of Agricultural Sciences &
Technology of Jammu-180 009
rks_2959@rediff mail.com

Kavita GUPTA

Principal Scientist
Division of Plant Quarantine
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
kavita.Gupta@icar.gov.in

Rakesh SINGH

Principal Scientist
Division of Genomic Resources
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
rakesh.singh2@icar.gov.in

Sheikh M. SULTAN

Principal Scientist & Officer-In-Charge
ICAR-NBPGR, Regional Station
Srinagar-190 005
Jammu & Kashmir
mohmmad.sheikh@icar.gov.in

Lalit ARYA

Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
lalit.arya@icar.gov.in

K. PRADHEEP

Principal Scientist
ICAR-NBPGR Regional Station - Thrissur, Vellanikkara,
KAU P.O. Thrissur-680656, Kerala
k.pradheep@icar.gov.in

Sherry Rachel JACOB

Senior Scientist
Division of Germplasm Conservation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
sherry.jacob@icar.gov.in

S. RAJKUMAR

Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
S.Rajkumar@icar.gov.in

Kuldeep TRIPATHI

Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
kuldeep.tripathi@icar.gov.in

Manjusha VERMA

Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
manjusha.verma@icar.gov.in

Amit SINGH

Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Amit.singh5@icar.gov.in

C.S. MOHANTY

Principal Scientist
CSIR-National Botanical Research Institute
436, Rana Pratap Marg, Prem Nagar, Hazratganj
Lucknow-226 001, Uttar Pradesh
cs.mohanti@nbri.res.in

Rakesh BHARDWAJ

Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Rakesh.Bhardwaj1@icar.gov.in

Rajiv KUMAR

Principal Scientist (Horticulture)
Division of Flower and Medicinal Crop
ICAR-Indian Institute of Horticultural Research
Hessaraghatta lake post, Bengaluru-560089, Karnataka
rajiv.kumar11@icar.gov.in

Somnath ROY

Scientist
Central Rainfed Upland Rice Research Station
ICAR-National Rice Research Institute
Hazaribag-825 301, Jharkhand
somnath.roy@icar.gov.in

CONTENTS

1. Potato Genetic Resources and their Utilization in India	1
<i>Satish K. Luthra and Vinod Kumar</i>	
2. Molecular Profiling of Erucic Acid Biosynthesizing <i>FAE1</i> Gene of Indian Mustard Varieties	20
<i>Rajesh Kumar, S. Rajkumar and J. Radhamani</i>	
3. High Popping Quality Finger Millet (<i>Eleusine coracana</i>) Genotypes	24
<i>Y. A. Nanja Reddy, P. Jayalakshmi, T. Lavanyabai, K. Geetha, M. Deepika and M. V. C. Gowda</i>	
4. Molecular Characterization of Garden Rose Germplasm using SSR Markers	31
<i>Shephalika Amrapali, Sunil Archak, Namita and Ambika B. Gaikwad</i>	
5. SSR Markers based Diversity Analysis in Elite Genotypes of Pearl Millet	39
<i>J. Jorben, Mukesh Sankar S., Anju M. Singh, C. Tara Satyavathi, Tripti Singhal, Thiribhuvan R. and S. P. Singh</i>	
6. Multi-crop Exploration in Unexplored Areas of Garo Hills, Meghalaya	47
<i>Sanjeev K. Singh, Ranbir S. Rathi, Kailash C. Bhatt, Subarna Hajong and Naorem A. Singh</i>	
7. Evaluation of Recombinant Inbred Lines of <i>Oryza glaberrima</i> and Improved Samba Mahsuri for Antixenosis and Tolerance against <i>Nilaparvata lugens</i> (Stal)	56
<i>Neha Chhabra, Preetinder S. Sarao, R. M. Sundaram and Gurjot Kaur</i>	
8. Collection, Characterization and Identification of Elite Genotypes of Wild/Semi-Domesticated Bitter Gourd (<i>Momordica charantia</i> var. <i>muricata</i>) for Utilization and Conservation	62
<i>Asna A. C., Jiji Joseph, Joseph K. John, Sainamole Kurien P and C. Beena</i>	
9. Evaluation of <i>Saccharum spontaneum</i> Clones for Water Deficit Stress Tolerance	73
<i>Vinu V., T. L. Pathy, Mahadevaswamy H. K., R. Valarmathi, Manju M. Paul and R. A. Kumar</i>	
10. Variability, Heritability, and Correlation Studies for Economic Traits in Grain Amaranth (<i>Amaranthus</i> spp.)	80
<i>Ved Prakash, Gajala Ameen, Vivek K. Sandilya and Jitendra K. Tiwari</i>	
11. Microsatellite Markers Reveal the Genetic Integrity of Stored Accessions of Cotton (<i>Gossypium arboreum</i> L.) in the Indian National Genebank	90
<i>Anto James, Shipra Deo, Anjali Kak and Mukesh K. Rana</i>	
12. Studies on Traditional Melon 'Vellari' (<i>Cucumis melo</i> Var. <i>momordica</i> L.) in Tamil Nadu, India	97
<i>Prabhu P, Anjula Pandey, S Rajkumar, Harish GD, Chithra Pandey and Rakesh Bharadwaj</i>	
13. Acclimatization Pattern of Cultivated <i>Capsicum</i> spp. in an Agro-Ecologically Diverse Habitat, Kerala, India	105
<i>Asish I. Edakkalathur, Presannakumari K.T., Latha M, Minimol J.S., Manju P, Pradeepkumar T., Krishnan S. and Sivaraj N.</i>	
14. Genetic Diversity, Variability, and Correlation Studies in South Indian Culinary Melon (<i>Cucumis melo</i> ssp. <i>agrestis</i> var. <i>acidulus</i>) Accessions	118
<i>Ratnakar M. Shet, Virupakshi Hiremata, Raghavendra Gunnaiah and Santosha Rathod</i>	
15. Performance of Exotic and Indigenous Coconut Genotypes for Growth, Fruit Yield, Fruit and Nut Characters under Assam Conditions of North East Region of India	125
<i>Leichombam S Singh, Niraj Vittal, Gobinda C Acharya and Manju Chaithra</i>	
Plant Germplasm Registration Notice	131
Author Guidelines	

REVIEW ARTICLE

Potato Genetic Resources and their Utilization in India

Satish K. Luthra^{1*} and Vinod Kumar²

Abstract

In India, ICAR-Central Potato Research Institute, Shimla presently holds a modest collection of over 4,669 accessions, comprising cultivated species, parental lines, indigenous varieties, advanced clones and wild/semi-wild tuber-bearing *Solanum* species. This is the largest potato collection in South Asia. The exotic *tuberosum*, *andigena* and wild species germplasm accessions have been imported from 40 countries based on requirements of resistance or tolerance to various biotic and abiotic stresses. Potato germplasm has been evaluated against several diseases and insect pests and also for morphological and yield traits. Donors have been identified against all the major diseases; some are resistant to two to three diseases. The utilization of indigenous and exotic genetic resources has resulted in the development and release of 70 indigenous potato varieties suitable for different agro-ecologies and 46 elite genetic stocks have been registered with ICAR-National Bureau of Plant Genetic Resources (NBPGR). This paper reviews the status of potato genetic resources and their utilization in India.

Keywords: Genetic stocks, Genetic resources, Potato, Utilization, Varieties.

¹ICAR-Central Potato Research Institute, Regional Station, Meerut, Uttar Pradesh, India.

²ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India.

***Author for correspondence:**

skluthra@hotmail.com

Received: 23/01/2023 **Revised:** 07/01/2024

Accepted: 12/01/2024

How to cite this article: Luthra SK and V Kumar. (2024) Potato Genetic Resources and their Utilization in India. *Indian J. Plant Genetic Resources*. 37(1): 1-19.
DOI: 10.61949/0976-1926.2024.v37i01.01

Introduction

Potato (*Solanum tuberosum* L.) is the most important non-grain food crop globally and is the most important crop for ensuring food security for developing countries, and a highly nutritious food providing more calories, vitamins and nutrients than any other staple food. Wide genetic resources are a high priority for any crop improvement program. Genetic resources are a collection of the large number of genotypes representing the genetic diversity of a crop species and its wild relatives. Genetic diversity is essential for crop improvement and maintaining the agro-ecosystem functioning. In the present climate change scenario, potato is an important crop for food and nutritional security. The long historical period of varietal development from its ancestors' native cultivars to modern, present-day potato varieties has become the treasure of potatoes. The centers of origin of crop species are the richest source of genetic diversity. Prof. S. M. Bukasov and his co-workers were the first to explore the centres of diversity of tuber-bearing *Solanum* species during 1925-26 and in subsequent years to collect from remote and non-accessible areas the old land races, and primitive and wild species. In later years, explorations were carried out by scientists from other countries as well and valuable genetic material was collected. The International Potato Centre (CIP), Lima, Peru, a CGIAR institute, holds the largest potato germplasm collection. Other important collections are available with N.I. Vavilov Institute of Plant Industry, St. Petersburg, Russia; United States Potato Introduction Project (NRSP-6), Sturgeon-Bay, Wisconsin, USA; Dutch German Potato Collection (CGN), Wageningen, the Netherlands; Leibniz Institute of Plant Genetics and Crop Plant Research (IPK),

Table 1: Indigenous and exotic potato varieties in India (Pushkarnath, 1969)

Indigenous varieties	Exotic varieties
Chamba Red, Coonoor White, Coonoor Red, Darjeeling Red Round, Desi, Dhantauri, Gola Type A, Gola Type B, Gola Type C, Phulwa, Phulwa Purple Splashed, Red Long Kidney, Sathoo, Shan and Silbilati	Ally, Arran Counsal, Ben Cruachan, Craig's Defiance, Dunbar Cavalier, Great Scot, Italian White Round, Late Carman, Magnum Bonum, Majestic, Northern Star, President, Raeburn's Gregor Cups, Red Rock, Royal Kidney and Upto-Date

Germany; Commonwealth Potato Collection (CPC) and Scottish Crop Research Institute (SCRI now the James Hutton Institute-JHI), Dundee, Scotland.

The total gene pool available for research and breeding purposes can be classified into five distinct classes, viz., i) present and past commercial varieties, ii) breeding lines and genetic stocks in breeding programs, iii) old land races, iv) primitive edible wild species and their hybrids, and v) wild species. The wild and primitive species are valuable for their resistance to a wide range of biotic and abiotic stresses. Landraces possess quality characteristics and varieties and hybrids are important because of their adaptation and agronomic characteristics. This paper reviews the status of potato genetic resources and their utilization in India.

Potatoes in India

The potato was believed to be introduced in India towards the beginning of the 17th century, most probably by Portuguese traders or British missionaries (Pushkarnath, 1976). The early history of the potato in India is obscure till the mid 18th century. From 1830 onwards, the potato has a history as a commercially grown crop in India. The earliest potato introduction in India resembled subsp. *andigena* were adapted to short days, had long dormancy and could withstand high temperatures in country stores. These were known by different names in local dialects depicting some character, viz., *Phulwa*-flowering in the plains, *Gola*-round potatoes, *Satha*-maturing in 60 days, etc. Between 1924 and the end of World War II, a large number of European varieties were introduced into India for adaptability. These, however, failed to make an impact as potato is grown in India in conditions very different from those in Europe.

Potato Germplasm Collections in India

In India, the first attempt to collect indigenous variability of potatoes was made in the 1940's. About 400 samples were collected from different parts of the country. Within this mass of variability, 16 varieties were identified as known exotic cultivars, while the rest were grouped into 16 distinct morphotypes whose original identity could not be established (Pal and Pushkarnath, 1951; Pushkarnath, 1969) (Table 1). These cultivars represented some of the earliest introductions and their clonal variants and were termed *desi* varieties. Morphologically, these varieties resembled subsp. *andigena*. Among indigenous varieties, Phulwa, Darjeeling Red Round and Gola were popular in the plains, whereas European varieties Craig's Defiance, Great Scot, Up-to-Date and Magnum Bonum were popular in the hills.

After the establishment of the Central Potato Research Institute (CPRI now ICAR-CPRI) in 1949, the collection, conservation, evaluation and documentation of potato germplasm and its utilization became a regular activity. Acquisition of exotic germplasm from different countries continued. This activity was accelerated after the establishment of the International Potato Centre (CIP) in Lima, Peru in 1972. Over a period of time, however, some of the old indigenous collections got riddled with viruses and were lost. Surveys were conducted from 1983 to 1992 in Uttar Pradesh, Bihar, West Bengal, Assam, Meghalaya, and Himachal Pradesh to retrieve these and any other variability not available in the collection. In all 621 samples were collected, studied for various morphological characters and grouped into 125 morphotypes. In India, the ICAR-CPRI presently holds a modest collection of over 4,669 accessions, comprising cultivated species (subsp. *tuberosum* and *andigena*), parental lines, indigenous varieties, advanced clones and wild/semi-wild tuber-bearing *Solanum* species (Table 2). This is the largest potato collection in South Asia. The exotic *tuberosum*, *andigena*, and wild species' germplasm accessions have been imported from 40 countries based on our requirements of resistance or tolerance to various biotic and abiotic stresses. The major source of this collection has been the International Potato Center (CIP), Lima, Peru and the USA Potato Gene bank, Sturgeon Bay, Wisconsin. Before the establishment of the CIP, potato germplasm was largely imported from the Commonwealth Potato Collection, Dundee, Scotland. Nearly 42% (1946 accessions) of genetic resources have been acquired from the International Potato centre Lima Peru (Figure 1). At present CIP holds nearly 7490 accessions comprising 4894 cultivated and 2596 wild relatives and it reflects the availability of nearly 26% CIP germplasm in India. The institute, at present, has in its collection about 540 accessions of 125 wild species consisting of diploids, triploids, tetraploids, pentaploids and hexaploids.

Conservation

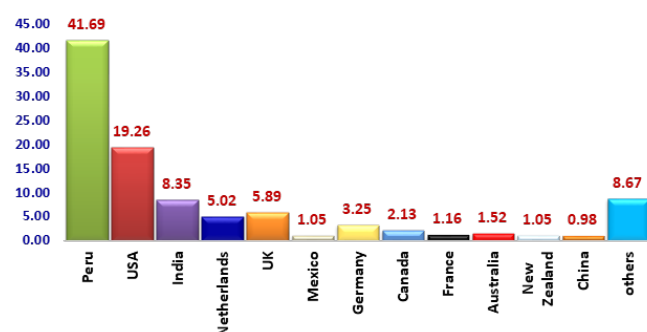
At ICAR-CPRI, the available germplasm is maintained by *in-vivo* clonal propagation, *in-vitro* clonal propagation, and sexual propagation.

Field gene bank or in-vivo clonal propagation

The germplasm is maintained through clonal propagation in glasshouses at Shimla and as duplicate sets in fields at Kufri and Jalandhar. All *S. tuberosum* subsp. *tuberosum* and a part

Table 2: Potato germplasm holding at ICAR-CPRI, Shimla

Material	No. of accessions				No. of donor countries
	Tuber	In-vitro	True seed	Total	
a) Tuberosum (Cultivars / parental lines)					
Indian					
Cultivars bred at CPRI	56	60		63	
Advanced hybrids	86	50	-	96	
Indigenous varieties	51	107	-	107	
Indigenous samples	97	42		97	
Exotic	1837	2754	-	3004	30
b) Andigena	701	77	-	762	5
c) Wild/ semi-cultivated sps.	119 (40 species)	130 (29 species)	294 (70 species)	540 (125 species)	5
Total germplasm				4669	

**Figure 1:** Country wise collection of potato germplasm at ICAR-CPRI, Shimla

of subsp. *andigena* accessions are maintained and multiplied to facilitate their evaluation for adaptability to different agro-climatic regions as well as for resistance/tolerance to various biotic/abiotic stresses. This is the traditional method of conservation and germplasm are exposed to viral and mycoplasmal diseases, resulting in the degeneration of germplasm stocks. Loss of material due to natural calamities and loss of correct identity due to mechanical mixtures or wrong labeling are the other risks associated with this method. Labor and maintenance costs are also high.

True potato seed or sexual propagation

True potato seeds (botanical seeds) produced through sexual propagation are easy to produce and maintain in disease-free conditions. The wild and semi-cultivated potato species are presently maintained in true seed form. True seeds are produced by selfing and/or sib-mating. Sib-mating is often resorted to in diploid species most of which are self-incompatible. True seeds for short-term storage are maintained at 10 to 15°C at ICAR-CPRI and long-term storage at the National Genebank, ICAR-National Bureau of Plant Genetic Resources, New Delhi. Preservation of germplasm as true seed is less laborious and inexpensive as moisture content is low and can be kept at low temperatures for many years. In addition, it is easier to maintain the material

free of pathogens as only a few viruses are known to be seed-transmitted.

In-vitro conservation

The ability of plants to grow under aseptic conditions has resulted in the development of *in-vitro* techniques for germplasm conservation. By this technique, nodal cuttings are micropropagated on MS media containing 40 g/litre sucrose and 20 g/litre mannitol. Plantlets are incubated under 16 hours photoperiod at 5 to 6°C. Under these conditions, potato plantlets can be preserved for up to 30 months without sub-culturing. This method has several advantages, viz., a) maintenance round the year in disease conditions, b) safety from natural calamities, c) the possibility of conserving the large number of genotypes in limited space, and d) easy exchange in *in-vitro* form. Presently, more than 3,200 accessions are conserved in this form. The disadvantage is that growth retardants may alter plant morphology and induce DNA methylation (Harding, 1994) and somaclonal variation (Kumar, 1994).

Cryo-preservation

This is the best method for long-term conservation of vegetatively propagated plants. By this method, plant material is frozen at an ultra-low temperature of around -196°C in liquid nitrogen. This technique was derived from the observations that plant species could survive below freezing temperatures in temperate areas. At ultra-low temperatures, cell division metabolic and biochemical processes are arrested; thus, the plant material can be stored without deterioration or modification for a long period. Tissues can be stored virtually indefinitely with low labor costs and little space. Work input is needed mainly at the beginning when samples are prepared and cooled. Once in storage, only refilling of liquid nitrogen is needed. Other advantages are the prevention of infections and genetic changes. Further, the cleanliness degree is higher for cryopreserved explants than *in-vitro* and field cultures. Cryopreservation is only useful for long-term storage

Table 3: Wild species as sources of resistance to various diseases

Diseases	Sources
Viruses - PVX	<i>S. acaule</i> , <i>S. berthaultii</i> , <i>S. brevicaula</i> , <i>S. chacoense</i> , <i>S. commersonii</i> , <i>S. curtilobum</i> , <i>S. phureja</i> , <i>S. sparsipilum</i> , <i>S. sucrense</i> , <i>S. tarijense</i> and <i>S. tuberosum</i> ssp. <i>andigena</i>
PVY	<i>S. acaule</i> , <i>S. chacoense</i> , <i>S. demissum</i> , <i>S. gourlayi</i> , <i>S. phureja</i> , <i>S. rybinii</i> , <i>S. stoloniferum</i> , <i>S. tuberosum</i> ssp. <i>andigena</i>
PLRV	<i>S. acaule</i> , <i>S. brevidens</i> , <i>S. chacoense</i> , <i>S. demissum</i> , <i>S. etuberosum</i> , <i>S. raphanifolium</i> , <i>S. stolonifrum</i> and <i>S. tuberosum</i> ssp. <i>andigena</i>
Late blight- Vertical	<i>S. cardiophyllum</i> , <i>S. demissum</i> , <i>S. edinense</i> , <i>S. stoloniferum</i> and <i>S. verrucosum</i>
Horizontal	<i>S. berthaultii</i> , <i>S. bulbocastanum</i> , <i>S. chacoense</i> , <i>S. circaeifolium</i> , <i>S. demissum</i> , <i>S. microdontum</i> , <i>S. phureja</i> , <i>S. pinnatisectum</i> , <i>S. polyadenium</i> , <i>S. stoloniferum</i> , <i>S. tarijense</i> , <i>S. tuberosum</i> ssp. <i>andigena</i> , <i>S. vernei</i> and <i>S. verrucosum</i>
Wart	<i>S. acaule</i> , <i>S. berthaultii</i>
Common scab	<i>S. chacoense</i> , <i>S. tuberosum</i> ssp. <i>andigena</i>
Bacterial wilt	<i>S. chacoense</i> , <i>S. microdontum</i> , <i>S. phureja</i> , <i>S. sparsipilum</i> and <i>S. stenotomum</i>
Cyst nematodes	<i>S. acaule</i> , <i>S. berthaultii</i> , <i>S. boliviense</i> , <i>S. bulbocastanum</i> , <i>S. capsicibaccatum</i> , <i>S. cardiophyllum</i> , <i>S. demissum</i> , <i>S. gourlayi</i> , <i>S. kurtzianum</i> , <i>S. leptophyes</i> , <i>S. multidissectum</i> , <i>S. oplocense</i> , <i>S. sparsipilum</i> , <i>S. spagazzinii</i> , <i>S. sucrense</i> , <i>S. tuberosum</i> ssp. <i>andigena</i> and <i>S. vernei</i>
Root knot nematode	<i>S. bulbocastanum</i> , <i>S. cardiophyllum</i> , <i>S. chacoense</i> , <i>S. curtilobum</i> , <i>S. hjertingii</i> , <i>S. kurtzianum</i> , <i>S. microdontum</i> , <i>S. phureja</i> , <i>S. sparsipilum</i> and <i>S. tuberosum</i> ssp. <i>andigena</i>
Aphids	<i>S. berthaultii</i> , <i>S. bukasovii</i> , <i>S. bulbocastanum</i> , <i>S. chomatophilum</i> , <i>S. infundibuliforme</i> , <i>S. lignicaule</i> , <i>S. marinasense</i> , <i>S. medians</i> , <i>S. multidissectum</i> , <i>S. neocardenasii</i> , and <i>S. stoloniferum</i>
Frost	<i>S. acaule</i> , <i>S. ajanhuiri</i>
Heat and drought	<i>S. acaule</i> , <i>S. bulbocastanum</i> , <i>S. chacoense</i> , <i>S. commersonii</i> , <i>S. gourlayi</i> , <i>S. megistacrolobum</i> , <i>S. microdontum</i> , <i>S. ochoae</i> , <i>S. papita</i> , <i>S. pinnatisectum</i> , <i>S. spagazzinii</i> and <i>S. tarijense</i>
High protein content	<i>S. phureja</i> and <i>S. vernei</i>

because the material is normally not ready for immediate utilization and re-warming and growth of plant material takes some time.

Evaluation

To make the best use of genetic resources in breeding programmes, it is necessary to have sufficient description and evaluation data on desirable as well as undesirable traits in a gene pool. Where such information is unavailable, passport data on characteristics of species' natural habitats are of great importance. For example, late blight-resistant species are found in the Mexican gene pool, where late blight fungus (*Phytophthora infestans*) has been found to reproduce sexually. Similarly, frost resistance is found in species capable of growing at altitudes above 3,500 meters. Some important sources of resistance to major potato diseases, pests, and abiotic stresses are listed in Table 3.

In the early stages of potato research in India, large numbers of European varieties were evaluated to identify cultivars adapted to temperate long-day conditions (hills) and sub-tropical short-day conditions (plains). Simultaneously, attention was paid to identifying suitable parental lines for Indian potato breeding program (Table 4). The germplasm accessions were thus evaluated for economic characters like adaptability (Luthra *et al.* 2008a, 2009a), resistance to late blight (Singh *et al.* 2001b; Kumar *et al.* 2005a, 2005b; Srivastava *et al.* 2012; Lal *et al.*

2013, 2018; Gujar *et al.* 2016; Luthra *et al.* 2018b), bacterial wilt (Upadhyaya *et al.* 1976; Chakrabarti *et al.* 1992; Nagesh *et al.* 1993; Gadewar *et al.* 2003), wart (Singh and Gopal, 1990, 1994; CPRI 2003-04), nematodes (CPRI 1983, CPRI 2003-04), potato tuber moth (CPRI 1992-93; CPRI 2003-04; Chandla *et al.* 2007), powdery scab (Dutt and Pushkarnath, 1960), charcoal rot (Paharia *et al.* 1962; Upadhyaya *et al.* 1977; Somani, 2008), hopper burn (Chaudhary *et al.* 1983; Malik and Luthra, 2007, Luthra *et al.* 2013), viruses (Garg and Gopal, 1994; Singh *et al.* 2001a), stem necrosis (Khurana 1997, Singh *et al.* 1998; Garg *et al.* 1999; Singh and Khurana, 2005; Somani, 2009), tuber dormancy (Joseph and Gopal, 1994; Luthra and Gopal, 1999; Luthra *et al.* 2003b), tuber dry matter and protein content (Gaur and Gupta, 1981; Gaur and Rana, 1982), nutrition (Luthra *et al.* 2018b), keeping quality (Gupta *et al.* 2015, Luthra *et al.* 2018c), early planting (Luthra *et al.* 2003a, Malik and Luthra, 2007, Luthra *et al.* 2013), foliage maturity (Kumar *et al.* 2005c), processing attributes (Marwaha *et al.* 2002; Gupta *et al.* 2014; Luthra *et al.* 2018b), cold sweetening (Pandey *et al.* 2005, Luthra *et al.* 2009b), frost tolerance (Luthra *et al.* 2007, 2008b) etc.

The germplasm accessions have been studied for flowering and fruiting behavior (Gopal, 1994; Kumar *et al.* 2005c) and true potato seed (TPS) attributes (Luthra *et al.* 2000, Kumar and Gopal, 2003b). These have also been characterized for morphological traits like tuber skin color,

Table 4: Some promising potato accessions having multiple-resistance

CP numbers	Variety	Characters
CP1363	AG-16 (X143) (USA)	Early maturity, resistance to late blight (tuber), good keeper, medium dry matter, good chipping quality, resistance to common scab.
CP1402	Bea (Netherlands)	Early maturity, adapted to plains, moderately resistant to late blight (foliage to tuber), immune to wart, resistance to PVX, resistance to stem necrosis, resistance to PVA, tolerance to heat.
CP1410	Gineke (Netherlands)	Immune to wart, highly resistant to stem necrosis, good chipping quality, medium dry matter, resistant to common scab, resistant to PVA, and tolerant to drought.
CP1447	Conchita (United Kingdom)	Highly resistant to late blight, resistance to PVX & PVY, resistance to <i>Globodera pallida</i> .
CP1461	Sieglinde (Germany)	Moderately resistant to PVX & PVY, resistance to <i>Globodera pallida</i> . Moderately resistant to late blight, highly resistant to stem necrosis, good keeper.
CP1474	Duquesa (Spain)	Medium maturity, resistance to late blight (foliage & tuber), resistance to PVX & PVY, immune to wart, good keeper.
CP1588	Cosima (Germany)	Adapted to normal & early planting to plains, resistance to late blight (foliage), moderately resistant to hopper burn & mites, good keeper.
CP1604	B5052-7 (USA)	Adapted to plains, resistance to late blight (foliage & tuber), immune to wart, moderately resistant to charcoal rot, resistance to PVX & PVY, resistance to ring rot, moderately resistant to common scab, resistance to stem necrosis.
CP1664	Royal Kidney (United Kingdom)	Adapted to plains, resistance to late blight (foliage & tuber), immune to wart, resistance to PVX & PVY, resistance to both spp of cyst nematodes
CP1673	Dr. McIntosh (Ireland)	Early maturity, adapted to hills and plains, resistance to late blight (foliage & tuber), moderately resistant to stem necrosis, immune to PVA, good keeper.
CP1690	Irish Cobbler (Canada)	Adapted to hills & plains, resistance to late blight (foliage & tubers), moderately resistant to stem necrosis, good keeper.
CP1729	La 1106-5 (USA)	Adapted to plains, resistant to late blight (foliage & tuber), resistant to cyst nematodes (both Spp.), good keeper.
CP1798	316.1 (USA)	Resistance to late blight (foliage to tuber), immune to wart, resistance to PVX, good chipping quality, medium dry matter.
CP1818	B 6039-1 (USA)	Immune to wart, tolerance to bacterial wilt, resistance to hopper burn, high dry matter, good keeper.
CP1927	B 6739-2 (USA)	Medium maturity, adapted to plains, resistance to late blight (foliage & tuber), resistance to stem necrosis, moderately resistant to hopper burn.
CP1971	Saturna (Netherlands)	Adapted to hills, immune to wart, resistance to scab, resistance to stem necrosis, resistance to hopper burn & mites, resistance to PVX & PVY, immune to PVA, resistance to common scab, high dry matter.
CP2011	CIP 676082 (Peru)	Adapted to hills & plains, resistant to late blight (foliage & tubers), moderately resistant to stem necrosis.
CP2018	CIP 750847 (Peru)	Adapted to hills & plains, resistant to late blight (foliage & tubers), immune to wart, and resistant to hopper burn.
CP2058	CIP 379386 (Peru)	Adapted to hills & plains, tolerant to heat, highly resistant to late blight (foliage), immune to wart, moderately resistant to charcoal rot, and resistant to hopper burn.
CP2118	Desiree (Netherlands)	Medium maturity, adapted to plains, resistance to PVX, tolerance to heat & drought, immune to wart, resistance to powdery scab.
CP2173	MS 82.80	Adapted to hills & plains, resistant to late blight (foliage & tubers), moderately resistant to termite, resistant to hopper burn.
CP2175	LT-5 (Peru)	Early maturity, adapted to hills & plains, resistance to late blight (foliage), immune to wart, resistance to stem necrosis, resistance to hopper burn, tolerance to heat.
CP2369	V-3 (Peru)	Medium maturity, adapted to plains, resistance to late blight (tuber), resistance to PVX, PVY & PLRV, moderately resistance to hopper burn & mites.
CP2371	LT-8 (Peru)	Early maturity, adapted to hills & plains, moderately resistant to late blight (tuber), immune to wart, resistant to PVX, high dry matter, and tolerant to heat.
CP2384	AGG 69.1 (Peru)	Medium maturity, adapted to hills and plains, resistance to late blight (foliage), resistance to cyst nematodes (both spp.), moderately resistant to PVA.

CP2385	AND 69.1 (Peru)	Medium maturity, adapted to hills & plains, resistance to late blight (foliage & tuber), resistance to PVY, high dry matter.
CP3088	Oblix (Netherlands)	Adapted to hills & plains, tolerance drought, resistance to PLRV, immune to wart, resistance to common scab and resistance to <i>Globodera rostochinesis</i> .
CP3091	Nicola (Netherlands)	Adapted to hills, resistance to late blight (tuber), immune to wart, tolerance to bacterial wilt, resistance to PVX & PVY, resistance to both spp of cyst nematodes, moderately resistance to common scab & drought.
CP3098	27/15 (Peru)	Early maturity, adapted to hills & plains, resistance to late blight (foliage & tuber), immune to wart.
CP3171	Bzura (Poland)	Early maturity, adapted to hills & plains, resistance to late blight (foliage & tuber), immune to wart, resistance to PLRV.
CP3187	BW-8 (Peru)	Adapted to hills & plains, resistance to late blight (tuber), resistance to PVX & PVY, resistance to cyst nematodes (both spp.)
CP3191	24/40 (Peru)	Early maturity, adapted to hills & plains, resistance to late blight (foliage & tuber).
CP3247	LB-2 (Peru)	Adapted to hills, resistance to late blight (foliage & tuber), resistance to PVX & PVY, resistance to cyst nematodes (<i>Globodera pallida</i>)
CP3251	LB-3 (Peru)	Adapted to hills, resistance to late blight (foliage & tuber) and resistance to PVX & PVY.
CP3290	Hope Hely (Hungary)	Adapted to hills & plains, resistance to late blight (foliage & tuber).

tuber shape, eye depth, flesh color and flower color as per descriptor of the International Board for Plant Genetic Resources (now IPGRI). The germplasm accessions found promising for various characters have also been studied for combining ability (Gaur *et al.* 1983, 1985, 1993; Gopal 1996a, 1996b; Gopal and Gaur, 1997; Kaushik *et al.* 1996; Pandey and Gupta, 1997; Luthra, 2001; Luthra *et al.* 2003a; Kumar and Gopal, 2006; Kumar *et al.* 2005b, Luthra *et al.* 2006a).

Documentation

The information on passport data, morphological characters and reaction to various biotic and abiotic stresses of subsp. *tuberosum* and subsp. *andigena* collections, available at the CPRI, has been published from time to time in the form of germplasm catalogs (Pal and Pushkarnath, 1951; Pushkarnath, 1964; Gaur *et al.* 1984; Gopal *et al.* 1992; Birhman *et al.* 1998; Kumar *et al.* 2005d; Kumar *et al.* 2008; Dalamu *et al.* 2021).

Utilization

The choice of parents in crossing depends on the objectives of the program. Breeders prefer to work with parents who have good agronomic attributes, adaptation, and other desired traits. Characters with high heritability and monogenic dominant control are the easiest to transfer. The use of germplasm for the selection of parents, in order of preference, is a) *S. tuberosum* subsp. *tuberosum* collection involving commercial varieties, breeding lines, stocks in ongoing breeding programs and old landraces, b) subsp. *andigena*, c) primitive cultivated species, d) wild tuber-bearing species, and e) wild non-tuber-bearing species.

Use of *S. tuberosum* subsp. *tuberosum*

Due to superior agronomic attributes and good adaptability, commercial varieties, parental lines and old landraces have

been extensively used in variety improvement programs all over the world. However, continuous breeding cycles and selection for similar economic attributes have resulted in fixing favorable alleles in the population, thereby reducing genetic variability in *S. tuberosum* subsp. *tuberosum* collections. This reduces the chances of recovering high heterosis for economic characters. Since distantly related lines are more complementary and produce heterotic effects, genetic distances are recommended for planning crosses in breeding programs (Gaur *et al.* 1978; Gopal and Minocha, 1997; Luthra *et al.* 2005, Luthra 2009). Luthra *et al.* (2005) and Luthra (2006, 2009) suggested the selection of parents based on genetic divergence followed by progeny tests for effective exploitation of heterosis in potatoes.

Use of *S. tuberosum* subsp. *andigena*

S. tuberosum subsp. *andigena* is a short-day adapted wild and weedy relative of cultivated subsp. *tuberosum*. Subsp. *tuberosum* is known to be evolved from subsp. *andigena*, through selection for good agronomic attributes and adaptability to long days. *S. tuberosum* subsp. *tuberosum* thus represents only a fraction of total genetic variability present in subsp. *andigena*. To augment the genetic variability of subsp. *tuberosum*, efforts have been made to further harness the genetic variability of subsp. *andigena*. In Europe, recurrent selection cycles for economic attributes and adaptation to long days were established in subsp. *andigena* populations. The final population developed in the process came to be known as 'Neo-tuberosum' population. Selections from this population resembling subsp. *tuberosum*, were subsequently involved in breeding programs. The *andigena* collection available in India possesses wide wealth of valuable traits such as resistance/tolerance to biotic and abiotic stresses, high starch and

Table 5: List of elite genetic stocks registered by ICAR-CPRI, Shimla with ICAR-NBPGR

S. No	Donor identity	IC/EC No	INGR No	Year	Pedigree	Novel unique features
1	EX/A680-16	IC296790	INGR01011	2001	Clone No 502-14 x Bulk Pollen)	Short days adapted with resistance to early and late blight.
2	QB/A 9-120	IC296650	INGR04057	2004	EX/A680-16 x Kufri Jyoti	High resistance to late blight and GCA for agronomic traits.
3	QB/B92-4	IC296651	INGR04058	2004	Kufri Red x CP 1755	High dry matter and low reducing sugars & good GCA.
4	PS/F-220	IC296661	INGR04059	2004	B-8695 x Kufri Jyoti	Resistant to potato stem necrosis.
5	MP/99-322	IC445068	INGR04109	2004	MCP-1x 48-1	High starch, dry matter, low amylose & resistance to late blight.
6	E/79-42	IC522200	INGR05022	2005	D42/9 x <i>S. vernei</i> clone vtn2 62-33-3	Combined resistance to cyst nematodes & late blight disease.
7	JW 96	IC524019	INGR05023	2005	Kufri Jyoti x CP1362	Early maturing (60 days).
8	JX 123	IC547013	INGR06021	2006	JE812 x CP2144	Resistance to early blight.
9	JN-189	IC553285	INGR07040	2007	Kufri Jawahar x <i>S. andigena</i>	Resistance to leaf hopper burn & potato stem necrosis tospovirus.
10	D4	IC567213	INGR09067	2009	Androgenic di-haploid of TPS parental line JTH/C-107	Flowering, male fertile androgenic dihaploid of tetraploid potato.
11	C-13	IC567214	INGR09068	2009	Androgenic di-haploid of Kufri Chipsona-2	Flowering, male fertile androgenic dihaploid of tetraploid potato, highly resistant to late blight.
12	JX 90	IC585711	INGR09069	2009	CP1346 (Krririnee) X MS/78-62	Horizontal resistant to late blight & early blight, high yield under early (75 days) & medium (90 days) crop duration.
13	SS-2040	EC460686	INGR09120	2009	Clonal selection from segregating progeny of the accession SS 2040 of <i>S. tuberosum</i> ssp. <i>andigena</i>	Higher frost tolerance introduced through ssp. <i>andigena</i> a cultivated clone.
14	SS-1725-22	EC412923	INGR09121	2009	Clonal selection from segregating progeny of the accession SS 1725 of diploid wild species <i>S. spengazzinii</i>	Higher frost tolerance introduced through a wild species clone of <i>S. spengazzinii</i> .
15	YY 6/3 C11	IC0586781	INGR10143	2010	Clonal selection from the segregating progeny of YY-6 x YY-3 using marker assisted selection	An elite parental line possessing potato virus Y (PVY) extreme resistance gene Ryadg in triplex (YYYy) condition.
16	E 1-3	IC0590089	INGR11050	2011	<i>S. tuberosum</i> dihaploid 'C-13' (+) Wild species <i>S. etuberosum</i>	Tetraploid somatic male fertile hybrid carrying resistance to potato virus introgressed from <i>S. etuberosum</i> .
17	P-7	IC0590090	INGR11051	2011	<i>S. tuberosum</i> dihaploid 'C-13' (+) Wild species <i>S. pinnatisectum</i>	Tetraploid, somatic male fertile hybrid carrying resistance to potato late blight introgressed from <i>S. pinnatisectum</i> .
18	SS 1735-02	IC0594469	INGR13048	2013	Clonal selection From the TPS population GLKS-269 (<i>S. demissum</i> ; 2n = 6x;4 EBN)	An elite wild potato clone possessing very high resistance against late blight and low cold induced sweetening even after 6 months of cold storage (2–4°C).

19	MP/97-921	IC0594470	INGR13049	2013	MP/92-154 x MP/91-65	High dry matter content (>24% in hills & >22% in plains); superior chip color (even after 6 months cold storage); low reducing sugar and sucrose content; highly resistant to late blight; ideal free amino acid and phenol content; extreme resistant to potato virus PVY.
20	JEX/A 785	IC0616582	INGR15059	2015	Clonal selection from segregating progeny of the acc. PI280868 of <i>S. tuberosum</i> spp. <i>andigena</i>	Suitable for cold chipping and resistance to cold induced sweetening.
21	JEX/A 911	IC0618556	INGR16010	2016	Clonal selection from segregating progeny of acc. CIPC700939 of <i>S. tuberosum</i> ssp. <i>andigena</i>	Suitable for making multicolor chips & tuber flesh attractive multicolored.
22	SM/00-120	IC0616580	INGR16022	2016	EB/A-304 x EX/A-680-16	A photo-insensitive high yielding hybrid with high resistance to late blight both in hills & subtropical plains.
23	SS 1652-09	IC0616581	INGR16023	2016	Selection from acc. PI No. GRA 338x381	SS/1652-09 is a clone of wild potato species <i>S. jamesti</i> ; highly resistant to late blight; low cold induced sweetening after 6 months cold storage.
24	VMT 5-1	IC623450	INGR17061	2017	K Lalima x VDS-81	Meiotic tetraploid (MT) with 2x genome from semi-cultivated species, <i>S. verrucosum</i> and other 2x from cultivated potato cv. K. Lalima. Highly resistant to late blight. Performs well under short & long day conditions.
25	Crd-6	IC623449	INGR17062	2017	Protoplast fusion between dihaploid <i>S. tuberosum</i> 'C-13' (+) <i>S. cardiophyllum</i> (P1341233)	Tetraploid and male fertile somatic hybrid. Resistance to potato late blight disease.
26	MS/6-1947	IC623447	INGR17063	2017	MS/82-638 x JX 576	Drought tolerant advanced potato clone with good keeping quality & high tuber yield.
27	MS/8-1565	IC623448	INGR17064	2017	MS/89-1095 x CP 3290	Purple skin colored specialty advanced potato clone with very good keeping quality & high tuber yield.
28	MP/6-39	IC623446	INGR17065	2017	Kufri Himsona x Kufri Pukhraj	Processing advanced hybrid. Excellent keeping quality. High tuber yield.
29	MSH/14-113	IC630606	INGR19101	2019	Interspecific potato somatic hybrid P8 (<i>S. tuberosum</i> + <i>S. pinnatisectum</i>) × Kufri Jyoti (<i>S. tuberosum</i>)	Diverse genetic base with very high resistance to late blight disease & High tuber dry matter content.
30	J.93-58	IC625993	INGR19103	2019	Kufri Pukhraj x MS/82-797	Better water use efficiency than popular cultivars and high yield.
31	BER57	IC635057	INGR20072	2020	Wild potato species: <i>S. berthaultii</i> ; Acc. PI 265857	Highly resistant to late blight disease. Diploid wild potato species with a wider genetic base.
32	PLD47	IC635058	INGR20073	2020	Wild potato species: <i>S. polyadenium</i> ; Acc. CGN17747	Highly resistant to late blight disease. Diploid wild potato species with a wider genetic base.
33	JAM07	IC635059	INGR20074	2020	Wild potato species: <i>S. jamesii</i> ; Acc. PI 498407	Highly resistant to late blight disease. Diploid wild potato species with a wider genetic base.

34	SM/11-120	IC637593	INGR21073	2021	CP2379 × Kufri Himalini	Highly resistant to both the species of potato cyst nematode (<i>G. pallida</i> and <i>G. rostochiensis</i>). Highly resistant to late blight and non-preference to white flies.
35	MSH/14-129	IC637594	INGR21074	2021	Kufri Gaurav × P2 (P2= <i>S. tuberosum</i> dihaploid 'C-13' + <i>S. pinnatisectum</i>)	Interspecific somatic hybrid derived clone with wider genetic base. High yield combined with moderate late blight resistance.
36	MCD24	IC637595	INGR21075	2021	Clone 'MCD24' belongs to wild potato species <i>S. microdontum</i> ; Acc. PI 218224	Highly resistant to late blight disease. Diploid wild potato species with diverse genetic base.
37	N/9-42	IC638884	INGR21111	2021	JN2207 × Kufri Pukhraj	Better nitrogen use efficiency than popular cultivars.
38	MSH/14-7	IC640713	INGR21169	2021	MSH/14-7 [Kufri Garima × Bulk pollen of somatic hybrids (<i>S. tuberosum</i> + <i>S. pinnatisectum</i>)]	Interspecific somatic hybrid-derived clone with a wider genetic base. High yield combined with moderate resistance to late blight under field conditions.
39	CPH62	IC640714	INGR21170	2021	<i>S. cardiophyllum</i> ; Acc. PI283062	Highly resistant to late blight disease. Diploid species with diverse genetic base. Suitable for protoplast fusion & somatic hybrid development.
40	PNT43	IC640715	INGR21171	2021	<i>S. pinnatisectum</i> ; Acc. CGN17443	Highly resistant to late blight disease. Diploid species with diverse genetic base. Suitable for protoplast fusion and somatic hybrid development.
41	STO61	IC640716	INGR21172	2021	<i>S. stoloniferum</i> ; Acc. PI225661	Approved: Highly resistant to late blight disease. Diploid species with diverse genetic base.
42	MSH/17-16	IC640717	INGR21173	2021	Kufri Garima × Crd10 (interspecific potato somatic hybrid derived from <i>S. tuberosum</i> dihaploid 'C-13' + wild <i>S. cardiophyllum</i>)	Interspecific somatic hybrid-derived potato hybrid with a wider genetic base. Yellow tuber flesh color hybrid with high carotenoid content.
43	NUE/15-8	IC640718	INGR21174	2021	Kufri Jyoti × Kufri Gaurav	High nitrogen use efficiency traits such as NUE, Agronomic NUE (AgNUE), nitrogen uptake efficiency (NUpE), & nitrogen utilization efficiency (NUE). High yield under low nitrogen (50 kg N/ha) supply under field conditions and suitable for low input agriculture.
44	MSP/15-26	IC644002	INGR22062	2022	Bareilly Red × CP3770	MSP/15-26 is an elite cultivated potato clone (<i>S. tuberosum</i> ; 2n = 4x = 48). Possessing high carotenoids in flesh. Yellow flesh color with red vascular ring.
45	MSP/15-51	IC644003	INGR22063	2022	Bareilly Red × CP3770	MSP/15-51 is an elite cultivated potato clone (<i>S. tuberosum</i> ; 2n = 4x; 48). High ascorbic acid in flesh. Distinct red purple flesh.
46	NUE/15-23	IC645767	INGR22188	2022	Kufri Jyoti × Kufri Gaurav	High nitrogen use efficiency traits such as NUE, Agronomic NUE (AgNUE), nitrogen uptake efficiency (NUpE), and nitrogen utilization efficiency (NUE). High tuber yield under low nitrogen fertilizer input under field conditions.

protein content, good keeping quality and response to fertilizers (Nagaich, *et al.* 1978; Nagaich, 1983; Chaudhary *et al.* 1983; Birhman *et al.* 1988; Luthra and Gopal, 1999; Shekhawat *et al.* 2005, Kumar *et al.* 2008). *Andigena* is also a good source of resistance to many diseases and pests, including resistance to late blight, *Phoma* blight, charcoal rot, root-knot nematodes and cyst nematodes. It also provides resistance to physiological stresses like drought and frost. The crosses involving subsp. *tuberosum* and subsp. *andigena* are known to exhibit heterosis for tuber yield and its components, though late maturity is often observed in progenies. The *andigena* are particularly suitable for potato improvement in sub-tropical Indo-gangetic plains in India (Kang and Birhman, 1993; Gopal *et al.* 2000; Kumar and Gopal, 2003a, Kumar and Kang 2006). Use of subsp. *andigena* has resulted in the development of varieties like Kufri Pukhraj, Kufri Chipsona-1 and Kufri Giriraj, which appear to have more durable resistance to late blight.

Use of cultivated and wild species

Only a few cultivated/wild species have been used in breeding programs. Even in these cases, the number of clones used from each species has been extremely limited. Further, these species have served as donors of only the desired dominant genes controlling disease resistance. Other characteristics in such crosses have been largely lost due to continued back-crossing with the *tuberosum* parent and correlated response to selection for desirable traits. The non-*tuberosum* species like *S. etuberosum* has been used through somatic hybridization.

Somatic hybridization has been used in potatoes to overcome the sexual barriers between the cultivated (*Solanum tuberosum* L.) and wild species. Symmetric protoplast fusion approaches involving diploid *Solanum* species combined with di-haploid *S. tuberosum* have been essentially used to develop tetraploid somatic hybrid potatoes with desirable introgression from wild relatives. This technology has led to the production of multiple resistant somatic hybrids. ICAR-CPRI, Shimla have developed three interspecific potato somatic hybrids using androgenic dihaploid clone 'C-13' (regenerated from *Solanum tuberosum* cv. Kufri Chipsona-2) and wild species *S. pinnatisectum* (1EBN) for adaptability, tuber traits, late blight resistance and keeping quality (Sarkar *et al.* 2011; Tiwari *et al.* 2013; Luthra *et al.* 2016), *S. cardiophyllum* (1EBN) for late blight resistance (Chandel *et al.* 2015, Luthra *et al.* 2019) and *S. tuberosum* (1EBN) for potato virus Y resistance (Tiwari *et al.* 2014). Further, these somatic hybrids have been utilized for the development of advanced stage clones in breeding programs. Elite genetic stocks of somatic hybrid, namely P-7 (late blight), Crd-6 (late blight) and E-1-3 (Potato virus), and somatic hybrid derived advanced clones, namely MSH/14-113, MSH/14-129 and MSH/17-16 (late blight) has been registered with NBPGR (Table 5).

Genetic Stocks Registered

Genetic stocks, defined as plants or populations developed and/or selected for genetic studies, represent a unique type of extremely valuable germplasm which, represents genetic resources of either transient or long-lasting value. Genetic stocks can be divided into three general groups: cytological stocks, mutants and germplasm sets. Genetic stocks are important components of the total conserved genetic resources of potatoes. In potato breeding, genetic stocks are breeding lines that contain specific desirable traits but lack some economic traits required for commercial exploitation. Genetic stocks are an asset as a parental line in the breeding program for the introgression of specific traits in the progenies. Since the inception of ICAR-Central Potato Research Institute, Shimla, in 1949, concerted breeding efforts have resulted in the identification and registration of 46 genetic stocks with ICAR-NBPGR, New Delhi (Table 5). These elite genetic stocks are valuable sources of resistance to biotic/abiotic stresses and also carry valuable genes for many other traits.

Potato Varieties and their Parentage Background

Information on the parental origin of potato varieties that have been cultivated or themselves used as parental lines for further selection provides a wealth of information on historical breeding choices (Van Berloo and Hutten, 2005). Such historical records allow a better understanding of the current population structure and can, therefore provide relevant data for breeders to use when making the right decisions in their respective breeding programs (Machida, 2015).

Institute has led to the development of 69 improved potato varieties and one TPS population (92-PT-27) over last 72 years for cultivation in diverse agro-climatic zones of the country. Of these, two varieties, viz., Kufri Safed and Kufri Red are clonal selections from indigenous '*desi*' varieties Phulwa and Darjeeling Red Round, respectively, whereas the remaining 68 are hybrids as they were derived from the mating of the female and male parent.

The parentage of 68 varieties shows that 26 varieties have both parents of Indian origin (Table 6), 28 have one parent of Indian origin and one of exotic origin (Table 7) and the remaining 14 have both parents of exotic origin (Table 8). In total, 103 parents have been used in the breeding program involving 55 female and 53 male parents. The most frequently used indigenous varieties or advanced clones are Kufri Jyoti (6 varieties), Kufri Red, Phulwa, MS/82-638 and MP/92-35 (3 varieties), Kufri Pukhraj, Kufri Alankar, Kufri Bahar, Kufri Chipsona-2, Kufri Himsona, Kufri Khyati and Kufri Kundan (2 varieties). The exotic cultivars/ clones that have figured more frequently as parents of Indian varieties are Craigs Defiance and Katahdin (3 varieties), (VTn)² 62.33.3, 27/40, Adina, Ekishirazu, EX/A 680-16, Irish

Table 6: Potato varieties developed using both parents from indigenous germplasm

S. No.	Variety	Original name	Year of release	Parentage
1	Kufri Sindhuri	C 140	1967	Kufri Red x Kufri Kundan
2	Kufri Chandramukhi	A 2708	1968	Seedling 4485 x Kufri Kuber
3	Kufri Neelamani	A 7871	1968	Kufri Kundan x 134-D
4	Kufri Badshah	JF 4870	1979	Kufri Jyoti x Kufri Alankar
5	Kufri Megha	SS/C-562	1989	SLB/K-37 x SLB/Z-73
6	Kufri Jawahar	JH 222	1996	Kufri Neelamani x Kufri Jyoti
7	Kufri Sutlej	JI 5857	1996	Kufri Bahar x Kufri Alankar
8	Kufri Giriraj	SM/85-45	1998	SLB/J-132 x EX/A 680-16
9	Kufri Anand	MS/82-717	1999	Kufri Ashoka x PH/F-1430
10	Kufri Arun	MS/92-2105	2005	Kufri Lalima x MS/82-797
11	Kufri Shailja	SM/87-185	2005	Kufri Jyoti x EX/A 680-16
12	Kufri Chipsona 3	MP/97-583	2006	MP/91-86 x Kufri Chipsona 2
13	92-PT-27	TPS population	2007	83-P-47 x D150
14	Kufri Himsona	MP/97-644	2008	MP/92-35 x Kufri Chipsona-2
15	Kufri Sadabahar	MS/93-1344	2008	MS/81-145 x PH/F-1545
16	Kufri Khyati	J/93-86	2008	MS/82-638 x Kufri Pukhraj
17	Kufri Frysona	MP/98-71	2010	MP/92-30 x MP/90-94
18	Kufri Neelima	OS/93-D-204	2010	E/79-15 x E/79-42
19	Kufri Garima	MS/99-1871	2012	PH/F 1045 x MS/82-638
20	Kufri Gaurav	JX576	2012	JE 812 x Kufri Jyoti
21	Kufri Ganga	MS/6-1947	2018	MS/82-638 x Kufri Gaurav
22	Kufri FryoM	MP/04-578	2020	Kufri Chipsona 1 x MP/92-35
23	Kufri Sangam	MP/6-39	2020	Kufri Himsona x Kufri Pukhraj
24	Kufri Thar 3	WS/05-146	2020	JN2207 x Kufri Jyoti
25	Kufri Lohit	MS/11-664	2021	Kufri Kanchan x Kufri Khyati
26	Kufri Bhaskar	HT/11-3	2022	Kufri Khyati x Kufri Surya

Table 7: Potato varieties developed using one parent from indigenous germplasm and one from exotic germplasm

S. No.	Variety	Original name	Year of release	Parentage
1	Kufri Kumar	S 1758	1958	Lumbri x Katahdin
2	Kufri Alankar	A 3649	1968	Kennebec x ON2090
3	Kufri Chamatkar	ON 1202	1968	Ekishirazu x Phulwa
4	Kufri Jeevan	SLB/E 427	1968	M109-3 x Seedling 698-D
5	Kufri Khasigaro	SLB/A-67	1968	Taborky x Seedling 698-D
6	Kufri Naveen	SLB/E-402	1968	3070d (4) x Seedling 692-D
7	Kufri Sheetman	C 3745	1968	Craigs Defiance x Phulwa
8	Kufri Dewa	C 3804	1973	Craigs Defiance x Phulwa
9	Kufri Bahar	E 3797	1980	Kufri Red x Gineke
10	Kufri Lalima	BS/C-1753	1982	Kufri Red x AG 14 (Wis. X 37)
11	Kufri Swarna	PCN/76-110	1985	Kufri Jyoti x (VTn) ² 62.33.3 (CP1974)
12	Kufri Ashoka	PJ 376	1996	EM/C-1020 x Allerfrüheste Gelbe
13	Kufri Pukhraj	JEX/C-166	1998	Craigs Defiance x JEX/B-687
14	Kufri Chipsona 1	MP/90-83	1998	MEX.750826 x MS/78-79
15	Kufri Chipsona 2	MP/91-G	1998	F-6 (CP2346) x QB/B 92-4

16	Kufri Kanchan	SE/I-1307	1999	SLB/Z-405 (a) x Pimpernel
17	Kufri Pushkar	JW 160	2005	QB/A 9-120 x Spatz
18	Kufri Surya	HT/92-621	2006	Kufri Lauvkar x LT1 (CP2066)
19	Kufri Girdhari	SM/93-237	2008	Kufri Megha x Bulk pollen of 10 genotypes
20	Kufri Mohan	MS/5-1543	2016	MS/92-1090 x Claudia (CP1704)
21	Kufri Sahyadri	OS/1-497	2018	D/79-56 x (VTn) ² 62.33.3 (CP1974)
22	Kufri Neelkanth	MS/8-1565	2018	MS/89-1095 x Hope Helly (CP3290)
23	Kufri Lalit	2001-P-55	2018	85-P-670 x 27/40 (CP3192)
24	Kufri Chipsona 4	MP/01-916	2020	Atlantic x MP/92-35
25	Kufri Karan	SM/00-42	2020	Cruza-27 x HB/83-39
26	Kufri Manik	PS/08-88	2020	Kufri Arun x 27/40 (CP3192)
27	Kufri Thar 1	J/92-167	2020	Kufri Bahar x Deodara (CP1785)
28	Kufri Chipsona 5	MP/9-45	2022	Kufri Himsona x CP1371 (B3556-12)

Table 8: Potato varieties developed using both parents from exotic germplasm

S. No.	Variety	Original name	Year of release	Parentage
1	Kufri Kisan	PS 454	1958	Up-to-date x Sd. 16
2	Kufri Kuber	ON 2236	1958	(<i>S. curtilobum</i> x <i>S. tuberosum</i>) x <i>S. andigenum</i>
3	Kufri Kundan	Hybrid-9	1958	Ekishirazu x Katahdin
4	Kufri Neela	A 1528	1963	Katahdin x Shamrock
5	Kufri Jyoti	SLB/Z-389(b)	1968	3069d (4) x 2814a (1)
6	Kufri Muthu	SLB/Z-785	1971	3046 (1) x M109-3
7	Kufri Lauvkar	A 7416	1972	Serkov x Adina
8	Kufri Sherpa	F 5242	1983	Ultimus x Adina
9	Kufri Himalini	SM/91-1515	2006	I-1062 (CP2184) x Tollocan (CP2132)
10	Kufri Lima	CP4054	2018	C90.266 x C93.154
11	Kufri Thar 2	CP4175	2020	CIP92.119 x CIP88.052
12	Kufri Kiran	HT/7-1329	2021	LT9 (CP2372) x Irish Cobler (CP1748)
13	Kufri Uday	CP4409	2021	CIP387521.3 x Aphrodite
14	Kufri Daksh	WS/07-113	2022	Irish Cobler (CP1748) x LT1 (CP2066)

Cobler, LT1, seedling 698-D, M109-3 9 (2 varieties). Among the 32 unreleased indigenous selections used as parents include 83-P-47, 85-P-670, D/79-56, D150, E/79-15, E/79-42, EM/C-1020, EX/A 680-16, HB/83-39, JE 812, JEX/B-687, JN2207, MP/90-94, MP/91-86, MP/92-30, MP/92-35, MS/78-79, MS/81-145, MS/82-638, MS/82-797, MS/89-1095, MS/92-1090, ON2090, PH/F-1045, PH/F-1430, PH/F-1545, Phulwa, QB/A 9-120, QB/B 92-4, SLB/J-132, SLB/K-37, SLB/Z-405 (a) and SLB/Z-73 were advanced improved clones. Some of these had reached the stage of multi-locational trials but could not be released as varieties.

Use of CIP Germplasm in Varietal Improvement

The germplasm received from International Potato Center, Lima, Peru accounts for nearly 42% of germplasm available in ICAR-CPRI repository and has contributed to the release of 19 potato varieties, including 10 varieties having one immediate parent in their pedigree, 6 varieties having one

or both parents in their pedigree and three varieties namely Kufri Lima, Kufri Thar-2 and Kufri Uday having both parents in their pedigree (Table 9). Kufri Lima, Kufri Thar-2 and Kufri Uday have been released in India following the evaluation of advanced clones received from CIP, Lima, Peru, under ICAR-CPRI and CIP collaborative program on potato improvement.

Limited Use of Genetic Resources

The limited use of genetic resources in potato variety improvement is due to several reasons. One of the reasons is that most of the collections have not been adequately evaluated and cataloged. Secondly, there have not been many efforts to develop parental lines from wild *Solanum* species as this is a long and difficult task owing to differences in ploidy, tight linkages with undesirable characteristics, and the non-crossability of some species. It is estimated that only 13 species have been used so far in variety of improvement programs all over the world. Wild species such as *S. demissum*,

Table 9: Use of germplasm derived from International Potato Center, Lima, Peru

Variety name	Year of release	Parentage	CIP parent	Year of receipt	Remarks
Kufri Swarna (PCN/76-110)	1985	Kufri Jyoti x (VTN) ² 62.33.3	(VTN) ² 62.33.3 (CIP800291)	1971/ 1973	Immediate parent
Kufri Chipsona-1 (MP/90-83)	1998	MEX.750826 x MS/78-79	MEX.750826 (CIP720124)	1987	Immediate parent
Kufri Chipsona-2 (MP/91-G)	1998	F-6 x QB/B 92-4	F-6 (CIP 377427.1)	1987	Immediate parent
Kufri Surya (HT/92-621)	2006	Kufri Lauvkar X LT-1	LT-1 (CIP 377257.1)	1980	Immediate parent
Kufri Chipsona-3 (MP/97-583)	2006	MP/91-86 x Kufri Chipsona-2 (F-6 x QB/B 92-4)	F-6 (CIP 377427.1) in pedigree of K. Chipsona-2	1987	In pedigree of one parent
Kufri Himalini (SM/91-1515)	2006	I-1062 x Tollocan	Tollocan (CIP 720054)	1984	Immediate parent
Kufri Himsona (MP/97-644)	2008	MP/92-35 x Kufri Chipsona-2	F-6 (CIP 377427.1) in pedigree of K. Chipsona-2	1987	In pedigree of one parent
Kufri Frysona (MP/98-71)	2009	MP/92-30 x MP/90-94; MP/92-30 (CIP378711.5 x AL575); MP/90-94 (CIP378711.5 MS/78-79)	Muziranaara (CIP378711.5) and AL575	1987	In pedigree of both parents
Kufri Chipsona-4 (MP/01-916)	2010	Atlantic x MP/92-35 (CIP378711.5 x CIP720125)	CIP378711.5 x CIP720125 in pedigree of MP/92-35	1987	In pedigree of one parent
Kufri Lalit (2001-P-55)	2013	85P670 x CP3192 (CIP380013.12)	CIP380013.12	1989	Immediate parent
Kufri Lima (CIP397065.28)	2018	(391 180.6 (C90.266) x 392820.1 (C93.154))	(391 180.6 (C90.266) x 392820.1 (C93.154))	2007	Both parents
Kufri Sahyadri (OS/1-497)	2018	D/79-56 x CP 1974 (VTN) ² 62.33.3)	(VTN) ² 62.33.3 (CIP800291)	1973	Immediate parent
Kufri Karn (SM/00-42))	2018	Cruza-27 (CP2376-575031) x HB/83-39	Cruza-27 (CIP575031)	1983	Immediate parent
Kufri Manik (PS/08-88)	2018	K. Arun x CP3192 (CIP380013.12)	CIP380013.12	1989	Immediate parent
Kufri Thar-2 (CIP397006.18)	2020	(389468.3 (92.1 19) x 88.052)	(389468.3 (92.1 19) x 88.052)	2008	Both parents
Kufri Uday (CIP392797.22)	2021	CIP387521.3 x APHRODITE	CIP387521.3	2012	Both parents
Kufri Chipsona-5 (MP/9-45)	2022	Kufri Himsona x CP1371 (B3556-12)	F-6 (CIP 377427.1) in pedigree of K. Himsona	1987	In pedigree of one parent
Kufri Bhaskar (HT/11-3)	2022	Kufri Khyati x Kufri Surya	LT-1 (CIP 377257.1) in pedigree of K. Surya	1980	In pedigree of one parent
Kufri Daksh (WS/07-113)	2022	Irish Cobler (CP1748) x LT1 (CP2066)	LT-1 (CIP 377257.1)	1980	Immediate parent

S. acaule, *S. chacoense*, *S. spegazzinii*, *S. stoloniferum*, *S. vernei* have been utilized for the development of several cultivars. Genes of *S. demissum* have been incorporated into more than 50% of the world's cultivars for resistance to late blight and PLRV. In most of these programs, dihaploids of subsp. *tuberosum* have been used as a bridge to transfer resistance from wild/cultivated species to cultivated potato. In pre-breeding programs involving hybridization and selection

at diploid level followed by tetraploidization of desirable selections, attempts are made to develop parents with the desirable genes at quadruplex or triplex level to ensure high-frequency transfer of resistance to progenies. In India, wild species *S. verrucosum* and *S. microdontum* have been used as donors of durable resistance (horizontal) to late blight (Sharma *et al.* 1982). Varieties like Kufri Jeevan, Kufri Jyoti, Kufri Khasigaro, Kufri Naveen, Kufri Neelamani,



Figure 2: Colored potato varieties: Kufri Manik, Kufri Neelkanth and Kufri Lohit



Figure 3: Most popular potato varieties of India: Kufri Jyoti, Kufri Bahar and Kufri Pukhraj

Kufri Muthu, Kufri Badshah, Kufri Megha and Kufri Jawahar were developed by incorporating resistance genes in indigenously developed material, through exotic material from UK having *S. demissum* genes. Similarly, *S. chacoense* has been used to provide resistance to charcoal rot (Upadhyaya *et al.* 1977). Resistance to cyst nematodes in the variety Kufri Swarna and Kufri Sahyadri has been derived from *S. vernei*.

Impact of Indigenous Potato Varieties

Among 70 varieties released so far, 10 are early, 46 are medium and 14 are late in maturity. Also, whereas 60 varieties possess white or yellow skin, nine varieties, viz., Kufri Red, Kufri Sindhuri, Kufri Lalima, Kufri Kanchan, Kufri Arun, Kufri Lalit, Kufri Manik (rich in iron & zinc), Kufri Lohit and Kufri Uday possess red tuber skin (Figure 2). The new potato variety Kufri Neelkanth (rich in antioxidants) produces attractive purple ovoid tubers with yellow flesh. Most of these varieties possess resistance/tolerance to major diseases and pests. About 90% of potatoes are grown in North Indian plains and commensurate with this area, the largest number (49) of varieties has been developed for this region. Varieties have also been developed for north Indian hills and other special problem areas, viz., Sikkim, north Bengal hills, and south Indian hills.

Three indigenous potato varieties, namely Kufri Pukhraj, Kufri Jyoti and Kufri Bahar (Figure 3) are the most popular among the farmers and occupy 33, 21 and 17% of areas in six major potato growing states (Pradel *et al.* 2019). Kufri Pukhraj, released two decades ago, has become the farmer's first choice in Bihar, Gujarat and Punjab, occupying 39, 85 and 64% of cultivated areas in these states. This variety is also popular in Uttar Pradesh and West Bengal, occupying about 28 and 19% of the total area under potato cultivation. The latest information on Kufri Pukhraj reveals that it is one

of the most popular short-duration varieties in the North Indian plains and is grown in nearly 33% of the potato area of the country. The annual economic surplus during 2020-21 has been estimated to be 4729 crores (at 2018 prices, DARE, ICAR, Significant achievement, 2021-22). Kufri Jyoti is another widely adapted variety and is grown throughout India in hills, plains and plateaus. It is the most popular variety in West Bengal and Karnataka, occupying about 56 and 94% of the area under potato cultivation. Kufri Bahar is the farmer's preferred choice in Uttar Pradesh, occupying about 45% of the area. These three Indian potato varieties viz., Kufri Pukhraj, Kufri Jyoti and Kufri Bahar, occupy 2nd, 5th and 6th place, respectively in South East Asian potato growing countries too (Gatto *et al.* 2018).

Farmers' preferences for red-skinned potatoes keep the demand for Kufri Sindhuri in Bihar high. Kufri Kanchan, a wart-immune variety, is popular among the farmers of north Bengal and Sikkim hills, where the wart is an endemic problem and there is a distinct preference for red skin tubers. Similarly, Kufri Swarna and Kufri Neelima, having resistance to cyst nematodes, is popular in Nilgiri hills. The late blight-resistant varieties developed by the institute, Kufri Himalini, initially released for Northern hills, is also becoming popular in plains and plateau areas, where late blight is a production constraint. New potato varieties Kufri Girdhari and Kufri Karn have also been developed for late blight resistance. In the sub-tropical plains of India, potato is one of the crops in multiple cropping systems. The Institute has developed new and improved varieties for the farmers of sub-tropical plains, which include Kufri Khyati, Kufri Mohan, and Kufri Ganga (Figure 4), which are becoming popular in sub-tropical plains. For expanding the crop area in the plateau region and the early planted crops in north India, varieties that can respond favorably to high-temperature conditions



Figure 4: Table potato varieties: Kufri Khyati, Kufri Mohan and Kufri Ganga



Figure 5: Heat tolerant potato varieties: Kufri Surya, Kufri Lima and Kufri Kiran

and possess resistance to hopper burn and mite damage are required. Kufri Surya, Kufri Lima (with extreme resistance to PVX and PVY), Kufri Kiran (Figure 5) and Kufri Bhaskar have been developed for high-temperature stress areas. These varieties are likely to pick up and become popular among farmers.

In the recent past, potato processing got a boost with the release of varieties suitable for chipping and the development of technology for storing potatoes for processing. The breeding work led to the development of eight varieties exclusively for processing purposes (Figure 6), namely Kufri Chipsona-1, Kufri Chipsona-2, Kufri Chipsona-3, Kufri Frysona, Kufri Chipsona-4, Kufri FryoM, Kufri Sangam (Dual purpose) and Kufri Chipsona-5 for cultivation in plains and Kufri Himsona for cultivation in hills. Among these varieties, Kufri Frysona and Kufri FryoM are suitable for French fries, while all others are chipping varieties. Besides being suitable for processing, these varieties also have high yields and resistance to late blight. The availability of such varieties will help stabilize the potato price fluctuations in the market and help in increasing the area and production of potatoes in the country. Recently, water-use efficient varieties (Figure 7), namely, Kufri Thar-1, Kufri Thar-2, Kufri Thar-3 and Kufri Daksh, have been released for cultivation in drought-prone areas of north Indian plains.

Currently, 28 varieties are under the institute's breeder/quality seed production program. The statistics of breeder seed of 18 varieties supplied by ICAR-CPRI during 2021 to different state government agencies reveal the maximum share of the popular potato variety Kufri Chipsona-1.

(17.28%) followed by Kufri Bahar (16.42%), Kufri Jyoti (14.11%), Kufri Pukhraj (11.36%), Kufri Khyati (7.27%), Kufri Mohan (7.06%), Kufri Chandramukhi (4.65%), Kufri Chipsona-3 (4.43%), Kufri Surya (4.10%), Kufri Himalini (3.97%), Kufri

Garima (2.11%), Kufri Frysona (1.90%), Kufri Anand (1.88%), Kufri Sindhuri (1.81%), Kufri Lauvkar (0.66%), K Badshah (0.37%), Kufri Lalit (0.36%) and Kufri Gaurav (0.25%). The virus-free *in-vitro* culture tubes of basic seed material of the listed 18 varieties and Kufri Lima, Kufri Karan, Kufri Sangam, Kufri Sahyadri, Kufri Neelkanth, Kufri Kanchan, Kufri Neelkanth, Kufri Ganga, Kufri Thar-1 and Kufri Thar-2 were also supplied to 18 different seed producing agencies in India.

The ICAR-CPRI varieties are well-adopted by farmers in different parts of the country. In India, nearly 95% area under potatoes is grown with indigenous improved varieties developed by the ICAR-CPRI. The potato varieties are suitable for different agro-climatic regions. In addition to these, the State Agricultural Departments have also released some potato cultures. These are ON1645, PS-555, K-122, and G-24 in Uttar Pradesh; Co-Shimla in Tamilnadu, and Gulmarg Special, Gulmarg Queen, Shalimar potato 1 (clonal selection, tubers white, round, shallow eyes, white-yellow flesh-2012) and Shalimar Potato 2 (clonal selection, tubers pink, round, shallow-medium eyes, cream flesh-2012) in Jammu & Kashmir.

Many Indian potato varieties have found favour in foreign countries. Indian varieties are grown in Mexico, Sri Lanka, Philippines, Madagascar, Bolivia and Vietnam (Table 10). For example Kufri Chandramukhi in Afghanistan, Kufri Jyoti in Nepal and Bhutan and Kufri Sindhuri in Nepal and Bangladesh. Many Indian clones have also been released as varieties in other countries. For example, I-654 as CCM-69.1 in Mexico, I-822 as Krushi and I-1085 as Sita in Sri Lanka, I-1035 as Montanosa and I-1085 as BSUP-04 in Philippines, I-1035 as Mailaka in Madagascar, and I-1039 as India and Red skin in Bolivia and Vietnam, respectively. The CIP advanced clone, CIP392797.22 released in India as Kufri



Figure 6: Potato varieties for processing: Kufri Chipsona-1, Kufri Frysona and Kufri Sangam



Figure 7: Water use efficient potato varieties: Kufri Thar-1, Kufri Thar-2 and Kufri Thar-3

Uday, had been released in different countries as Unica (Peru, 1998), Qingshu 9 (China, 2011), Tajikiston (Tajikistan, 2014), Yusi Maap (Bhutan, 2017), Mkanano (Africa, 2018) and Unica (CIP392797.22) (Nigeria, 2023). In Afghanistan, Kufri Chipsona 4 and Kufri Himalini have been released as Sadaf-20 and Bamyan-20, respectively. As Indian potato enjoys a high degree of consumer preference in neighboring countries, there is enormous scope for the export of seed and table potatoes.

The availability of indigenous varieties, good quality seeds and the right package of agronomic practices triggered a revolution in potato productivity, causing very fast growth in the area, production and productivity. The potato production in India during 2020-21 was 54.23 million tonnes from 2.25 million ha area with a productivity of 24.12 t/ha as compared to 1949 when India used to produce 1.54 million tons potatoes from 0.23 million ha area at an average productivity level of 6.59 t/ha. It is the hard work of potato farmers, scientists and policymakers that potato production, area and productivity increased over more than seven decades by 35.21, 9.78 and 3.66 times, respectively. India is the second largest annual producer of potatoes after China. Considering all other factors involved in this quantum jump in potato productivity, we can safely assume that at least 50% of the contribution is due to the release of improved, high-yielding varieties possessing resistance/tolerance to various biotic and abiotic stresses. It is pertinent to mention that potato varieties developed at ICAR-CPRI contributed 57,512 crores annually to the gross value added (GVA) at the current price.

Future Thrusts

ICAR-Central Potato Research Institute, Shimla, is India's National potato germplasm collection repository. Efforts are

Table 10: Indian potato varieties/hybrids being grown in other countries

Country	Varieties/Hybrids
Afghanistan	Kufri Chandramukhi, Kufri Chipsona – 4 as Sadaf-20 Kufri Himalini as Bamyan-20
Bangladesh	Kufri Sindhuri
Bhutan	Kufri Jyoti
Bolivia	I-1039 as cv. India
Madagascar	I-1035 as Mailaka
Mexico	I-654 as CCM-69.1
Nepal	Kufri Jyoti, Kufri Sundhuri
Philippines	I-1035 as cv. Montanosa, I-1085 as cv. BSUP-04
Sri Lanka	I-822 as cv. Khrushi, I-1085 as cv. Sita
Vietnam	I-1039 as cv. Red skin

being made to improve quarantine facilities to handle large import of germplasm to augment the available collection. Infra-structural facilities are also being strengthened to maintain the large collections of *in-vitro* plants. The present-day Indian potato varieties have a narrow genetic base for most of the economically important characters. The genetic base of 70 potato varieties developed over the past 70 years can be traced back to only 103 parents. Most of these parents represent tetraploid potato cultivars with a negligible representation of *S. tuberosum* subsp. *andigena* and wild/cultivated species. There is a need for better utilization of *S. tuberosum* subsp. *andigena*, adapted to short days and suitable for subtropical plains. Agronomically improved parental lines with acceptable tuber shape, color, depth of eyes and maturity needs to be developed from *andigena* source and assessed for combining ability for economic characters for better utilization in breeding programs.

Potato tuber moth and bacterial wilt are major problems of the crop in mid-hills and the plateau region. So far no reliable resistance sources have been reported for both of them. Hence, the available potato genetic resources need to be extensively evaluated for these traits. Other characteristics of interest are processing attributes, including cold chipping and nutritional components for which the collection needs to be exploited. The under-exploitation of wild and cultivated species in various improvement programs is primarily due to the long time required to develop desirable parental lines. Gene bank collections, therefore, need to be transformed into "working collections". In this context, biotechnology can offer opportunities for the horizontal introgression of genes into cultivated potatoes across trans-specific barriers. Characterization of accessions for specific genes in terms of their allelic constitution is also required. Work on DNA fingerprinting needs to be strengthened to have a catalog for monitoring the genetic integrity of germplasm collection from time to time to make the system WTO and TRIPS compatible. In a nutshell, a core collection and focused approach hold the key to utilizing potato genetic resources in the future.

References

- Birhman RK, J Gopal, SK Kaushik, GS Kang, R Kumar, TA Joseph and SK Luthra (1998) Inventory of Potato Germplasm (Group *Andigena*) Collection, CPRI, Shimla, 51p.
- Birhman RK, MLH Kaul and HC Sharma (1988) Phenotypic and biochemical diversity in *Andigena* potato. *J. Indian Potato Assoc.* 15: 115-130.
- Dalamu, B Chaudhary, JK Tiwari, V Bhardwaj, SK Luthra, Nimisha, S Sood, AK Sharma, V Kumar, RK Singh and M Kumar (2021) Catalogue of Indigenous Potato Varieties based on Morphological Descriptors eTechnical Bulletin-8, ICAR-CPRI, Shimla, India, 138p.
- Chandel P, JK Tiwari, S Ali, S Devi, S Sharma, S Sharma, SK Luthra and BP Singh (2015) Interspecific potato somatic hybrids between *Solanum tuberosum* and *S. cardiophyllum*, potential sources of late blight resistance breeding. *Plant Cell, Tissue and Organ Culture*. 123: 579-589
- Chandla VK, J Gopal and RS Chandel (2007) Evaluation of potato for their resistance to potato tuber moth, *P. operculella* (Zeller). *Potato J.* 34: 89-90.
- Chakrabarti SK, GS Shekhawat and J Gopal (1992) Comparative tolerance of potato clones to *P. solanacearum*. *J. Indian Potato Assoc.* 19: 180-183.
- Chaudhary R, M Singh and SK Anand (1983) Variation in leafhopper burn incidence in *S. tuberosum* and *andigena* collection. *Indian J. Ento.* 45: 493-497.
- CPRI (1983) Annual Scientific Report, Central Potato Research Institute (CPRI), Shimla, p13.
- CPRI (1992-93) Annual Scientific Report, Central Potato Research Institute (CPRI), Shimla, p15.
- CPRI (2003-04). Annual Scientific Report, Central Potato Research Institute (CPRI), Shimla, p16.
- Dutt BL and Pushkarnath (1960) Resistance of potato varieties to powdery scab. *Indian Potato J.* 2: 78-82.
- Gadewar AV, GS Shekhawat and J Gopal (2003) Response of potato genotypes to bacterial wilt and colonization by *R. solanacearum*. *J. Indian Potato Assoc.* 30: 131-132.
- Garg ID and J Gopal (1994) *Virus, status of indigenous potato germplasm collection*. Ann. Conf. Indian Phytopathological Society (North Zone) and Indian Society of Plant Pathologist, 10-11 November 1994, CCS HAU, Hissar, Haryana, India, 42p.
- Garg ID, MN Singh, SMP Khurana, J Gopal (1999) Virus analysis of indigenous potato germplasm collection. *J. Indian Potato Assoc.* 26: 111-117
- Gatto M, G Hareau, W Pradel, V Suarez, J Qin (2018) Release and adoption of improved potato varieties in Southeast and South Asia. International Potato Center (CIP), Social Sciences Working Paper No. 2018-2. Lima, Peru. 42p.
- Gaur PC, J Gopal and MS Rana (1983) Combining ability studies for yield, its components and tuber dry matter in potato. *Indian J. Agri. Sci.* 53: 876-879.
- Gaur PC, J Gopal and MS Rana (1985) Combining ability performance of some recently developed potato hybrids. *J. Indian Potato Assoc.* 12: 195-198.
- Gaur PC and PK Gupta (1981) Evaluation of potato germplasm for tuber dry matter and protein content. *J. Indian Potato Assoc.* 8: 92-95.
- Gaur PC, PK Gupta and H Kishore (1978) Studies on genetic divergence in potatoes. *Euphytica*. 27: 361-368.
- Gaur PC, PC Misra and NM Nayar (1984) Catalogues of Potato Germplasm Collection Group Tuberosum. Central Potato Research Institute (CPRI), Shimla, India, p38.
- Gaur PC, SK Pandey and SV Singh (1993) Combining ability study in the development of potato hybrids suitable for processing. *J. Indian Potato Assoc.* 20: 144-149.
- Gaur PC and MS Rana (1982) Variation for tuber dry matter in *Andigena* potatoes. *J. Indian Potato Assoc.* 9: 88-90.
- Gopal J (1994) Flowering behaviour, male sterility and berry setting in tetraploid *S. tuberosum* germplasm. *Euphytica*. 72: 133-142.
- Gopal J (1996a) *In-vitro* selection, genetic divergence and cross prediction in potato. Ph.D Thesis. Punjab Agricultural University, Ludhiana, XVIII+215p.
- Gopal J (1996b) *Inheritance in potato of resistance to early blight (Alternaria solani)*. National Symposium on molecular approaches in plant disease management, 14-15 November 1996, CPRI, Shimla, 29p.
- Gopal J, RK Birhman and CL Khushu (1992) Inventory of Potato Germplasm (Group *Tuberosum*) Collection, CPRI, Shimla, 47p.
- Gopal J, GS Chahal and JL Minocha (2000) Progeny mean, heterosis and heterobeltiosis in *Solanum tuberosum x tuberosum* and *S. tuberosum x andigena* families under a short day sub-tropic environment. *Potato Res.* 43: 61-70.
- Gopal J and PC Gaur (1997) Potato genetic resources in India. *Indian J. Plant Genetic Resources*. 10: 205-212.
- Gopal J and Minocha JL (1997) Genetic divergence for cross prediction in potato. *Euphytica*. 97: 269-75.
- Gupta VK, SK Luthra and BP Singh (2014) *Breeding potatoes for value addition: A comprehensive approach for sustainable potato production*. National seminar on emerging problems of potato, 1-2 November 2014, CPRI, Shimla, HP, 159 p.
- Gupta VK, SK Luthra and BP Singh (2015) Storage behaviour and cooking quality of Indian potato varieties. *J. Food Sci. and Technol.* 52(8): 4863-4873,
- Gujar MS, S Sharma and V Kumar (2016) Phenotyping of potato

- accessions for stable resistance to late blight. *Indian Phytopath.* 69(2): 141-144.
- Harding K (1994) The methylation status of DNA derived from potato plants recovered from the slow growth. *Plant Cell Tissue and Organ Culture.* 37: 31-38.
- Joseph TA and J Gopal (1994) Variation in tuber dormancy of andigena potato (*Solanum tuberosum* ssp. *andigena*). *Indian J. Agric. Sci.* 64: 240-243.
- Kang GS and RK Birhman (1993) Potato breeding for the plains. In: Chadha, KL and JS Grewal (Ed.) *Advances in Horticulture Vol. 7, Potato*. Malhotra Publishing House, New Delhi, pp 51-84.
- Khurana SMP (1997) Genetic manipulation of potato varieties for virus resistance. In: KR Aneja et al. (Ed.) *Glimpses in Plant Science*. Prof. RS Mehrotra Comm., pp 173-180
- Kaushik SK, RK Birhman, BP Singh and J Gopal (1996). *Combining ability and heterosis for field resistance to late blight in potato*. In: National Symposium on Molecular Approaches in Plant Disease Management, 14-15 November 1996, CPRI, Shimla, 31p.
- Kumar A (1994) Somaclonal variation. In: Bradshaw, J.E. and G.R. Mackay (Ed.) *Potato Genetics*. CAB International, Wallingford, UK, pp 197-212.
- Kumar R and J Gopal (2003a) Combining ability of andigena accessions for yield components and tuber dry matter in third clonal generation. *J. Indian Potato Assoc.* 30: 3-4.
- Kumar V and J Gopal (2003b) Genetic parameters and association among characters important to TPS production. *J. Indian Potato Assoc.* 30: 23-24
- Kumar V, J Gopal and V Bhardwaj (2005a) Evaluation of exotic potato (*Solanum tuberosum* ssp. *tuberosum*) germplasm in Northwestern hills of India. *Indian J. Plant Genetic Resources* 18: 94-95.
- Kumar V, J Gopal and KR Dhiman (2005b) Combining ability analysis for tuber yield and late blight. *Potato J.* 32: 129-130.
- Kumar V, J Gopal and KR Dhiman (2005c) Evaluation of exotic potato germplasm for foliage maturity and flowering characters under field and glass house conditions. *Indian J. Plant Genetic Resources.* 18: 94-95.
- Kumar V, J Gopal, R Kumar, SK Luthra, SK Kaushik and SK Pandey (2005d). Inventory of cultivated potato germplasm, Technical Bulletin-70, CPRI, Shimla, India, p162.
- Kumar R and GS Kang (2006) Usefulness of Andigena (*S.tuberosum* ssp. *andigena*) genotypes as parents in breeding early bulking potato cultivars. *Euphytica.* 150: 107-115
- Kumar R, V Kumar, J Gopal, SK Luthra and SK Pandey (2008) Inventory of Potato Germplasm (Group *Andigena*) Collection, Technical Bulletin-86, CPRI, Shimla, India, p100.
- Machida-Hirano R (2015) Diversity of potato genetic resources. *Breed. Sci.* 65: 26-40.
- Malik K and SK Luthra (2007) Screening of potato germplasm for hopper and mite burn under early planting conditions of west central plains. *Haryana J. Hort. Sci.* 36(3&4): 361-362.
- Marwaha RS, SK Sandhu and J Gopal (2002) Characterization of potato (*S. tuberosum* ssp. *tuberosum*) genotypes based on genetic divergence and processing attributes. *Indian J. Plant Genetic Resources.* 15: 40-45.
- Nagesh M, GS Shekhawat, AV Gadewar, J Gopal and SK Chakrabarti (1993) *Screening of potato clones for resistance against bacterial wilt in presence of Meloidogyne incognita*. National Symposium on recent approaches in integrated management of Agriculture crops, 6-7 August 1993, CCSHAU, Hissar, Haryana, India, 52-53p.
- Lal M, SK Luthra, BP Singh and S Yadav (2013) Screening of genotypes against potato late blight. *Potato J.* 40(1): 80-83.
- Lal M, SK Luthra, VK Gupta and S Yadav (2018) Evaluation of Potato Genotypes for Foliar and Tuber Resistance against *P. infestans* Causing Late Blight of Potato under Subtropical Plains of India. *Int. J. Current Microbiol. Applied Sci.* 7(3): 1234-1242.
- Luthra SK (2006) Selection of superior parents and crosses based on progeny mean and heterosis in potato (*S. tuberosum* L.). *Haryana J. Hort. Sci.* 35(3&4): 306-309.
- Luthra SK (2009) Genetic divergence of germplasm accessions in potato (*S. tuberosum* subsp. *tuberosum*). *Indian J. Plant Genetic Resources.* 22(2): 98-101.
- Luthra SK and J Gopal (1999) *Tuber dormancy behaviour of Andigena potatoes*. In: Global Conference on Potato, 6-11 December 1999, IPA, CPRI, Shimla, and New Delhi, 168p.
- Luthra SK, J Gopal, BP Singh and SK Pandey (2009a) Stability of tuber yield and its components in potato (*S. tuberosum* L.). *Potato J.* 36(1-2): 20-24.
- Luthra SK, J Gopal, D Kumar, BP Singh and SK Pandey (2009b) *Solanum* wild and cultivated species as source of resistance to cold induced sweetening. *Potato J.* 36(3-4): 115-120.
- Luthra SK, J Gopal, P Manivel, V Kumar, BP Singh and SK Pandey (2007) Screening of wild and cultivated species of potato for frost tolerance in north-central plains of India. *Potato J.* 34(1-2): 45-46.
- Luthra SK, J Gopal and SK Pandey (2003a) Selection of superior parents and crosses in potato for developing cultivars suitable for early planting in UP. *J. Indian Potato Assoc.* 30: 1-2.
- Luthra SK, J Gopal and PC Sharma (2005) Genetic divergence and its relationship with heterosis in potato. *Potato J.* 32: 37-42
- Luthra SK, J Gopal, V Kumar, BP Singh and SK Pandey (2008b) Evaluation of potato (*S. tuberosum* subsp. *tuberosum*) germplasm for frost tolerance. *Indian J. Hort.* 65(3): 344-246.
- Luthra SK, J Gopal, SK Pandey and BP Singh (2008a) Evaluation of potato germplasm for adaptability under West-Central Plains. *Indian J. Hort.* 65(4): 446-451.
- Luthra SK, IA Khan and J Gopal (2003b) *Tuber dormancy behaviour of tuberosum potatoes under west-central plains*. In: Conference on Processing and export potential of potatoes with in Asia. 10 March 2003, CPRI, Modipuram, Meerut, 41-42p.
- Luthra SK, JK Tiwari, V Kumar and M Lal (2018a) Evaluation of interspecific somatic hybrids of potato (*S. tuberosum*) and wild *S. cardiophyllum* for adaptability, tuber dry matter, keeping quality and late blight resistance. *Agri. Res.* 8(2): 158-164
- Luthra SK, JK Tiwari, M Lal, P Chandel, V Kumar and BP Singh (2016) Breeding potential of potato somatic hybrids: Evaluations for adaptability, tuber traits, late blight resistance, keeping quality and back-cross (BC₁) progenies. *Potato Res.* 59: 375-391.
- Luthra SK, JK Tiwari, V Kumar and M Lal (2019) Evaluation of interspecific somatic hybrids of potato (*Solanum tuberosum*) and wild *S. cardiophyllum* for adaptability, tuber dry matter, keeping quality and late blight resistance. *Agric. Res.* 8(2): 158-164.
- Luthra SK, PC Sharma and J Gopal (2000) Performance of parents for true potato seed attributes. In: Khurana SMP, GS Shekhawat, BP Singh and SK Pandey (Ed.) *Potato; Global Research and*

- Development- Volume-I*. IPA, CPRI Shimla, pp 705-707.
- Luthra SK, PC Sharma and J Gopal (2006a) Identification of superior parents and crosses in potato (*S. tuberosum* L.) by combining ability analysis. *Indian J. Agri. Sci.* 76(3): 205-208.
- Luthra SK, K Malik, VK Gupta and BP Singh (2013) Evaluation of potato genotypes under high temperature stress conditions. *Crop Improv.* 40(1): 74-80.
- Luthra SK, VK Gupta, B Kaundal and JK Tiwari (2018b) Genetic analysis of tuber yield, processing and nutritional traits in potato (*S. tuberosum*). *Indian J. Agri. Sci.* 88(8): 1214-1221.
- Luthra SK, VK Gupta, M Lal and JK Tiwari (2018c) Genetic parameters for tuber yield components, late blight resistance and keeping quality in potato (*S. tuberosum* L.). *Potato J.* 45(2): 107-115.
- Malik K and SK Luthra (2007) Screening of potato germplasm for hopper and mite burn under early planting conditions of west-central plains. *Haryana J. Hort. Sci.* 36(3&4): 361-362.
- Nagaich BB, V Singh and IP Chaubey (1978) Multiple disease resistance lines obtained from *tuberosum x andigena* crosses. *J. Indian Potato Assoc.* 5: 26-31.
- Nagaich BB (1983) Disease Resistance in Potato in India. *Indian Phytopath.* 36: 1-10.
- Pal BP and Pushkarnath (1951) Indian potato varieties, Misc. Bulletin, ICAR, New Delhi, India, pp 62-63.
- Pushkarnath (1969) Potato in India-Varieties. ICAR, New Delhi, 493p.
- Paharia KD, Pushkarnath and MJ Deshmukh (1962) Resistance of potato varieties to charcoal rot. *Indian Potato J.* 4: 84-87.
- Pandey SK and BP Singh (2005) *Potato in India: Achievements and Challenges*. In: Souvenir: National Conference on IPR and Management of Agriculture, 27-29 August 2005, ICAR-IPA, NASC Auditorium, New Delhi, pp 40-48.
- Pandey SK and PK Gupta (1997) Genetic divergence and combining ability studies on true potato seeds (TPS) in potato (*S. tuberosum* L.). *J. Indian Potato Assoc.* 24: 1-16.
- Pradel W, M Gatto, G Hareau, SK Pandey and V Bhardwaj (2019) Adoption of potato varieties and their role for climate change adaptation in India. *Climate Risk Manag.* 23: 114-123.
- Pushkarnath, (1964) Potato in India- Varieties, ICAR, New Delhi, 466p.
- Pushkarnath. (1969) Potato in India-Varieties, ICAR, New Delhi, 493p.
- Pushkarnath. (1976) *Potato in Sub-tropics*, Orient Longman, New Delhi, 289p.
- Sarkar D, JK Tiwari, S Sharma, Poonam, S Sharma, J Gopal, BP Singh, SK Luthra, SK Pandey and D Pattanayak (2011) Production and characterization of somatic hybrids between *Solanum tuberosum* L. and *S. pinnatisectum* Dun. *Plant Cell, Tissue and Organ Culture.* 107(3): 427-440.
- Sharma KP, SK Pandey and BR Tyagi (1982) Breeding for field resistance to late blight of potato. In: *Potato in Developing Countries*. IPA, CPRI, Shimla, pp 92-95.
- Shekhawat GS, J Gopal, SK Pandey, GS Kang and GJ Randhawa (2005) Potato. In: Dhillan, BS, RK Tyagi, S Saxena and GJ Randhawa (Ed.) *Plant Genetic Resources: Horti. Crops*. Narosa Publishing House Pvt. Ltd., New Delhi, pp 89-107.
- Singh PH and J Gopal (1990) Indian potato varieties and wart resistance. *J. Indian Potato Assoc.* 17: 209-211.
- Singh PH and J Gopal (1994) Wart resistance in exotic potato germplasm. *J. Indian Potato Assoc.* 21: 163-165.
- Singh MN, SMP Khurana, K Mukherjee and J Gopal (2001a) Screening of potato germplasm for resistance to potato virus X and Y. *J. Indian Potato Assoc.* 28: 99-100.
- Singh PH, BP Singh, J Gupta, LC Sikka and SK Pandey (2001b) Evaluation of late blight resistance in B-population of potato. *J. Indian Potato Assoc.* 28: 92-93.
- Singh, RB and SMP Khurana. 2005 Potato cultivars resistant to stem necrosis tospovirus. *Potato J.* 32: 123-124.
- Singh RB, SMP Khurana, SK Pandey and KK Srivastava (1998) Screening germplasm for potato stem necrosis resistance. *Indian Phytopath.* 51: 222-224.
- Singh N, T Phukan, PL Sharma, K Kabyashree, A Barman, R Kumar, RV Sonti, S Genin and SK Ray (2018) An innovative root inoculation method to study *R. solanacearum* pathogenicity in tomato seedlings. *Phytopath.* 108(4): 436-442.
- Srivastava, AK, V Kumar, TA Joseph, S Sharma, TK Bag and BP Singh (2012) Screening potato germplasm for stable resistance against late blight (*P. infestance*). *Potato J.* 39(2): 177-184.
- Somani AK (2008) Resistance in potato against charcoal rot and incidence of tuber rots. *Potato J.* 35: 94-96.
- Somani AK (2009) Stem necrosis disease resistance in exotic potato germplasm. *Potato J.* 36: 57-60.
- Tiwari JK, Poonam, V Kumar, BP Singh, S Sharma, SK Luthra and V Bhardwaj (2013) Evaluation of potato somatic hybrids of dihaploid *S. tuberosum* (+) *S. pinnatisectum* for late blight resistance. *Potato J.* 40(2): 176-179.
- Tiwari JK, P Chandel, BP Singh, V Bhardwaj (2014) Analysis of plastome and chondriome genome types in potato somatic hybrids from *Solanum tuberosum* and *Solanum etuberosum*. *Genom.* 57: 29-35
- Upadhyaya MD, SK Anand, V Kishore, SK Pandey and GS Shekhawat (1976) Final Technical Report on Breeding Potato Varieties Resistant to Brown Rot, CPRI, Shimla, p24.
- Upadhyaya MD, CL Khushu, SK Bhattacharjee and S Ray (1977) Final Technical Report. Breeding Potato Varieties Resistant to Charcoal Rot, CPRI, Shimla, p31.
- Van Berloo R and RCB Hutten (2005) Peditree: Pedigree Database Analysis and Visualization for Breeding and Science. *J. Hered.* 96: 465-468.

RESEARCH ARTICLE

Molecular Profiling of Erucic Acid Biosynthesizing *FAE1* Gene of Indian Mustard Varieties

Rajesh Kumar*, S. Rajkumar and J. Radhamani

Abstract

Indian mustard is a major contributor to the edible oil supply in India. Traditional Indian mustard varieties contain very high proportion of 18C polyunsaturated fatty acids and large amounts of long-chain (20C and more) monounsaturated fatty acids, mainly erucic acid. The composition of fatty acids in oil determines its end usage. Erucic acid, though an important feedstock for industrial applications, is an undesirable property for cooking oil due to its potential health hazard. Erucic acid is synthesized by condensing enzyme fatty acid elongase 1 (FAE1). The present study aimed to gain insight into the molecular profile of FAE1 gene in Indian mustard varieties. The detailed characterization of a full-length coding sequence of FAE1 gene revealed a near absence of uniqueness among haplotypes of paralogous in Indian mustard varieties. The absence of variation among haplotypes in FAE1 paralogous in the studied Indian mustard varieties plausibly indicates the use of germplasm/varieties having a narrow genetic base towards the development of such varieties.

Keywords: FAE1, Indian mustard, Molecular profiles, Erucic acid.

ICAR-National Bureau of Plant Genetic Resources, Pusa campus, New Delhi, India.

***Author for correspondence:**

rajesh.kumar13@icar.gov.in

Received: 03/09/2020 **Revised:** 22/07/2021

Accepted: 04/10/2021

How to cite this article: Kumar R, S Rajkumar and J Radhamani. (2024) Molecular Profiling of Erucic Acid Biosynthesizing *FAE1* Gene of Indian Mustard Varieties. *Indian J. Plant Genetic Resources*. 37(1): 20-23.
DOI: 10.61949/0976-1926.2024.v37i01.02

Introduction

The five fatty acids, palmitic (16:0), stearic (18:0), oleic (18:1), linoleic (18:2) and linolenic (18:3), considered “usual” fatty acids, are the most widely occurring fatty acids in seeds of higher plants. Interestingly, the same fatty acids constitute a structural component of all cellular membranes. Their synthesis and accumulation in seed tissues is a relatively simple modification of the general pathways of fatty acid and glycerolipid synthesis in plants (Voelker and Kinney, 2001). While seed triacylglycerol (TAG) vary widely in fatty acid composition among species, 18-carbon unsaturated and polyunsaturated fatty acids generally predominate. To date more than 300 naturally occurring fatty acids with various functional groups such as hydroxy, epoxy or double bonds in unusual positions have been reported in seed oils of various plant species (Badami and Patil, 1980). Due to their special functional groups or double bond position, they have many industrial end-uses, such as components of plasticizers, adhesives, paints or as a precursor of nylon and composite materials (Jaworski and Cahoon, 2003). Since their chemical structure deviates significantly from usual fatty acids, they are termed “unusual” fatty acids and are largely excluded from polar lipids and cell membranes (Millar and Kunst, 1997). Very long chain fatty acids (VLCFA), with 20 to 30Cs, are mostly required for the synthesis of wax that forms a protective covering of epidermal cells of plants also qualify as unusual fatty acids.

The seed oil of *Brassica* species, in addition to the above-mentioned “usual” fatty acids, also contains significant amounts of VLCFA, mainly erucic acid (C22:1), catalyzed by FAE1 enzyme (Millar

and Kunst, 1997), is stored primarily in storage TAG molecule of seeds. Though erucic acid serves as a useful industrial feedstock for the manufacturing of adhesives, plasticizers, lubricants, etc. (Millar and Kunst, 1997 and references therein), nutritionally, it is an undesirable fatty acid as it poses a health hazard (Metzger and Bornscheuer, 2006).

The biosynthesis of erucic acid (22:1) takes place by the endoplasmic reticulum resident fatty acid elongase enzyme complex and the major rate-limiting enzyme is 3-ketoacyl-CoA synthase (KCS), also known as fatty acid elongase 1 (FAE1) which catalyzes initial condensation step (Millar and Kunst, 1997). *FAE1* gene has been cloned and characterized in many brassica species. In the present study, *FAE1* gene of Indian mustard varieties was examined to explore allelic diversity, if any, among themselves.

Materials and Methods

DNA Extraction and PCR Condition

Indian mustard varieties [Basanti (IC 305113), Pusa Jagannath (IC 427782) Pusa Agrani (IC 73187), Coral-432 (IC 574232), JM-2 (IC 471177), Kranti (IC 113116), Krishna (IC 113117) and Laxmi (IC 305061)] were selected for the present study. The seeds of above mustard varieties, procured from NBPGR Gene-Bank, were allowed to germinate on wet filter paper placed inside petri dishes. The genomic DNA was isolated from 10 days old seedlings according to 2xCTAB protocol (Lukowitz *et al.*, 2000). The polymerase chain reaction (PCR) condition for amplification was as follows: initial denaturation at 94°C for 5 minutes; 30 cycles at 30 seconds at 94°C, 30 seconds, at 56°C and 1.5 minutes at 72°C and final extension at 72°C for 10 minutes. The primers of *FAE1* (F- 5'ATGACGTCCATTAACGTAAAG3'; R- 5'TTAGGACCGACGTTTGGAC 3') were designed based on published sequence information of *FAE1* gene of *Brassica*. For PCR, the reaction volume of 20 µL included 1U Ex-Taq DNA polymerase (Takara) 1x PCR buffer (Takara), 0.5 µM primers (IDT), 0.2 mM of dNTP mix (Takara) and 1-µL of dissolved DNA as template. The total volume was adjusted with nuclease-free water (Gibco). After PCR, the amplified products were electrophoresed on 1% native agarose gel.

Cloning and Sequence Analyses

The genomic fragment of *FAE1*, which included complete coding sequences (CDS), was amplified from genomic DNA. An extraction kit eluted the expected size fragment from gel (Zymo Research). The gel-purified fragment was finally dissolved in the requisite volume of nuclease-free water. The purified product was subsequently cloned in PCR2.1 vector (Invitrogen) according to manufacturer protocol. The positive clones, obtained after colony PCR, were subjected to plasmid isolation by using kit (Zymo Research). The expected size (~1.5 kb) of cloned *FAE1* gene fragments was further verified by PCR using vector-born primers. The purified

plasmids were then subjected to bi-directional sequencing (Sanger method). Sequence analyses was carried out on VectorNTI software (Invitrogen) and NCBI blast service.

Results and Discussion

Although *de novo* fatty acid synthesis occurs inside plastids in the plant kingdom, desaturation and elongation predominantly occur on endoplasmic resident enzymes encoded by *FAD2*, *FAD3* and *FAE1* genes (Figure 1). VLCFA, such as erucic acid (22:1) and eicosenoic acid (20:1), being regarded as unusual fatty acids and thus stored primarily in seed TAG as the ectopic expression of *FAE1* resulted in severely altered morphology of plant due to incorporation of VLCFA in polar lipids of membranes (Millar *et al.*, 1998).

Brassica juncea (AABB) is amphidiploid and composed of genomes of both *B. rapa* (AA) and *B. nigra* (BB). Accordingly, two paralogous of *FAE1* gene were identified in *B. juncea* having 1521 base pairs (bp) long coding sequence (CDS) (Gupta *et al.*, 2004). *B. napus*, another amphidiploid oilseed species of *Brassica* also reported to contain two *FAE1* paralogous belonging to A and C (*B. oleracea*) genome, respectively having 1521 bp long CDS sharing ~98% identity at nucleotide level (Wang *et al.*, 2010). Both *B. juncea* and *B. napus* contain very high levels of erucic acid in seeds. Erucic acid (22:1), is synthesized by β-Ketoacyl CoA synthase encoded by *FAE1* gene (Millar and Kunst, 1997) (Figure 1).

In the present study, *FAE1* gene fragments from Indian mustard varieties were cloned to study the polymorphism in Indian mustard varieties. The sequence analyses of full-length coding sequences (CDS) of *FAE1* gene revealed the presence of two paralogues (*FAE1-A* and *FAE1-B*) in both Basanti (1) and Pusa Jagannath (8) varieties of Indian mustard. It was based on the nucleic acid alignment of full-length CDS of *FAE1* paralogous of Indian mustard varieties of the present study with that of a published sequence of *FAE1* of *B. rapa* and *B. juncea* cv. Varuna, the two paralogous were named *FAE1-A* and *FAE1-B*, respectively.

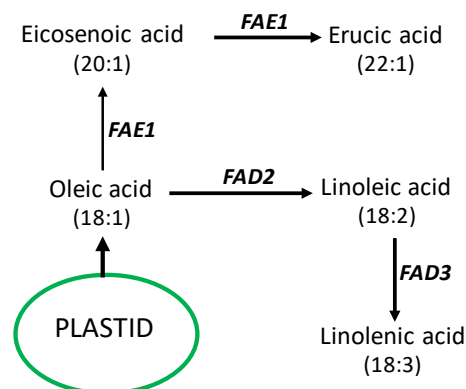


Figure 1: Simplified outline of fatty acid biosynthesis pathway in *Brassica* oilseed. (FAE1 = Fatty acid elongase1; FAD2 = Oleate desaturase, FAD3 = Linoleate desaturase)

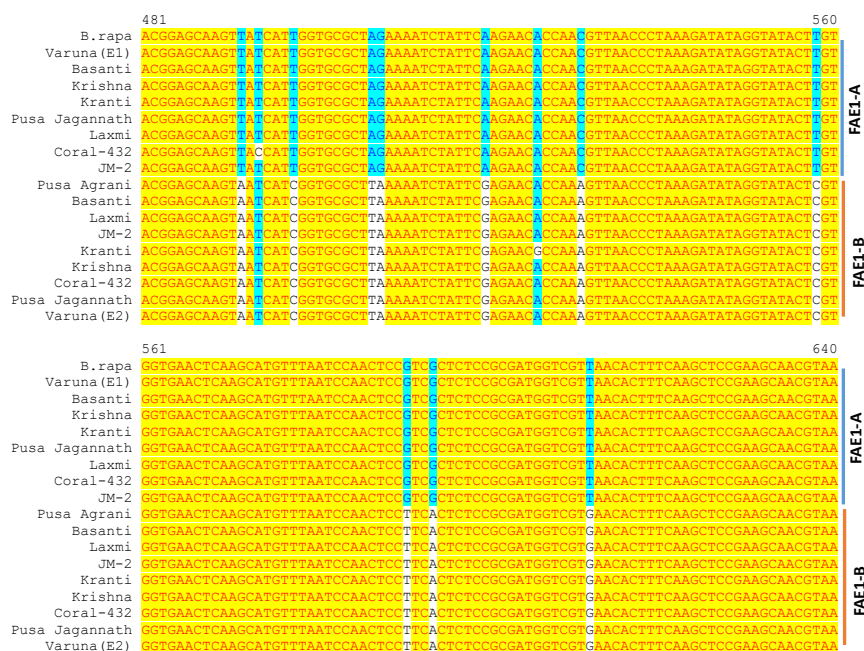


Figure 2: A representative nucleic acids alignment of *FAE1* genes of Indian mustard (*B. juncea*) varieties. The NCBI accession number of Indian mustard varieties for *FAE1-A* were [JM-2 (KP074961), Coral-432 (KP074959), Laxmi (KP074957), Pusa Jagannath (KP074955), Kranti (KP074953), Krishna (KP074951) and Basanti (KP074949)] and for *FAE1-B* [Pusa Agrani (KP074963), Basanti (KP074950), Laxmi (KP074958), JM-2 (KP074962), Kranti (KP07954), Krishna (KP074952), Coral-432 (KP074960) and Pusa Jagannath (KP074956)]. The published *FAE1* sequences of *B. rapa* (AF490461) and *B. juncea* cv. Varuna (E1-AJ558197 and E2-AJ558198) were used for alignment.

In contrast to the occurrence of two *FAE1* paralogues in Basanti and Pusa Jagannath, in Pusa Agrani (19), only one paralogue, i.e., *FAE1-B*, was found. However, to verify our non-occurrence of other paralogue in Pusa Agrani, a similar study was extended to five more Indian mustard varieties (Coral-432, JM-2, Kranti, Krishna and Laxmi). From analyses, it was found that each of these five varieties contained two paralogues of *FAE1*, unlike Pusa Agrani thus concluding that Indian mustard possess two paralogues of *FAE1*. The finding of only one paralogue in Pusa Agrani might be due to the analysis of sequences with fewer clones.

The *FAE1* paralogues in all varieties examined had 1521 bp long CDS with no intron. The paralogues' similarity in each variety was ~ 96% at the nucleotide level. However, haplotypes of each paralogous were nearly ~100% identical at the nucleotide level across the Indian mustard varieties examined (Figure 2). The generated *FAE1* gene sequences of above varieties have been submitted to NCBI (KP074949-KP074963). The absence of variation in *FAE1* paralogous in the studied Indian mustard varieties largely indicates the exploitation of narrow genetic base germplasm/varieties towards the development of such varieties.

Both *FAE1* paralogues encode 506 amino acids long polypeptides in all the eight Indian mustard varieties studied. However, in an earlier study, the two *FAE1* paralogous of Pusa Bold, a variety of Indian mustard, were reported to encode 509 and 510 amino acids long polypeptide, respectively

(Yadav *et al.*, 2003). Like Indian mustard, both the *FAE1* paralogous of *B. napus* also encode 506 amino acids long polypeptide (Wang *et al.*, 2010), a report consistent with our present finding. Moreover, the genetic study with low erucic acid (LEA) Indian mustard variety have clearly demonstrated the additive and differential contribution of *FAE1* paralogous towards the accumulation of erucic acid in seed (Saini *et al.*, 2019).

When coding sequence (CDS) of *B. napus* (AACC) *FAE1-A* (EU543282) was aligned with *FAE1-A* paralogues of Indian mustard varieties (JM-2, Coral-432, Laxmi, Pusa Jagannath, Kranti, Krishna and Basanti), they all shared ~ >99% identity at the nucleotide level. Such a high degree of conservation of *FAE1* gene originating from *B. rapa* (AA) genome in both the amphidiploids i.e. *B. napus* (AACC) and *B. juncea* (AABB), seemingly explain the evolutionary advantage for retaining large amounts of erucic acid in seed. However, CDS of *FAE1-B* paralogous of the above-mentioned Indian mustard varieties were only ~95% identical with *B. napus* *FAE1-A* (EU543282).

The seed oil of *B. juncea* oil contains 10 to 15% oleic acid, 10 to 15% linoleic acid and 14 to 16% linolenic acid and 50 to 60% erucic acid (Suresha *et al.*, 2012). However, oil is significantly rich in oleic acid (18:1), preferably in the range of 70 to 80%, along with the optimal ratio of linoleic (18:2) to linolenic (18:3) acids and almost zero level of erucic acid (22:1) will be most desirable cooking oil commodity due to its balanced nutritional fatty acid composition.

Conclusion

The result of *FAE1* paralogues study in Indian mustard varieties clearly indicates narrow genetic differences among themselves. This further suggests the plausible reason for the near absence of significant differences in erucic acid content in the seeds of mustard varieties examined. It is also important to note that *FAE1* is a key biosynthetic gene for seed erucic acid accumulation. Therefore, the generation of null or hypomorphic alleles of both *FAE1* paralogous and/or associated structural changes/disruption in the upstream promoter region offers some of the approaches for diversifying the genetic base of Indian mustard varieties. Such measures may ensure the breeding of cooking-compatible, healthy vegetable oil that contains elevated levels of oleic acid and near absence of erucic and eicosenic acid in seeds.

Acknowledgments

The authors thank the Director, ICAR-NBPGR for providing institutional funds to conduct research.

References

- Voelker T and AJ Kinney (2001) Variations in the biosynthesis of seed-storage lipids. *Annu. Rev. Plant Biol.* 52(1): 335-361.
- Badami RC and KB Patil (1980) Structure and occurrence of unusual fatty acids in minor seed oils. *Prog. Lipid Res.* 19(3-4): 119-53
- Jaworski J and EB Cahoon (2003) Industrial oils from transgenic plants. *Curr. Opin. Plant Biol.* 6(2): 178-84.
- Millar AA and L Kunst (1997) Very-long-chain fatty acid biosynthesis is controlled through the expression and specificity of the condensing enzyme. *Plant J.* 12(1): 121-131.
- Metzger JO and U Bornscheuer (2006) Lipids as renewable resources: current state of chemical and biotechnological conversion and diversification. *Appl. Microbiol. Biotechnol.* 71(1): 13-22.
- Lukowitz W, CS Gillmor and WR Scheible (2000) Positional cloning in *Arabidopsis*. Why it feels good to have a genome initiative working for you. *Plant Physiol.* 123: 795-806.
- Millar AA, M Wrischer and L Kunst (1998) Accumulation of very-long-chain fatty acids in membrane glycerolipids is associated with dramatic alterations in plant morphology. *Plant Cell.* 10(11): 1889-1902.
- Gupta V, A Mukhopadhyay, N Arumugam, YS Sodhi, D Pental and, AK Pradhan (2004) Molecular tagging of erucic acid trait in oilseed mustard (*Brassica juncea*) by QTL mapping and single nucleotide polymorphisms in *FAE1* gene. *Theor. Appl. Genet.* 108(4): 743-749.
- Yadav P, SR Bhat and VL Chopra (2003) Cloning, Sequencing and Characterization of *FAE1* Genes of *Brassica juncea* cv Pusa Bold and the Mutant *fae1* of *B. rapa* cv Tobin. *J. Plant Biochem. Biotechnol.* 12(1): 19-23.
- Wang N, L Shi, F Tian, H Ning, X Wu, Y Long and J Meng (2010) Assessment of *FAE1* polymorphisms in three *Brassica* species using EcoTILLING and their association with differences in seed erucic acid contents. *BMC Plant Biol.* 10(1): 137.
- Saini N, MK Koramutla, N Singh, S Singh, R Singh, S Yadav and DK Yadava (2019) Promoter polymorphism in *FAE1. 1* and *FAE1. 2* genes associated with erucic acid content in *Brassica juncea*. *Mol. Plant Breed.* 39(5): 75.
- Suresha GS, RD Rai and IM Santha (2012) Molecular cloning, expression analysis and growth temperature dependent regulation of a novel oleate desaturase gene (*fad2*) homologue from *Brassica juncea*. *Aust. J. Crop Sci.* 6: 296-308.

RESEARCH ARTICLE

High Popping Quality Finger Millet (*Eleusine coracana*) Genotypes

Y. A. Nanja Reddy^{1*}, P. Jayalakshmi¹, T. Lavanyabai¹, K. Geetha², M. Deepika¹ and M. V. C. Gowda¹

Abstract

Finger millet grains are rich in micronutrients, but their bioavailability to the human body is limited by its anti-nutritional factors. The popping of grain is one of the easy and economical household processing techniques that reduce the anti-nutritional factors. The popped grain can be used in the preparation of value-added products like weaning foods, noodles, and ready-to-eat products. In order to identify finger millet genotypes for high popping quality, grains of 85 genotypes were evaluated for popping quality using an iron frying pan by adjusting the grain moisture content to 19%. The popping ranged from 16.6% (*Pichakaddi ragi*) to 87.1% (Co-10) with a mean of 54.1%. Genotypes Co-10, Indaf-3 and *Karikaddi ragi* showed a high popping percentage (>80.0%). The brown-colored grain was better for popping (55.7%) than white grain (34.5%), and the freshly harvested grains were better than grain stored for three years.

Keywords: Finger millet, Popping, Grain color, Landraces, Stored grain.

¹All India Coordinated Small Millets Improvement Project, University of Agricultural Sciences, GKVK, Bangalore, Karnataka, India

²All India Coordinated Research Project on Home Science, Department of Crop Physiology & University of Agricultural Sciences, GKVK, Bangalore, Karnataka, India

***Author for correspondence:**

yanreddy61@gmail.com

Received: 03/10/2022 **Revised:** 18/09/2023

Accepted: 31/01/2024

How to cite this article: Reddy YAN, P Jayalakshmi, T Lavanyabai, K Geetha, M Deepika and MVC Gowda. (2024) High Popping Quality Finger Millet (*Eleusine coracana*) Genotypes. *Indian J. Plant Genetic Resources*. 37(1): 24-30. DOI: 10.61949/0976-1926.2024.v37i01.03

Introduction

Finger millet is known for its health benefits and is a staple food in southern Karnataka, India and many parts of eastern and central Africa. It is a rainfed crop cultivated under adverse conditions (Davis *et al.*, 2019). It is rich in calcium, iron, zinc, fiber and essential amino acids like lysine and has several health benefits (Chethan and Malleshi, 2007; Chandra *et al.*, 2016; Hiremath *et al.*, 2018). Finger millet is consumed as ragi balls, lumps, porridge, malt and rotis (Indian flatbread). However, the anti-nutritional factors such as phytic acid, tannin, oxalic acid and trypsin inhibitor activity in the seed coat decrease the bioavailability of micronutrients like iron and zinc (Chauhan and Sarita, 2018). Products prepared from popped grains were found to increase the bio-accessibility of iron (5%) and zinc (18%) as compared to whole grain products (Krishnan *et al.*, 2012; Chauhan and Sarita, 2018). Popped grain is used extensively in the preparation of value-added products like weaning foods, noodles, and ready-to-eat products that are crunchy and porous (Singh and Raghuvanshi, 2012). Besides, the popped products will have a pleasant aroma and an acceptable taste (Lewis *et al.*, 1992; Mirza *et al.*, 2015). The popping increases the solubility and digestibility of starch and leads to a low bulk density and pleasing texture (Ramashia *et al.*, 2019). Popping enables easy digestion due to the pre-cooked hydrolysis of proteins and structural changes. Genotypes with superior popping quality can be effectively utilized in the food processing industry to ensure enhanced nutrient availability in the products. Hence, the present investigation aimed to identify the best-popping varieties amongst the released varieties of finger millet in the country and study the factors influencing the popping quality.

Materials and Methods

Popping is the simplest, inexpensive, and quickest traditional method of processing of finger millet grain. The most widely used popping technique in rural households is by heating the sand mixed with a small quantity of grain in an iron frying pan. The principle involved in popping is that, during heating the grains will experience a high temperature for a short period (HTST). During heating, super-heated vapors develop inside the grain, the grain is cooked, and the endosperm expands. During the expansion of the endosperm, the vapors will escape through the micropores with great force, leading to the popping of grains.

Grains of 85 finger millet genotypes (including land races) grown during *Kharif* 2013 in two replications at the All India Coordinated Small Millets Improvement Project on Small Millets were pooled, cleaned and used for popping. The process of popping was carried out in three replications at the All India Coordinated Research Project on Food and Nutrition, University of Agricultural Sciences, GKVK, from March to April 2014. The initial grain moisture content was measured by taking 10 g of sample from each variety and oven-drying at 105°C for four hours.

$$\text{Moisture content (\%)} = \frac{\text{Initial weight (g)} - \text{Oven-dried weight (g)}}{\text{Initial weight (g)}} \times 100$$

After determining the initial grain moisture content for each variety, 20 g of grain samples in three replications were sprayed, with the required volume of water to adjust the grain moisture to 19%. Such samples were mixed well and equilibrated for 24 hours in desiccators (Malleshi and Desikachar, 1981) and used for popping. These grains were placed in the iron frying pan containing fine sand (0.85 mm) as a heat exchange medium, mixed and heated as sufficient for popping (approx. 270°C). When the popping sound stopped, the pan was removed immediately from the flame, cooled, and sieved through a 0.85 mm sieve to remove the sand. The leftover popped grains in the sieve were separated into completely popped, partially popped and un-popped grains manually, weighed, and the popping percentage was calculated. The data were analyzed in a completely randomized design in OPSTAT statistical software replications (Sheoran *et al.*, 1998).

$$\begin{aligned} \text{Complete Popping yield (\%)} &= \frac{\text{Weight of completely popped grains}}{\text{Weight of popped (complete + partial) grains + un-popped grains}} \times 100 \\ \text{Partial Popping yield (\%)} &= \frac{\text{Weight of partially popped grains}}{\text{Weight of popped (complete + partial) grains + un-popped grains}} \times 100 \\ \text{Total Popping yield (\%)} &= \frac{\text{Weight of popped (complete + partial) grains}}{\text{Weight of popped (complete + partial) grains + un-popped grains}} \times 100 \end{aligned}$$

Pearson correlations were performed between initial grain moisture content and popping percentage using the data on

popping percentage. The brown and white-grain genotypes were separated and compared for their popping quality.

Furthermore, to compare the freshly harvested grain with stored grain for a given period, the popping performance of three years old (aged) seeds of six genotypes grown in *Kharif*, 2016 (harvested in January 2017) were collected and popped during May-June, 2020. In another sub-study, the seeds of cv. GPU-28 and PR-202 grown during *Kharif*, 2016, 2018, and 2019 (harvested in Jan 2017, 2019, and 2020, respectively) were collected and popped during May-June 2020.

Results and Discussion

Genetic Diversity in Popping Performance

The productivity of finger millet is higher than that of major rainfed crops like sorghum (www.indiaagristat.com) and has superior nutritional qualities (Chandra *et al.*, 2016). However, the use of whole grains has a limitation on the bioavailability of micronutrients. Processing whole grain by popping and preparing products out of popped grain can improve the bioavailability of micronutrients by reducing the anti-nutritional factors (Krishnan *et al.*, 2012). In the present study, the popping percentage differed significantly amongst 85 genotypes and ranged from 16.6 (cv. *Picha kaddi ragi*) to 87.1% (cv. Co-10), with a mean of 54.1% (Table 1). Similarly, a wide range of popping from 31.0 to 76.0% (Hiremath and Geetha, 2019), 55.0 to 84.0% (Chaturvedi and Srivastava, 2008) and 68 to 74% (Sneha *et al.*, 2018 in white finger millet) has been reported previously. The majority of genotypes (56 out of 85) recorded >50% popping (Table 1). The genotypes Indaf-3, *Karikaddi ragi* and Co-10 were high-popping types with > 80% (Table 1). Malleshi and Desikachar (1981) also reported that cv. Indaf-3, Purna and PR-202 were high-popping types. The genotypes *Picha kaddi ragi*, PRM-802 and *Jenu Bonda ragi* were poor popping genotypes (<20%; Table 1).

Completely popped grains are preferred over partially popped grains in the preparation of ready-to-eat and other products. Among the popped grains, the mean weight of completely popped grains was high (31.8%) when compared to the partially popped grains (22.3%). The completely popped grains were highest in cultivated cv. Co-10 (55.9%), followed by Indaf-3 (58.1%), GN-4, PRM-2, Indaf-9, Purna and KMR-301 in addition to a landrace *Karikaddi ragi* with more than 62.2% (Figure 1; Table 1). The higher popping quality of grain could be due to grain hardness, hydration capacity and higher protein solubility (Mirza *et al.*, 2015). These selected genotypes are better for both household and industrial use.

Effect of Grain Moisture Content on Popping Performance

As grain moisture content is important in determining the popping quality, the influence of initial grain moisture

Table 1: Genotypic variation in popping quality (%) of finger millet

Sl. No.	Genotype	Year of release	Parentage	State	Moisture (%)	Complete (%)	Partial (%)	Total (%)
1	GPU-28 (check)	1998	Indaf-5 x IE-1012	Kar	10.2	29.7	27.2	56.9
2	PR-202 (check)	1976	Selection	AP	11.4	33.6	45.2	78.8
3	Co-10	1976	Selection	TN	10.0	55.9	31.2	87.1
4	Indaf-3	1976	Cauvery x IE-927	Kar	11.1	58.1	25.2	83.3
5	Kari kaddi ragi*		Local	Kar	10.7	62.2	19.6	81.8
6	GN-4	2000	Selection	Gujarath	11.0	57.5	20.2	77.7
7	ES-11	1939	Selection from Gidda ragi	Kar	11.1	45.2	28.6	73.8
8	PRM-2	2010	Pure line selection	UK	10.5	54.4	19.1	73.5
9	GPU-66	2009	PR-202 x GPU-28	Kar	11.6	46.6	25.8	72.4
10	Indaf-9	1985	K-1 x IE-980 R	Kar	10.2	53.3	18.2	71.5
11	Purna	1959	Co-1 x Aruna	Kar	8.2	52.5	18.8	71.3
12	RAU-3			Bihar	10.9	34.5	36.5	71.0
13	Hullubele*			Kar	11.4	47.7	23.0	70.7
14	BM-1	1985	Pureline selection	Bihar	10.8	44.2	26.0	70.2
15	Co-12	1985	Selection from PR-722	TN	9.4	48.6	21.6	70.2
16	Co-14	2004	Malawi-1305 x Co-13	TN	11.0	46.8	23.4	70.2
17	Indaf-8	1982	Hullubele x IE-929	Kar	9.7	51.5	18.4	69.9
18	Dapoli-1	1994	Selection from mutant	MR	11.7	36.8	32.9	69.7
19	KMR-301	2009	MR-1 x GE-1409	Kar	10.1	52.8	16.8	69.6
20	Bhairabi	1999	Mutant of Bhudha Madua	Odisha	11.2	41.6	27.4	69.0
21	Co-13	1989	Co-7 x TAH-107	TN	10.8	47.2	21.8	69.0
22	Paiyur-2	2008	VL-145 X Selection-10	TN	12.3	41.4	26.5	67.9
23	PES-110	1985	Pureline selection	Bihar	10.3	40.2	27.3	67.5
24	HR-911	1985	UAS-1 x IE-927	Kar	11.2	41.8	25.7	67.5
25	RAU-8	1989	BR-407 x Ranchi local	Bihar	10.5	42.4	23.9	66.3
26	Saptagiri	1995	MR-1 x Kalyani	AP	10.1	50.3	14.1	64.5
27	VR-708	1998	Pure line selection-local	AP	11.0	46.3	17.6	63.9
28	TRY-1	1989	Pureline selection from HR-374	TN	10.3	39.6	23.2	62.8
29	A-404	1993	Introd. From AP	Bihar	10.3	36.0	26.6	62.6
30	Nashini			MR	10.0	40.9	21.7	62.6
31	Kalyani	1972	Pureline selection from CR-652	AP	10.0	35.6	26.0	61.6
32	VR-762	2006	Pureline selection from VMVC-134	AP	10.4	41.3	20.3	61.6
33	PRM-1	2006	Selection-Local	UK	11.0	33.2	28.3	61.5
34	VL-149	1991	VL-204 x IE-882	UK	10.3	39.2	21.9	61.1
35	Shakti	1972	R-0013 x H-22	Kar	12.4	32.3	28.2	60.5
36	GE-4			UP	9.0	34.7	25.6	60.3
37	Hasiru kaddi ragi*			Kar	10.6	28.2	32.0	60.2
38	GPU 70			Kar	10.3	33.8	26.0	59.8
39	VR-847	2009	GPU-26 x L-5	AP	11.4	43.7	16.0	59.7
40	KMR-305			Kar	10.3	34.7	24.1	58.8
41	MR-6	2004	African White x ROH-2	Kar	11.5	33.5	24.3	57.8
42	Indaf-5	1977	Cauvery x IE-929	Kar	10.7	33.8	23.3	57.1
43	Dibyasinha	1971	Mutant of AKP-7	Odisha	11.2	33.9	23.1	57.0
44	MR-1	1990	Hamsa x IE-927	Kar	11.0	29.4	25.8	57.2
45	Chilka	2001	GE-68 x GE-156	Odisha	10.4	29.7	27.2	56.9

46	L-5	1999	Malawi x Indaf-9	Kar	9.3	39.5	16.9	56.4
47	Co-7	1953	Pureline selection from Cuddaph	TN	11.0	31.1	25.4	56.5
48	KMR-204	2012	GPU-26 x GE-1409	Kar	12.0	29.5	26.3	55.8
49	GPU-76			Kar	9.4	38.7	17.1	55.8
50	Co-9	1970	EC-4336 x PLR-1	TN	10.3	38.3	16.9	55.2
51	GPU-67	2009	Selection from GE-5331	Kar	11.4	28.4	26.0	54.4
52	JWM-1(Old)				11.5	28.4	25.9	54.3
53	GPU-26	1997	Indaf-5 x Indaf-9 x IE-1012	Kar	11.3	28.3	25.0	53.3
54	VL-146	1995	VL-201 x IE-882	UK	10.2	30.8	20.3	51.1
55	Hasiru Dundaga ragi*			Kar	10.6	17.6	33.2	50.8
56	GPU-45	2001	GPU-26 x L-5	Kar	10.5	26.5	23.9	50.4
57	GPU-48	2005	GPU-26 x L-5	Kar	8.9	35.2	14.7	49.9
58	Hamsa	1967	Pureline selection	Kar	11.0	24.1	19.4	43.5
59	BM-2	1995	Pure line selection	Bihar	11.3	19.8	23.2	43.0
60	HR-374	1975	EC-4840 x IE-927	Kar	11.5	24.6	17.7	42.3
61	GN-5	2009	Pure line selection	Gujarath	11.5	24.7	17.5	42.2
62	Sharada	1971	Pureline selection	AP	11.2	19.9	22.2	42.1
63	CO-11	1982	Pureline selection from MS-2584	TN	11.0	26.4	19.0	45.4
64	HPB-7-6	1976	Hamsa x Poorna	Kar	10.3	17.8	23.8	41.6
65	VL-330			UK	11.4	13.2	27.6	40.8
66	MR-2	1994	Indaf-5 x PR-202	Kar	10.5	16.8	23.0	39.8
67	Bonda ragi*			Kar	10.6	15.9	23.4	39.3
68	VL-324	2006	VL-162 x IE-3808	UK	11.5	22.1	17.1	39.2
69	Srichaithanya	2009	GPU-26 x L-5	AP	10.6	17.6	21.5	39.1
70	OUAT-1			Odisha	10.9	16.0	22.9	38.9
71	Bili kaddi ragi*			Kar	10.8	14.5	24.0	38.5
72	Nilachal	1985	Mutant of IE-642	Odisha	10.6	15.0	20.9	35.9
73	Indaf-15	1991	IE-67 X IE-927	Kar	10.7	14.8	20.7	35.5
74	GPU-75			Kar	11.4	16.3	19.2	35.5
75	Hejje ragi*			Kar	9.4	13.8	17.6	31.4
76	PRM-901			UK	10.9	15.3	16.0	31.3
77	VL-315	2004	SDFM-69 x VL-231	UK	8.9	14.8	14.7	29.5
78	VL-351			UK	11.4	9.7	17.9	27.6
79	JWM-1(new)				11.1	12.9	13.4	26.3
80	GN-1	1976	Pureline selection	Gujarath	9.8	10.6	15.3	25.9
81	KOPN-933			MR	9.5	12.2	11.3	23.5
82	Indaf-11			Kar	11.0	4.4	17.1	21.5
83	Jenu Bonda ragi*			Kar	10.7	6.8	11.5	18.3
84	PRM-802			UK	11.0	6.0	11.5	17.5
85	Pichakaddi ragi*			Kar	10.6	7.9	8.7	16.6
	Mean				10.7	31.8	22.3	54.1
	SEM $\pm$					1.9	1.4	2.9
	CD (P < 0.05)					5.4	3.9	8.1
	C.V. (%)					14.4	17.0	9.4

*: Land races, Kar: Karnataka, AP: Andhra Pradesh, TN: Tamil Nadu, UK: Uttara Khand, MR: Maharastra, UP: Uttara Pradesh. `

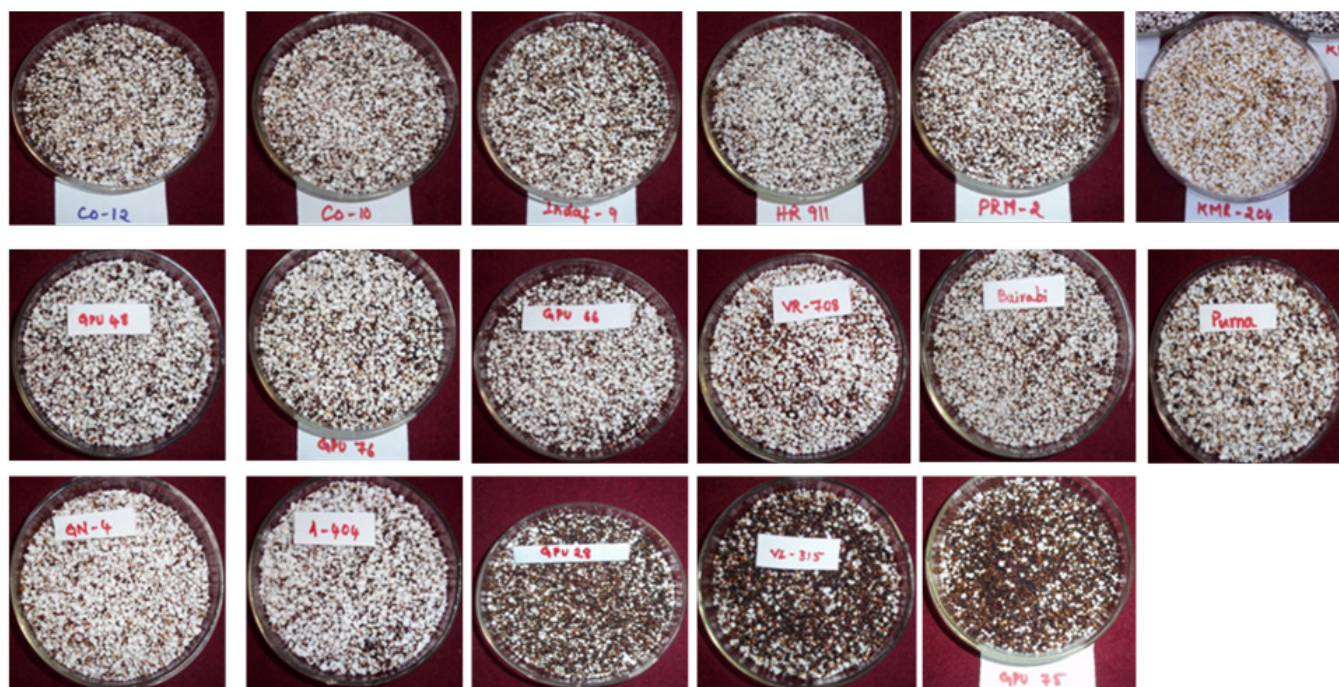


Figure 1: Contrasting finger millet varieties for popping performance

content on popping quality was studied. The initial grain moisture content was measured and used to calculate the adjusted moisture content (19%). The initial grain moisture content ranged from 8.2 (Cv. Purna) to 12.4% (Cv. Shakti), with a mean of 10.7% (Table 1). Varieties possessing 8 to 10% initial moisture content showed less than 50% popping, 10 to 12% moisture content showed a wide range from 18.6 to 88.2% popping and moisture content with >12.0% showed a popping percent of 55.8 to 67.8% (Table 1). However, no significant relationship was observed between initial grain moisture content and popping percent (Figure 2). These results infer that the general grain storage moisture content (8–10%) does not influence the popping performance of finger millet and hence, irrespective of the grain moisture content under storage, the grain should be equilibrated to 19% moisture as preconditioning during the start of popping process for achieving the maximum popping (Malleshi and Desikachar, 1981).

Influence of Seed Coat Color on Popping Performance

Among 85 genotypes, most of the brown grains showed a higher popping percent as compared to the white grain genotypes like Co-9 (55.2%), Hamsa (43.5%), GN-5 (42.2%), OUAT-1 (38.9%), PRM-901 (31.3%), JWM-1 (26.3%), Indaf-11 (21.5%), and PRM-802 (17.5%; Table 1). Shukla *et al.* (1986) had reported that the brown grain varieties have a higher popping percentage (>90%) as compared to the white grain varieties ($\leq 66\%$). Mirza *et al.* (2015) also reported that the reddish-brown seeds had relatively higher popping percent and popping volume when compared to yellow or white grain. However, Sneha *et al.* (2018) reported a high

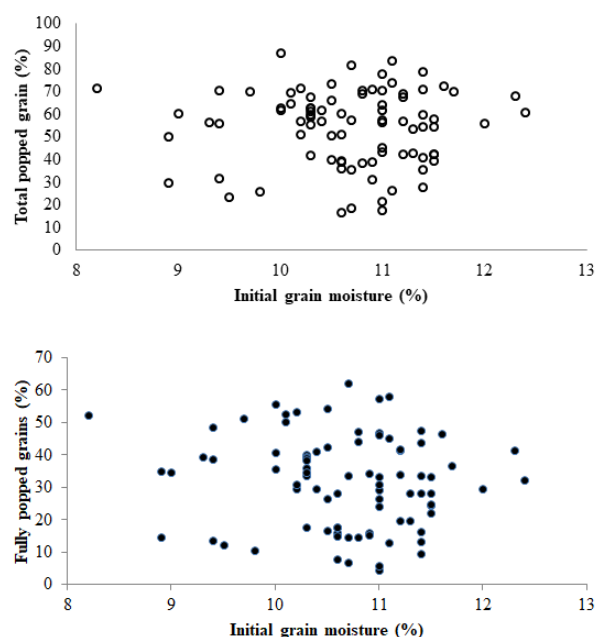


Figure 2: Relationship between initial grain moisture content and popping percent

popping percentage of 68 to 84% in new and only three genotypes of white ragi. Hence, the popping could be genotype-dependent based on grain composition rather than grain color alone.

Influence of Grain Storage on Popping

Grain stored for three years showed a decrease in the popping quality, and it was genotype-dependent. For

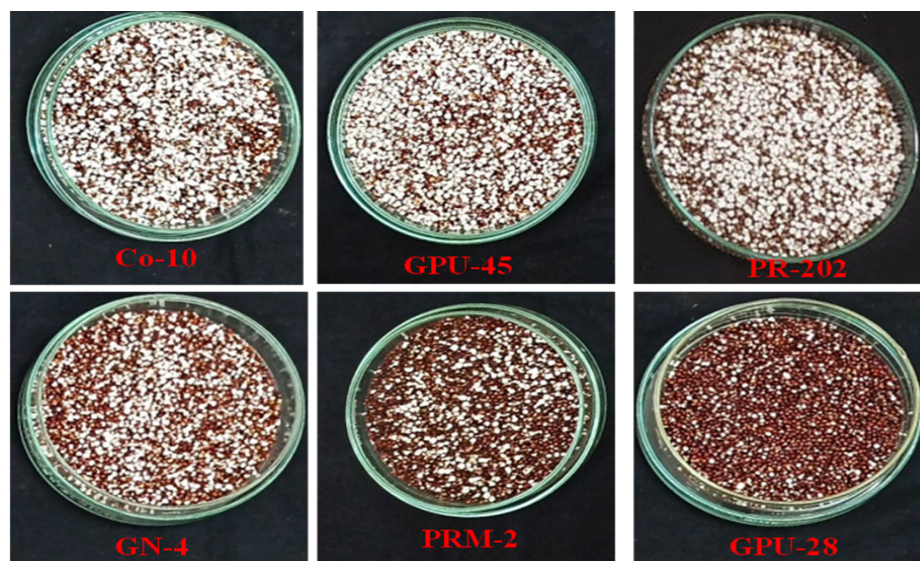


Figure 3: Genotypic variation in popping performance of three years old grains of finger millet

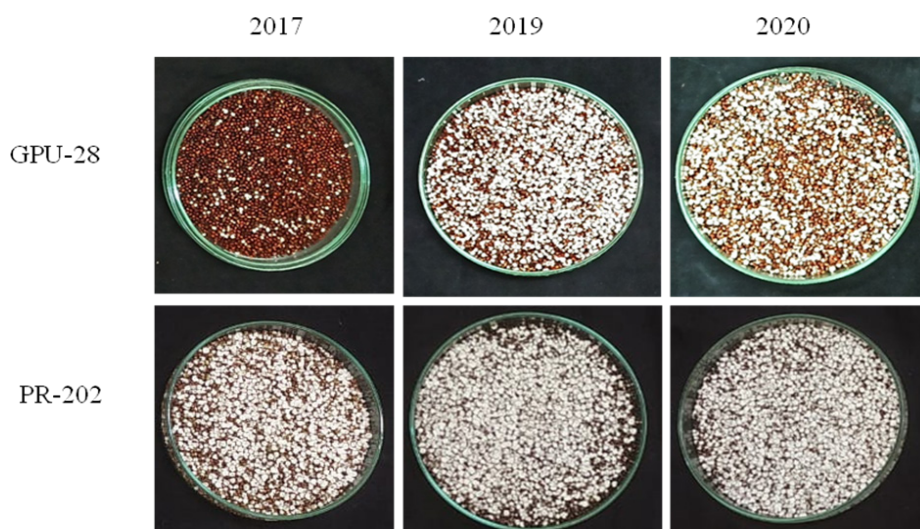


Figure 4: Effect of storage period on popping performance in cv. GPU-28 and PR-202 (2020, 2019 and 2017 are fresh, one and three years old grains, respectively)

instance, even after three-year storage, genotypes Co-10, GPU-45 and PR-202 had better-popping quality when compared to GN-4, PRM-2 and GPU-28 (Figure 3). Further, the recently harvested grains have shown a higher popping quality when compared to grain stored for three years (Figure 4). Therefore, freshly harvested grain is appropriate for popping, and the popping quality is not related to the grain moisture content as grain moisture will be equilibrated to 19% at the time of the popping process.

Conclusion

The present study evaluated a large number of genotypes (85) for popping quality and infers that stored grain moisture content does not limit the popping quality. The grain moisture content needs to be equilibrated to 19%

while processing. The freshly harvested grains were found to be better for higher popping quality. The finger millet genotypes with higher popping (>65%) are Co-10, Indaf-3, *Karikaddi ragi*, PR-202, Purna, GN-4, ES-1 and PRM-2, can be exploited at the industrial level.

Acknowledgment

Authors are thankful to the International Development Research Centre (IDRC), PO Box BP 8500, Ottawa, ON, Canada, and DHAN Foundation, Madurai, Tamil Nadu, for funding under Revalorizing Small Millets in the Rainfed Regions of South Asia (RESMISA Project, 2010 - 2014), the ICAR-All India Coordinated Small Millets Improvement Project and the University of Agricultural Sciences, Bangalore. The authors thank Ms. Dhruvashree for having initiated the work and

Mr. M. Karthikeyan, Programme leader DHAN Foundation for cooperation during the project period.

References

- Chandra D, S Chandra, Pallavi and AK Sharma (2016) Review of finger millet (*Eleusine coracana* (L) Gaertn): A power-house of health benefiting nutrients. *Food Sci. Hum. Wellness*. 5: 149-155.
- Chaturvedi R and S Srivastava (2008) Genotype variation in physical, nutritional and sensory quality of popped grains of amber and dark genotypes of finger millet. *J. Food Sci. Technol.* 45: 443-446.
- Chauhan ES and Sarita (2018) Effects of processing (germination and popping) on the nutritional and anti-nutritional properties of finger millet (*Eleusine coracana*). *Curr. Res. Nutr. Food Sci.* 6(2): 566-572.
- Chethan S and NG Malleshi (2007) Finger millet polyphenols: Characterization and their nutraceutical potential. *Amer. J. Food Technol.* 2: 582-592.
- Davis KF, A Chhtr, ND Rao, D Singh and R De Fries (2019) Sensitivity of grain yields to historical climate variability in India. *Environ. Res. Lett.* 14: 064013, <http://www.indiaagristat.com/table/agriculture/sown-area-under-various-kharif-crops-india-2019-20/1373263>
- Hiremath N, K Geetha, SR Vikram, YA Nanja Reddy, N Joshi and HB Shivaleela (2018) Minerals content in finger millet [*Eleusine coracana* (L.) Gaertn.]: A future grain for nutritional security. *Int. J. Curr. Microbiol. Appl. Sci.* 7: 3448-3455.
- Hiremath SP and K Geetha (2019) Nutritional composition of raw, malted and popped finger millet (*Eleusine coracana*) varieties. *Int. J. Curr. Microbiol. Appl. Sci.* 8(2): 966-974.
- Krishnan R, D Usha and NG Malleshi (2012) Influence of decortication, popping and malting on bio-accessibility of calcium, iron, and zinc in finger millet. *LWT - Food Sci. Technol.* 48: 169-174.
- Lewis KD, K Lorenz and R Tribelhorn (1992) Puffing quality of experimental varieties of proso millets (*Panicum miliaceum*). *Cereal Chem.* 69(4): 359-365.
- Malleshi NG and HSR Desikachar (1981) Varietal differences in puffing quality of ragi (*Eleusine coracana*). *J. Food Sci. Technol.* 26: 26-28.
- Mirza N, N Sharma, S Srivastava and A Kumar (2015) Variation in popping quality related to physical, biochemical, and nutritional properties of finger millet genotypes. *Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci.* 85(2): 507-515.
- Ramashia SE, TA Anyasi, ET Gwata, S Meddows-Taylor and AIO Jideani (2019) Processing, nutritional composition and health benefits of finger millet in sub-Saharan Africa. *Food Sci. Technol.* 39(2): 253-266.
- Shukla SS, OP Gupta and YK Sharma (1986) Puffing quality of characteristics of some ragi (*Eleusine coracana*) cultivars. *J. Food Sci. Technol.* 23: 329-330.
- Singh P and S Raghuvanshi (2012) Finger millet for food and nutritional security. *Afr. J. Food Sci.* 6(4): 77-84.
- Sneha S, R Usha and P Ravishankar (2018) Effect of processing methods on phytic acid content in selected white finger millet varieties. *Int. J. Curr. Microbiol. Appl. Sci.* 7(2): 1829-1835.
- Sheoran OP, DS Tonk, LS Kaushik, RC Hasija and RS Pannu (1998) Statistical software package for agricultural research workers. Recent advances in information theory, statistics, and computer applications. Department of Mathematics and Statistics, CCS HAU, Hisar. pp. 139-143.

RESEARCH ARTICLE

Molecular Characterization of Garden Rose Germplasm using SSR Markers

Shephalika Amrapali^{1*}, Sunil Archak², Namita³ and Ambika B. Gaikwad²

Abstract

A set of 205 garden rose germplasm consisting of 87 hybrid tea, 111 floribundas, and seven wild species were evaluated using 20 simple sequence repeat (SSR) primers. A total of 109 bands were generated from 205 rose cultivars. The average polymorphism for 205 cultivars tested with 20 SSR primers was 88%. On average, 1.78 unique alleles (N_a) and 1.46 expected number of alleles (N_e) were discovered. The genetic diversity analysis showed an excess of observed heterozygosity over expected. AMOVA revealed that 98% of total molecular variance occurred within groups, with only 2% occurring between groups. Principal coordinate analysis and cluster analysis were carried out to investigate the genetic relatedness of cultivars. The scatter plot did not reflect the grouping of cultivars used for analysis, indicating that the cultivars of different garden rose classes are related to each other. A dendrogram is also produced to better understand the presence of a grouping pattern and three major clusters were found. However, the clustering pattern does not correspond to the horticultural classifications that group accessions. The study suggests higher genetic similarity among the rose cultivars across different classes of garden roses and a need to broaden the genetic base. There is unexploited rose germplasm, which has the potential to broaden the overall gene pool of rose breeding programs in general. The wild species of roses used in the study showed considerably higher dissimilarity with almost all the cultivars and can be used to broaden the genetic base.

Keywords- Garden rose, Rose cultivar, Genetic diversity, Molecular marker, SSR.

¹ICAR-NBPGR, Regional Station Ranchi, Jharkhand, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India

³ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India

***Author for correspondence:**

shephalika.amrapali@icar.gov.in

Received: 20/12/2020 **Revised:** 09/08/2023

Accepted: 10/01/2024

How to cite this article: Amrapali S, S Archak, Namita and AB Gaikwad. (2024) Molecular Characterization of Garden Rose Germplasm using SSR Markers. *Indian J. Plant Genetic Resources*. 37(1): 31-38.
DOI: 10.61949/0976-1926.2024.v37i01.04

Introduction

A rose (*Rosa* sp.) is a woody perennial flowering plant cultivated for over 2,000 years. During the 1800s, aggressive breeding initiatives resulted in a huge growth in rose cultivation. Gardening, cutting flowers, house plants (pot rose), oil production, and medicinal use are the primary goals of the rose improvement programs. In the 1950s, improved breeding techniques and extensive testing of new cultivars resulted in roses with longer vase lives and higher yield quality. However, it has been stated that only a small %age of the variability has been employed in breeding programs because most breeders begin crossing with a limited number of cultivars as parents (Dutta, 2018; Byrne *et al.*, 2005). Zlesak (2006), reported that the fertility of modern roses is generally poor due to the meiotic abnormalities and the accumulation of deleterious recessive genes as a result of the long crossing history of polyploid and heterozygous parents. Hence, selecting a more diverse parent for making crosses is necessary. Genetic diversity plays an important role in developing hybrids as progenies of genetically diverse parents reveal greater heterosis compared to the progenies of genetically related parents (Dutta, 2015). Selecting genetically diverse parents for crossing needs estimation of genetic diversity, which has been successfully done in rose using various marker systems such as amplified fragment length polymorphism (AFLP)

(Baydar *et al.*, 2004; Pirseyedi *et al.*, 2005), random amplified polymorphic DNA (RAPD) (Jan *et al.*, 1999; Kiani *et al.*, 2007; Tabaei-Aghdaei *et al.*, 2007; Kaul *et al.*, 2009; Henuka *et al.*, 2015) micRosatellite (Babaei *et al.*, 2007; Kaul *et al.*, 2009; Nadeem *et al.*, 2014; Singh *et al.*, 2017; Velluru *et al.*, 2019) markers. Among molecular markers, SSRs are useful over others because of high reproducibility, a high degree of polymorphism, co-dominant inheritance, and uniform distribution in the genome. Scariot *et al.*, (2006) showed that micRosatellite markers are useful in describing genetic diversity and relationships among roses. These are reserved between closely related species; they could provide a marker database for phylogenetic and evolutionary studies (Esselink 2003). SSR markers have been developed in roses by many researchers and had been used for various diversity studies in rose species and varieties (Esselink *et al.*, 2003; Kimura *et al.*, 2006; Scariot *et al.*, 2006; Zhang *et al.*, 2006; Babaei *et al.*, 2007; Hibrand-Saint Oyant *et al.*, 2008; Kaul *et al.*, 2009; Samiei *et al.*, 2009; Smulders *et al.*, 2009). Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, is maintaining more than 200 rose cultivars frequently used to develop new cultivars. In this study, 205 garden rose germplasm were evaluated using sSimple sequence repeat (SSR) markers to understand genetic relatedness among the cultivars using SSR markers.

Material and Method

Plant Material

The plant material consisted of 205 cultivars of rose germplasm (Table 1) maintained at the Division of Floriculture and Landscaping, ICAR-IARI, New Delhi. These cultivars mostly comprised Indian and exotic cultivars of rose and some of the rose species, which form the basis of the rose improvement program at ICAR-IARI, New Delhi, the pioneer institute working for the development of rose cultivars for various traits.

DNA Exwtraction and SSR Analysis

Each accession's fresh, young, and healthy leaves were harvested, fixed in liquid nitrogen, and stored at -80°C until use. The total genomic DNA was extracted using cetyl trimethyl ammonium bromide (CTAB) method (Doyle and Doyle, 1990) with some modifications. A total of 68 primers were screened for polymorphism and optimum amplification, of which 20 polymorphic primers (Table 2) were selected for further analysis. Each 20 µL PCR mix contained 2 µL Taq buffer, 0.5 µL MgCl₂, 2 µL dNTPs, 1 U Taq polymerase, 0.5 µL SSR primer, and 2 to 3 µL of genomic DNA. The PCR procedure was as follows: initial denaturation at 95°C for 4 minutes followed by 35 cycles of denaturation at 95°C for 30 seconds, primer annealing at respective annealing temperatures of primer pair for 30 seconds, and primer extension at 72°C for 45 seconds was done. The

final extension was carried out at 72°C for 10 minutes. The PCR product was separated on 3% agarose gel, prepared in 0.5x TBE buffer stained with 4 µL ethidium bromide (Life Technology PVT Ltd, India) per 100 mL of gel. The resolved amplification products were visualized and photographed using a gel documentation system. DNA amplification was visualized as the presence and absence of a band and was compared with the DNA ladder of 500 bp to quantify the bands. Allelic data were recorded in a binary data matrix as one for presence and 0 for absence.

Data Analysis

The molecular data generated using 20 SSR markers for 205 cultivars were analyzed using Gen-Alex software ver. 6.5 to estimate genetic diversity parameters including band pattern, percent polymorphism, number of different alleles, the effective number of alleles, Shannon information index, expected heterozygosity and unbiased expected heterozygosity, and analysis of molecular variance. DARwin 6.0.21 software was used to estimate the diversity index and create a dendrogram.

Result and Discussion

Results

Using 20 SSR primers, a total of 109 bands were generated from 205 rose cultivars, ranging from 2 to 8 bands per locus. Floribunda had 108 bands, hybrid tea had 98, and wild species had 87. The band pattern is shown in Figure 1. The percent polymorphism, the effective and observed number of alleles (allelic richness), Shannon Information index, and heterozygosity parameters were calculated (Table 3). The average polymorphism for 205 cultivars tested with 20 SSR primers was 88%. On average, 1.78 unique alleles (Na) and 1.46 expected number of alleles (Ne) were discovered. The Shannon information index (I) has an average value of 0.41. The expected (He) and unbiased expected (uHe) heterozygosity were 0.269 and 0.276, respectively. The Jaccards dissimilarity index ranged from 0.15 to 0.82, with an average value of 0.51 (Figure 2). AMOVA revealed that 98% of total molecular variance occurred within groups, with only 2% occurring between groups (Figure 3 and Table 4). The principal coordinate analysis is performed, and a 2D scatter plot for PCoA is generated, as shown in Figure 4, which does not reflect the grouping pattern of cultivars used for analysis. A dendrogram is generated using the Jaccards dissimilarity index, as shown in Figure 5, to understand the presence of any grouping pattern. Cluster I had 94 cultivars, cluster II had 47, and cluster III had 64 cultivars. The grouping of cultivars is given in Table 5.

Discussion

The genetic relatedness of the accessions was revealed by molecular characterization using SSR markers. AMOVA found

Table 1: Rose germplasm used in the study

S.No.	Classification	Cultivars	No. of cultivars
I	Floribunda	Akash sundari, American hero, Andora, Anita, Anne Elizabeth, Aruna, Arunima, Atago, Ave maria, Bacardi, Banjaran, Black Chanakya, Black lady, Brides dream, Bronze star, Camara, Camaray, Charleston, Cherry parfait, Chingari, Christian Dior, Deepak, Delhi brightness, Delhi princess, Dil ki rani, Double knock out, Dr. Benjamin pal, Dr. Hue, Ico, Edmond rose, Else Polson, Emma Harkness, Flamenco, Gemini, Granada, Himalayan wonder, Hoot and howler, Iceberg, Imperator, Ingel horst, Jaimbra, Jantar mantar, Jogan, June bride, Krishna, Kungfu, Lahar, Legar field, Liebehour, Loree, Louisiana, Madhura, Magic central, Manas, Manasi, Manmatha, Marcel pangle, Mist, Moon drop, Mrs. K B Sharma, Navneet, Neelambari, Oh la la, Paraben nandjee, Pearl Polson, Pinata, Pink knock down, Pink parfait, Prema, Punchu, Pusa Ajay, Pusa Baramasi, Pusa Garima, Pusa Komal, Pusa Manhar, Pusa Manjis, Pusa Muskaan, Pusa Pitambar, Pusa Shatabdi, Pusa Urmil, Queen Elizabeth, Raja S. S. of Nalagarh, S S Bhatnagar, Sadabahar, Sea pearl, Shabnam, Shahastradhara, Shailaij Mukharjee, Shanti pal, Sheer delight, Skati metal, Stainless steel, Suchitra, Surabhi, Surdas, Suryakiran, Suryoday, Table Mountain, Tequila, Tarang, Taichung sunset, Tipus flame, Twin balad, Zine borner, Zizi	111
II	Hybrid tea	Abhisharika, American heritage, Angelique, Arjun, Ashwini, Balat spirit, Barbara bush, Bharat ram, Bheem, Borolina, Brandy, Kardinal, Carmousine, Chambe di kali, Command performance, Dr. B. P. Pal, Dr. M S Randhawa, Dulhan. Folk lore, Folklore drakshi, Ganga, Grand gala, Grand Mughal, Gulzar, Haseena, Hollywood, Homaze, Imperetice farah, Jacaranda, Jawani, Kiss of fire, Konrad honki, Lady X, Lalima, Lynn Anderson, Madam Delbert, Madhosh, Melody perfume, Montreal, Mother Teresa, Mridula, Nagabelle, Nayika, Nehru centenary, Olympiad, Parody of England, Pasadina, Priyadarshini, Pusa Abhishek, Pusa Arun, Pusa bahadur, Pusa Gaurav, Pusa Mohit, Pusa Priya, Pusa Sonara, Pusa Veerangana, Raja Ram Mohan Rai, Raktgandha, Scarlet Elizabeth, Soma, Sonia Meiland, Surekha, Surkhhab, White Elizabeth, Woods of Windsor, Yankee doddle	87
III	Wild species	<i>R. indica</i> var. major, <i>R. macrophylla</i> , <i>R. multiflora</i> , <i>R. slancensis</i> , <i>R. tomentosa</i> , <i>R. wichuriana</i> , <i>R. dumalis</i>	7

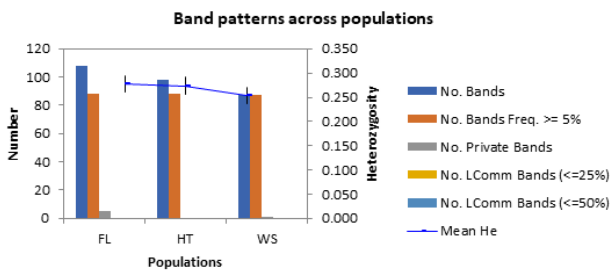


Figure 1: Band patterns across populations

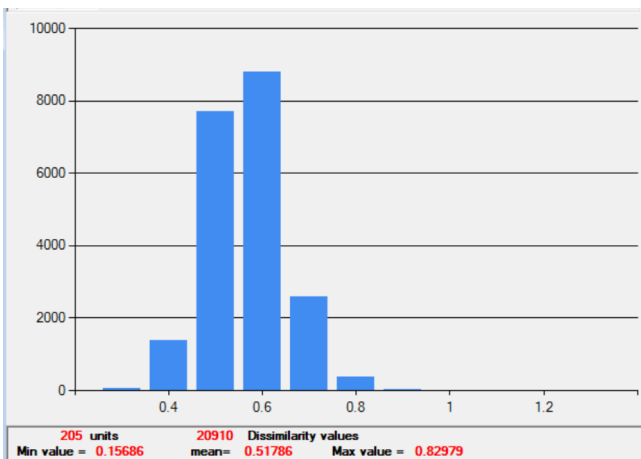


Figure 2: Distribution of Jaccard's dissimilarity coefficients

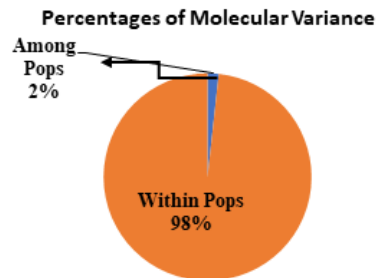


Figure 3: Percentage of molecular variance

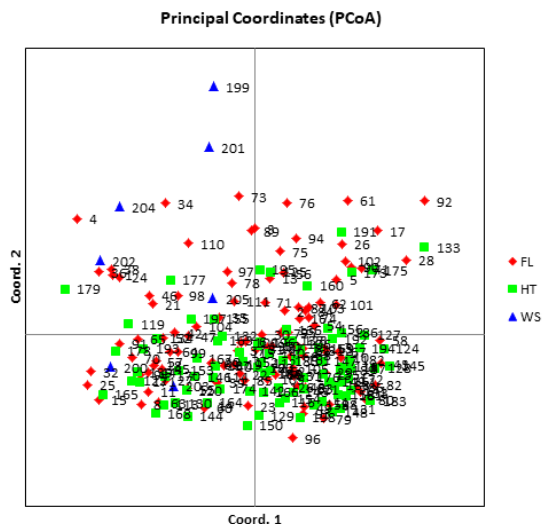


Figure 4: Principal coordinate analysis of 205 rose germplasm based on SSR markers

Table 2: List of selected SSR primers used in the study

S. No.	Marker	Forward (5'→3') Reverse (5'→3')	Expected Band Size (bp)	Ta (°C)	Reference
1	RH93	F-GCTTTGCTGCATGGTTAGGTTG R-TTCTTTTGTCTGTTCTGGGATGTG	251, 273, 275	54	Yan <i>et al.</i> , 2005
2	RH78	F-AAAGAAACGCGAAATCTATGATGC R-TCTGGATGGGATTTAAAAGACAGG	216, 250	51	
3	RH50	F-TGATGAAATCATCCGAGTGTCAG R-TCACTTTCATTGGAATGCCAGAAT	336, 339, 340, 343	54	
4	RH58	F-ACAATTTAGTGCGGATAGAACAAC R-GGAAAGCCCGAAAGCGTAAGC	248, 252, 254, 269	54	
5	Rhb510	F-AAACGATAGGTGAATCTGTGGGT R-CACTCAACCTTGCCACTCCTAAT	159, 161	54	
6	RH73	F-GGTTAGACGGGTGGAAGAAG R-ACTGCCGATAGAAGTATTCATCA	160, 162, 172	54	
7	RW54n22	F-CTCAACTTCCCCGCCTTATC R-CTGGCAGCTCCACTATCTC	169	55	Oyant <i>et al.</i> , 2008
8	CI3881	F-GACAACGACCACCACTTGG R-CCAAAGCAACATTGTCAAAGA	241	55	
9	RW23F13	F-TGCATTATCCCTCTCACTG R-TCAAATGCATGCTGAAAGGA	172	59	
10	H2F12	F-TGGCCAACCTCTCTGTCT R-TCCCAGCTTCGCTTTGTAT	247	55	
11	RW25J16	F-TGGACCTTCCCTTTGTTCC R-GCTTGCCACATATTGTTGA	177	50	
12	H22C01	F-TCATAACCAACCATCTCCATCA R-AGGATTTACCCAGAACACG	228	55	
13	H22EO4	F-GACATCACCACCACACAAG R-AACCAAGGTTTCCAGTTCCA	241	55	
14	CL2980	F-CCCTATTCGATTCGAGTG R-ACTTGCTCGACGGATACAC	234	55	
15	H10D03	F-CAATTCAAACACCGCTCT R-CGCAGAGTCAACGAACCATA	226	55	
16	H23017	F-ACACCAAGCAAACCAAAACC R-AGCACGAAAACCGAGAGAGA	218	55	
17	RW35C24	F-GGCGAATCGAGATTCAGAGA R-GGATTAGCCCAAGTCCAGGT	247	55	
18	RW52D4	F-GGCAGTTGCTGTGCAGTG R-TTGTGCCGACTCAAATCAA	174	55	
19	RW62D8	F-CCTGACTTAACCTCGTGCT R-TCCATCATCAACTTCGTCTG	123	56	
20	RW15D15	F-CGGCTAGCAATCAGTGACAA R-GGTCTTCCCTAATGCCCAAT	203	55	

that within-population variation is greater, with only 2% variation between populations. PCoA and cluster analysis are used to investigate the genetic relatedness of crops. The scatter plot did not exhibit a distinct grouping pattern, indicating that the cultivars are related to each other. The genetic relatedness of cultivars could be attributed to their open outcrossing nature, which results in free gene flow among populations, contributing to more genetic variety within groups (Akond *et al.* 2012; DeVries and Dubois 1996). Hybrid tea cultivars were the first group of modern rose

cultivars derived from crosses of hybrid perpetuals (derived from *R. chinensis*, *R. gallica*, and *R. centifolia*) and tea roses (originated from *R. chinensis* and *R. gigantea*) whereas other modern rose class 'Floribundas' was developed from the crosses of hybrid teas and polyantha roses (latter developed from species *R. multiflora* and *R. wichuriana*) (Marriott 2003) which explains the relatedness between floribunda and hybrid tea cultivars. The addition of genetic material from the polyantha group of roses in floribundas could be attributed to slightly higher heterozygosity within this

Table 3: Summary statistics of genetic diversity

Pop		%P	N	Na	Ne	I	He	uHe
Floribunda (Group 1)	Mean	99.08	111.0	1.982	1.472	0.424	0.279	0.280
	SE		0.00	0.018	0.034	0.022	0.017	0.017
Hybrid tea (Group 2)	Mean	89.91	87.00	1.798	1.468	0.414	0.274	0.276
	SE		0.00	0.058	0.035	0.024	0.018	0.018
Wild species (Pop3)	Mean	76.15	7.00	1.560	1.428	0.384	0.254	0.273
	SE		0.00	0.078	0.035	0.025	0.018	0.019
Total	Mean	88.38	68.33	1.780	1.456	0.407	0.269	0.276
	SE	6.66	2.46	0.034	0.020	0.014	0.010	0.010

Table 4: Summary of AMOVA Table

Source	df	SS	MS	Est. Var.	%
Among Pops	2	60.000	30.000	0.270	2
Within Pops	202	3118.283	15.437	15.437	98
Total	204	3178.283		15.707	100

group as compared to the hybrid teas. Similarly, Azeem *et al.* (2012) and Rusanov *et al.* (2005) reported lower genetic variability of cultivated roses using RAPD and SSR markers. Akond *et al.* (2012) using SSRs also observed higher similarity and narrow genetic base of modern cultivars (Miniature roses and hybrid breeding lines) as compared to their wild relatives. Smulders *et al.* (2009) also used 11 micRosatellite markers to characterize 734 hybrid tea cultivars and found that they had relatively close genetic links.

A dendrogram is also produced to better understand the presence of a grouping pattern. Three major clusters were found. The first cluster consists primarily of Indian-bred rose cultivars and a few wild species. The second cluster consists primarily of exotic varieties, whereas the third cluster has both Indian and exotic cultivars. These classifications do not correspond to the horticultural classifications used to group the accessions. Some investigations on garden rose varieties have also revealed a similar pattern (Vainstein *et al.*, 1993; Ben-Meir and Vainstein, 1994; Debner *et al.*, 1996; Panwar *et al.*, 2006; Rai *et al.*, 2015; Velluru *et al.* 2019). Debner *et al.* (1996) discovered that rose cultivars did not cluster according to the groups to which their parents belonged. The hybrid tea and the floribunda groups share the highest genetic similarity. Similar results were also reported by

Table 5: Clustering of cultivars based on SSR data

Cluster No.	Cultivars	No. of cultivars
Cluster I	Oh lala, Navneet, June Bride, Haseena, Pusa Muskan, Pusa Gaurav, Mother Teresa, Grand Mughal, Sugandha, Thaichun Sunset, Memorial Day, Lalima, Pusa Mahak, Montezuma, Pusa Sonara, Pusa Shatabdi, Kiss of Fire, Surekha, Arjun, Soma, Shashtradhara, Tajmahal, Pusa Garima, Manas, Folklore, Sheer Delight, Yankee doodle, Borolina, Imteretice Farah, Dil Ki Rani, Chambe di Kali, Angelique, Taquilla, Pinata, Anita, Black Lady, Blue moon, Camara, Gemini, Ingel horst, Magic central, Hollywood, Tarang, Pusa komal, Camaray, Jaimbra, Pusa Manhar, Madhura, Pusa Ajay, Pusa Veerangana, Pusa Mohit, Jawahar, Anurag, Krishna, Pusa Pitamber, Aruna, Raktagandha, Bharat Ram, Dr B P pal, Surdas, Dr Benjamin Pal, Raja Ram Mohan Rai, Raja S S of Nalagarh, Ranjana, Pusa Arun, Iceberg, Nehru Centenary, Dulhan, Delhi Brightness, Jawani, Pusa Manjis, Homaze, Pusa Bahadur, Pusa Abhishek, Dr M S Randhwa, Pusa Urmil, Jantar Mantar, Mrs. K. B. Sharma, Baccardi, Pink Parfait, Lahar, Twin Balad, Folklore Drakshi, Brandy, Jadis, Balat Spirit, Century II, White Elizabeth, NoorJanah(HT), Legarfield, Kardinal, Ganga, Pearl Polson, Delhi Princess	94
Cluster II	Atago, Midas Touch, Double Knockout, Moon Drop, Karen Blixen, Konred Honki, Christian Dior, Lynn Anderson, Nagabelle, Carmousine, Andora, Madam Delbert, Bewitched, <i>Rosa salascensis</i> , Jwala, <i>R. tomentosa</i> , <i>R. macrophylla</i> , Mist, Shola, Table Mountain, Suchitra, Marcel pangel, Grandgala, Granada, Parady of England, Louisiana, Melody perfume, Leibeheour, Ico, American Hero, Cherry Parfait, Ave Maria, Lady X, Paraben Nandjee, Sonia Meiland, Barbara Bush, Anne Elizabeth, Pasadina, Impereter, Sea Pearl, Brides Dream, Superstar, Command performance, Montreal, Jogan, Maid of Honour, Velvet Fragrance	47
Cluster III	Black Chanakya, Akash Sundari, Emma Harkness, Shantipal, Jaccaranda, Scarlet Elizabeth, Noorjahan (D), <i>R. dumalis</i> , Pink knockdown, Manmatha, Ashwini, Shailaize Mukherjee, Nayika, Banjaran, Okhlahoma, Bonne nuit, Pusa Aradhan, Skati metal, Olympiad, Surkhab, Stainless steel, American Heritage, Zine borner, Kungfoo, Bronze Star, Edmond rose, Zizi, Bheem, Woods of Windsor, Tipus Flame, Neelambari, Priyadarshini, Surabhi, Pusa Priya, Deepak, Raktima, Flamenco, Charleston, Else polson, Ranisahiba, Loree, Arunima, Sadabahar, Punchu, Pusa Barahmasi, Rose sherbet, Manasi, Madhosh, Gulzar, S S Bhatnagar, Himalayan Wonder, Abhisarika, Suryoday, Suryakiran, Shabnam, Prema, Mridula, Chingari, <i>R. multiflora</i> , Dr. Hue, <i>R. wichuriana</i> , Queen Elizabeth, Hoot and howler, <i>R. indica</i> var major	64
Total		205

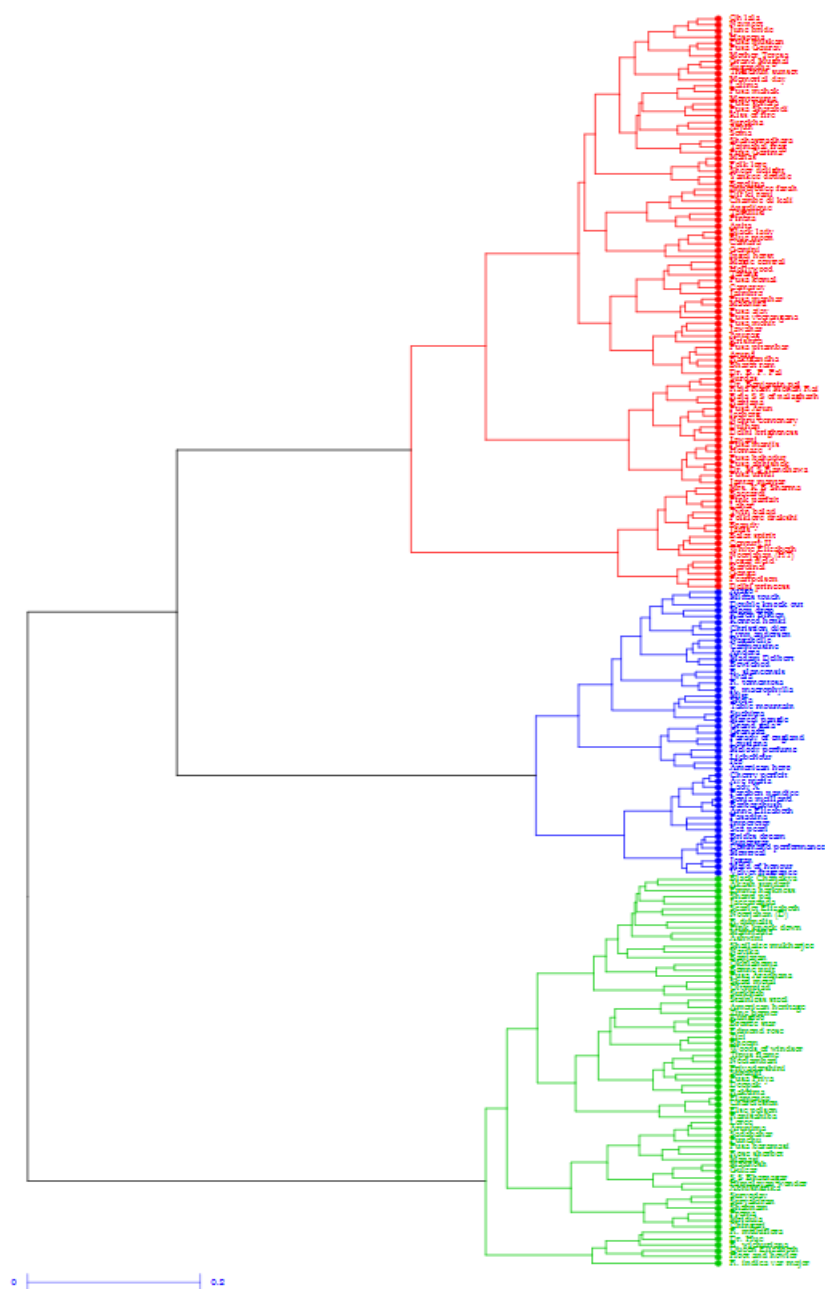


Figure 5: Clustering of cultivars

Vainstein *et al.* (1993). The lack of clear distinction between different groups may be due to the complex hybrid nature of rose cultivars. The majority of the cultivars used in the present study belong to modern rose classes (Hybrid Teas and Floribundas).

The polymorphism observed can be attributed to its polyploidy and heterozygous nature. Roses are highly heterozygous and show a wide range of variability in the color and form of rose flowers in the seedlings obtained (Dutta 2018). However, the basic material for the development of new cultivars is limited. Interspecific

hybridization in roses (*Rosa* spp.) has generated thousands of cultivars with commercial value, but only eight to ten species are commonly represented in the pedigrees of modern cultivars even though there are hundreds of rose species reported (Bryne 2005). Modern classes of rose hybrids (Hybrid Teas, Floribundas, and Grandifloras, and Miniatures) are also products of such hybridizations. The majority of the rose species are products of the natural hybridization of one or more hybrids.

The study suggests genetic similarity among the rose cultivars across different horticultural classes, indicating

the decreasing genetic base of hybrid roses. There is unexploited rose germplasm, which has the potential to broaden the overall gene pool of rose breeding programs in general (Akond *et al.*, 2012). The most diverse cultivars should be used as parents to exploit the heterosis. The wild rose species showed higher dissimilarity with almost all the cultivars and can be used to broaden the genetic base. The dissimilarity coefficient for Queen Elizabeth and Surkhab had a maximum (82%) and cultivar Suchitra and Barbara Bush (15%) had a minimum dissimilarity coefficient. The cultivars Queen Elizabeth and rose species *Rosa indica* var. *major*, *Rosa macrophylla*, and *Rosa multiflora* are found to show higher dissimilarity coefficients ranging from 50 to 80% with almost all the cultivars and can be used as parents in the crossing program.

Conclusion

The study suggests genetic similarity among the rose cultivars across different horticultural classes, indicating the decreasing genetic base of hybrid roses. There is unexploited rose germplasm, which has the potential to broaden the overall gene pool of rose breeding programs in general (Akond *et al.*, 2012). The most diverse cultivars should be used as parents to exploit the heterosis. The wild rose species showed higher dissimilarity with almost all the cultivars and can be used to broaden the genetic base. The dissimilarity coefficient for Queen Elizabeth and Surkhab had a maximum (82%) and cultivar Suchitra and Barbara Bush (15%) had a minimum dissimilarity coefficient. The cultivars Queen Elizabeth and rose species *Rosa indica* var. *major*, *Rosa macrophylla*, and *Rosa multiflora* are found to show higher dissimilarity coefficients ranging from 50 to 80% with almost all the cultivars and can be used as parents in the crossing program.

Acknowledgment

During the period of study, Shephalika Amrapali was supported by study leave for the doctoral program at the Discipline of Plant Genetic Resources, ICAR-IARI, New Delhi. Sunil Archak was supported by the ICAR National Fellowship. The authors also acknowledge the field facilities of the Division of Floriculture and Landscaping, ICAR-IARI, and laboratory facilities at the Division of Genomic Resources, ICAR-NBPGR.

References

- Akond M, S Jin and X Wang (2012) Molecular characterization of selected wild species and miniature roses based on SSR markers. *Sci. Hort.* 147: 89-97.
- Babaei A, R Tabaei-Aghdahi, M Khosh-Khui, R Omidbaigi, M Naghavi, GD Esselink and MJM Smulders (2007) MicRosatellite analysis of Damask rose (*Rosa damascena* Mill.) accessions from various regions in Iran reveals multiple genotypes. *Plant Biol.* 7: 12.
- Baydar GN, H Baydar and T Debener (2004) Analysis of genetic relationships among *Rosa damascena* plants grown in Turkey by using AFLP and micRosatellite markers. *J. Biotech.* 111: 263-267.
- Ben-Meir H and A Vainstein (1994) Assessment of genetic relatedness in roses by DNA fingerprint analysis. *Sci. Hort.* 58: 158-164.
- Bryne DH (2005) Rose breeding and genetics research at Texas A&M University. *Indian Rose Annu.* XXI, 52-56.
- Debener T, C Bartels and L Mattiesch (1996) RAPD analysis of genetic variation between a group of rose cultivars and selected wild rose species. *Mol. Breed.* 2: 321-327.
- Debener T and L Mattiesch (1999) Construction of a genetic linkage map for roses using RAPD and AFLP markers. *Theor. Appl. Genet.* 99(5): 891-899.
- Datta SK (2015) Indian Floriculture: Role of CSIR, Regency Publications, A Division of Astral International (P) Ltd., New Delhi, India, 454p.
- Datta SK (2018) Breeding of new ornamental varieties: Rose. *Curr. Sci.* 114: 6p.
- Esselink GD, MJM Smulders, and B Vosman (2003) Identification of cut-rose *Rosa hybrida* and rootstock varieties using robust Sequence Tagged MicRosatellite markers. *Theor. Appl. Genet.* 106: 277-286.
- Henuka R, DVS Raju, T Janakiram, Namita, SG Krishnan and J Rana (2015) Characterization and analysis of genetic diversity among different species of rose (*Rosa* species) using morphological and molecular markers. *Indian J. Agric. Sci.* 85(2): 240-245.
- Jan CH, DH Byrne, J Manhart and H Wilson (1999) Rose germplasm analysis with RAPD markers. *Hort. Sci.* 342: 341-345.
- Kaul K, S Karthigeyan, D Dhyani, N Kaur, RK Sharma and PS Ahuja (2009). Morphological and molecular analyses of *Rosa damascena* × *R. bourboniana* interspecific hybrids. *Sci. Hort.* 1222: 258-263.
- Kaicker US (1982) Mutation breeding in roses. *Indian Rose Annu.* II+ pp 35-42.
- Kaicker US (1992) Rose breeding in India and cytology of induced mutants of H.T.cv Folklore. *Acta Hort.* 320: 105-112.
- Kiani M, Z Zamani and A Khalighi (2007) Wide genetic diversity of *Rosa damascena* Mill germplasm in Iran as revealed by RAPD analysis. *Sci. Hort.* 115: 386-392.
- Kimura T, C Nishitani, H Iketani, Y Ban and T Yamamoto (2006) Development of micRosatellite markers in rose. *Mol. Ecol. Resour.* 63: 810-812.
- Nadeem M, X Wang, M Akond, FS Awan, A Riaz and A Younis (2014) Hybrid identification, morphological evaluation and genetic diversity analysis of 'Rosa x hybrida' by SSR markers. *Aust. J. Crop Sci.* 8(2): 183.
- Oyant HSL, L Crespel, S Rajapakse, L Zhang and F Foucher (2008) Genetic linkage maps of rose constructed with new micRosatellite markers and locating QTL controlling flowering traits. *Tree Gen. Genom.* 4: 11-23.
- Panwar S, KP Singh, H Sonah, PK Deshmukh, B Namita, KV Prasad and Sharma TR (2015) Molecular fingerprinting and assessment of genetic diversity in rose. *Indian J. Biotechnol.* 14: 518-524.
- Pirseyedi SM, M Mardi and S Davazdahemami (2005) Analysis of the genetic diversity between 12 Iranian Damask rose (*Rosa damascena* Mill) using amplified fragment length

- polymorphism markers. *Iran J. Biotechnol.* 3: 225-230.
- Prasad KV, S Kumar, and ML Choudhary (2006) Molecular characterization of fragrant rose cultivars. *Indian J. Hort.* 63: 229-234
- Qi W, X Chen, P Fang, S Shi, J Li, X Liu, X Cao, N Zhao, H Hao, Y Li, Y Han and Z Zhang (2018) Genomic and transcriptomic sequencing of *Rosa hybrida* provides micRosatellite markers for breeding, flower trait improvement and taxonomy studies. *BMC Plant Biol.* 18: 119
- Samiei L, R Naderi, A Khalighi, A Bushehri, V Mozaffarian, GD Esselink and MJM Smulders (2009) In search of genetic diversity in *Rosa foetida* Herrmann in Iran. *Acta Hort.* 836: 25-30.
- Scariot V, A Akkak and R Botta (2006) Characterization and genetic relationships of wild species and old garden roses based on micRosatellite analysis. *J. Am. Soc. Hort. Sci.* 131: 66-73
- Singh S, D Dhyani, A Nag and RK Sharma (2017) Morphological and molecular characterization revealed high species level diversity among cultivated, introduced, and wild roses *Rosa* sp. of western Himalayan region. *Gen. Resour. Crop Evol.* 643: 515-530
- Smulders MJM, P Arens, CSF Koning-Boucoiran, VW Gitonga, FA Krens, A Atanassov, I Atanassov, KE Rusanov, M Bendahmane, A Dubois, O Raymond, JC Caissard, S Baudino, L Crespel, S Gudín, SC Ricci, N Kovatcheva, J Van Huylbroeck, L Leus, V Wissemann, H Zimmermann, I Hensen, G Werlemark and H Nybom (2011) *Rosa*. In: Kole, C. (Ed.), *Wild Crop Relatives: Genomics and Breeding Resources Plantation and Ornamental Crops*. Springer Verlag, Berlin, Heidelberg, pp 243-275.
- Tabaei-Aghdai SR, A Babaei, M Khosh-Khui, K Jaimand, MB Rezaee, MH Assareh and MR Naghavi (2007) Morphological and oil content variations amongst Damask rose (*Rosa damascena* Mill.) landraces from different regions of Iran. *Sci. Hort.* 1131: 44-48.
- Vainstein A, H Ben-Meir and A Zucker (1993) *DNA fingerprinting as a reliable tool for the identification and genetic analysis of ornamentals*. In: Proceedings of XVIIth eucarpia symposium on "creating genetic variation in ornamentals", San Remo. pp 63-68
- Yan Z, C Denneboom, A Hattendorf, O Dolstra, T Debener, P Stam, and PB Visser (2005) Construction of an integrated map of rose with AFLP, SSR, PK, RGA, RFLP, SCAR and morphological markers. *Theor. Appl. Genet.* 110: 766-777
- Zhang LH, DH Byrne, RE Ballard and S Rajapakse (2006) MicRosatellite marker development in rose and its application in tetraploid mapping. *J. Am. Soc. Hort. Sci.* 131: 380-387
- Zlesak DC (2006) *Rosa x hybrida* L. In: NO Anderson (Ed.) *Flower Breeding and Genetics: Issues, Challenges, and Opportunities for the 21st Century*. Springer, The Netherlands, pp. 695-738.

RESEARCH ARTICLE

SSR Markers based Diversity Analysis in Elite Genotypes of Pearl Millet

J. Jorben, Mukesh Sankar S., Anju M. Singh, C. Tara Satyavathi¹, Tripti Singhal, Thribhuvan R. and S. P. Singh*

Abstract

Analysis of genetic diversity was carried out using 32 genotypes of pearl millet using SSR markers and phenotypic data of 10 morphological traits. Significant differences were observed for all the traits recorded in the study, indicating the availability of sufficient genetic variability in the materials. Among the 69 simple sequence repeat (SSR) primers screened, 44 primers were found polymorphic. These polymorphic primers amplified 151 alleles. The number of alleles per SSR marker varied from 2 to 5 per locus. Polymorphism information content values (PIC) ranged from 0.058 to 0.608 per locus with an average of 0.375. Genotypes were grouped into three clusters based on molecular and phenotypic data, and the genotypes' distribution was similar in both. Principal coordinate analysis further corroborated the grouping of genotypes obtained on phenotypic and molecular data. Structure analysis was also observed to be in line with cluster grouping as well as principal coordinate analyses.

Keywords: A₄ maintainers and restorers, Dendrogram, Diversity, *Pennisetum glaucum*, Polymorphism information content, Simple sequence repeats.

Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India.

¹ICAR-Indian Institute of Millet Research, Rajendranagar, Hyderabad, Telangana, India.

***Author for correspondence:**

sumerpalsingh@yahoo.com

Received: 18/07/2023 **Revised:** 29/02/2024

Accepted: 01/03/2024

How to cite this article: Jorben J, MS Sankar, AM Singh, CT Satyavathi, T Singhal, R Thribhuvan and SP Singh. (2024) SSR Markers based Diversity Analysis in Elite Genotypes of Pearl Millet. *Indian J. Plant Genetic Resources*. 37(1): 39-46. DOI: 10.61949/0976-1926.2024.v37i01.05

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is the staple food of the majority of the poor and small landholders. It is also used as feed and fodder for livestock in the rain-fed regions of the country. It requires less input and matures in a short duration. Pearl millet is a highly nutritious cereal with high levels of energy and protein and a more balanced amino acid profile (Andrews and Kumar, 1992). It can play an important role not only in contributing to the food and nutritional security of the poor in the pearl millet growing areas of India and sub-Saharan Africa but could also have potential health value for the affluent (Rai *et al.*, 2012; Jorben *et al.*, 2020). Recognizing its value, the Government of India has declared the year 2018 as the 'National Year of Millets' and UN also declared 2023 as the 'International Year of Millets'. It is a drought-tolerant warm-season cereal grown in dry land agriculture on more than 27 million ha in some of the harshest environments in Africa's arid and semi-arid tropical regions (17 million ha) and Asia (10 million ha). In these regions, pearl millet is a staple food of more than 90 million people. In India, pearl millet is the third most widely cultivated food crop after rice and wheat. The area of pearl millet in India was estimated to be 6.93 million hectares, with an average production of 8.61 million tons and productivity of 1391 kg/ha (Directorate of Millets Development, 2020).

Many researchers (Lakshmana *et al.*, 2009; Sharma, 2016) estimated the diversity based on phenotypic traits in pearl millet. But, these data are more influenced by the environment

and other factors and are considered less reliable. Hence, molecular markers have emerged as a more reliable tool for studying the genetic diversity of genotypes. The study of morphological markers and polymerase chain reaction (PCR) based co-dominant markers like simple sequence repeats (SSRs) are often considered to be one of the most suitable and reliable markers in applied breeding programs. These markers have been extensively utilized to assess the extent of genetic diversity among various crops such as sorghum, maize, wheat, barley and cotton (Chandra *et al.*, 2014; Gupta *et al.*, 2015). Molecular diversity analysis in pearl millet has been studied often in the recent genomics era (Nepolean *et al.*, 2012; Satyavathi *et al.*, 2013; Chandra *et al.*, 2014; Bashir *et al.*, 2015; Gupta *et al.*, 2018). Most of these studies have relied on morphological or molecular interpretation. Some studies in other crops (Wang *et al.*, 2006; Hegay *et al.*, 2014) are also available, wherein morphological and molecular data have been jointly studied. However, information on the estimation of genetic diversity using both morphological and molecular markers is limited in pearl millet. The present study attempts to classify the elite maintainers and restorers belonging to A₄ cytoplasm using morphological and molecular markers.

Materials and Methods

For the assessment of genetic diversity, six seed parents (B-Lines)/maintainers and 26 A₄ restorers (R-Lines) were obtained from ICRISAT, Patancheru, India. Details of these parental lines are given in Table 1. All 32 genotypes were sown at ICAR-Indian Agricultural Research Institute, New Delhi, and evaluated in randomized complete block design with three replications. In the case of phenotypic evaluation, observations were recorded using standard methods on ten agro-morphological traits, which ultimately contributed to the plant yield. Observations on each genotype were recorded for yield and related characters on five randomly selected competitive plants from each replication, except for days to 50% flowering, days to maturity and grain yield, which were recorded on plot basis. The average values were used for statistical analysis.

DNA was isolated from young expanding leaves of 32 genotypes using the modified CTAB method (Saghai Maroof *et al.*, 1984) with suitable modification. About 69 SSR primers developed for pearl millet were selected in such a way as to have 8 to 10 primers from each of the seven chromosomes (Rajaram *et al.*, 2013). The utility of a marker for detecting genetic variation was estimated using power marker software as reported by Liu and Muse, (2005). It includes a) polymorphism information content (PIC), which is equal to $1 - \sum P_{ij}^2$ where P_{ij} is the frequency of j^{th} allele at i^{th} locus summed across all alleles in the locus, b) observed heterozygosity c) genetic diversity and d) allelic richness which means the number of alleles per primer.

A simple matching allele frequency-based distance matrix was used in the DARwin-6.0 program (Perrier *et al.*, 2003) to construct a tree diagram to examine the genetic structure and diversity among maintainer and restorer lines using molecular marker scores. The grouping into clusters and sub-clusters was done at 5% dissimilarity level with a bootstrap analysis of 1000 times for statistically supporting the branches of the cluster. Similarly, using morphological data, pair-wise genetic distance comparisons of genotypes were calculated by Euclidean distance coefficients (Bakonyi and Johnson, 1995) using SAS 9.3 program (SAS Institute, Cary NC). Based on an average linkage algorithm (UPGMA, unweighted pair group method with arithmetic average), clustering of genotypes was done to depict the similarity or dissimilarity among groups or individual genotypes.

Bayesian clustering model was also performed using STRUCTURE software version 2.3.4 (Pritchard *et al.*, 2000). A continuous series of K were tested from 1 to 10 in 10 independent runs. The initial burn-in period for each run was set to 1,50,000, followed by 1,50,000 Markov Chain Monte Carlo (MCMC) iterations. The online available program, STRUCTURE HARVESTR (Earl and von Holdt, 2012) was used to calculate the optimum k value based on an ad hoc quantity ΔK proposed by Evanno *et al.*, 2005 based on second order rate of change of the likelihood function with respect to K estimated to get the final population structure.

Results and Discussion

Assessment of Phenotypic Diversity

The mean, range, and coefficient of variation of 10 phenotypic traits recorded on 32 genotypes were estimated. Significant differences were observed for all the 10 traits recorded, indicating the existence of sufficient genetic variability in the material (Figure 1). Information on the genotypic coefficient of variation, phenotypic coefficient of variation, heritability in a broad sense and genetic advance were also obtained. The genotypic coefficient of variation varied from 4.29 to 47.12. The range of phenotypic coefficient of variation was 4.33 to 47.32. High heritability estimates were observed for all the traits except the number of productive tillers per plant. The highest heritability (99.17%) was observed for blast score and the lowest for the number of productive tillers per plant (67.05%). In the same way, the highest genetic advance was observed for blast score and it was lowest for days to maturity. Similar results for phenotypic diversity were also reported by Shanmuganathan *et al.*, 2006, Lakshmana *et al.*, 2009 and Sharma, 2016. The clustering based on Euclidean distance distributed the genotypes in three different clusters at 1.0 Euclidean coefficient. On the basis of morphological data, most diverse genotype was ICMB 03999, placed in cluster III alone. The distribution of genotypes was not found in

Table 1: Details of genotypes used for morphological and molecular characterization

S. No.	Genotype	Parentage/pedigree
1	ICMB 99111	(843B x ICTP 8202-161-5)-17-1-2-B-1
2	ICMB 99444	(SPF3/S91-327 x SPF3/S91-5)-6-2-2
3	ICMB 03999	ICMB 89111 x IP 9402-2-1-1-2)-31-1-B-B
4	ICMB 04111	(81B x 4017-5-4-B)-12-3-1-3
5	ICMB 05888	(SRC II C3 S1-1-1-2 x HHVBC)-5-1-1-2
6	ICMB13222	[(ICMB 95111 x 9035/S92-B-3)-17-5-1-B-B-B x ICMB 99111]-3-2-1-3
7	ICMR 06111	MC 94 C2-S1-3-1-3-3-2-2-B
8	ICMR 06222	SDMV 90031-S1-3-3-2-1-3-2-2-1-B
9	ICMR 06333	SDMV 90031-S1-93-3-1-1-3-2-2-1-1-B
10	ICMR 06444	[[(MC 94 S1-34-1-B x HHVBC)-16-2-1) x (IP 19626-4-2-3)]-B-37-1-1-1-2-B
11	ICMR 07222	MRC HS-130-6-1-1-B-B-B-B-B
12	ICMR 07555	ICMS 8511 S1-17-2-1-1-4-1-B-3-2-2-B
13	ICMR 08888	ICMS 7704 S1-52-3-1-2-1-2-1-6-B-B
14	ICMR 08999	JBV 3 S1-18-2-2-1-3-2
15	ICMR 09666	[[(IP 12322-1-2) x B-Lines)-B-14) x (MRC S1-156-2-1-B)]-B-1-3-3-B-B
16	ICMR 09777	JBV 3 S1-35-2-1-2-B
17	ICMR 09888	[[(MC 94 S1-34-1-B x HHVBC)-16-2-1) x (IP 19626-4-2-3)]-B-34-1-3-3-1-1-B-2
18	ICMR 10888	ICMV 93074-S1-9-1-1-1-3-B-B-B-B
19	ICMR 12222	JBV-3-S1-33-2-1-3-3-B-3-B-1-B
20	ICMR 12333	(E 298 x LCSN 282-4-1-2)-12-2-1-2-B-B-B-1
21	ICMR 12444	(ICMS 7704-S1-127-5-1 x RCB-2 Tall)-B-19-3-2-1-1-1-B
22	ICMR 12555	(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-28-1-1
23	ICMR 13444	(IAC-ISC TCP6 S1-9-1-2-B-4-2-B x AIMP 92901-S1-488-2-1-1-4-B-B)-B-11-3-1-B
24	ICMR 13555	GB 8735-S1-15-3-1-1-3-4-2-2-1-1-B-B
25	ICMR 13666	ICMS 8511-S1-17-2-1-1-4-1-B-3-2-3-2-B-1-1-B
26	ICMR 13999	MDMRRC S1-329-1
27	A ₄ RT-13-2/DPR 7	PPMI 2354 x PPMI 112/PPMI 217-89-52-2-2
28	A ₄ RT-15-13	(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-28-1-1-B
29	A ₄ RT13-3/DPR 8	P1977x P85/PPMI 69-2310-256-5-3-1
30	A ₄ RT-13-5	(ICMS 7704-S1-127-5-1 x RCB-2 Tall)-B-19-3-3-1-2-1
31	A ₄ RT-15-10	(IPC 337 x SDMV 90031-S1-84-1-1-1-1)-12-5-2-4-B-B-B
32	A ₄ RT-15-12	(MC 94 C2-S1-3-2-2-2-1-3-B-B x AIMP 92901 S1-488-2-1-1-4-B-B)-B-23-4-4-2

accordance with pedigree and source/origin of genotypes. It may be because environmental conditions highly influence morphological traits.

Yadav *et al.* (1994) also did not find accordance between phenotypic diversity and pedigree/origin of genotype.

Informativeness of SSR Markers

Total 69 SSR loci were analyzed to differentiate among 26 restorers and 6 maintainers of A₄ cytoplasm. About 44 SSR markers were found to be polymorphic and data derived from these polymorphic SSR markers was used for further statistical analysis, which gave amplicons in the range of 130 to 340 bp. Total number of alleles observed were 151 and the number of alleles per locus varied from 2 to 5 with an average number of 3.43 alleles per locus. The gels for visualizing the amplification products of two primers are shown in Figure 2. PIC ranged from 0.058 to 0.608 per locus with an average PIC of 0.375. PIC calculated was highest for four SSR primers viz. PSMP 2081 (0.61), PSMP 2237 (0.59), IPES 191 (0.58) and IPES 233 (0.58) and lowest for the primer IPES160 and IPES175 (0.06) (Table 2). Seven out of the 44 SSR markers revealed heterozygosity in different inbreds. The seven SSR primers viz., IPES 200, IPES 225, IPES 236, IPES 198, IPES 208, PSMP 2089 and PSMP 2235 have detected heterozygosity. The observed heterozygosity per primer ranged from 0 to 0.81. PIC values observed in the study were comparable with those reported by Satyavathi *et al.*, 2009, Sumanth *et al.*, 2013, Chandra *et al.*, 2014 and Kifouli *et al.*, 2017. The number of alleles detected per marker and the gene diversity of markers depend on the number of genotypes analyzed, which were comparably less in the present study.

Assessment of SSR Marker-based Genetic Diversity

Simple matching dissimilarity coefficients were calculated using SSR primer amplification scoring data generated in 32 genotypes using Darwin 6. Accordingly, these genotypes were placed in three clusters at 5% dissimilarity coefficient

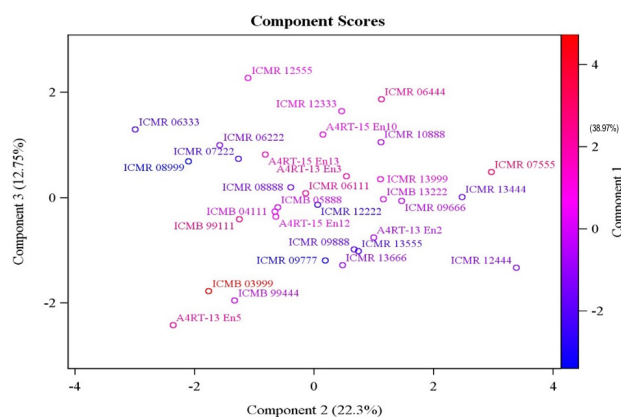


Figure 1: PCA plot based on phenotypic diversity analysis of 32 genotypes using 10 morphological traits

Table 2: List of SSR primers, their allelic size range, allelic richness, major allele frequency, gene diversity, PIC and observed heterozygosity

S. No.	SSR loci	Allelic richness	Allele size range	Major allele freq.	Gene diversity	Observed heterozygosity	PIC
1	IPES230	3	10 (170–180)	0.84	0.28	0	0.26
2	IPES076	4	30 (200–230)	0.78	0.37	0	0.35
3	IPES210	4	20 (170–190)	0.81	0.33	0	0.31
4	IPES017	3	10 (140–150)	0.72	0.43	0	0.38
5	IPES144	3	20 (140–160)	0.84	0.27	0	0.25
6	IPES219	3	20 (130–150)	0.91	0.17	0	0.17
7	IPES174	3	20 (230–250)	0.88	0.23	0	0.21
8	IPES200	3	20 (170–190)	0.52	0.53	0.03	0.42
9	IPES225	3	10 (250–260)	0.81	0.32	0.06	0.30
10	IPES185	4	20 (150–170)	0.69	0.47	0	0.42
11	IPES166	4	20 (210–230)	0.75	0.42	0	0.39
12	IPES206	3	10 (230–240)	0.84	0.28	0	0.26
13	IPES087	3	10 (220–230)	0.63	0.53	0	0.47
14	IPES089	4	20 (310–330)	0.69	0.48	0	0.44
15	IPES236	4	20 (210–230)	0.45	0.6	0.22	0.51
16	IPES198	4	20 (300–320)	0.52	0.63	0.09	0.57
17	IPES195	3	10 (180–190)	0.56	0.52	0	0.41
18	IPES151	4	20 (170–190)	0.88	0.23	0	0.22
19	IPES213	4	20 (220–240)	0.75	0.41	0	0.39
20	IPES127	4	20 (270–290)	0.63	0.55	0	0.50
21	IPES208	2	10 (280–290)	0.64	0.46	0.03	0.35
22	IPES175	2	10 (270–280)	0.97	0.06	0	0.06
23	IPES095	4	20 (200–220)	0.88	0.23	0	0.22
24	IPES118	3	10 (180–190)	0.63	0.52	0	0.45
25	IPES229	2	10 (180–190)	0.81	0.3	0	0.26
26	IPES154	2	10 (300–310)	0.84	0.26	0	0.23
27	IPES233	4	20 (230–250)	0.53	0.63	0	0.58
28	IPES191	4	20 (260–280)	0.56	0.62	0	0.58
29	IPES186	4	30 (270–300)	0.69	0.48	0	0.44
30	IPES160	2	10 (150–160)	0.97	0.06	0	0.06
31	IPES093	4	110 (40–150)	0.75	0.4	0	0.36
32	IPES052	4	20 (260–280)	0.44	0.64	0	0.57
33	IPES019	5	30 (250–280)	0.56	0.61	0	0.56
34	PSMP2081	4	40 (180–220)	0.41	0.67	0	0.61
35	PSMP2089	3	10 (270–280)	0.8	0.33	0.03	0.30
36	PSMP2077	5	30 (150–180)	0.59	0.59	0	0.54
37	PSMP2229	4	20 (230–250)	0.84	0.28	0	0.26
38	PSMP2235	3	10 (140–150)	0.53	0.55	0.81	0.45
39	PSMP2246	4	30 (150–180)	0.69	0.49	0	0.45
40	PSMP2237	4	20 (270–290)	0.53	0.64	0	0.59
41	PSMP2090	4	20 (150–170)	0.72	0.45	0	0.41
42	PSMP2030	2	10 (170–180)	0.84	0.26	0	0.23
43	PSMP2202	3	20 (170–190)	0.72	0.43	0	0.38
44	PSMP2027	3	20 (250–270)	0.78	0.37	0	0.34
Mean		3.4		0.71	0.42	0.03	0.37

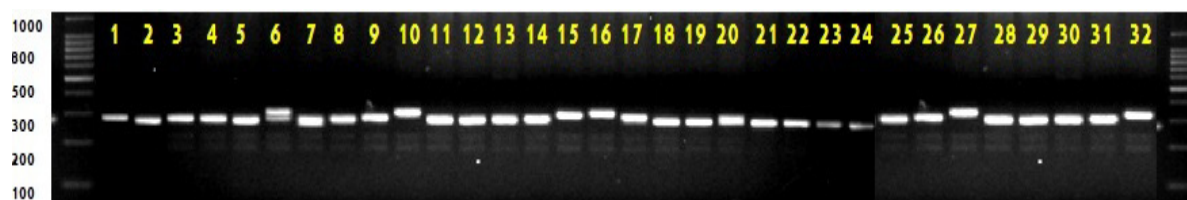


Figure 2: Ethidium bromide-stained DNA amplification profile of 32 genotypes of pearl millet using microsatellite marker PSMP 2237

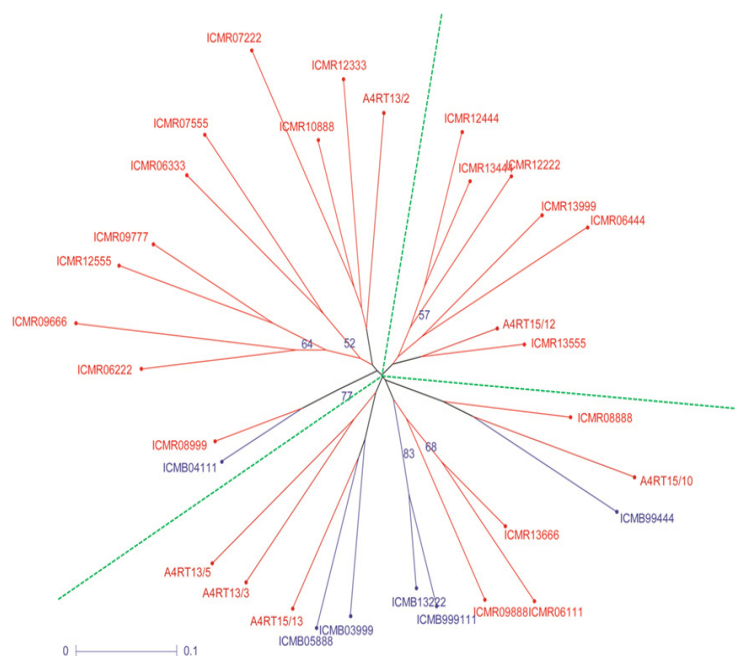


Figure 3: Unweighted neighbor-joining tree based on a simple matching dissimilarity matrix for allele sizes, detected by 44 SSR primers across 32 genotypes (B-lines are shown in blue and R-lines in red color).

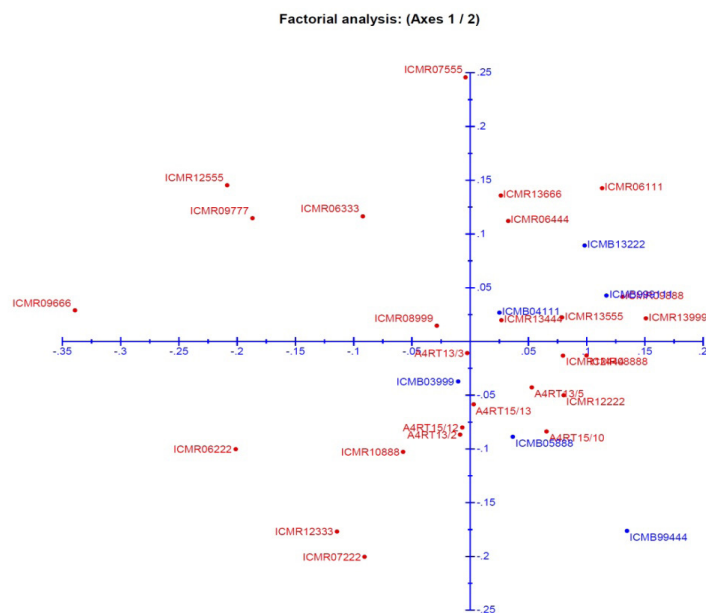


Figure 4: Factorial analysis of 32 genotypes using 44 SSR primers (B-lines are shown in blue and R-lines in red color)

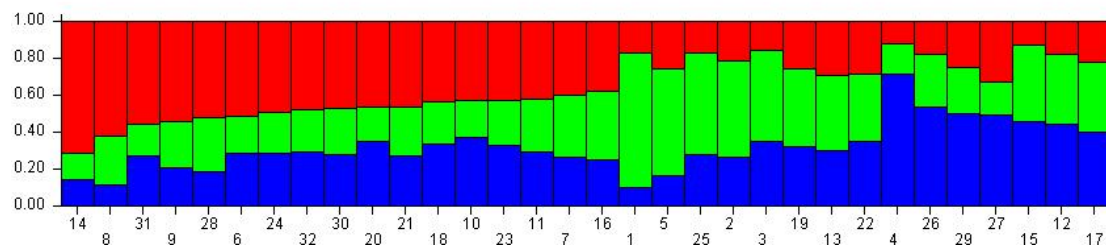


Figure 5: Bar diagram for 32 genotypes arranged based on inferred ancestry at $K = 3$; Color codes represent the three subpopulations. Values in the left indicate the membership coefficient (Q). Proportions of colors in each bar indicate the allelic affiliation of the sub-populations

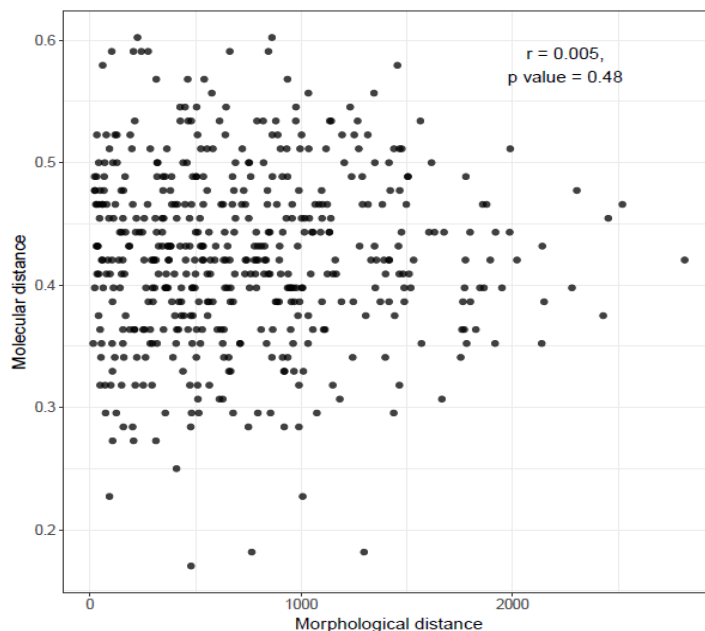


Figure 6: Correlation between morphological and molecular genetic distance matrices values (X Label: Euclidian similarity distance & Y Label: Simple matching dissimilarity distance)

(Figure 3). On the basis of molecular grouping, in cluster I, five maintainers viz., ICMB 99444, ICMB13222, ICMB 99111, ICMB 03999 and ICMB 05888 were placed with eight restorers namely A4RT15/13, ICMR 08888, ICMR 06111, ICMR 13666, ICMR 09888, A4RT15/10, A4RT13/5, and A4RT13/3. This indicates these maintainers and restorers are genetically more similar and hybrid developed using female parents of these maintainers and restorers may not result in a heterotic combination. One maintainer (ICMB04111) was placed in cluster II along with 11 restorers (ICMR07555, A4RT13/2, ICMR06333, ICMR08999, ICMR10888, ICMR07222, ICMR12333, ICMR09666, ICMR06222, ICMR09777 and ICMR12555). This again indicates a similarity between this maintainer and these 11 restorers. These eleven restorers can be crossed with 5 maintainers placed in cluster I. Similarly, restorers available in cluster I can be crossed with a female parent of the maintainer placed in cluster II. Seven restorers, namely ICMR13444, ICMR06444, ICMR13999, ICMR13555, ICMR12444, ICMR12222, and A4RT15/12, which were placed in the third and last cluster, can be crossed with a female parent of

maintainers available in cluster II and cluster II. This analysis indicates that genetic diversification of parental lines should be given priority for realizing maximum heterosis.

Based on molecular data, the dissimilarity was again subjected to factorial analysis to explore and establish similarity or dissimilarity coefficient matrices among groups or individual genotypes. The same trend of genotype distribution was observed as shown in a dendrogram. There were only six restorer lines, which were not grouped with any maintainers. These lines are ICMR 06333, ICMR 07555, ICMR 08999, ICMR 09666, ICMR 09777 and ICMR 12555. A cross between these lines and the female parent of maintainers included in this study may result into a heterotic one

Principal Coordinate Analysis

Using same similarity coefficient, principal coordinate analysis was performed. The total genetic variation existing in the material was divided into principal components. Principal components 1, 2, and 3 explained the 73.84% total variability used to plot the genotypes (Figure 4). Based on

colors and position, the same trend in the distribution of genotypes was observed as depicted in the dendrogram.

The dissimilarity coefficient matrices were again subjected to factorial analysis to explore and establish similarity or dissimilarity among groups or individual genotypes. The same trend of genotype distribution was observed as shown in the dendrogram. Clustering pattern as well as PCoA formed three groups which broadly clustered the majority of B- and R-lines into two separate clear-cut groups with minor exceptions, as shown by AMOVA also, indicating that B- and R-lines exist as two distinct broad-based gene pools.

Structure Analysis

Population structure refers to all genetic patterns of individuals within a population. In fact, the genetic structure in a natural population is characterized by the number of possible subpopulations within it, the frequencies of different alleles in each subpopulation, and the degree of genetic isolation of the subpopulations. The population structure of the 32 genotypes was analyzed based on generated polymorphism data of each marker system and pooled data using STRUCTURE analysis for $K = 1$ to $K = 10$. In all the analyses, the results obtained by STRUCTURE HARVESTER indicated that maximum ΔK was reached at $K = 3$ (Figure 5). At this K , all accessions were assigned to three main subpopulations. The inferred population structure for $K = 3$ indicated that most of the accessions had a membership coefficient (q_i) to one of the subpopulations equal or higher than 0.6 ($q_i = 0.6$). These results further confirmed the PCoA and cluster analysis.

Correlation between Phenotypic and SSR-based Genetic Distance Matrix

Mantel's correlation test statistic (Z) was applied to determine the relationship between molecular marker-based and phenotypic marker-based distances. This test indicated a non-significant association between phenotypic and molecular-based analysis. The overlapping trend of dots was not observed, indicating low correlation between two types of matrices. The present study revealed a low correlation between phenotypic traits and SSR-based matrices, indicating that the two methods were different in assessing genetic diversity. Furthermore, the simple correlation between both the genetic distance matrices was also low ($r = 0.005$) (Figure 6). This indicates that both morphological and molecular data should be utilized in the estimation of genetic diversity in pearl millet. Despite the low correlation, many genotypes were placed together in the same clusters in both the dendrograms.

Low association between phenotypic and molecular diversity may be due to fewer morphological traits (10 traits) and fewer polymorphic markers (44 only), which may also be from non-genic regions. Morphological traits are also highly influenced by environmental factors and may be

a cause of low association between morphological and molecular diversity analysis. As in the present study, weak correlation between phenotypic data and molecular data was reported by Vinu *et al.*, 2016 and Karuri *et al.*, 2009 in mustard and sweet potato. The low association indicated that molecular markers (SSR) did not adequately sample the relevant genomic regions for phenotypic differentiation. In contrast to the present study, Rahman *et al.*, 2011, and Hegay *et al.*, 2014 reported a significant association between phenotypic and molecular diversity in rice and common bean. The co-phenetic correlation can be further improved by considering the trait-linked molecular markers, particularly from genic regions such as SNPs.

Conclusion

Fundamental of any crop improvement program is existence of genetic diversity among parental lines. Exploitation of genetic diversity will result into the development of hybrids and varieties with high yield potential. In current study, high genetic diversity was observed among 32 restorers and maintainers of A4 cytoplasm using morphological and molecular data. Placement of maintainers and restorers into different clusters indicates that they are highly diverse and may be used for generating hybrids and transgressive segregants with higher yield potential.

Acknowledgment

The first author gratefully acknowledges the support provided by Post Graduate School, ICAR- Indian Agricultural Research Institute, New Delhi. The corresponding author is highly thankful to Dr S.K. Gupta, Principal Scientist (ICRISAT, Patancheru) for providing the A₄ maintainers and restorers used in the present study.

References

- Andrews DJ and KA Kumar (1992) Pearl millet for food, feed, and forage. *Adv. Agrono.* 48: 89-139.
- Bakonyi M and CR Johnson (1995) The Euclidean distance matrix completion problem. *SIAM J. Matrix Anal. Appl.* 16: 646-54.
- Bashir EMA, MA Abdelbagi, MA Adam, El Tahir I. Mohamed, Albrecht E. Melchinger, Heiko K. Parzies and Bettina IG Haussmann (2015) Genetic diversity of Sudanese pearl millet [*Pennisetum glaucum* (L.) R. Br.] landraces as revealed by SSR markers, and relationship between genetic and agromorphological diversity. *Genet. Resour. Crop Evol.* 62: 579-91.
- Chandra S (2014) Inheritance of fertility restoration in A1 based CGMS and genetic diversity analysis of maintainers and restorers in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. M.Sc. Thesis. IARI, New Delhi, India, 60p.
- Directorate of Millets Development (2020) Available online at: <http://millets.dacfw.nic.in>
- Earl DA and BM vonHoldt (2012) Structure harvester: a website and program for visualizing structure output and implementing the Evanno method. *Conservation Genet. Resour.* 4: 359-61.
- Evanno G, S Regnaut and J Goudet (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol. Ecol.* 14(8): 2611-2620.

- Gupta SK, T Nepolean, SM Sankar, A Rathore, RR Das and KN Rai (2015) Patterns of molecular diversity in current and previously developed hybrid parents of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Amer. J. Plant Sci.* 6: 1697–12.
- Gupta SK, T Nepolean, CG Shaikh, KN Rai, CT Hash, R Rani Das and A Rathore (2018) Phenotypic and molecular diversity-based prediction of heterosis in pearl millet [*Pennisetum glaucum* L. (R.) Br.]. *Crop J.* 6: 271–81.
- Hegay S, M Geleta, T Bryngelsson, A Asanaliev, Gustavsson, LG, HP Hovmalm and R Ortiz (2014) Genetic diversity analysis in *Phaseolus vulgaris* L. using morphological traits. *Genet. Resour. Crop. Evol.* 61: 555–66.
- Jorben J, SP Singh, CT Satyavathi, SM Sankar, JS Bhat, K Durgesh, and M Mallik (2020) Inheritance of fertility restoration of A4 cytoplasm in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Indian J. Genet. Plant Breed.* 80(1): 64–69.
- Karuri HW, EM Ateka, R Amata, AB Nyende and AWT Muigai (2009) Characterization of Kenyan sweet potato genotypes for SPVD resistance and high dry matter content using simple sequence repeat markers. *Afr. J. Biotechnol.* 8: 2169–75.
- Kifouli A, D Dustave, E Ebenezer, B Thierry, S Sylvain, R Alain and J Estelle (2017) Assessment of genetic diversity among cultivated pearl millet [*Pennisetum glaucum* (L.) R. Br.] accessions from Benin, West Africa. *Afr. J. Biotechnol.* 16(15): 782–90.
- Lakshmana D, BD Biradar and SK Deshapande (2009) Genetic divergence studies in Indian and exotic accessions of pearl millet. *Karnataka J. Agric. Sci.* 22(5): 1080–83.
- Liu K and SV Muse. 2005. Power Marker: Integrated Analysis Environment for Genetic Marker Data. *Bioinformatics.* 21: 2128–29.
- Nepolean T, SK Gupta, SL Dwivedi, R Bhattacharjee, KN Rai and CT Hash (2012) Genetic diversity in maintainer and restorer lines of pearl millet. *Crop Sci.* 52(6): 2555–63.
- Perrier X, A Flori and F Bonnot (2003) Data Analysis Methods. In: Hamon P., Seguin, M., Perrier, X. and Glaszmann, J.C., (Eds.) *Genetic diversity of cultivated tropical plants*. Science Publishers, Enfield, pp 43–76.
- Pritchard JK, M Stephens and P Donnelly (2000) Inference of population structure using multi-locus genotype data. *Genet.* 155(2): 945–59.
- Rahman MM, MA Rahman, A Hossain and G Rasul (2011) Comparative study on morphological, physiological and molecular genetic diversity analysis in rice (*Oryza sativa* L.). *Libyan Agric. Res. Cen. J. Int.* 2(2): 85–93.
- Rai KN, M Govindaraj and AS Rao (2012) Genetic enhancement of grain iron and zinc content in pearl millet. *Qual. Assur. Saf. Crops Foods.* 4: 119–25.
- Rajaram V, T Nepolean, S Senthilvel, RK Varshney, V Vadez, RK Srivastava, M Shah, A Supriya, S Kumar, BR Kumari, A Bhanuprakash, ML Narasu, OR Lizarazu and CT Hash (2013) Pearl millet [*Pennisetum glaucum* (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. *BMC Genom.* 14: 15.
- Saghai-Maroo MA, KM Soliman, RA Jorgensen and RW Allard (1984) *Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics*. Proceedings of the National Academy of Sciences. December 1984, PNAS, USA. 81(24): pp 8014–18.
- Satyavathi CT, S Tiwari, C Bharadwaj, AR Rao, J Bhat and SP Singh (2013) Genetic diversity analysis in a novel set of restorer lines of pearl millet [*Pennisetum glaucum* (L.) R. Br.] using SSR markers. *Vegetos.* 26(1): 72–82.
- Satyavathi CT, S Begum, BB Singh, KV Unnikrishnan and C Bharadwaj (2009) Analysis of diversity among cytoplasmic male sterile sources and their utilization in developing F₁ hybrids in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Indian J. Genet.* 69: 352–60.
- Shanmuganathan M, A Gopalan and K Mohanraj (2006) Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm for dual Purpose. *J. Agri. Sci.* 2(1): 73–80.
- Sharma PN. (2016). Studies of fertility restoration of various male sterile cytoplasm and genetic diversity of elite restorers and maintainers in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. M.Sc. Thesis, IARI, New Delhi, India. p67.
- Sumanth M, P Sumathi, NK Vinodhana and M Sathya (2013) Assessment of genetic distance among the inbred lines of pearl millet (*Pennisetum glaucum* (L.) R. Br.) using SSR markers. *Int. J. Biotechnol. Allied Fields.* 1: 153–62.
- Vinu V, N Singh, S Vasudev, SC Giri, R Singh, B Dass and DK Yadava (2016) Relationship of molecular and phenotypic divergence with hybrid performance in Indian Mustard (*Brassica juncea*). *Indian J. Agric. Sci.* 86(9): 1158–63.
- Wang JF, EB Graham, A Kilian, CH Balatero, DM Hautea, A Cameille, P Besse, N Hidayati, TX Jaunet, V Dittapongpitch, SM Huang, THH Truong, RC de la Peña and PM Hanson (2006) *Mapping quantitative resistance loci to bacterial wilt in tomato line Hawaii 7996*. Tomato Breeders Round Table and Tomato Quality Workshop. 7–11 May 2006, Tampa, Florida, USA, 43p.
- Yadav OP (1994) Genetic divergence in pearl millet accessions of Indian and exotic origin. *Indian J. Genet.* 54: 89–93.

RESEARCH ARTICLE

Multi-crop Exploration in Unexplored Areas of Garo Hills, Meghalaya

Sanjeev K. Singh^{1*}, Ranbir S. Rath¹, Kailash C. Bhatt^{1*}, Subarna Hajong² and Naorem A. Singh³

Abstract

A multi-crop exploration trip in difficult and unexplored areas falling under South Garo Hills, West Garo Hills and South West Garo Hills districts of Meghalaya was conducted to collect the diversity in different agri-horticultural crops, their wild relatives and other economically important plants. During exploration, 170 diverse germplasm belonging to cereals, millets and pseudo-cereals, pulses, oilseeds, vegetables, tuber crops, citrus etc., were collected from 10 development blocks from 21st to 30th November 2018. Rice is the main staple crop of the area. Interestingly, the germplasm collected included aromatic, sticky, and medicinal rice landraces with tremendous variability. Of the landraces collected in different crops, 29 landraces of paddy and 14 of maize are the new addition to the National Gene bank from the area. In addition, some less known ethnically important plants being cultivated in kitchen gardens/homesteads collected with traditional knowledge were *Corchorus capsularis* (as vegetable), *Clerodendrum colebrookianum* (a source of treating high blood pressure), *Aegle marmelos* (source of local tea), *Citrus indica* locally known as *Memang Narang* (cure for jaundice and stomach ailments) and also information on preparation of local liquor from sticky rice and Job's tears. Due to the spread of new technology, the use of high-yielding varieties, and the introduction of new crops, many traditional varieties are eroding. Hence, conserving the available diversity from such unexplored and difficult areas is of tremendous importance and value.

Keywords: Garo hills, Germplasm, Multi-crop, Unexplored areas, Wild relatives.

¹National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India.

²National Bureau of Plant Genetic Resources Regional Station, Umiam, Meghalaya, India.

³Krishi Vigyan Kendra, (ICAR), West Garo Hills Tura, Meghalaya, India.

***Author for correspondence:**

kailash.bhatt@icar.gov.in, sanjeev.singh1@icar.gov.in

Received: 03/08/2023 **Revised:** 21/12/2023

Accepted: 21/12/2023

How to cite this article: Singh SK, RS Rath, KC Bhatt, S Hajong and NA Singh. (2024) Multi-crop Exploration in Unexplored Areas of Garo Hills, Meghalaya. *Indian J. Plant Genetic Resources*. 37(1): 47-55.
DOI: 10.61949/0976-1926.2024.v37i01.06

Introduction

Meghalaya, one of the states of North-eastern hill (NEH) Region, is considered a hot spot of India's biodiversity (Mittermeier *et al.*, 2011). The inhabitants of the state have different cultural backgrounds, various food habits, and inhabit in adverse climatic situations resulted in the cultivation of diverse crops. The agricultural production system, characterized by large variation in cropping intensity, mono-cropping and subsistence farming, is complex, diverse and risk-prone. Shifting cultivation, locally known as *jhum*, is the mainstay of the economy in most of the parts of NEH states, including Meghalaya. Keeping in view the richness of genetic diversity and gap analysis of conserved germplasm, multi-crop germplasm collection trips were conducted mainly in unexplored localities of South Garo Hills, West Garo Hills and South West Garo Hills districts of Meghalaya, located between 25° 10' & 25° 35' N latitude and 90° 15' & 91° 0' E longitude. The average altitude of the explored area ranged between 300 to 1000 above msl. Over 1800 accessions of various agri-horticultural crops, wild relatives and other economic species were collected from Garo Hills, while only over 800 accessions could be collected and conserved from explored districts.

Garo tribe (*Sangma*, *Marak*, *Momin*) is the inhabitant of surveyed area. The tribe has two divisions, one inhabits the hilly mountains,

and the other lives in the plain areas and valleys. Besides this tribe, *Koches*, *Rabhas*, *Hajongs*, and Banars also reside in these districts. Plants and plant products play an important role in folk life of inhabitants and thus are an integral part of their culture (Jaiswal, 2010). Agriculture (*Jhum* or slash & burn and settled agriculture) is the main occupation of local tribes. Generally, mixed cropping is done in hilly areas, which the inhabitants opt to produce their household food and to fulfill nutrition needs from their own farm. Rice is the main crop grown both in *jhum* land and plain areas. They brew local beverages (beer) known as *Mi-Bitchi* or *Chubitchi* or *Minil Bichi* or *Chubok*, using local sticky/glutinous rice for consumption and also to offer their deity '*Saljong*' (Sun) during '*Wangla*' (festival of harvest). It is also served during *Dosi Dodoka* (wedding festivities) and religious rituals and as a refreshment drink for weary field laborers and guests. The local beverage has a great significance in the social and cultural life of the Garos (Marak *et al.*, 2021). Besides rice, the other major crops grown in the areas are maize, ginger, turmeric, vegetables, foxtail millet, *Coix*, rice bean, cowpea, pigeon pea, areca nut, taro, yam, Indian bay leaf, and some fruit crops such as banana, citrus, pineapple, coconut and cashew nut.

The forests of Meghalaya provide a large number of plants, the economic parts of which make an important contribution to the diet of local tribes, particularly those living near forests. About 70% of the state's total area is covered by forest, and the tribal communities own 90% of this (Kayang, 2007). The study of such useful plant wealth could be helpful in the identification of alternative sources of food and future crops for domestication. The explored area belongs to the outer territory of "Nokrek Biosphere Reserve", which is located on the Tura range. Evergreen and semi-evergreen deciduous forests dominate the landscape,

while some patches of bamboo forest can also be found in the lower altitudes. The reserve is also known for the occurrence of rich diversity of *Citrus* spp. including *C. indica* (Indian wild orange), endemic to this region, hence has been designated as 'Citrus Gene Sanctuary', covering an area of 47 sq. km, provides a gene-pool for the improvement of citrus. Collecting and conserving the available genetic diversity from such important and under-explored difficult areas are, thus of tremendous importance and value.

Materials and Methods

As per National Exploration Plan 2018-19, two explorations were planned and inputs about areas and crops were obtained during a workshop organized on the conservation of plant genetic resources of Meghalaya, involving Krishi Vigyan Kendras (KVK's), officials from state agriculture and horticulture departments, local research organizations and progressive farmers of Meghalaya. During the survey, ten development blocks (Zikzak, Dalu, Dagenggiri, Rongram, Selsella, Gasuapara, Baghmara, Rongra, and Chokpot) belonging to South Garo Hill, West Garo Hill and South West Garo Hill districts were extensively explored during 21st to 30th November 2018. The route followed and areas covered in the exploration and germplasm collection trip have been depicted in Figure 1. Standard germplasm exploration and collection procedures developed by ICAR-NBPGR, New Delhi (Tyagi *et al.*, 2016) were followed. Whereas, individual and selective sampling methods were adopted for horticultural crops, and a random sampling method was adopted for agricultural crops with an aim to capture all the alleles from the represented population. In the majority of cases, the germplasm was sampled from the farmer's field; however, the germplasm was also collected from threshing yards/farmer stores as and when required.

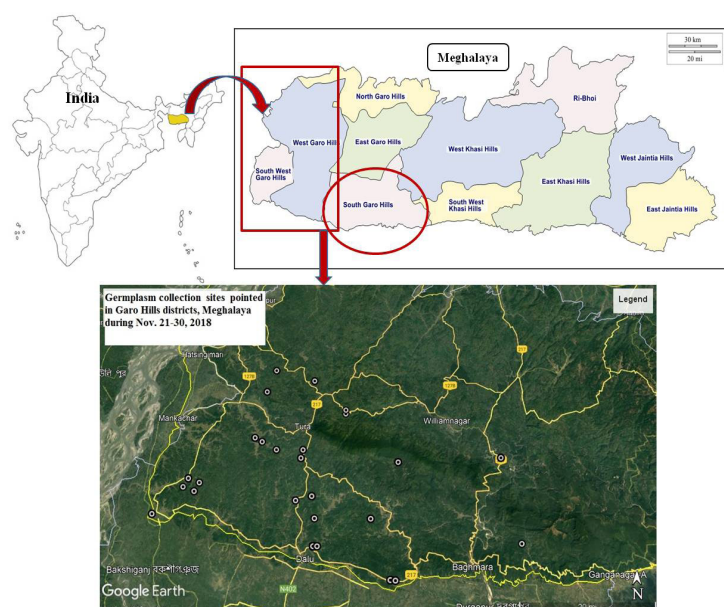


Figure 1: Area covered and route followed during exploration and germplasm collection programme undertaken in parts of Garo hills

Natural and partly-disturbed habitats were sampled for collections of wild useful plants and crop wild relatives. The samples were collected in the form of seeds, fruits, bulbs, corms, rhizomes, tubers, etc., based on their mode of propagation. Tribal markets or weekly *haats* were also visited to record the plants and plant products sold there. For recording ethnobotanical information, discussions were held with the headman (Nokma's) and head of the families of villages surveyed. The passport data were recorded as per standard passport datasheet, and the collector number was allotted to each collected sample. One set of the collected germplasm samples along with passport data were deposited in the National Genebank, ICAR-NBPGR, New Delhi for assigning IC numbers and conservation, while another set was retained for characterization and multiplication at a suitable site.

Results and Discussion

As per available records, over 5000 accessions of different agri-horticultural crops, wild relatives and other economic species have been collected from Meghalaya, of these over 1900 accessions are from Garo Hills. Among the three districts of Garo Hills, South Garo Hills is the least explored district, with only 110 accessions collected and conserved, while West Garo Hills also shows same trend. During the present exploration trips, a total of 170 diverse crop germplasm comprising rice (85), maize (17), millets (17), *Coix lacryma-jobi* (2), amaranth (3), pulses (4), oilseeds (7), vegetables (19) and others (16) have been collected as presented in Table 1. As far as the availability of rice landraces in NEH region, including Meghalaya, is concerned, thousands of rice landraces are being cultivated under lowland, upland and deep-water conditions (Hore, 2005). The farming communities of NEH region are still growing local landraces despite the impact of changes in climate, food habits and various demographic changes. A total of 85 accessions of rice with significant variability for grain & kernel size, shape and husk color, aroma, and early and late types were collected from surveyed areas (Figure 2A). Details of variability observed in 85 landraces comprising of scented or aromatic, sticky type, upland rice, and early types are given in Table 2. Of these, 29 landraces, namely *Babu jaha*, *Chaging minil*, *Chaging*, *Jaha gapok*, *Jarong*, *Kotchu ghisim*, *Kutchia ghisim*, *Lakhipur*, *Minil aringa*, *Minil gachcha*, *Minil gambal*, *Minil kakua*, *Minil michmopok*, *Minil mikongsi*, *Minil midambak*, *Minil nasket*, *Minil pappu*, *Mima buring*, *Mi kotchu*, *Mi kudep*, *Mima mianjke*, *Mi phisa*, *Mi wasit*, *Nal bini*, *Raha bini*, *Rong chram*, *Tairol*, *Thepra*, *Tulsimala* are new addition to the National Gene bank. The inhabitants of the study area consume rice as daily meal; however, sticky rice is eaten only in breakfast. Some of the local recipes prepared from rice are *Mimagorum*, *Jahagipok* (consumed both as regular meal and as special recipes during festivals); *Jahagitchak* rice landrace

is mainly cooked during festivals or on special occasions; '*Pura*'- a traditional recipes prepared from a scented/ aromatic rice landrace *Jahagisim* is also supposed to be medicinal to cure *mibangnapa* (weakness); while cooked rice is wrapped with a banana leaf known as '*Rongjanggi*' and is given to the patient the sticky rice landraces are used to make local recipes called '*Pitha*' (steamed rice cake), '*Jakep*' (a mixture of rice flour and sesame seeds), and '*Sakin*' (rice is soaked in water for overnight the roasted sesame seeds are mixed in it while sugar is added for taste, which is wrapped by banana leaves and placed in a pot for cooking); a local liquor '*Mibitchi*' is also prepared by fermented sticky rice landraces. But at present, the above-mentioned recipes are hardly prepared by the inhabitants as most of the landraces have been eroded, except in a few pockets in and around the *jhum* lands of the Garo Hills.

Maize is the second most important food grain crop of entire NEH region. The availability of rich maize diversity in the region supports the consideration of the secondary centre of maize diversity (Singh, 1977). Being a part of the eastern Himalayas, Meghalaya also has remarkable diversity in maize. Diverse germplasm accessions with variability in grain color (yellow, cream, white and reddish black), grain shape (flint, dent, flat, beaked, pop) and grain size (small, medium, bold) were collected (Table 3). As per the existing genebank data, out of 17 collected maize landraces, 14 are new addition to the National genebank. Maize is consumed in different preparations like steamed and roasted grains cooked with rice and is also considered a good feed for animals and poultry.

In foxtail-millet, variability was collected (Table 4; Figure 2B) in panicle for grain color (black, yellowish and greyish) and size (10–20 cm). The tribals consume its grains as rice or make it into porridge, which is considered light and nutritive food. *Coix* is also very nutritive food of the area and generally cooked with rice and pulses; its grains are also used to brew local liquor and its roots are used as medicine. A specific plant type of *Coix* landrace having red grain has been collected from *Jhum* field in the Rondong area of Baghmara, South Garo Hills (Figure 2C). In the entire surveyed region the area of cultivation under *Coix* and little millet (*Panicum sumatrense*) is gradually declining due to change in food habits and adoption of remunerative cash crops by the farming community. In pulses, a rare type of soybean was collected with unique morphological characteristics like bushy plant habit, height up to 75 cm, profusely branched, 2.5 cm long, hairy pods with 2 to 3 seeds, grain small, flat, dull-white, greenish. Perennial pigeon pea is generally found to grow mainly in homesteads and *jhum* fields with rice, and it has been collected with variability in grain color, shape and size. In turmeric and ginger, the tribal people are cultivating local landraces on a large scale as commercial crops.

Table 1: Crop group wise collected accessions during exploration and collection from Garo Hills of Meghalaya

Crop group	Botanical name	Crop name	Vernacular name	No. of accs.
Cereals (102)	<i>Oryza sativa</i>	Rice	Mi, Mi ma	85
	<i>Zea mays</i>	Maize	Maraku, Meraku	17
Millets & pseudo-cereals (22)	<i>Coix lacryma-jobi</i>	Job's tear	Mairukku, Megaru	2
	<i>Setaria italica</i>	Finger millet	Misi	14
	<i>Amaranthus</i> spp.	Amaranth	Dangasak	3
	<i>Panicum sumatrense</i>	Little millet	Suji	1
	<i>Sorghum bicolor</i>	Jowar	Gonggit	2
Pulse crops (3)	<i>Cajanus cajan</i>	Pigeonpea	Mendu	1
	<i>Vigna umbellata</i>	Ricebean	Bil'lik	1
	<i>V. mungo</i>	Black gram	Maskalai	1
Oilseed crops (6)	<i>Brassica juncea</i>	Mustard	Me'jak	1
	<i>Sesamum indicum</i>	Sesame	Spin	4
	<i>Glycine max</i>	Soybean	Do'dim	1
Vegetable crops (16)	<i>Abelmoschus esculentus</i>	Okra	Dorai	1
	<i>Benincasa hispida</i>	Ash gourd	Akarukobok	1
	<i>Solanum melongena</i>	Brinjal	Mantau/Baring a'rongga	5
	<i>Capsicum annum</i>	Chilli	Jal'lik/Murich	5
	<i>Cucumis melo</i> var. <i>conomon</i>	Oriental pickling melon	Bangi	1
	<i>Luffa acutangula</i>	Ridge gourd	Zinkha Daring	1
	<i>L. hermaphrodita</i>	Satputia	Satpuli-jinga	1
	<i>L. cylindrica</i>	Sponge gourd	Sawil	1
Tuber/bulbs, rhizomatous (6)	<i>Allium tuberosum</i>	Garlic chives	RasinChisik	1
	<i>Alocasia indica</i>	Giant taro	Kimachu/Kachchu	1
	<i>Colocasia esculenta</i>	Arvi	Ta'a	1
	<i>Curcuma longa</i>	Turmeric	Holdi	1
	<i>Zingiber officinale</i>	Ginger	E'ching	2
Fiber crops (2)	<i>Corchorus capsularis</i>	Jute	Nalia Pat	1
	<i>Gossypium arboreum</i>	Cotton	Kil	1
Fruit crops (11)	<i>Citrus medica</i> ; <i>C. indica</i> ; <i>C. xlatifolia</i> ; <i>C. x limon</i> ; <i>C. latipes</i> ; <i>C. aurantium</i> ; <i>C. hystrix</i> ; <i>Citrus</i> hybrid	Citrus	Gancheng	11
Other crops (2)	<i>Clerodendrum colebrookianum</i>	East Indian Glory/Bhrangi	Dongum	1
	<i>Trichosanthes wallichiana</i>	Wild snake gourd	Trichosanthes	1

North eastern region holds over 23 species, 01 sub-species and 68 varieties of citrus, including wild and natural hybrids (Malik *et al.*, 2012; Sharma *et al.*, 2004). From Nokrek Biosphere Reserve, a total of 11 accessions of citrus species (*Citrus medica*, *C. indica*, *C. xlatifolia*, *C. latipes*, *C. aurantium*, *C. hystrix* and *Citrus* hybrid) were collected. The details of the characteristics recorded in different species are given in Table 5. *Citrus indica* (Figure 2D), locally known as *Memang Narang* is supposed to be the most primitive species and perhaps the progenitor of cultivated *citrus* occurring here (Tanaka, 1937). It is an endangered endemic species of this region; hence, is considered an important and unique germplasm. Garo tribe also used this species as medicine to

cure jaundice and stomach ailments (Malik *et al.*, 2006). Good variability in collected germplasm of citrus (Figure 2E) was observed for fruit shape (oval, oblong, pyriform, spherical), fruit weight (50–1300 g) and fruit color (yellow, orange, pale yellow) with smooth shining and rough peel as also reported by Singh and Singh (2006) from Garo hills.

Use of both wild and cultivated vegetables is an integral part of the food habit of local tribal communities (Samati, 2004; Kayang, 2007, Singh *et al.*, 2012). They consume different vegetables either raw or cooked and with non-vegetarian food preparations. As the tribals in the study area are largely dependent on wild plants and plant products for their existence, while their local markets can be seen with full

Table 2: Characters recorded at collection site in rice (*Oryza sativa*) landraces

Landrace name	IC/Collector No.	Remarks (Trait-specific characters)
<i>Babujaha</i>	IC-0635671	Small and bold grain, scented, kernel white, non-sticky
<i>Chaging/Chagingminil</i>	IC-0629109	Grain bold, leaves broad, tall 3.5- 4ft., tillers 8-12, plant strong, upland rice, normal type
<i>Champali</i>	IC-0637008	Grain yellowish & medium, kernel white, plant thin & weak tall up to 3.5ft., tillers 6-12, normal, low land rice landrace with good taste
<i>Ganji</i>	KC/SK/AS-59	Sticky, grown in rainy season (saalidhan)
<i>Goriya</i>	IC-0631761	Blackish husk, kernel reddish (pre-kharif season crop locally called Ashudhan), early in maturity, require fertilizer for good yield
<i>Halai</i>	IC-0635676	Bold grains, good in taste
<i>Jahaghisim</i>	IC-0635673	Scented, aromatic, black husk, kernel white, elongated grain, small sized, easy in threshing
<i>Jahagapok</i>	IC-0635672	Plant height is medium, maturity 4 months, whitish or yellowish grain color, rice grain is smaller and finer, slightly sticky, two types of <i>Jahagapok</i> , because of having , smaller and bigger sized grains. The aroma of smaller grain <i>Jahagapok</i> is stronger than the bigger sized grain, yield upto 3.0-3.5 qtl./bigha.
<i>Jarong</i>	IC-0629108	Grain light brown & bold, tall up to 4.5ft., plant strong, upland rice, medium maturity
<i>Kalajira</i>	IC-0637005, IC-0635677	Highly scented, black husk, kernel white, small and elongated, low yielder tall up to 4.5 ft., scented
<i>Kala bini</i>	IC-0631763	Good in taste
<i>Kishor mi</i>	IC-0631760, KC/SK/AS-47	Non-sticky, awned, kernel reddish white, good yielder, grain small, golden
<i>Kotchughisim</i>	KC/SK/AS-24, KC/SK/AS-46	Less sticky, scented, with strong aroma, blackish husk, kernel white grows well on medium lowland, plant ht. 140-150 cm, lodging prone, low yielder, medium, yield 3.0-3.5 qtl./ bigha
<i>Kuchia</i>	RSR/SH-18-20	Lowland, late type, grain bold, leaves broad, tall 4 – 5ft., tillers 10-15, strong plant.
<i>Lakhipur</i>	RSR/SH-18-10	Lowland, late type, grain bold, light brown, plant ht. 3ft.
<i>Malbhog</i>	IC-0637002, IC-0635674	Creamy husk, kernel white non-sticky, scented, soft and tasty, plant ht. 4 ft., scented, lowland type
<i>Malschira</i>	IC-0637003	Grain husk brown, sticky, plant weak, leaf narrow, plant ht. 3 ft., tillers 8-10
<i>Mekudep</i>	IC-0631765	Early in maturity (six months), golden yellow husk, kernel white
<i>Mikudep</i>	IC-0631742	Non-sticky and scented
<i>Memietimgitchak</i>	IC-0631766	Husk light golden, kernel reddish. Considered good for rice beer
<i>Mikatchu</i>	IC-0629116, IC-0631747	Golden husk, oval, kernel white, used for preparation of rice beer 'Chubak', tall up to 4ft, best for <i>jhum</i> cultivation, early type, maturity in August
<i>Miron</i>	IC-0629111	Husk colour pale yellow/ straw color, grain bold, plant tall up to 3.5ft., awned, irrigated, lowland rice
<i>M chandak</i>	IC-0635682	Light golden husk, grain flat, kernel white, good in taste
<i>Mi bisaa</i>	IC-0631757	Grains small, oval, husk blackish, kernel white
<i>Mi kotchu</i>	IC-0631752	-
<i>Mi kudap</i>	IC-0631751	Less sticky, flat, light yellow/reddish grain husk
<i>Mi ma</i>	IC-0631754	Flat, golden yellow husk, kernel white
<i>Mi miraka</i>	IC-0631767	Husk light reddish, kernel white
<i>Mi phisa</i>	IC-0629117	Grain husk brown, kernel white, tall up to 4ft, best for <i>jhum</i> cultivation, early type, maturity in August
<i>Mi wasit</i>	IC-0635668	Sticky, scented, grains reddish, elongated, kernel white
<i>Mi maboldok</i>	IC-0629120, IC-0631748, IC-0635667	Whitish yellow husk, grain bold, pale yellow/straw color, kernel white, sticky, plant tall up to 4ft., best for <i>jhum</i> cultivation, early type, maturity in August
<i>Mi maburing</i>	IC-0635670	Golden yellow grains, scented, non-sticky
<i>Mi machureng</i>	IC-0629113	Old rice landrace, grain light brown normal, kernel white, tall up to 4ft. good yielder, upland rice, early, maturity in August
<i>Mi maghisim</i>	IC-0635666	Husk black, kernel white, scented
<i>Mi maghisim</i>	IC-0631749	Husk black, grain oval, sticky, tasty

Cont....

<i>Mi maghisim</i>	IC-0635669	Blackish husk, flat, small, reddish kernel
<i>Mi magitchak</i>	IC-0631744, IC-0631746, IC-0631755	Flat, blackish husk, kernel white, also used for medicinal purpose
<i>Mi magorum</i>	IC-0631768	Grain with golden husk, flat, kernel white, scented, also used as medicine. Rare in dry areas but grown in moist localities in Jhum.
<i>Mima mi</i>	KC/SK/As-14	Grain oval, bold, taste is good, kernel white
<i>Mi mamianjke</i>	IC-0629121	Grain light brown in color, medium bold, white kernel, plant tall up to 3.5–4ft., best for <i>jhum</i> cultivation, late type, maturity in Nov.
<i>Mima misokmal</i>	IC-0629118	Kernel white, plant tall up to 4 ft, best for <i>jhum</i> cultivation, early type, maturity in August
<i>Minil agunia</i>	IC-0637011	Grain husk brownish red, plant tall up to 3.5–4 ft., strong, sticky, low land rice, early type
<i>Minil aringa</i>	KC/SK/AS-28	Reddish husk, grain elongated, sticky
<i>Minil danggap</i>	IC-0629110	Grain bold, plant tall up to 5.5 ft, strong, tillers 8–12, low land rice
<i>Minil dokdang</i>	IC-0631769	Golden yellow husk, sticky, kernel white. Used in preparation of rice beer “Chhu”
<i>Minil gachcha</i>	IC-0629114	Grain husk pale yellow/ straw color, kernel red and long, plant tall up to 4ft, early, maturity in Sept., best for <i>jhum</i> cultivation, sticky rice, considered best for break fast meal
<i>Minil gambal</i>	IC-0629115	Grain husk yellow, bold, kernel white, plant tall up to 4 ft, best for <i>jhum</i> cultivation, early type, maturity in August, aromatic rice, good in taste
<i>Minil gapok</i>	IC-0629119	Kernel white, plant tall up to 4 ft, best for <i>jhum</i> cultivation, early type, maturity in August, sticky rice, best for break fast meal
<i>Minil ghipok</i>	KC/SK/AS-10	Fine, elongated grains, sticky, golden husk
<i>Minil gisam</i>	IC-0637006	Grain husk dark brown, plant tall up to 5 ft., strong, sticky, late type rice landrace
<i>Minil gitckak</i>	IC-0637010, IC-0631743, IC-0631753	Grain husk brown, kernel red rice, sticky, scented, grain slim, plant tall up to 4 ft., tillers 5–8, low land yield 2.0–2.5 qtl./bigha
<i>Minil guhati</i>	IC-0631759	Sticky, brought from Guwahati, used only for breakfast. Good for rice beer, easy in threshing
<i>Minil kakua</i>	IC-0637009	Kernel light black & medium fine grain, plant thin & week, tall up to 4 ft., tillers 5–10, normal sticky, low land rice
<i>Minil mikongsi</i>	IC-0631756	Reddish husk, elongated. It is considered best for rice beer and prepared during festival <i>Wangla</i> , also fetch good price
<i>Minil michmopok</i>	IC-0631745	Highly sticky, reddish husk, scented
<i>Minil midambak</i>	KC/SK/AS-49	Reddish, kernel white, elongated, sticky
<i>Minil mikohgken</i>	IC-0631764	Husk light golden, kernel white, sticky, tasty, used for making cake by mixing seeds of sesame
<i>Minil nasket</i>	KC/SK/AS-50	Reddish husk, grooves prominent, oval, bold, sticky, kernel white.
<i>Minil pappu</i>	IC-0631741	Sticky rice, scented, very much preferred by local people
<i>Nalbini</i>	IC-0635675, IC-0635680	Sticky, kernel long, reddish
<i>Purabini</i>	IC-0637001	Grain black, plant ht. 4 ft., tillers 8–15, sticky, lowland rice
<i>Purabini</i>	IC-0635681	Husk maroon, kernel white. It is considered as oldest paddy, grown in small scale. Used for making kheel/moodi
<i>Rahabini</i>	IC-0631762	Husk black, kernel reddish, sticky. Offered to guest, also cooked with milk
<i>Rangabhog</i>	IC-0635679	Fine grained, scented, kernel reddish, good yielder
<i>Rongchram</i>	IC-0635665	Easy in threshing, awned, scented
<i>Sarang</i>	RSR/SH-18-21	Grain medium brown, tall 4–5 ft., tillers 10, low land rice, late type
<i>Sillgutti</i>	IC-0637004	Grain husk pale yellow/straw color, plant tall up to 5ft, late type
<i>Tairol</i>	IC-0631758	Light yellow, kernel white, elongated
<i>Thepra</i>	IC-0631750, KC/SK/ AS-15	Fine grains, husk reddish, kernel white, elongated
<i>Tulsimala</i>	IC-0637007	Grain black & small, plant thin & week tall up to 3.5 ft., tillers 6–12, aromatic
	IC-0635678	Golden husk, oval in shape, kernel creamy white, good yielder, grown in large scale, less sticky, good in taste

Table 3: Characters recorded at collection site in maize (*Zea mays*) landraces.

Landrace name	IC/Collector No.	Remarks (Trait-specific characters)
Minilgitchak	KC/SK/AS-1	Reddish brown grains, sticky, cobs small
Mirakuwabok	KC/SK/AS-2	Creamy white grains, medium sized cobs
Gippok	KC/SK/AS-8	Small, 8–10 cm long cob, grain creamy white, sticky
Binimaku	KC/SK/AS-73	Sticky, medium sized cobs, grains maroon
Mirakujagiting	KC/SK/AS-82	Plant dwarf in height (up to knee height), cobs small (2 per plant), light yellow grains, early in maturity (Sown in March– April and harvested in May last)
Mirakuagatchi	KC/SK/AS-83	Medium sized plant, cobs 2–3 per plant with yellow grains, reddish grains at bottom of cobs, when boiled in water it turns red, sticky grains
Mirakuashok	KC/SK/AS-88	Medium sized cobs, 3–4 cobs/ plant, grains sticky
Meraku	RSR/SH-18-16	Grain orange in color & bold, plant ht. 6–7 ft., cob length 12–15 cm, March–April sowing & August harvesting months
Meraku	RSR/SH-18-17	Grain yellow & medium in size, sticky & aromatic, plant ht. 5–6 ft., cob length 12–15cm, April –May sowing & September maturity months
Merakusobok	RSR/SH-18-18	Sowing March & October (twice in a year), harvesting in Jan–Feb & May–June, Sobok means banana, spade in shape
Merakminil	RSR/SH-18-19	Sowing March & October (twice in a year), harvesting in Jan–Feb & June, aromatic maize
Mikop	RSR/SH-18-48	Kernel white, medium, pl. ht. 5–6 ft., roasted cobs eaten, sowing in March–April & harvesting in July, sticky, very sweet in taste, oldest landrace
Meraku Burma	RSR/SH-18-65	Kernel yellow & medium, sowing in March–April & harvesting in July–August, sticky
Meraku Agra	RSR/SH-18-66	Kernel mottled, white, sticky, sweet, strong/hard and boiled cobs/grains eaten
Merakubadur	RSR/SH-18-67	Kernel creamy, medium sized, sticky, sweet in taste, cob length up to 15 cm, boiled & eaten
Merakuminil	RSR/SH-18-68	Kernel reddish black, medium, sticky sweet in taste, cob length 6–8 cm, boiled & eaten, farmer cultivating it more than 100 years

Table 4: Characters recorded at collection site in foxtail millet (*Setaria italica*) landraces

Landrace name	IC/Collector No.	Remarks
Missi	IC-0631458, IC-0631460	Small brown grain, rice are eaten after mixing with rice or also made into porridge
Missidongji	IC-0631464	Grains brown, panicles without bristles
Missighisim	IC-0631462, IC-0631465	Grain & panicle black, panicle 15–20 cm long, bristles less
Missijongsi	IC-0631467	Panicles small, 12–16 cm long, elongated, bristles present, grains brown
Misijongsu	IC-0631456,	Small seeded, Black seeded panicle with bristles like caterpillar, cooked as rice
Missijongsu	IC-0631463, IC-0631466, IC-0631468,	Panicle 20–25 cm long with bristles, grains brown, good in taste, cooked with rice
Missisarang	IC-0631461	Brown seeded, long panicle
Samcheng/Missi	IC-0631517	Panicles small, 12–16 cm long, elongated, suitable for <i>jhum</i> cultivation, rice cooked and eaten
Missiwangal	IC-0631519, IC-0631459	Panicles black 20 cm long, grain husk black, kernel white, good yielder under <i>jhum</i> cultivation, rice cooked and eaten, rice very tasty

of wild edibles for sale. Some of the important wild species consumed and sold in local market by the inhabitants are *Bauhinia purpurea*, *Begonia palmata*, *B. roxburghii*, *Centella asiatica*, *Corchorus olitorius*, *Diplazium esculentum*, *Eryngium foetidum*, *Flemingia procumbens*, *Homalomena aromatica*, *Phlogacanthus thyriformis*, *Solanum violaceum*, *S. nigrum*, *Spilanthes acmella*, *Clerodendrum colebrookianum*, *Zanthoxylum khasianum*, *Baccaurea sapida*, *Castanopsis indica*, *Docynia indica*, *Elaeagnus latifolia*, *Garcinia paniculata*,

Myrica esculenta, *Rhus javanica* etc. indicating their popularity and future potential. During the present exploration, an interesting/new information from the farmers of Sadolpara village of West Garo Hill district was recorded on the use of fruit rind of *Aegle marmelos* (Bael). Its dried rind is used as a substitute for tea leaves, producing the same color as tea leaves (Figure 2), which is Tea from bael rind is considered as medicine medicinal and useful for stomach disorders.

Table 5: Characters recorded at collection site in *Citrus* species

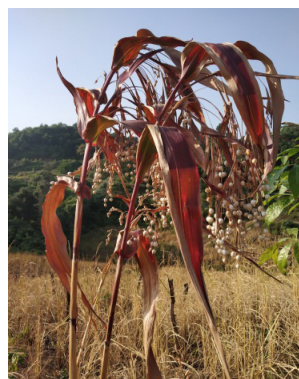
IC/Collector No's.	Botanical Name	Vernacular name	Trait-specific characters
IC0628827	<i>Citrus x limon</i>	Komla/Khasi mandarin	Fruit medium in size, the fruit turns pale-yellow when ripe, peel/rind is very soft and shinning
IC0629323	<i>Citrus aurantium</i>	Bomsim	Ripe fruit yellow in color, fruit appearance same as orange but ridges on fruit
IC0629326	<i>Citrus hystrix</i>	Matchadu	Medium size pyriform fruit (300 g), yellow ripe, rind thick & rough, tree tall 4-5 m
IC0629327	<i>Citrus hybrid</i>	Memang	Fragrant fruit oblong, aromatic, tree tall up to 5 m
IC0628824	<i>Citrus indica</i>	Memangnarang	Wild citrus species, fruit spherical & orange in color, peel/rind is very soft and shinning
IC0628825	<i>Citrus x latifolia</i>	Sohkymphor (Khasi)	Tree looks like Khasi mandarin
RSR/ SH-18-40	<i>Citrus latipes</i>	Surengki	30-year-old tree, tree ht. 10–12 m. fruit appearance same as orange, fruit sour, used as flavouring agent in non-veg preparations, semi wild
RSR/ SH-18-22	<i>Citrus medica</i>	Slongga	Fruit big (1300 g), sour in taste, used to eaten, Pl. Ht. 5–7 m, 5–6-year-old tree
IC0629324 RSR/ SH-18-73	<i>Citrus medica</i>	Gancheng	Large fragrant citrus fruit with a thick rind, resemble like rough lemon, tree tall up to 5 m, ripe fruit yellow in color & oblong, fruit weight 300–400 g
IC0629325	<i>Citrus medica</i>	Thematchu	Large fragrant citrus fruit oblong pyriform, resemble like rough lemon, tree tall 5–6 m



(A)



(B)



(C)



(D)



(E)



(F)

Figure 2: Diversity in grains of rice landraces (A), panicles of foxtail millet (B), specific grain and plant type in coix landrace, collected from *Jhum* field in Rondong area of Baghmara, South Garo Hills (C), big size fruits of *Citrus indica* (D), *Citrus* species collected in nearby areas of Nokrek Citrus Gene Sanctuary (E) and dried rind of *Aegle marmelos* (Bael) used as a substitute of tea leaves (F)

Conclusion

The widespread loss of global biodiversity is one of today's most serious crises. Population explosion, climate change, deforestation, urban development, various developmental activities, and the introduction of improved varieties are some of the major causes of biodiversity loss. As hotspots of biodiversity, the North-eastern hill region is also facing genetic erosion in the diversity of crops, economically useful species and associated indigenous knowledge mainly due to shifting cultivation. Now, the inhabitants have started cultivation of cash crops like strawberry, ginger, pineapple, large cardamom and other commercial crops like areca nut, rubber, cashew nut, black pepper, tea, and coffee, which are responsible for replacing the traditional varieties, crops and associated agricultural practices. Efforts have been made to collect and conserve the available diversity of crop landraces, wild relatives and wild economic species from the surveyed areas for use in breeding new varieties. Some significant collections made from the area were 29 named rice landraces unrepresented to the National gene bank; bushy type soybean landrace; perennial pigeon pea with variation in grain color, shape & size; and a specific plant type having red grain in *Coix lacryma-jobi*.

The collected germplasm should be characterized to identify promising germplasm as well as to plan an extensive survey for the further collection of trait-specific germplasm. The wild species being domesticated in homesteads need to be popularized through the development of suitable agro-techniques, which can boost the economic condition of local tribal communities. Efforts should also be initiated for *in-situ* on-farm conservation of landraces facing erosion and for establishing community seed banks to safeguard and promote the utilization of local landraces.

Acknowledgments

The authors would like to thank the Director of the ICAR-NBPGR in New Delhi for his help and guidance. We are grateful to the Head, Krishi Vigyan Kendra, West Garo Hills, Meghalaya for their steadfast assistance on the ground throughout the exploration. A special thanks also goes to all the farmers who donated their seeds and time for the germplasm collection and conservation.

References

- Hore DK (2005) Rice diversity collection, conservation and management in North-eastern India. *Genet. Resour. Crop Evol.* 52: 1129–1140.
- Jaiswal V (2010) Culture and ethnobotany of Jaintia tribal community of Meghalaya, Northeast India - a mini-review. *Indian J. Trad. Know.* 9(1): 38–44.
- Kayang H (2007) Tribal knowledge on wild edible plants of Meghalaya, Northeast India. *Indian J. Trad. Know.* 6(1): 177–178.
- Malik SK, R Chaudhury, S Kumar, OP Dhariwal and DC Bhandari (2012) Citrus genetic resources in India: present status and management. National Bureau of Plant Genetic Resources, New Delhi, India, 184p.
- Malik SK, R Chaudhury and OP Dhariwal (2006) Collection and Characterization of *Citrus indica* Tanaka and *C. macroptera* Montr.: Wild Endangered Species of North-eastern India. *Genet. Resour. Crop Evol.* 53: 1485–1493.
- Marak Silba R, D Sharma and H Sarma (2021) Ethnic preparation of Chubitchi, an alcoholic beverage of the Garo tribe of Meghalaya: a socio-cultural analysis. *J. Ethn. Food.* 8: 29.
- Mittermeier RA, WR Turner, FW Larsen, TM Brooks and C Gascon (2011) Global biodiversity conservation: the critical role of hotspots. In: FE Zachos and JC Habel (Eds.) *Biodiversity hotspots: Distribution and Protection of Conservation Priority Areas*. Springer Berlin, Heidelberg, pp 3–22.
- Samati H (2004) Kitchen Garden plants of Pnar tribe in Jaintia Hills District, Meghalaya. *Ethnobotany.* 16(1&2): 125–130.
- Sharma BD, DK Hore and SG Gupta (2004) Genetic resources of *Citrus* of north-eastern India and their potential use. *Genet. Resour. Crop Evol.* 51: 411–418.
- Singh B, BK Sinha, SJ Phukan, SK Borthakur and VN Singh (2012) Wild edible plants used by Garo tribes of Nokrek Biosphere Reserve in Meghalaya, India. *Indian J. Trad. Know.* 11(1): 166–171.
- Singh IP and S Singh (2006) Exploration, collection and characterization of citrus germplasm—a review. *Agric. Rev.* 27(2): 79–90.
- Singh B (1977) Races of Maize in India. Indian Council of Agricultural Research, New Delhi, pp 62–66.
- Tanaka T (1937) Citrus fruits of India. *Allahabad Farmer*, 2: 53–57.
- Tyagi RK, A Agrawal, R Pandey, VC Chalam and Bhag Mal (2016) Guidelines for management of plant genetic resources, India, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India.

RESEARCH ARTICLE

Evaluation of Recombinant Inbred Lines of *Oryza glaberrima* and Improved Samba Mahsuri for Antixenosis and Tolerance against *Nilaparvata lugens* (Stal)

Neha Chhabra¹, Preetinder S. Sarao^{2*}, R. M. Sundaram³ and Gurjot Kaur¹

Abstract

The selected recombinant inbred lines (RILs) of *Oryza glaberrima*, improved Samba Mahsuri (ISM), resistant (Ptb33) and susceptible (TN1) checks were evaluated for antixenosis and tolerance against brown planthopper (BPH), *Nilaparvata lugens* under glasshouse conditions for two wet crop seasons of 2020 and 2021. The mean least number of nymphs were recorded on a resistant check, Ptb33 (7.04) followed by resistant parent, *O. glaberrima* acc. IR75870 (9.04), while highest nymphs were settled on the susceptible check, TN1 (15.63). IR75870 and homogenous resistant line (HRL) were least preferred by adult BPH males (3.25 and 3.40, respectively) and females (2.85 and 3.28, respectively) for settling. In tolerance studies of different germplasm lines against BPH, Ptb33, IR75870, and HRL, it took more time (19.40–23.00 days) to completely wilt. The mean lowest functional plant loss index (FPLI) was recorded from Ptb33 (19.28%), followed by IR75870 (21.32%) and HRL (21.77%), whereas the highest mean FPLI was recorded from TN1 (76.93%). A similar trend was observed among germplasm lines in case of plant dry weight loss index.

Keywords: *Oryza glaberrima*, Recombinant inbred lines, Brown planthopper, Brown planthopper adult settling, BPH nymph settling, Functional plant loss index, Plant dry weight loss index.

¹Department of Entomology, Punjab Agricultural University, Ludhiana, Punjab, India.

²Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab, India.

³ICAR-Indian Institute of Rice Research, Hyderabad, Telangana, India.

***Author for correspondence:**

preetento@pau.edu

Received: 27/10/2023 **Revised:** 21/12/2023

Accepted: 26/12/2023

How to cite this article: Chhabra N, PS Sarao, RM Sundaram and G Kaur. (2024) Evaluation of Recombinant Inbred Lines of *Oryza glaberrima* and Improved Samba Mahsuri for Antixenosis and Tolerance against *Nilaparvata lugens* (Stal). *Indian J. Plant Genetic Resources*. 37(1): 56-61. DOI: 10.61949/0976-1926.2024.v37i01.07

Introduction

Rice is a staple food for a substantial portion of the world's population, particularly in East, South, and Southeast Asia, making it the second most consumed cereal grain. More than 90% of the world's rice is cultivated and consumed in Asia, which has 60% of the world's population. It is grown on around 154 million hectares per year, accounting for 11% of the world's cultivated land (Udayasree *et al.*, 2021). Rice crop is attacked by more than a hundred insect species, of which 20 are economically important and brown planthopper (BPH); *Nilaparvata lugens* (Stal)) is one of them (Prakash *et al.*, 2007). This phloem sap feeder is one of Asia's most destructive and notorious rice pests, capable of causing up to 60% yield loss under epidemic conditions (Roy *et al.*, 2021). BPH nymphs and adults suck sap from the lower portion of the plant, resulting in yellowing of leaves, reduction in tiller number, plant height, and, finally, chaffy grains (Seo *et al.*, 2009). Feeding also causes a reduction in chlorophyll and protein content of leaves followed by a reduced rate of photosynthesis, in case of severe attack, it causes extensive plant mortality referred to as the 'hopper burn' symptom (Kusumawati *et al.*, 2018). BPH also acts as a vector and transmits rice grassy stunt virus (GSV) and ragged stunt virus (RSV) (Khush and Brar, 1991).

Among the various methods (cultural, use of resistant varieties, biological and chemical control) available for managing BPH at

farmers' fields. The most commonly adopted method is the use of insecticides and for many years, synthetic chemicals have been the mainstay of BPH control. As a result of the widespread and extensive use of pesticides, BPH has developed significant levels of resistance to several of the major types of insecticides (Zhang *et al.*, 2016). Overall, BPH has evolved resistance to 29 compounds used in insecticide formulations (Sparks and Nauen, 2015), making chemical control one of the most insignificant approaches. Along with that, lack of proper planning and injudicious use of insecticides destroys the natural balance between BPH and natural enemies in rice agro-ecosystem (Sandhu and Sarao, 2020). Furthermore, it will also lead to increased production costs. Host plant resistance (HPR) is considered to be the most economical and eco-friendly strategy to manage the BPH. Therefore, a breeding programme for the development of BPH-resistant varieties with a different mode of host plant resistance is extremely important.

The exploration for the source of BPH resistance gene started back in 1967 and so far, more than 42 BPH resistance genes have been identified in Indica varieties, African cultivars, landraces and several species of wild rice germplasms (Kaur *et al.*, 2022). The International Rice Research Institute (IRRI) has commercially released numerous BPH-resistant varieties for Asian farmers, but in recent years, these improved varieties have lost their resistance due to the emergence of new BPH biotypes. Therefore, incorporating new rice germplasm for identifying new resistance genes from novel sources against BPH in the breeding program will act as saviour against this most destructive pest of rice. So far, no BPH resistance gene have been designated and identified from *Oryza glaberrima* Steud. *O. glaberrima*, commonly known as African rice, is one of the two domesticated rice species and is tolerant to low phosphorus, acidic soils, drought and other biotic stresses such as African gall midge, nematodes and blast. Keeping this objective in mind, present experiments were conducted for the evaluation of recombinant inbred lines (RILs) of *O. glaberrima* as a novel source for antixenosis and tolerance resistance against *N. lugens*. The goal is to incorporate these resistant traits into pre-breeding programs for the development of varieties resistant to BPH.

Materials and Methods

The selected recombinant inbred lines (RILs) of *O. glaberrima* and Improved Samba Mahsuri (ISM) after screening against BPH has been evaluated for antixenosis and tolerance against *N. lugens* under glasshouse conditions in the Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana (30°90' latitude and 75°81' longitude) for two wet crop seasons of 2020 and 2021.

Test Plants

The seeds of ISM, *O. glaberrima* (acc. IR75870), Ptb33 (resistant check), TN1 (susceptible check) and 260 F₅

recombinant inbred lines were received from the Indian Institute of Rice Research (formerly Directorate of Rice Research), Hyderabad, India. The selected homogeneous resistant and homogeneous susceptible recombinant lines along with parents and checks after screening against BPH were used for the studies. The pre-sprouted seeds of these lines were planted in either seed boxes or pots, depending on the specific experiment. The containers thoroughly filled with nutrient-rich, well-puddled soil were placed in a glasshouse designed to prevent the entry of any insect pests before exposure to BPH.

BPH Rearing

The 30 days old TN1 plants were used for the rearing of BPH population under glasshouse conditions at the Rice Research Laboratories, Department of Plant Breeding and Genetics, positioned at 30° 54' N and 75° 48' E at (28 ± 2°C), 75% ± 5% relative humidity and 14 hours light/10 hours dark photoperiod (Heinrichs *et al.*, 1985). These TN1 plants were sown in earthen pots (20 cm diameter) filled with nutrient-rich, well-puddled soil and replaced with fresh ones after the complete wilting of plants owing to insect feeding. To prevent the BPH population from escaping, the earthen pots were placed in rearing cages (68 x 50 x 50 cm) covered with nylon mesh, sewn along the four edges of the frame, and connected at the top with rope.

Antixenosis Resistance

BPH nymph settling

The seeds of each test germplasm were sown in lines randomly in rows at a spacing of 3.5 cm in seed box (45 x 35 x 10 cm) containing nutrient-rich well-puddled soil (Photo 1). Each row had 10 seedlings and the experiment was repeated thrice. 2nd – 3rd instar BPH nymphs @ 10 nymphs per seedling were released on 30 days old seedlings (3–4 leaf stage). After 1st, 2nd and 3rd days of release, the number of settled nymphs was counted. The seedlings were disturbed after each count for reorientation of the hopper nymphs. Six rows were randomly assigned to each seed box such that each replicate had a distinct arrangement of the rows, and the settling behavior of the nymphs was recorded using an average of three replications.

BPH adult settling

The seeds of test germplasms were sown in small pots (10 cm diameter, 15 cm height) and kept in a water trough in a complete randomized design with five replications (a single potted plant represented one replicate). All plastic pots were placed inside a small net house (120 × 80 × 40 cm) in a completely randomized design. On 30 days old seedlings (3–4 leaf stage), 100 pairs of one day old macropterous adults were released under free choice test. The number of male and female adults settled on the tested lines were counted 4, 8, 12, 24, 48 and 96 hours after release. For the

reorientation of the insects, the seedlings were disturbed after each count.

Germplasm Tolerance to BPH

This study was carried out in a series of five replications to determine the tolerance of germplasm lines to BPH. Like previous experiments, 30 day-old seedlings of each germplasm line were covered with cylindrical mylar cages with well-ventilated windows (Photo 2). About 25, 2nd-3rd instar BPH nymphs were released on each tested germplasm seedling and allowed to feed. The plant wilting was recorded when they started drying. Simultaneously, plants that were unexposed to BPH were also maintained as a check. The experiment was terminated after 40 days of nymphs release and the number of plants that did not wilt at the end of study was recorded.

Upon seedling wilting, planthoppers were killed by spraying insecticide and dead BPH were collected and then oven dried for 48 hours at 55°C and weighed using a digital balance. Infested and uninfested seedlings were also collected at the same time washed properly to remove soil and oven-dried at 70°C for 72 hours and thereafter weighed. Functional plant loss index (FPLI, %) and plant dry weight loss index (PDWLI, mg) to BPH were calculated by using the formula of Panda and Heinrichs (1983) as given below:

$$\text{Functional Plant Loss Index (FPLI, \%)} = 1 - \frac{\text{Dry weight of infested plants}}{\text{Dry weight of uninfested plants}} \times 100$$

$$\text{Plant dry weight loss index (PDWLI, mg)} = \frac{\text{Dry weight of uninfested plant} - \text{Dry weight of infested plant}}{\text{Dry weight of BPH progeny on infested plant}}$$

Statistical Analysis

Data from different experiments were subjected to analysis of variance following statistical software SPSS v 20.0. Statistical analysis was done using complete randomized design (CRD). Means and standard errors were calculated for comparison purposes at 5% level of significance. The arc

sine ($\sqrt{\text{percentage}}$) and square root transformations were used for different data before statistical analysis to meet the normalization requirement.

Results

Antixenosis Resistance

BPH nymph settling

The mean nymph settling among germplasm lines differed significantly during different data recording days during both study years. After one day of nymph release the settling differed significantly on tested germplasm lines with a minimum number of nymphs were recorded on Ptb33 and highest on TN1 ($F_{5,12} = 190.541$, $p \leq 0.0001$). Similarly, after two days of BPH release, nymph settling was lowest on Ptb33 followed by IR75870, whereas the maximum number of nymphs were observed on TN1 followed by Improved Samba Mahsuri (ISM) and homogenous susceptible line (HSL) ($F_{5,12} = 2261.00$, $p \leq 0.0001$). Likewise, after three days of release, least nymphs were recorded on Ptb33 and highest on TN1 ($F_{5,12} = 738.09$, $p \leq 0.0001$) (Figure 1). Overall, the mean number of nymphs settled 54.96% less on Ptb33, 42.16% less on resistant parent (IR75870) and 40.31% less on homogenous resistant line (HRL) than on TN1 ($F_{5,12} = 2067.00$, $p \leq 0.0001$) (Table 1).

BPH adult female settling

The mean adult female settling among germplasm lines differed significantly during different time durations of data recording during both the years of study. After 4 hours of release a significantly minimum number of female adults were recorded on Ptb33, whereas the highest number of female adults were recorded on TN1 followed by ISM and HSL ($F_{5,24} = 140.24$, $p \leq 0.0001$). A similar trend was observed after 8 hours of release ($F_{5,24} = 208.41$, $p \leq 0.0001$). After

Table 1: Antixenosis studies on selected rice germplasm lines against *N. lugens* (mean of 2020 and 2021)

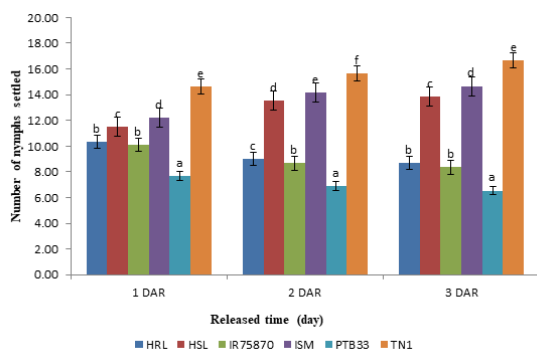
Germplasm line	Mean number of settled nymphs [#] (Mean ± SE)	Mean number of settled adult female [#] (Mean ± SE)	Mean number of settled adult male [#] (Mean ± SE)
Homogenous resistant line	9.33 ± 0.05 ^c (3.21)	3.28 ± 0.05 ^c (2.07)	3.40 ± 0.06 ^b (2.10)
Homogenous susceptible line	12.95 ± 0.11 ^d (3.73)	6.60 ± 0.04 ^d (2.75)	6.08 ± 0.05 ^c (2.66)
<i>O. glaberrima</i> (IR75870)	9.04 ± 0.02 ^b (3.17)	2.85 ± 0.07 ^b (1.96)	3.25 ± 0.06 ^b (2.06)
Improved Samba Mahsuri (ISM)	13.68 ± 0.06 ^e (3.83)	7.05 ± 0.07 ^e (2.84)	6.47 ± 0.04 ^d (2.73)
Ptb33	7.04 ± 0.06 ^a (2.84)	1.15 ± 0.07 ^a (1.47)	1.80 ± 0.08 ^a (1.67)
TN1	15.63 ± 0.10 ^f (4.08)	8.52 ± 0.03 ^f (3.08)	7.90 ± 0.18 ^e (2.98)
LSD (p = 0.05)	(0.03)	(0.04)	(0.05)

Figures in parentheses are the means of $\sqrt{n+1}$ transformations; Means within a column followed by the same letter are not significantly different at $p \leq 0.05$

Table 2: Tolerance studies on selected rice germplasm lines against *N. lugens* (mean of 2020 and 2021)

Germplasm line	Days to wilt (days)* (Mean $\pm$ SE)	Functional plant loss index (%)* (Mean $\pm$ SE)	Plant dry weight loss index (mg)* (Mean $\pm$ SE)
Homogenous resistant line	19.40 $\pm$ 0.53 ^b (4.52)	21.77 $\pm$ 0.44 ^b (27.80)	17.38 $\pm$ 0.25 ^b (4.29)
Homogenous susceptible line	13.40 $\pm$ 0.19 ^c (3.79)	61.50 $\pm$ 0.56 ^c (51.63)	97.24 $\pm$ 0.25 ^c (9.91)
<i>O. glaberrima</i> (IR75870)	20.50 $\pm$ 0.63 ^b (4.63)	21.32 $\pm$ 0.57 ^b (27.48)	16.71 $\pm$ 0.17 ^b (4.21)
Improved Samba Mahsuri	12.70 $\pm$ 0.30 ^c (3.70)	66.15 $\pm$ 0.53 ^d (54.40)	104.93 $\pm$ 0.53 ^d (10.29)
Ptb33	23.00 $\pm$ 0.42 ^a (4.90)	19.28 $\pm$ 0.22 ^a (26.04)	14.40 $\pm$ 0.37 ^a (3.92)
TN1	10.60 $\pm$ 0.29 ^d (3.40)	76.93 $\pm$ 0.61 ^e (61.28)	126.74 $\pm$ 0.93 ^e (11.30)
LSD (p = 0.05)	(0.14)	(0.97)	(0.09)

Figures in parentheses are the means of $\sqrt{n+1}$ transformations; *Figures in parentheses are the means of arc sine $\sqrt{\text{percentage}}$ transformations; Means within a column followed by the same letter are not significantly different at $p \leq 0.05$



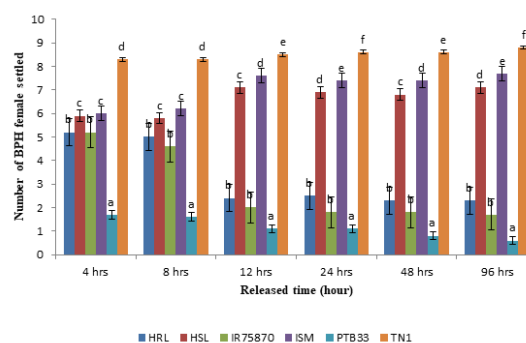
DAR – Days after release; HRL – Homogenous resistant line; HSL – Homogenous susceptible line; ISM – Improved Samba Mahsuri; Different letters represent significant difference at the 0.05 level for each DAR separately; Bar represents the standard error

Figure 1: Number of *N. lugens* nymphs settled on rice germplasm lines (mean of 2020 & 2021)

12 hours of release, least number of female adults were observed on Ptb33 followed by IR75870 and HRL whereas the maximum number of female adults were recorded on TN1 ($F_{5,24} = 463.79$, $p \leq 0.0001$). After 24 ($F_{5,24} = 494.29$, $p \leq 0.0001$), 48 ($F_{5,24} = 374.98$, $p \leq 0.0001$) and 96 ($F_{5,24} = 420.93$, $p \leq 0.0001$) hours of release, trend was similar as in the previous observations (Figure 2). Overall, the number of female adult settled 86.70% less on Ptb33, 66.71% less on IR75870 and 61.50% less on HRL than on TN1 ($F_{5,24} = 2469.00$, $p \leq 0.0001$) (Table 1).

BPH adult male settling

The mean adult male settling among germplasm lines differed significantly during different days of observations during both years of study. After 4 hours of release settling, adult males differed significantly and minimum number of male adults were recorded on Ptb33, the highest on TN1, followed by HSL ($F_{5,24} = 92.62$, $p \leq 0.0001$). A similar trend was observed after 8 hours of release ($F_{5,24} = 111.24$, $p \leq 0.0001$).



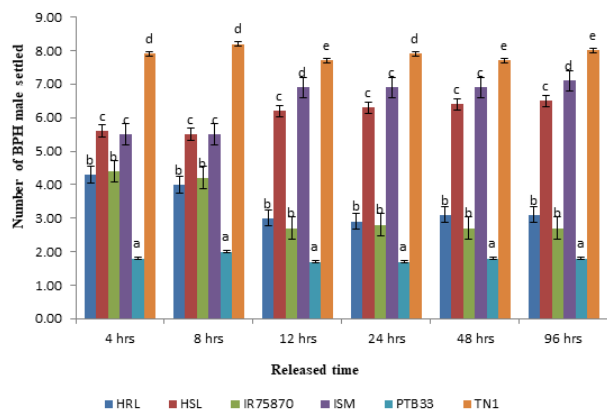
HRL – Homogenous resistant line; HSL – Homogenous susceptible line; ISM – Improved Samba Mahsuri; Different letters represent significant difference at the 0.05 level for each DAR separately; Bar represents the standard error

Figure 2: Number of *N. lugens* females settled on rice germplasm lines (mean of 2020 & 2021)

After 12 hours of release, least number of male adults were observed on Ptb33 followed by IR75870 and HRL, whereas maximum on TN1 ($F_{5,24} = 196.80$, $p \leq 0.0001$). After 24 ($F_{5,24} = 114.77$, $p \leq 0.0001$), 48 ($F_{5,24} = 304.06$, $p \leq 0.0001$) and 96 ($F_{5,24} = 185.03$, $p \leq 0.0001$) hours of release, similar results were obtained (Figure 3). Overall, the number of male adult settled 77.22% less on Ptb33, 58.86% less on IR75870 and 56.96% less on HRL than on TN1 ($F_{5,24} = 658.92$, $p \leq 0.0001$) (Table 1).

Germplasm tolerance to BPH

The germplasm tolerance to BPH among germplasm lines differed significantly during both years of study. The resistant germplasm lines such as Ptb33, IR75870 and HRL took significantly more time to wilt as compared to susceptible germplasm lines like TN1, ISM and HSL ($F_{5,24} = 140.70$, $p \leq 0.0001$) (Table 2). Similarly, the functional plant loss index (FPLI) was lowest in Ptb33 followed by IR75870 and significantly differ from TN1 ($F_{5,24} = 2739.00$, $p \leq 0.0001$) (Table 2). Likewise, the plant dry weight loss index over



HRL – Homogenous resistant line; HSL – Homogenous susceptible line; ISM – Improved Samba Mahsuri; Different letters represent significant difference at the 0.05 level for each DAR separately; Bar represents the standard error

Figure 3: Number of *N. lugens* male settled on rice germplasm lines (mean of 2020 & 2021)

the years differed significantly among the germplasm lines. It was least in Ptb33 followed by IR75870 and HRL ($F_{5,24}=1135.00$, $p \leq 0.0001$) (Table 2).

Discussion

Host plant resistance (HPR) is an effective, economical, and eco-friendly method of pest management and is a core of integrated pest management programmes. The host choice test indicates the antixenotic factor, which is used to evaluate the germplasm. Different antixenosis studies have shown that BPH nymphs and adults tend to move to susceptible genotypes with thriving exposures. Therefore, it appears that antixenosis is preferably driven by feeding response because genotype with high phosphorus, potash and polyphenols are less preferred by planthopper (Mote and Shahane, 1994). The results of nymph and adult settling experiments are corroborated with the findings of Sable *et al.* (2014), Bhanu *et al.* (2014), Sarao and Bentur (2016), Sandhu and Sarao (2020) and Roy *et al.* (2021). Sarao and Bentur (2016) reported that nymph, adult female, and adult male settling was significantly lower on RP2068-18-3-5 and Ptb33 among nine genotypes tested. Similarly, Roy *et al.* (2021) evaluated 26 West Bengal rice landraces to study antixenosis resistance mechanism against BPH. Nymph settling was significantly less on Kalabhat, Ptb33 and Badshabhog than on susceptible check Swarna, whereas adult females settling was less on Ptb33, Janglijata and Gamra than on susceptible check Swarna.

Few QTLs or genes linked to different parameters of antixenotic resistance against BPH are reported in rice (Haliru *et al.*, 2020). Kamolsukyonyong *et al.* (2013) reported that the sesquiterpene synthase gene in the rice cultivar Rathu Heenati affects the behavior of BPH during the first five days of BPH interaction with the rice plant. Prahalada *et al.* (2017) also reported that BPH nymph load was lowest on CR2711–76

harboring *Bph31* gene as compared to susceptible line Jaya and TN1, which possess no BPH-resistant gene.

In our studies we observed that among germplasm lines, Ptb33 harboring three genes such as *bph2+Bph3+Bph32* performed better than *O. glaberrima* (IR75870) and HRL in terms of nymphs settling, female settling as well as male settling. However, IR75870 and HRL are significantly at par with each other however in contrast, the susceptible check (TN1) and susceptible parent (ISM) with no resistance gene performed significantly poor. HRL performed far better than HSL as both are of F_5 generation and in this filial generation, almost 99% genetic homozygosity for desired traits will be achieved. Thus HRL showed similar results with that of the resistant parent (IR75870), whereas HSL showed results similar to that of the susceptible parent (ISM). Thus our findings demonstrated that BPH nymphs and adults less settled on IR75870 and HRL than on susceptible lines. Thus, IR75870, as a resistant parent, possesses an antixenosis mechanism which prevents BPH from settling on it, unlike ISM which BPH preferred.

Tolerance is the ability to grow and reproduce in spite of supporting a population approximately equal to that damaging a susceptible host (Painter, 1951). Panda and Heinrichs (1983) identified rice cultivars like Triveni, Kanchana and UtriRajapan with tolerance as a predominant component of BPH resistance through the elaborate development of the functional plant loss index (FPLI) method. Later, Alam and Cohen (1998) further refined the tolerance parameter as plant dry weight loss (PDWL) per unit dry weight of BPH gained. Similarly, Geethanjali *et al.* (2009) proposed a simple test of days to wilt for the tolerance parameter which is being readily accepted and is being followed by Ramesh *et al.* (2014) and Sarao and Bentur (2016). Roy *et al.* (2021) reported that under the continual pressure of BPH, days to wilt varied greatly between the test landraces. When compared to the susceptible check Swarna, the wilting of Badshabhog, Ptb33, and Kalabhat occurred substantially later. The link of genetic constituents with the tolerance component of plant resistance against BPH has already been confirmed by Qiu *et al.* (2014), who reported that the gene *bph7* in rice variety T12 majorly contribute to the resistance component of resistance against BPH.

Summary of tolerance studies showed that among the six tested rice germplasm lines, a new novel source from *O. glaberrima* (IR75870), Ptb33 and HRL possessed good tolerance against BPH. It is well established that the tolerant plant exerts less selection pressure on insect population and thus are useful for preventing the development of insect biotypes. It can be concluded from these experiments that settling and feeding of BPH on rice can be affected by the selection of a host plant. The restless behavior of BPH on resistant cultivars also makes them more vulnerable to natural enemies.

Conclusion

Finally, it is concluded that the accession IR75870 act as a novel source of *O. glaberrima* and HRL with high levels of antixenosis and tolerance against BPH. This will provide better opportunities for plant breeders and biotechnologists to develop resistant varieties from novel sources like *O. glaberrima* against BPH, which has AA genome as *O. sativa* L. also has good tillering and panicle bearing capacity. Spikelets are generally awnless and non-shattering. Our study shows that the development of a variety that can exhibit high levels of antixenosis and tolerance mechanisms against BPH could play a pivotal role in BPH management strategies.

Acknowledgment

We are thankful to Dr RM Sundaram, Director of Indian Institute of Rice Research, Hyderabad for providing the required material and in charge of the Rice section, Department of Plant Breeding and Genetics, PAU, Ludhiana for providing facilities for the conduct of experiments.

Conflicts of Interest

The authors declare that they have no conflict of interest.

References

- Alam SN and MB Cohen (1998) Detection and analysis of QTLs for resistance to the brown planthopper, *Nilaparvata lugens* in a doubled haploid rice population. *Theor. Appl. Genet.* 97(8): 1370.
- Bhanu KV, PV Satyanarayana, PS Reddy and AVV Reddy (2014) MTU IJ 206-7-4-1 (BM 71), a new brown planthopper resistant donor with high levels of antixenosis and antibiosis effects. *Int. J. Innov. Appl. Res.* 2(12): 35-41.
- Geethanjali S, P Kadirvel, K Gunathilagaraj and M Maheswaran (2009) Detection of quantitative trait loci (QTL) associated with resistance to whitebacked planthopper, *Sogatella furcifera* in rice (*Oryza sativa* L.). *Plant Breed.* 128(2): 130-136.
- Haliru BS, MY Rafii, N Mazlan, SI Ramlee, II Muhammad, I Silas Akos, J Halidu, S Swaray and Y Rini Bashir (2020) Recent strategies for detection and improvement of brown planthopper resistance genes in rice: A review. *Plants* 9(9): 1202-1206.
- Heinrichs EA, FG Medrano and HR Rapusas (1985) *Genetic evaluation for insect resistance in Rice*. International Rice Research Institute, Los Baños, Philippines, 365p.
- Kamolsukyonyong W, W Sukhaket, V Ruanjaichon, T Toojinda and A Vanavichit (2013) Single-feature polymorphism mapping of isogenic rice lines identifies the influence of terpene synthase on brown planthopper feeding preferences. *Rice* 6: 1-9.
- Kaur P, K Neelam, PS Sarao, A Babbar, K Kumar, Y Vikal, R Khanna, R Kaur, GS Mangat and K Singh (2022) Molecular mapping and transfer of a novel brown planthopper resistance gene *bph42* from *Oryza rufipogon* (Griff.) to cultivated rice (*Oryza sativa* L.). *Mol. Biol. Rep.* 49(9): 8597-8606.
- Khush GS and DS Brar (1991) Genetics of resistance to insects in crop plants. *Adv. Agron.* 45: 223-274.
- Kusumawati L, P Chumwong, W Jamboonsri, S Wanchana, JL Siangliw, M Siangliw, S Khanthong, A Vanavichit, W Kamolsukyonyong and T Toojinda (2018) Candidate genes and molecular markers associated with brown planthopper (*Nilaparvata lugens* Stål) resistance in rice cultivar Rathu Heenati. *Mol. Breed.* 38: 1-16.
- Mote UN and AK Shahane (1994) Biophysical and biochemical characters of sorghum varieties contributing resistance to delphacid, aphid and leaf sugary exudations. *Indian J. Entomol.* 56: 113-122.
- Oerke EC (2005) Crop losses to pests. *J. Agric. Sci.* 144(1): 31-43.
- Painter RH (1951) *Insect resistance in crop plants*. The Macmillan Company, New York, USA, 504p.
- Panda N and EA Heinrichs (1983) Levels of tolerance and antibiosis in rice varieties having moderate resistance to the brown planthopper, *Nilaparvata lugens* (Stål) (Homoptera: Delphacidae). *Envir. Ent.* 12(4): 1204-1214.
- Prahalada GD, N Shivakumar, HC Lohithaswa, DK Sidde Gowda, G Ramkumar, SR Kim, C Ramachandra, S Hittalmani, T Mohapatra and KK Jena (2017) Identification and fine mapping of a new gene, *BPH31* conferring resistance to brown planthopper biotype 4 of India to improve rice, *Oryza sativa* L. *Rice* 10(1): 1-15.
- Prakash A, J Rao, ON Singh, JP Tyagi, S Singh and PC Rath (2007) *Rice: the Queen of Cereals*. Applied Zoologist Research Association Publication, Cuttack, 15p.
- Qiu YF, JP Guo, SQ Jing, LL Zhu and GC He (2014) Fine mapping of the rice brown planthopper resistance gene *Bph7* and characterization of its resistance in the 93-11 background. *Euphytica* 198: 369-379.
- Ramesh K, G Padmavathi, R Deen, MK Pandey, VJ Lakshmi and JS Bentur (2014) Whitebacked planthopper *Sogatella furcifera* (Horvath) (Homoptera: Delphacidae) resistance in rice variety Sinna Sivappu. *Euphytica* 200: 139-148.
- Roy D, G Chakraborty, A Biswas and PK Sarkar (2021) Antixenosis, tolerance and genetic analysis of some rice landraces for resistance to *Nilaparvata lugens* (Stål). *J. Asia-Pac. Entomol.* 24(1): 448-460.
- Sable A, S Suresh and SM Kumar (2014) Antixenosis Mechanism of Resistance to brown planthopper *Nilaparvata lugens* (Stål) in selected rice genotypes. *J. Biosci.* 7: 1594-1598.
- Sandhu RK and PS Sarao (2020) Evaluation of antixenosis resistance in wild rice germplasms against brown planthopper, *Nilaparvata lugens* (Stål). *Int. J. Trop. Insect Sci.* 41: 65-73.
- Sarao PS and JS Bentur (2016) Antixenosis and tolerance of rice genotypes against brown planthopper. *Rice Sci.* 23(2): 96-103.
- Seo BY, YH Kwon, JK Jung and GH Kim (2009) Electrical penetration graphic waveforms in relation to the actual positions of the stylet tips of *Nilaparvata lugens* in rice tissue. *J. Asia-Pac. Entomol.* 12(2): 89-95.
- Sogawa K, GJ Liu and JH Shen (2003) A review on the hypersusceptibility of Chinese hybrid rice to insect pests. *Chin. J. Rice Sci.* 17(ZK): 23.
- Sparks TC and R Nauen (2015) IRAC: Mode of action classification and insecticide resistance management. *Pestic. Biochem. Physiol.* 121: 122-128.
- Udayasree M, P Rajanikanth, NR Varma and M Sreedhar (2021) Antibiosis and tolerance of certain elite rice genotypes against brown Planthopper *Nilaparvata lugens* (Stål). *J. Pharm. Innov.* 10: 1057-1061.
- Zhang X, X Liao, K Mao, K Zhang, H Wan and J Li (2016) Insecticide resistance monitoring and correlation analysis of insecticides in field populations of the brown planthopper *Nilaparvata lugens* (Stål) in China 2012-2014. *Pestic. Biochem. Physiol.* 132: 13-20.

RESEARCH ARTICLE

Collection, Characterization and Identification of Elite Genotypes of Wild/Semi-Domesticated Bitter Gourd (*Momordica charantia* var. *muricata*) for Utilization and Conservation

Asna A. C.^{1*}, Jiji Joseph², Joseph K. John³, Sainamole Kurien P⁴ and C. Beena⁵

Abstract

Fifty genotypes of wild/semi-domesticated bitter gourd collected from major bitter gourd growing tracts of India were characterized for various qualitative, quantitative and biochemical traits to record the existing variability and genetic resources available for utilization and conservation. Wide variability was observed for fruit and seed characteristics. The preliminary screening of accessions under natural field conditions for their reaction to powdery mildew and viral infection resulted in the identification of five accessions viz., IC 213312, AC-16/1, AC-16/4, AC-16/9, and AC-16/21 as potent resistant sources. Principal component analysis grouped the entire collection into four genetically diverse clusters irrespective of the origin or place of collection of accessions. The four better performing wild/semi-domesticated genotypes of bitter gourd viz., AC-16/1, AC-16/16, IC 467681 and JJNS-15/65 should be further tested in large-scale yield trials and recommended for commercial cultivation, especially for homestead farming.

Keywords: Wild/semi-domesticated genotypes, Characterization, Principal component analysis, Screening, Resistant sources.

¹Department of Plant Breeding and Genetics, Cashew Research Station, Kerala Agricultural University, Thrissur, Kerala, India,

²Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University, Thrissur, Kerala, India,

³National Bureau of Plant Genetic Resources-Regional Station, Thrissur, Kerala, India,

⁴Department of Plant Pathology, College of Horticulture, Kerala Agricultural University, Thrissur, Kerala, India,

⁵All India Coordinated Research Project on Medicinal and Aromatic Plants, College of Agriculture, Kerala Agricultural University, Thrissur, Kerala, India

***Author for correspondence:**

asna.ac@kau.in; asna.ac@gmail.com

Received: 01/08/2022 **Revised:** 22/06/2023

Accepted: 15/01/2024

How to cite this article: Asna AC, J Joseph, JK John, SP Kurien and C Beena. (2024) Collection, Characterization and Identification of Elite Genotypes of Wild/Semi-Domesticated Bitter Gourd (*Momordica charantia* var. *muricata*) for Utilization and Conservation. *Indian J. Plant Genetic Resources*. 37(1): 62-72. DOI: 10.61949/0976-1926.2024.v37i01.08

Introduction

Bitter gourd/bitter melon/balsam pear (*Momordica charantia* L.), belonging to the family Cucurbitaceae, is an important commercial vegetable crop grown in India, Sri Lanka, Philippines, Thailand, Malaysia, China, Japan, Australia, tropical Africa, South America and the Caribbean. The genus *Momordica* is indigenous to the Paleotropics (Robinson and Decker-Walters, 1997). *Momordica charantia*, the most widely cultivated species in this genus, has been highly valued for its nutritive and medicinal properties. Bitter gourd has been used for centuries in the traditional systems of medicine of India, China, Africa, and Latin America. The fruits are known to possess antioxidant, anti-microbial and anti-diabetic properties (Raman and Lau, 1996).

Bitter gourd was originally described by Linnaeus (1753) from Peninsular India and it is now found naturalized in all tropical and subtropical regions. Two varieties of *M. charantia* are reported in India viz., *M. charantia* var. *charantia* and *M. charantia* var. *muricata* (Chakravarty, 1990). The wild variety, *M. charantia* var. *muricata*, is considered as the progenitor of the cultivated type (Degner, 1947) with small and round fruits having markedly sculptured seeds and *M. charantia* var. *charantia* is the cultivated type which produces large fusiform fruits having feebly sculptured seeds (Chakravarty, 1990). The first authentic document on the Flora of Malabar, Hortus

Malabaricus, illustrated four *Momordica* entities, of which "Pavel" and "Pandi-Pavel" refer to small-fruited bitter gourd and are reported to have been extensively cultivated by the natives of India in the past (Roxburgh, 1832). The large-fruited *charantia* types replace this because of its large or heavy fruits and high-yielding potential. Now, the cultivation of small-fruited bitter gourds is restricted to few homestead gardens and under wild conditions in disturbed open forest and have practically escaped the attention of farmers and breeders alike (John and Antony, 2009).

Compared with the highly vulnarebale cultivated types, wild/semi-domesticated *muricata* types are endowed with resistance/tolerance to some of cucurbits' common pests and diseases (Bharathi and John, 2013). The *muricata* types are even reported to have potent antioxidant and free radical scavenging activities (Wu and Ng, 2008). Since both botanical varieties are readily crossable, chance mating between them may result in semi-domesticated cultivars. Thus, the small-fruited wild bitter gourd is on the verge of extinction in Kerala and rest of Southern peninsular India. In view of their excellent nutritional quality and tolerance to biotic and abiotic stresses, these wild types need to be collected and conserved from the whole range of their distribution across India and evaluated for the identification of promising lines to create new cultivars with commercial value and adaptability to adverse growing conditions.

In this context, the present study was taken up to showcase the genetic wealth and existing variability of wild/semi-domesticated bitter gourd in India and thereby identify elite wild types with promising quality attributes that can be out-rightly recommended for cultivation or further crop improvement programs in bitter gourd. Multivariate

data analysis, being a powerful statistical technique for analyzing genetic relationships from morphological traits, was used to discover the contribution of phenotypic traits to the total diversity in a germplasm collection. This article gives an insight into the extent of domestication in the wild genotypes, which may facilitate better conservation of this underutilized vegetable.

Materials and Methods

Plant Material

Fifty accessions of wild/semi-domesticated bitter gourd (*M. charantia* var. *muricata*) collected from the Regional Station of ICAR-National Bureau of Plant Genetic Resources (NBPGR), Thrissur, farmer's fields and wild habitats across Kerala, Karnataka and Tamil Nadu formed the material for the study. The plant materials from NBPGR comprised 24 accessions, of which five each were collected from Madhya Pradesh and Mizoram, two each from Rajasthan and Punjab, four from Kerala and three from Andaman and Nicobar (Figure 1). During the study period, a preliminary survey was conducted in Kerala and 12 sites of districts viz., Thrissur, Palakkad, Kannur, Kottayam, Wayanad and Idukki were visited and 16 indigenous genotypes of wild/semi-domesticated bitter gourd were collected (Figure 1). Six collections from Tamil Nadu and four from Karnataka were added to cover a potentially higher variability (Figure 1).

Characterization Trials

Morphological characterization

The 50 *M. charantia* var. *muricata* accessions were raised in an augmented block design (Federer, 1956) along with three

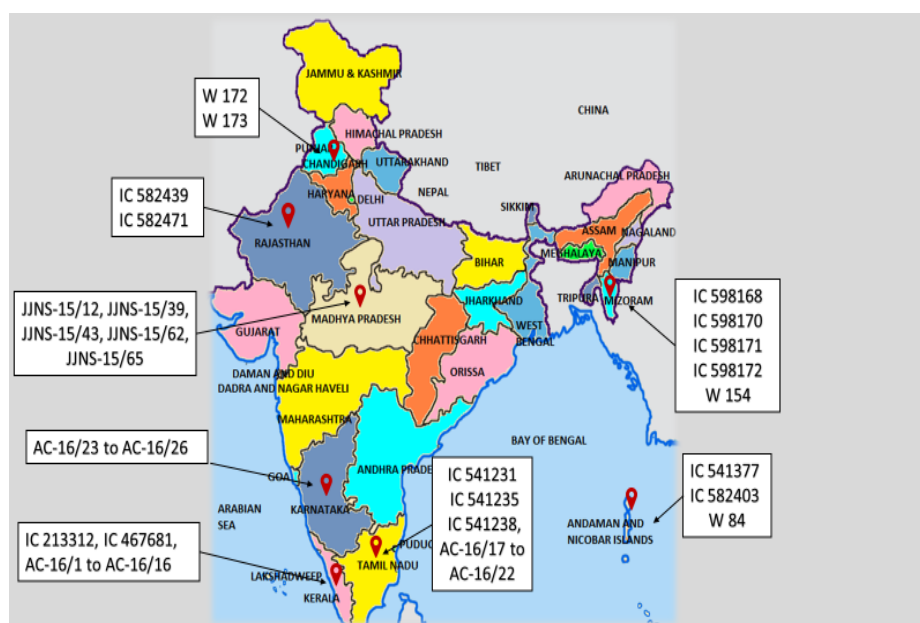


Figure 1: Map showing the collection sites of bittergourd accessions

check varieties viz., Preethi, Priyanka and Pusa Purvi. Preethi and Priyanka are the two most popular varieties of bitter gourd, belonging to *M. charantia* var. *charantia*, released by Kerala Agricultural University (KAU) whereas Pusa Purvi is the first small fruited bitter gourd variety developed by ICAR-Indian Agricultural Research Institute (IARI), New Delhi. It is the only variety of *muricata* type released from India. Data on the germplasm were recorded during two seasons of 2015 and 2016 in the experimental fields of the Department of Plant Breeding and Genetics, KAU, Vellanikkara, Thrissur, Kerala. There were 10 blocks and each block had 5 accessions of wild/semi-domesticated bitter gourd and three check varieties. The collected accessions were planted in pits 60 x 60 x 30 cm in size. The spacing between the pits and row was 3 x 3 m. Five plants were maintained per accession. All the recommended agronomic practices were followed as per the Kerala Agricultural University's package of practices (KAU, 2011) for raising a good and healthy crop. The plants were supported by installing pandals with bamboo and nets.

Plant characters and data recording

The data were recorded on 28 traits, of which 11 viz., days to first pistillate flower, days to first fruit harvest, number of pistillate flowers, number of fruits per plant, a yield of fruits per plant (g), fruit weight, length and width, flesh thickness (cm), cavity size (cm) and number of seeds per fruit were measured quantitatively, while another 17 traits viz., early plant vigor (EVP), plant growth habit (GH), the twining tendency (TT), leaf margin, leaf shape, leaf size (LS), fruit shape (FSH), fruit color (FC), fruit size (FS), fruit ends (FE), nature of tubercles (NT), seed color (SC), seed luster (SL), seed shape (SSH) and seed size (SS) were assessed qualitatively on different scales. All the traits were measured/assessed based on the descriptor list developed by NBPGR (2001).

All the accessions were scored for their susceptibility to biotic stresses like powdery mildew and viral infection. The disease severity of powdery mildew was recorded by using 0–9-point scale of TNAU (1980), where (0) no lesions, (1) Small sized powdery specks infecting < 1% leaf area, (2) Enlarged irregular powdery growth covering > 1 to 5% leaf area, (3) Powdery growth to form big patches covering > 5 to 25% leaf area, (4) Powdery growth covering > 25 to 50% leaf area followed by yellowing, (5) >50 to 100% leaf area

covered with powdery growth, yellowing and dropping of infected leaves. A modified 0 to 5 scale of Arunachalam *et al.* (2002) based on disease symptoms, was used to score the viral infection, where (0) no symptoms, (1) Minute chlorotic/mosaic specks on leaf, (2) Wide area of mosaic symptoms on whole leaf without distortion, (3) Mosaic symptom with reduction of 0 to 25% of leaf area, (4) Mosaic symptom with reduction of >25 to 75% of leaf area, and (5) Mosaic symptom with reduction of >75 to 100% of leaf area. Based on the disease score, level of resistance/susceptibility of the accessions to the disease were determined by percent disease severity (PDS) following the formula of McKinney (1923). The accessions were grouped into six categories based on the PDS of powdery mildew disease (Naik and Kulkarni, 2018) and viral infection (Arunachalam *et al.*, 2002) as given in Table 1. Each accession that showed resistance was tested twice to confirm the reaction.

Biochemical characterization

The collected genotypes were evaluated using standard procedures for four biochemical parameters: vitamin C, iron, fiber, and total antioxidant capacity. The vitamin C and crude fibre content of the fruits of bitter gourd accessions were estimated by volumetric, acid, and alkaline digestion methods, respectively, as Sadasivam and Manickam (1996) suggested. The fruits of 53 samples of bitter gourd were dried, powdered and digested with concentric nitric acid in a microwave digester. Iron content of the digest was then estimated in AAS using the hydride vapor generator method suggested by Jackson (1973). The phosphomolybdenum method (Prieto *et al.*, 1999) was used to estimate bitter gourd's total antioxidant capacity (TAC).

Organoleptic evaluation

Immediately after harvest, sensory evaluation of mature fruits from each genotype was done to identify the most accepted accession among them. Freshly harvested mature fruits of each accession were cut into small pieces and steamed for 5 minutes after adding a pinch of salt. Minimum processing was done in order to retain the flavor, color, taste and other qualities of the bitter gourd genotypes. Organoleptic parameters, namely, appearance, color, texture, flavor, odor, taste, after taste and overall

Table 1: Classification of accessions based on PDS of powdery mildew and mosaic diseases

Classification based on PDS of powdery mildew disease		Classification based on PDS of mosaic disease	
PDS	Disease response	PDS	Disease response
0	Immune (I)	0–5	Highly resistant (HR)
< 1	Highly resistant (HR)	>5–10	Resistant (R)
>1–10	Resistant (R)	>10–20	Moderately resistant (MR)
>10–25	Moderately resistant (MR)	>20–40	Moderately susceptible (MS)
>25–50	Moderately susceptible (MS)	>40–70	Susceptible (S)
>51–100	Highly susceptible (HS)	>70–100	Highly susceptible (HS)

acceptability of all the 53 bitter gourd genotypes, were evaluated by 20 semi-trained panel members between the age group of 18 to 40 years as suggested by Jellinek (1985) using a nine-point hedonic scale which arranged from 1 to 9. Hedonic ratings were then converted to rank scores, and rank analysis was done using Kendall's coefficient of concordance. Cumulative organoleptic score (COS) was also calculated for all the accessions by adding the mean rank recorded for each parameter.

Identification of better-performing wild/semi-domesticated genotypes

A modified method of Arunachalam and Bandyopadhyay (1984) was used to rank the genotypes, where each character's score was allotted based on its importance. The value of each accession for each trait was worked out by multiplying the score with the mean value of each character. These values were added across characters to provide a final/cumulative score for each accession. Based on the final scores, the entries were ranked on their performance over a set of characters. Thus, the better-performing bitter gourd genotypes among 50 wild/semi-domesticated accessions with respect to economically important characters were identified by ranking them using the selection index (SI) as enumerated below.

$$SI = [Y*10] + [FW*8] + [COS*6] + [NV*5] - [PM*8] - [M*8]$$

Where, Y-yield/plant, FW-fruit weight, COS-cumulative organoleptic score, NV-nutritive value, PM-percent disease severity of powdery mildew, M-percent disease severity of mosaic

Statistical Analysis

The germplasm accessions were evaluated in an augmented block design with three standard check varieties in 10 blocks. Analysis of variance was done for each of the quantitative characters observed using the free online Statistical Package for Augmented Designs (SPAD) developed by Indian Agricultural Statistical Research Institute (IASRI). The data obtained on various traits were further analyzed by principal component analysis (PCA) (Eriksson *et al.*, 1999), using the R based statistical software GRAPES version 1.14.02 (Gopinath, 2020) to quantify the contribution of each variable towards total genetic divergence in bitter gourd.

Results

Frequency Distribution for Qualitative and Quantitative Traits

Wide variability was present among the accessions for all the traits measured qualitatively. Early plant vigor recorded 30 days after sowing, which determines the subsequent growth of plant, was poor to good for 85% accessions. Long

vine growth habit was observed for 79% of accessions, indicating the wild nature and 21% were medium vine type. The twin tendency was found to be slight in 53% of accessions and intermediate in the remaining ones. Leaf margin and leaf shape was uniform in all the genotypes, multifold and cordate, respectively, as reported by Sidhu and Pathak (2016). More than 50% of accessions had smaller leaves with intermediate pubescence.

The qualitative characteristics of fruits, like shape, end shape, size, color, nature of tubercles etc. showed variability among the accessions. About 66% of the accessions produced small fruits, while 28% were natural intermediates with medium-sized fruits. Only 6% of the genotype produced large fruits. The fruit shape of bitter gourd was disc in 2%, rhomboid in 13%, cylindrical in 4%, spindle-shaped in 7.5%, elliptical in 36%, oblong in 30%, and globular in 7.5% accessions. In all the accessions evaluated, fruit ends were pointed either at both ends or only at the blossom end, except in one (AC-16/25), where both ends were round (blossom end shape is blunt). The surface of the fruit was highly tubercled with long green ridges. Sharp and pointed tubercles were found in 48% of accessions, followed by soft and raised tubercles. Green-colored fruit was present in all the accessions with different light-to-dark green intensities. In the present investigation, remarkable variability was observed with respect to the qualitative characteristics of bitter gourd seeds. A wide range of seed colors was obtained: Straw-colored, black, black and brown patched, brownish tan and whitish brown. However, straw-colored seeds (60%) with intermediate glossiness (58%) were predominant. The seeds of all the genotypes evaluated had a squarish oval shape, except 4% of accessions, which are round in shape. More than 50% of genotypes produced very small-sized seeds.

All the 53 accessions of bitter gourd were screened for their response to two important biotic stresses in Kerala like powdery mildew and viral infection based on standard disease score charts. PDS values were calculated during two consecutive crop seasons and resistant genotypes were identified. Based on the preliminary screening for powdery mildew resistance, two genotypes (Preethi and Priyanka) were found to be highly susceptible (PDS- 51.84 and 59.67, respectively), 24 were resistant, 19 were moderately resistant, three were moderately susceptible and five were highly resistant (PDS- 0.29–0.85). Whereas one (AC-16/4) was found to be highly resistant, five were resistant, nine were moderately resistant, 25 were moderately susceptible, 11 were susceptible and two were highly susceptible to viral infection. Five wild/semi-domesticated genotypes, IC 213312, AC-16/1, AC-16/4, AC-16/9 and AC-16/21, with high resistance to both powdery mildew and viral infection, were identified.

Frequency distribution graphs for quantitative traits depicted in Figure 2 showed that more than 50% of

accessions fall in the medium group of days to first pistillate flower (50–60 days) and days to first fruit harvest (50–70 days). The number of pistillate flowers and the number of fruits per plant revealed wide variation ranging from 179.71 to 17.78% and 14.32 to 168.39%, respectively. The highest range of fruit length (10.1–20.0 cm) and fruit width (4.1–5.0 cm) was observed in less than 10% of accessions. High variability was recorded for fruit yield per plant (124.05–8568.61 g). The average weight of individual fruit varied significantly among accessions and ranged from 3.53 to 420.61 g where only 4% of accessions produced the heaviest fruit (>100 g). The flesh thickness was 0.11 to 0.50 cm for 68% of the accessions, while the cavity size was 1.01 to 2.0 cm for 51% of the accessions. The majority of accessions had 10 to 20 number of seeds per fruit.

Principal Component Analysis

The principal component analysis was performed based on the nine yield contributing characters viz., number of pistillate flowers per plant, number of fruits per plant, fruit yield per plant, fruit weight, fruit length, fruit width, flesh thickness, cavity size and number of seeds per fruit. The cumulative variance, factor scores and contribution

Table 2: Eigen values, factor loadings and contribution of variations by yield attributing characters in bitter gourd

Variables	PC1	PC2	PC3
No. of pistillate flowers	-0.225	-0.654	0.022
No. of fruits per plant	-0.216	-0.664	0.047
Fruit yield plant	0.342	-0.193	0.489
Fruit weight	0.356	-0.089	0.505
Fruit length	0.402	-0.043	-0.016
Fruit width	0.376	-0.157	-0.324
Flesh thickness	0.379	-0.031	0.191
Cavity size	0.327	-0.22	-0.45
No. of seeds per fruit	0.323	-0.102	-0.399
Variance (%)	58.62	18.73	12.66
Cumulative variance (%)	58.62	77.35	90.01

of variation of each of the characters is presented in Table 2. In response to principal components, the scree plot revealed that the first three principal components had eigen eigenvalue > 1, accounting for 90.01% of the total variation. The first principal component (PC1) comprised of fruit yield per plant, fruit weight, fruit length, fruit width and flesh thickness and explained 58.62% of the total variation, whereas the PC2 comprised of a number of pistillate flowers and a number of fruits per plant and explained 18.73% of total variation. The PC3 accounted for 12.66% of variability and featured cavity size and number of seeds per fruit (Table 2).

The clustering of 53 accessions of bitter gourd based on the first two principal components formed four major distinct clusters (Figure 3). Cluster IV included the highest number of collections (46) and cluster I and III contained two accessions each. The score plot indicated that cluster I (Priyanka, Preethi), and II (AC-16/1, AC-16/16, IC467681) positioned at the first quadrant on the positive side of PC1 and PC2, exhibited their superiority over other clusters. The accessions grouped as cluster I belong to var. *charantia* and were superior to other clusters with preferred yield contributing attributes. Cluster II consisted of three collections that stand as elite wild/semi domesticated bitter gourd lines with good fruit yield per plant and weight. The two accessions in cluster III were superior with respect to number of pistillate flowers and fruits per plant.

Biochemical Characterization

Biochemical evaluation of 53 genotypes of bitter gourd based on vitamin C, iron, fiber content and antioxidant activity were done following standard procedures. A significant difference was observed among the accessions based on the analysis of variance. The average vitamin C content among 53 genotypes of bitter gourd was 94.14 mg/100 g, ranging from 76.53 mg/100 g (AC-16/25) to 125.67 mg/100 g (W 154). W 172 had the lowest (1.48 mg/100 g)

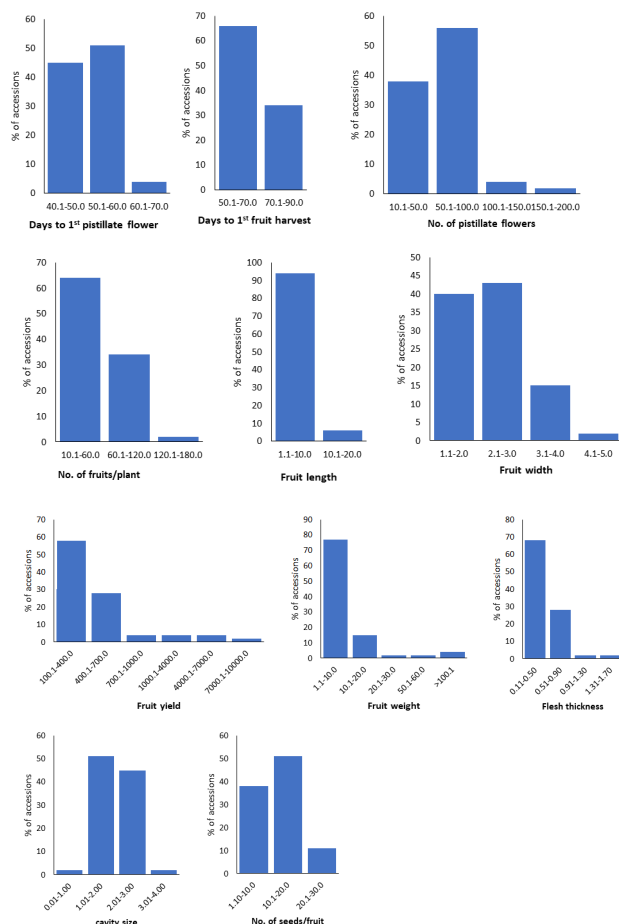


Figure 2: Frequency distribution of bitter gourd accessions for quantitative traits

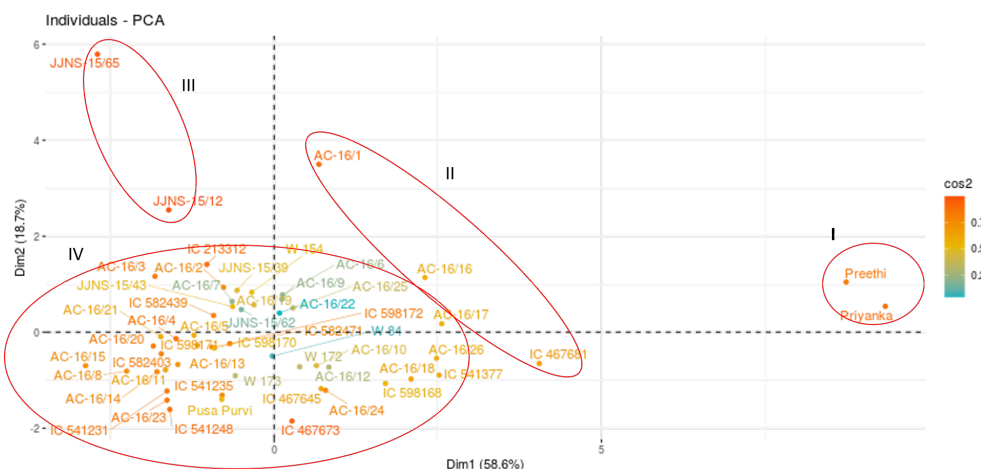


Figure 3: Score plot based on first two principal components of bitter gourd accessions

and AC-16/6 had the highest iron content (3.31 mg/100 g). The crude fibre content ranged from 12.17% in IC 598170 to 30.44% in IC 582403. The antioxidant capacity varied from 41.88 to 92.01 mg AAE/g.

Organoleptic Evaluation

The sensory profile of most preferred bitter gourd accessions is presented in Figure 4. Priyanka, Preethi, AC-16/1, IC467645, JJNS-18/43 and IC598168 ranked higher for their texture, taste, flavor, odor, after taste, appearance, color and overall acceptability. The maximum score for all the organoleptic parameters except taste and flavor were observed for Priyanka. The maximum taste and flavor scores were observed for AC-16/24 (43.75) and IC 598168 (43.40), respectively. Among the wild/semi-domesticated genotypes, the maximum score for appearance was found in AC-16/12 (43.75). Similarly, the accessions AC-16/18, AC-16/1, AC-16/21, and W 154 scored maximum for texture, color, odor and aftertaste, respectively. A cumulative score was also calculated by adding the scores obtained for all eight parameters. The overall acceptability was high for the cultivated types like Priyanka (52.05) and Preethi (47.10) followed by the wild accession AC-16/1(39.25) with a cumulative score of 288.60. The cumulative organoleptic score (COS) was the lowest in W 173 (130.25). Therefore, when the accessions were ranked based on organoleptic evaluation, first rank was recorded for Priyanka, followed by Preethi and AC-16/1 and last rank was recorded for W 173.

Identification of Elite Wild/Semi-domesticated Bitter Gourd Genotypes

All the 50 wild genotypes were ranked based on the selection index (Table 3) and better performing wild/semi-domesticated genotypes were identified with respect to higher yield, fruit weight, acceptability, nutritive value and resistance to biotic stresses. When the wild/semi-domesticated accessions were ranked based on yield, fruit weight, organoleptic score, nutritive value and resistance,

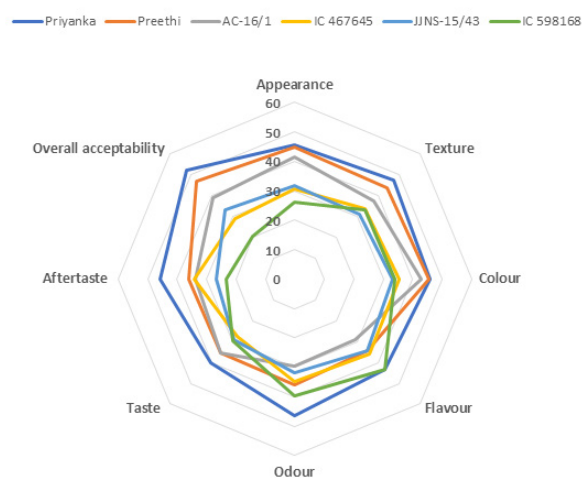


Figure 4: Organoleptic evaluation of most preferred bitter gourd collections

the best genotypes were AC-16/1, followed by AC-16/16, IC 467681 and JJNS-15/65. So, these accessions can be further tested in large-scale yield trials and recommended for commercial cultivation, especially for homestead farming.

Discussion

Bitter gourd is the highly nutritious and most popular vegetable throughout the tropics and subtropics of Asia (Reshmika *et al.*, 2019). The economic and breeding gains from germplasm collections can be easily derived by morphological characterization (Bekele *et al.*, 2006). Dey *et al.* (2006) and Paul *et al.* (2010) have also studied the genetic diversity of bitter gourd based on morphological characters. Chakravarty (1990) reported that plants belonging to different species of *Momordica* showed differences in morphological characters such as flower color, fruit shape, fruit color, fruit size and leaf shape. The simplified phenotypic approach has been found useful for preliminary characterization and discrimination of accessions to understand the level of genetic diversity (Szilagyi *et al.*, 2011).

Table 3: Ranking of accessions based on selection index

<i>Accessions</i>	<i>FY</i>	<i>FWt</i>	<i>COS</i>	<i>VIT C</i>	<i>FE</i>	<i>FIBRE</i>	<i>TAC</i>	<i>PM</i>	<i>VI</i>	<i>Rank</i>
AC-16/1	1493.88	14.19	288.6	98.89	2.79	19.5	70.03	0.29	6.95	1
AC-16/16	1058.62	19.11	226.55	83.65	2.19	15.7	48.32	12.17	27.83	2
IC 467681	969.44	50.15	225.4	99.56	2.18	13.6	86.93	38.82	14.34	3
JJNS-15/65	900.38	5.35	195.35	100.51	2.04	15.71	81.33	16.24	6.67	4
AC-16/9	642.33	9.38	205.4	86.21	2.73	19.52	41.88	0.46	5.84	5
IC 213312	570.27	6.94	178.75	85.11	3	17.39	67.47	0.365	7.34	6
JJNS-15/12	561.91	5.42	187.75	94.25	2.18	14.36	86.45	7.44	18.84	7
W 84	504.69	11.89	233.15	94.37	2.54	13.17	92.01	11.14	32.34	8
AC-16/3	485.33	5.87	236.85	95.58	2.9	13.11	78.83	6.57	13.84	9
AC-16/12	472.72	14.99	237.75	120.63	2.16	14.65	86.43	5.71	39	10
AC-16/5	508.05	8.18	214.65	92.44	2.67	20.15	83.72	1.89	50.84	11
AC-16/2	496.94	7.09	218.85	101.23	2.16	14.3	69.73	28.37	37.17	12
AC-16/6	454.88	6.91	233.15	96.37	3.31	15.03	54.83	4.46	10.17	13
JJNS-15/39	477.15	6.83	195.85	86.75	2.19	15.06	70.13	11.28	16.67	14
IC 598168	441.48	22.82	250.4	95.3	3.05	14.35	83.22	10.52	44.17	15
W 154	437.27	6.21	234.45	125.67	2.94	21.5	64.39	16.48	36.5	16
AC-16/25	455.42	7.36	189.35	76.53	2.27	17.39	78.21	7.02	30.17	17
JJNS-15/62	421.94	6.92	218.45	88.5	2.94	16.21	84.52	12.54	33	18
JJNS-15/43	401.79	6.24	251.25	84.43	2.05	17.83	87.33	21.95	27.67	19
AC-16/10	391.21	10.46	206.8	90.57	2	21.04	84.04	16.98	12.5	20
AC-16/17	399.85	10.57	198.6	100.54	2.74	21.58	73.9	13.34	35.17	21
AC-16/22	420.03	7.29	188.15	93.38	2.18	19.88	49.33	13.38	36.83	22
AC-16/19	393.84	6.09	194.3	97.12	2	19.46	90.36	7.32	44.17	23
IC 598172	359.43	7.09	230.15	80.47	2.58	15.64	63.37	3.41	29.67	24
AC-16/26	367.92	13.27	233.7	80.51	2.16	16.3	64.1	4.13	50.84	25
IC 582471	331	6.62	245.4	104.52	2.57	20.92	65.19	5.11	40.67	26
W 173	374.06	8.19	130.25	95.5	2.51	14.39	75.13	19.82	14.84	27
IC 598171	354.51	6.56	165.5	82.94	3.15	18.69	60.91	8.26	25.67	28
W 172	300.69	7.29	211.75	106.71	1.48	24.83	84.74	8.29	28.34	29
IC 598170	310.36	5.97	238.15	112.43	2.99	12.17	64.9	13.98	37.67	30
AC-16/4	283.26	5	212.5	100.06	2.55	19.25	71.6	0.36	3.51	31
AC-16/11	317.96	6.05	203.45	98.79	2.53	12.94	75.11	4.52	39.34	32
AC-16/13	315.42	6.44	194.15	110.47	2.02	19.62	64.29	3.11	36	33
IC 582439	303.03	4.77	236.6	78.93	2.95	19.33	49.62	4.04	28.17	34
AC-16/20	288.61	4.77	221.1	99.7	3.07	15.43	68.37	5.31	24.67	35
IC 541377	289.11	13.04	178.3	91.64	2.14	17.61	80	6.89	15.5	36
AC-16/24	268.7	9.08	240.05	92.51	2.85	15.83	70.49	1.45	41.5	37
AC-16/21	220.31	3.59	245.95	100.1	2.17	14.58	82.7	0.85	10	38
AC-16/8	254.06	4.97	195.3	85.49	3.17	20.33	87.38	14.09	24.33	39
IC 467645	220.14	8.19	261.05	89.88	1.94	19.82	64.92	3.81	73.84	40
AC-16/7	246.75	4.1	193.65	83.82	3.07	16.47	59.41	23.67	32.67	41
IC 582403	203.46	3.53	159.65	91.45	2.11	30.44	68.45	2.69	24.17	42
AC-16/18	192.79	9.29	225.15	97.94	2.4	15.1	49.63	33.78	42.67	43
AC-16/14	193.03	4.01	148.05	102.48	2.89	15.6	83.18	11.57	34	44

AC-16/23	159.87	4.17	171.6	95.14	1.94	17.46	88.51	3.76	18.83	45
AC-16/15	182.53	3.17	152.35	99.57	2.05	15.68	58.01	9.67	23.34	46
IC 541235	124.27	4.06	212.8	83.32	1.94	22.21	73.8	7.87	33.84	47
IC 541231	140.06	3.73	182.25	106.73	2.63	15.67	83.84	24.87	40.84	48
IC 467673	124.05	7.23	233.75	86.59	2.04	20.13	71.11	3.75	76.33	49
IC 541248	127.67	3.97	221.35	80.46	1.99	14.22	70.61	19.72	45	50

*FY- Fruit yield, FWt- Fruit weight, COS- Cumulative organoleptic score, VitC- Vitamin C content, Fe- Iron content, Fibre- Fibre content, TAC- Total antioxidant capacity, PM- PDS of Powdery mildew, M- PDS of viral infection

This study describes one of the large-scale phenotypic characterization of wild/semi-domesticated bitter gourd landraces of India. The germplasm collected in this study presented wide range of genetic variability for 30 traits among 53 accessions. The frequency distribution obtained for these characters showed the presence of maximum possible range of variability expected in the Western Ghats of Kerala. This survey showed that wild/semi-domesticated bitter gourd co-exists with cultivated varieties in adjacent habitats or under wild conditions in disturbed open forests. Specific cases of home garden cultivation of small-fruited wild genotypes were also noticed. In West Bengal, Andaman Island and Tamil Nadu, the small-fruited *muricata* types were even cultivated commercially for market supply (John and Antony, 2009).

Plant growth habits were found to vary from medium viny nature in cultivated varieties to long viny in wild cultivars. The short internodal length and a greater number of nodes per plant in the wild/semi-domesticated genotypes have given a more compact mat-like growth habit in which the vines spread like a carpet and easily cover the support (Asna, 2018). Even though the plants grow as an annual crop, the long viny wild *muricata* types have longer lifecycle and can extend beyond one season. The robustness and size of leaves and stem were greater in *M. charantia* var. *charantia* and progressively reduced to *M. charantia* var. *muricata*. These observations are in agreement with studies conducted by Bharathi and John (2013).

Among different traits, fruit characteristics are the major determinant of consumer's preference. In this study, marked variation was observed in fruit size ranging from very small to large with green color in varying tonalities. The preference for fruit size and color was found to be region-specific. The north Indians prefer long or medium long spindle-shaped glossy green fruits, whereas south Indians require long but white fruits. In eastern parts of the country, small and dark green-colored wild *muricata* types are preferred (Dey *et al.*, 2010). Similar observations on fruit bitterness, color, shape and size preference have been recorded worldwide (Dhillon *et al.*, 2014; Rao *et al.*, 2021). This suggests that differences exist between different regional cultivar groups in bitter gourd, reflecting the distinct consumer preferences in different countries and introgression from cultivars back to

wild accessions and vice-versa. Population resequencing revealed the divergence between wild and South Asian cultivars about 6,000 years ago, followed by the separation of the Southeast Asian cultivars about 800 years ago, with the latter exhibiting more extreme trait divergence from wild progenitors and stronger signs of selection on fruit traits (Matsumura *et al.*, 2020).

Rajput *et al.* (1996) and Rasul *et al.* (2004) found a wide range of variation among the genotypes of bitter gourd in respect of flowering habits. Bitter gourd is a monoecious plant, naturally inducing a greater number of staminate flowers than the pistillate flowers. This is a common problem in bitter gourd cultivation, since this flowering behavior results in lower fruit set and yield. In order to have higher yield, the staminate and pistillate flower ratio needed to be synchronized (Ram *et al.*, 2000). So, the germplasm lines viz., JJNS-16/65 having higher sex ratio than cultivated varieties have an important role in breeding programs for developing high-yielding crop varieties. The days to first fruit harvest were the least in the accession AC-16/25 (57 days) because of the earlier initiation of the first pistillate flower (40 days).

The wild, semi-domesticated and cultivated types have fallen in different classes of performance for yield per plant. Yield per plant itself is not a trait but a product of complex interaction of fruit traits such as fruit length, diameter, weight, number, and flesh thickness (Dey *et al.*, 2005; Rani *et al.*, 2015). In this study, the yield components like, fruit length ranged from 2-16 cm, fruit width from 1 to 4 cm, fruit weight from 3 to 420 g and the number of fruits per plant from 14 to 168. The flesh thickness of the fruit ranged from 0.15 to 1 cm, reflecting the quality and edible portion of bitter gourd fruit.

Apart from fruit traits, the variation found in number of seeds per fruit was significantly wider in the collected accessions. The seed size can easily identify the wild and cultivated genotypes. Wild bitter gourd produces small seeds resembling cockroach eggs whereas, genotypes belonging to *charantia* develop comparatively large, broadly rectangular, heavily or feebly sculptured seeds with sub-tridentate ends (Bharathi and John, 2013). It was noticed that the wild/semi-domesticated genotypes are more highly seeded than the *charantia* types. Seediness is a wild character that helps in surviving and producing

more offspring. The cultivated check varieties like Preethi and Priyanka, with long fusiform fruits and high fruit weight, produced only 21.58 and 19.81 seeds, respectively. While even the accession with lowest weight *i.e.*, IC 582403 (3.53 g), produced 9.57 seeds per fruit. The smaller size and highly seeded nature of *muricata* types may be the reason for the consumers' low acceptability of this highly medicinal variety of bitter gourd. Reduced seed content of fruits is desirable in bitter gourd (Islam *et al.*, 2009). Even though, the number and size of seeds of the wild/semi-domesticated genotypes was lower than that of the var. *charantia*, the proportion of the seeds to the total fruit biomass was higher. So, when the seeds are removed the consumable portion of the fruit becomes very small in *muricata* types. Hence, these fruits are preferred for cooking during immature stage itself along with the seeds.

Though there is no formal infraspecific system of classification, the extensive work done by Walters and Decker-Walters (1988) and Yang and Walters (1992) have given an insight into the difference between wild and domesticate types of bitter gourd as fruits of wild plants are 2 to 7 cm long, pointed at both ends and have small grey to nearly black seeds that often have scattered darker black patches whereas the fruits of domesticate are upto 60 cm long, are sometimes flattened at the proximal end, and have larger brown seeds. In the present study, 42 collections had fruit lengths of 2 to 7 cm and can be considered wild types. Eight accessions with a fruit length above 7 cm and seed characters similar to cultivated types represent the degree of domestication in bitter gourd genotypes.

Although beneficial to health, dietary phytonutrients in bitter gourd are bitter, acidic and/or astringent in taste, reducing consumer choice and acceptance of bitter gourd during food selection (Snee *et al.*, 2011). But the role of this bitter melon in treating diabetes increases its acceptability. Since higher fruit yield leads to decrease in ascorbic acid, iron and calcium content (Tendulkar, 1997; Dey *et al.*, 2005), small fruited accessions (*M. charantia* var. *muricata*) should be preferred over large fruited ones (*M. charantia* var. *charantia*) for better availability of ascorbic acid, iron and calcium content with increased fruit number. The small size of fruits and the belief that the bitterness increases with the intensity of green color can be a reason for low acceptability of *muricata* types, even though it is endowed with high nutritional values. Organoleptic scoring aided in selecting the most superior genotypes with better appearance, texture, color, flavor, odor, taste and aftertaste. Even though, the cultivated types surpassed wild genotypes in organoleptic evaluation, AC-16/1 with good COS and better organoleptic qualities can be selected as the best wild/semi-domesticated bitter gourd genotype which can be commercialized in future.

Grouping large number of germplasm accessions into few numbers of homogenous clusters facilitates the

selection of diverse parents. Similarity indices and pattern of relationships obtained through genetic diversity and PCA are useful to evaluate potential breeding value of germplasm through traits loaded on various components (Keneni *et al.*, 2005). Principal component analysis grouped the cultivated types separately from wild/semi-domesticated types. The wild/semi-domesticated accessions *viz.*, AC-16/1, AC-16/16 and IC 467681, having preferred attributes as that of cultivated stypes stand as elite collections for utilization and conservation.

Besides, understanding the nature and magnitude of genetic diversity obtained through different traits, it is desirable to identify the accessions having resistance against most prevalent pests and diseases. The bitter gourd has been reported to be the natural host of many viruses (Tiawari *et al.*, 2010) like cucumber mosaic virus (CMV), potyvirus and bitter gourd distortion mosaic virus (BDMV) (Ashwini *et al.*, 2016). The simultaneous occurrence of different viruses in bitter gourd plants resulted in the development of a mosaic complex. Here we simultaneously screened the accessions for powdery mildew disease, which cause yield loss up to 80% during December – January (AICRP on vegetable crops, 2014) and viral infection. Although bitter gourd is vulnerable to many pest and disease problems demanding high chemical control and consequent pesticide residues, wild genotypes of this crop is endowed with resistance/tolerance to some of the common diseases and pests of bitter gourd (Bharathi and John, 2013). PDS at peak disease level distinguished the resistant from the susceptible ones well. Duration of the crop is yet another factor that influences the susceptibility/tolerance reaction level. It was observed in the present study that early-maturing genotypes were relatively more susceptible to the disease than late-maturing genotypes, in conformity with the earlier reports by Kolte (1985) and Hiremath (1976). The five wild/semi-domesticated bitter gourd accessions, namely, IC 213312, AC-16/1, AC-16/4, AC-16/9 and AC-16/21, showed tolerance/resistance response to both powdery mildew and viral infection during two consecutive crop seasons were identified as good resistant sources for future breeding programs.

Wild/semi-domesticated materials were found to be at the verge of extinction due to competition from large fruited bitter gourds, destruction of homestead ecosystem, changed consumer culture, and reduction in a number of traditional farmers and farm holdings. The bird-mediated dispersal of seed is also much reduced as they are harvested at the immature stage. Thus, the identification of lines suitable for the eco-friendly production of this valuable vegetable is necessary. Four accessions (AC-16/1, AC-16/16, IC 467681 and JJNS-15/65) with superior yield, nutritional value and resistance can be profitably grown in organic way as an ideal homestead vegetable in every homestead across extreme environments and diverse ecosystems.

Conclusion

Wild/semi-domesticated bitter gourd is a relict vegetable of southern Peninsular India with tremendous potential for commercial cultivation in India. Great variability exists in both morphological and biochemical attributes with excellent culinary traits and perceived tolerance to abiotic and biotic stresses. The superior types satisfying consumer quality filtered out through cluster analysis and selection index need to be conserved for further confirmation studies and location trials. Thus, the study revealed that the wild landraces are comparable with the best-known varieties and even excel in nutritive values and resistance. This heritage crop needs to be popularized to diversify the diet and conserve biodiversity and nutritional security.

Acknowledgment

Kerala Agricultural University, Thrissur, Kerala fully funded this research. The facilities, help and advice of KAU faculty are sincerely acknowledged.

References

- All India Coordinated Research Project Vegetable Crops (2014) Annual Report. Indian Institute of Vegetable Research (ICAR-IIVR), Varanasi, India, 376p.
- Arunachalam P, VV Radhakrishnan, SK Mathew and SPG Kumar (2002) Reaction of bitter gourd genotypes against distortion mosaic virus. *Veg. Sci.* 29(1): 55-57.
- Arunachalam V and A Bandyopadhyay (1984) A method to make decisions jointly on a number of dependent characters. *Indian J. Genet. Plant Breed.* 44(3): 419-424.
- Ashwini KN, V Louis, AK Cherian and N Devi (2016) Bitter gourd mosaic: a complex virus disease in Kerala. *Int. J. Agric. Innov. Res.* 4(4): 737-739.
- Asna AC (2018) Characterization and distant hybridization for biotic stress tolerance in bitter gourd (*Momordica charantia* L.). PhD Thesis, Kerala Agricultural University, Thrissur, Kerala, 243p.
- Bekele FL, I Bekele, DR Butler and GG Bidaisee (2006) Patterns of morphological variation in a sample of cacao (*Theobroma cacao* L.) germplasm from the International Cocoa Gene Bank, Trinidad. *Genet. Resour. Crop Evol.* 53(5): 933-948.
- Bharathi LK and KJ John (2013) *Momordica Genus in Asia: An Overview*. Springer, New York, 147p.
- Chakravarty HL (1990) Cucurbits of India and their role in the development of vegetable crops. In: Bates DM, Robinson RW, Jeffrey C (Eds.) *Biology and Utilization of Cucurbitaceae*. Cornell University Press, Ithaca, New York, pp. 325-334.
- Degner O (1947) *Flora Hawaiiensis*. Book 5, Privately published, Honolulu, 185 p.
- Dey SS, TK Behera and C Kaur (2006) Genetic variability in ascorbic acid and carotenoids content in Indian bitter gourd (*Momordica charantia* L.) germplasm. *Cucurbit. Genet. Coop. Rep.* 28: 91-93.
- Dey SS, TK Behera and AD Munshi (2010) Gynoecious inbred with better combining ability improves yield and earliness in bitter gourd (*Momordica charantia* L.). *Euphytica* 173: 37-47.
- Dey SS, TK Behera, A Pal and AD Munshi (2005) Correlation and path coefficient analysis in bitter gourd (*Momordica charantia* L.). *Veg. Sci.* 32: 173-176.
- Dhillon NP, S Phethin, CC Lin, W Chen, JF Wang, CS Kousik and JD McCreight (2016) Preliminary evaluation of resistance to powdery mildew (*Podosphaera xanthii*) in AVRDC collections of bitter gourds (*Momordica charantia* L.). Proceedings of the Regional Symposium on Sustaining Small-Scale Vegetable Production and Marketing Systems for Food and Nutrition Security (SEAVEG2014), 25-27 February 2014, Bangkok, Thailand, 11: 137-140.
- Eriksson L, E Johansson, N Kettaneh-Wold and S Wold (1999) Introduction to multi- and megavariable data analysis using projection methods (PCA & PLS). Umetrics AB, Umea.
- Federer WT (1956) Augmented designs. *Hawaiian Planters' Record* LV (2): 191-208.
- Gopinath PP, R Parsad and B Joseph (2020). GRAPES: General Rshiny Based Analysis Platform Empowered by Statistics. <https://www.coagrapes.com/home>. version 0.1.0
- Hiremath RV (1976) Studies on disease of *Sesamum* 1. Incidence of powdery mildew on some varieties. *Oilseeds J.* 6(3): 18-25.
- Islam MR, MS Hossain, MSR Buhiyan, A Husna and MA Syed (2009) Genetic variability and path coefficient analysis of bitter gourd (*Momordica charantia* L.). *Int. J. Sustain. Agric.* 1: 53-57.
- Jackson ML (1973) *Soil Chemical Analysis*. Prentice Hall of India Private Limited, New Delhi, 171p.
- Jellinek G (1985) *Sensory evaluation of food: theory and practice*. Ellis Horwood Ltd., Chichester, UK, 429p.
- John JK and VT Antony (2009) Collection and preliminary evaluation of small bitter gourds (*Momordica charantia* L.) a relict vegetable of southern Peninsular India. *Genet. Resour. Crop Evol.* 56: 99-104.
- KAU (2011) *Package of Practices Recommendations: Crops*. Kerala Agricultural University, Directorate of Extension, Thrissur, India, 169p.
- Keneni G, M Jarso, T Wolabu and G Dino (2005) Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces: 1. Field pea (*Pisum sativum* L.). *Genet. Resour. Crop Evol.* 52: 539-549.
- Kolte SJ (1985) Disease of annual edible oilseed crops. In: *Rapeseed, mustard and sesame diseases*, CRS press, Florida, pp 83-127.
- Linnaeus C (1753) *Species Plantarum* Vol. 1 London, p392.
- McKinney HH (1923) Influence of soil, temperature and moisture on infection of wheat seedlings by *Helminthosporium sativum*. *J. Agric. Res.* 26: 195-217.
- Matsumura H, H Min-Chien, A Toyodac, N Taniaid, K Tarorad, N Urasakid, SS Anand, NPS Dhillon, R Schafleitnerf and L Cheng-Ruei (2020) Long-read bitter gourd (*Momordica charantia*) genome and the genomic architecture of nonclassic domestication. Proceedings of the National Academy of Sciences, 23 June 2020, PNAS 117(25): 14543-14551.
- Naik HP and S Kulkarni (2018) Screening of cucumber genotypes against powdery mildew. *Int. J. Curr. Microbiol. Appl. Sci.* 7(4): 414-418.
- NBPGR (2001) *Minimal Descriptors of Agri-Horticultural Crops. Part-II. Vegetable Crops*. National Bureau of Plant Genetic Resources (NBPGR), Pusa, New Delhi, 262p.
- Paul A, S Bandyopadhyay, P Acharyya and SS Raychaudhuri (2010) Studies on genetic diversity of twelve accessions of *Momordica charantia* L. using morphological, RAPD and SCAR markers. *Asian J. Plant Sci.* 9: 471-478.
- Prieto P, M Pineda and M Aguilar (1999) Spectrophotometric quantitation of antioxidant capacity through the formation of a phosphomolybdenum complex: specific application to

- the determination of vitamin E1. *Anal. Biochem.* 269: 337-341.
- Rajput JC, SP Paranjape and BM Jamadagni (1996) Variability, heritability and scope of improvement for yield components in bitter gourd (*Momordica charantia* L.). *Ann. Agric. Res.* 17: 90-93.
- Raman A and C Lau (1996) Anti-diabetic properties and phytochemistry of *Momordica charantia* L. (Cucurbitaceae). *Phytomedicine* 2: 329-362.
- Ram D, S Kumar, MK Banerjee and G Kalloo (2000) Occurrence, identification and preliminary characterization of gynoeceum in bitter gourd (*Momordica charantia* L.). *Int. J. Agric. Sci.* 72: 348-249.
- Rani RK, S Raju and KR Reddy (2015) Variability, correlation and path analysis studies in bitter gourd (*Momordica charantia* L.). *Agric. Sci. Digest* 35(2): 106-110.
- Rao GP, TK Behera, AB Gaikwad, AD Munshi, A Srivastva, G Boopalakrishnan and Vinod (2021) Genetic analysis and QTL mapping of yield and fruit traits in bitter gourd (*Momordica charantia* L.). *Sci. Rep.* 11: 4109.
- Rasul MG, M Hiramatsu and H Okubo (2004) Morphological and physiological variation in Kakrol (*Momordica dioica* Roxb.). *J. Faculty Agric.* 49: 1-11.
- Reshmika PK, T Pradeepkumar, S Krishnan and P Sureshkumar (2019) Evaluation of bitter gourd hybrids. *Electron. J. Plant Breed.* 10(4): 1617-1623.
- Robinson RW and DS Decker-Walters (1999) *Cucurbits*. CABI Publishing, Wallingford, UK, 101p.
- Roxburgh W (1832) *Flora Indica*. Today and Tomorrow's Publishers, New Delhi.
- Sadasivam S and A Manickam (1996) *Biochemical Methods*. New Age International Publications, New Delhi, India, 169p.
- Sidhu GK and M Pathak (2016) Genetic diversity analysis in bitter gourd (*Momordica charantia* L.) using morphological traits. *Int. J. Agric. Innov. Res.* 41: 59-63.
- Snee LS, VK Nerurkar, DA Dooley, JT Eford, AC Shovic and PV Nerurkar (2011) Strategies to improve palatability and increase consumption intentions for *Momordica charantia* (bitter melon): a vegetable commonly used for diabetes management. *Nutr. J.* 10: 78-88.
- Szilagyi L, S Taygar and M Ciuca (2011) Evaluation of genetic diversity in common bean (*P. vulgaris* L) using RAPD markers and morpho-agronomic traits. *Rom. Biotechnol. Lett.* 16(1): 98-10.
- Tendulkar S (1997) Heterosis, combining ability and gene action in bitter gourd (*Momordica charantia* L.). Ph.D. Thesis. IARI, New Delhi, 219p.
- Tiwari AK, PK Sharma, MS Khan, SK Snehi, SK Raj and GP Rao (2010) Molecular detection and identification of Tomato leaf curl New Delhi virus isolate causing yellow mosaic disease in Bitter gourd (*Momordica charantia*), a medicinally important plant in India. *Med. Plants* 2(2): 121-138.
- TNAU (1980) *Score Chart for Crop Diseases*. Tamil Nadu Agricultural University (TNAU), Coimbatore, India, 129p.
- Walters TW and DS Decker-Walters (1988) Balsam pear (*Momordica charantia*, Cucurbitaceae). *Econ. Bot.* 42: 286-288.
- Wu AJ and LT Ng (2008) Antioxidant and free radical scavenging activities of wild bitter gourd (*Momordica charantia* var. abbreviate Ser.) in Taiwan. *LWT.* 41: 323-330.
- Yang SL and TW Walters (1992) Ethnobotany and the economic role of the Cucurbitaceae in China. *Econ. Bot.* 46: 349-367.

RESEARCH ARTICLE

Evaluation of *Saccharum spontaneum* Clones for Water Deficit Stress Tolerance

Vinu V.^{1*}, T. L. Pathy¹, Mahadevaswamy H. K.¹, R. Valarmathi¹, Manju M. Paul² and R. A. Kumar¹

Abstract

About 4 *Saccharum spontaneum* accessions were evaluated for water deficit stress tolerance in augmented design along with three standards. After 90 days of the planting water stress was imposed by withholding the irrigation for a period of eight weeks. Morphological traits viz., plant height and number of tillers per clump and physiological traits viz., relative water content, membrane injury index and chlorophyll and carotenoid contents were recorded periodically. Total fresh biomass and dry biomass were recorded after harvesting the crop at the 11th month of the crop growth. Nine genotypes viz., IND 08 – 1491, IND 99 – 848, IND 99 – 847, IND 99 – 863, IND 99 – 849, IND 99 – 882, IND 02 – 1186, SES 121A and IND 99- 850 were found to be superior for maximum no. of drought tolerance related traits. From the correlation analysis among the traits recorded during stress it is found that apart from the plant height and number of tillers per clump, chlorophyll 'a' (0.343^{*}), total chlorophyll (0.326^{*}) and carotenoid (0.320^{*}) contents during stress had a significant positive correlation with total dry biomass. Relative water content had significant positive correlation (0.320^{*}) with the plant height during stress. The correlated traits can be used to identify the drought tolerant genotypes. The identified tolerant genotypes can be evaluated further in replicated trial and can be utilized in sugarcane improvement programmes.

Key words: *Saccharum spontaneum*, Water deficit stress, Morphological traits, Physiological traits, Correlation.

¹ICAR-Sugarcane Breeding Institute, Coimbatore, Tamil Nadu, India.

²College of Agriculture, Padannakkad, Kerala, India.

***Author for correspondence:**

vinu.v@icar.gov.in

Received: 07/08/2023 **Revised:** 15/01/2024

Accepted: 17/01/2024

How to cite this article: Vinu V, TL Pathy, HK Mahadevaswamy, R Valarmathi, MM Paul and RA Kumar. (2024) Evaluation of *Saccharum spontaneum* Clones for Water Deficit Stress Tolerance. *Indian J. Plant Genetic Resources*. 37(1): 73-79. DOI: 10.61949/0976-1926.2024.v37i01.09

Introduction

Sugarcane is an important source of sugar and bio energy in the world. Drought stress is becoming a major threat to sugarcane production worldwide in view of climate change. Water deficit stress affects the growth and development of the plant by altering different physiological, biochemical and molecular processes. The dry matter production in plants is directly associated with the water used by them (Tollenaar and Aguilera, 1992; Qing *et al.* 2001). The formative phase (tillering and grand growth stage) of sugarcane is the critical period for water use and water deficit stress during this stage can lead to severe yield loss. Breeding of crop varieties with high yield under unfavorable environmental conditions is a major challenge in view of growing population and changing climate scenario. Among the wild species of sugarcane, *Saccharum spontaneum* is well adapted to unfavourable natural environments and constitutes the primary source of genes for tolerance to biotic and abiotic stresses. However, the utilization of this genetic resources in developing commercial varieties with stress tolerance is hindered by the lack of knowledge about their genetic and phenotypic properties.

S. spontaneum is a perennial grass that can grow well in marginal soils and highly adaptable to various stress conditions. It is also characterised by its high vigor, ratooning ability, high biomass producing ability, resistance to pests and diseases. It is a

highly diverse species with a reported 30 cytotypes from Indian subcontinent with a varying chromosome number from $2n = 40$ to 128 (Sreenivasan *et al.* 1987) and has wide distribution in India from the sub-Himalayan regions to the peninsular region. Co 205, the first interspecific hybrid variety of sugarcane which leads to a revolution in sugarcane agriculture worldwide was derived from the cross between *S. officinarum* clone Vellai and *S. spontaneum* clone Coimbatore local. Modern sugarcane cultivars are complex aneuployploids derived from the interspecific crosses involving *S. officinarum* and *S. spontaneum*. By understanding the importance of *S. spontaneum* in sugarcane improvement programs, explorations for *S. spontaneum* in India was started in the year 1933 (Amalraj and Balasundaram, 2006) and still it is continuing. Presently ICAR- Sugarcane Breeding Institute, Coimbatore is the custodian of world's largest field gene bank of *S. spontaneum* with 1963 accessions. This *S. spontaneum* collection is attributed with wide range of phenotypic variations (Kandasami *et al.* 1983; Rao and Vijayalakshmi 1963; Sreenivasan *et al.* 2001; Govindaraj *et al.* 2014).

At present, a very few *S. spontaneum* genotypes have been utilized in commercial sugarcane breeding programmes. The trait specific characterization and extensive utilization of germplasm collections are lacking behind, albeit the availability of a large germplasm collection. Incorporating new germplasm lines in the breeding programme not only release huge genetic variation but also lead to broadening of the genetic base. Hence this study was aimed to identify drought tolerant *S. spontaneum* accessions for further exploitation to combat with climate change challenges.

Materials and Methods

A set of 40 *S. spontaneum* accessions were planted in augmented design along with three standards viz., Ponape 1, Pampa and Taiwan 96 during 2017-18 crop season at ICAR-Sugarcane Breeding Institute, Coimbatore. The plant material consisted of genotypes collected from different states of India viz., Kerala, Tamil Nadu, Andhra Pradesh, Telangana, Rajasthan and Karnataka as a part of germplasm exploration and collection. Each genotype was planted in a 3 m row with spacing of 2.4 m in between the rows. Standard package of practices was followed to raise a good and healthy crop. At 90 days of crop growth plant height (cm), no. of tillers per clump, leaf midrib thickness (mm) and leaf lamina width (cm) were recorded. Plant height was measured from the soil surface to the first fully expanded leaf. After 90 days of the crop growth, during the tillering stage, drought was imposed by withholding the irrigation for eight weeks.

Plant height and number of tillers per clump were recorded just before the imposition of drought (at 90 days of crop growth) and four and eight weeks after commencement of the drought. The same observations

were recorded after the crop revived from the stress at 210th days of the plant growth. The growth rates for plant height and no. of tillers per clump during the stress period were calculated as follows,

(The observed value at the end of the drought period – The observed value at the start of the drought period) / total number of days in the drought stress period.

Since the measurements had been recorded on the same experimental units repeatedly over time, data recorded at different time intervals tend to be highly correlated. The analysis of variance for these two traits was done using repeated measures analysis in R software. Different variance-covariance structures such as compound symmetry (CS), autoregressive 1 (AR 1) and the unstructured (UN) were employed for obtaining the best fit. To identify the best model information criteria viz., the Akaike (AIC) and Bayesian (BIC) were used. Parameters were estimated by the method of restricted maximum likelihood (REML). Random coefficient models were constructed for both these traits, where measurements were recorded over time periods. In these models, time was considered as fixed effect and genotypes were taken as random. This mixed model equations were analysed in lme4 package (Bates *et al.* 2015) in R. The random slope effects were then used for constructing the biplot, by considering slope effects for plant height and tiller number on X and Y axis, respectively.

Relative water content (RWC) of the excised fresh leaves were estimated during the stress period according to the method of Barrs and Weatherley (1962) based on the following formula:

$$\text{RWC (\%)} = \frac{[(\text{Fresh weight} - \text{Dry weight}) / (\text{Turgid Weight} - \text{Dry Weight})] \times 100.}$$

After taking the fresh weight, the leaves were soaked in water for four hours at room temperature for recording the turgid weight. Dry weight was recorded after drying the leaves at 80°C for 48 hours.

The chlorophyll and carotenoid content in the leaves were estimated using dimethyl sulphoxide (DMSO) method (Hiscox and Israelstam, 1979) during the drought stress and the revival period. The absorbance of the aliquot obtained after DMSO extraction, was measured at 663, 645 and 470 nm using UV visible spectrophotometer. Chlorophyll 'a' and 'b', and total chlorophyll content were calculated according to Arnon's (1949) and carotenoid content was calculated according to Lichtenthaler and Wellburn (1983) and expressed as mg g⁻¹ fresh weight.

Membrane injury index was estimated as per Deshmukh *et al.* (1991); wherein 100 mg fresh leaf samples were collected from the 3rd leaf of the drought induced plants and placed in a test tube containing 10 mL of double distilled deionized water. Tubes were incubated at 45°C in water bath for 30 minutes and electrical conductivity (C1)

of the solution was measured with EC meter. The test tubes were subsequently shifted to boiling water bath (100°C) for 10 minutes and cooled at room temperature and conductivity (C2) was measured again. The membrane injury index was calculated as given below:

$$\text{Membrane injury index} = \frac{C1}{C2} \times 100$$

Where,

C = conductivity in millisiemens

Drought scoring of each genotype was done during stress period using a 0 to 9 scale (Table 1) according to Ishaq *et al.* (2008). Besides this, the proportion of dryness was calculated by counting the dried and green leaves in each genotype. The percent dryness was calculated as follows:

$$\text{Proportion of dryness (\%)} = \frac{\text{Number of dried leaves in the plant}}{\text{Total no. of leaves in the plant}}$$

The total fresh and dry biomasses were recorded after harvesting the crop at the 11th month. Pearson's correlation coefficients between the traits recorded during drought stress were calculated. Analyses of variance for all the observations except plant height and no. of tillers per clump were done by using the SPAD software package for the augmented design. Rest of the analyses were performed in Microsoft excel, unless specified.

Results and Discussion

The analysis of variance for all the observed traits during the stress and revival period showed that the genotypes taken for this study had significant genetic variation. The growth rate during the stress period (8 weeks) was calculated for the plant height and number of tillers per clump. As compared to the plant height growth rate for the tiller count was less and it ranged from -0.19 to 0.16. This can be attributed to tiller mortality during this phase, wherein only certain tillers would mature to form shoots. This tiller mortality is more

Table 1: Scale used for drought scoring in sugarcane according to Ishaq *et al.* 2008

Scale	Description	Rate
0	No symptoms	Highly tolerant
1	Slight tip drying	Tolerant
3	Tip drying extended to 25% length in most leaves	Moderately tolerant
5	25% to 50% of all leaves fully dried	Moderately susceptible
7	More than 66% of all leaves fully dried	Susceptible
9	All plants apparently dead	Highly susceptible

Table 2: Covariance structures and information criteria for no. of tillers per clump and plant height

Information criteria	Variance- covariance structures		
	CS	AR1	UN
No.of tillers per clump			
AIC	1239.67	1245.22	1238.41
BIC	1616.37	1621.69	1626.28
Plant Height			
AIC	1262.78	1249.26	1231.62
BIC	1639.25	1625.73	1619.49

pronounced in the case of drought. The lowest growth rate for the no. of tillers per clump was recorded in the genotype IND 02-1194 and the highest was in IND 08- 1491. The growth rate for plant height ranged from 0.01 (IND 03-1224) to 1.32 (SES 121A). During the stress period, the plant height and no. of tillers per clump were measured in monthly intervals. Since the measurements had been recorded on the same experimental units repeatedly, the data recorded at different time intervals were highly correlated and the data were subjected to repeated measures analysis. Among the analysed variance – covariance structures, compound symmetry was the ideal one to get best fit for no. of tillers per clump and in case of plant height it was unstructured, as they had corresponding lower AIC and BIC values. The covariance structures and information criteria were presented in Table 2.

The ANOVA (Table 3) showed that the time x treatment interaction was significant for no.of tillers per clump as well as plant height at 1% level of significance. It indicated that there was significant influence of drought on both the traits as the genotypes varied for their height and tiller numbers across the time periods. In case of plant height, there was no or very little improvement in a few genotypes viz., IND 02-1194, IND- 03-1224, IND 03-1226, IND 03-1227, IND 03-1247 and Ponape 1, whereas genotypes like SES 121A, IND 99-847, IND 99-849, IND 99-850, IND 99-863 and IND 02-1166 exhibited a considerable growth in plant height during stress period. There was a general reduction in the number of tillers in all the genotypes during stress period. Severe reduction in the no. of tillers was observed in genotypes like IND 08-1492, IND 99-882, IND 03-1224, IND 02-1214 and IND 02-1186. Genotypes viz., IND 99-863, Taiwan 96, SES 121A, IND 03-1250 and IND 08-1491 reported comparatively less reduction in tiller number during drought stress.

Random coefficient models were constructed by considering time period as fixed effect and genotypes as random, assuming both random intercepts and random slopes for plant height and tiller number. Overall slope of fixed effect was positive for plant height, whereas for tiller number it was negative, indicating gradual decrease in tiller number over time, because of tiller mortality. Large variance of random effects for plant height as compared

Table 3: Analysis of variance for number of tillers per clump and plant height using restricted maximum likelihood (REML) method

	DF		F-value		p-value	
	No. of tillers	Plant height	No. of tillers	Plant height	No. of tillers	Plant height
Replication	1	1	3.81	1.165	0.0530	0.2824
Time	2	2	107.41	148.69	<0.0001	<0.0001
Genotypes	42	42	3.36	8.667	<0.0001	<0.0001
Time x Treatment	84	84	1.60	2.012	0.0081	0.0002

Table 4: Genotypes with higher growth rate for number of tillers per clump than the best standard

Accessions	No. of tillers/plant	Plant height
IND 08-1491	0.16	0.12
SES 121A	0.12	1.32
IND 99-864	0.10	0.30
IND 99-850	0.07	0.55
IND 99-849	0.06	0.57
Taiwan 96	0.05	0.14

to tiller number highlighted that the accessions highly differed for increase in plant height (growth rate) before start of the drought period as compared to tiller number. On similar basis, slope variances were larger for plant height indicating varied differential response of genotypes for the trait in contrast to tiller number. Random slope estimate is the measure that relatively evaluates genotypes for their performance during the time period. In this scenario, positive slope estimates indicated that there has been increase in the trait value over time and vice versa. Hence, the genotypes IND 99 – 848, IND 99 – 849, IND 99 – 850, IND 99 – 851, IND 99 – 881, IND 99 – 882 having positive slope estimates for both the traits can be considered superior, by virtue of their increasing height and tillers during drought period (Figure 1). Although SES 121A had highest slope for plant height, there was a marginal reduction in tillers during this period.

From the above data, it is observed that number of tillers

per clump was more affected by the drought stress than the plant height. High tillering is one of the peculiarities of this wild relative of sugarcane and the effect of water deficit stress on this trait may have a major impact on the total biomass production. The reduction in plant height and no. of tillers per clump may be due to the reduction in the cell enlargement and increased leaf senescence under water stress as reported by Munawarti *et al.* (2014). Reduction in plant height and number of millable canes in sugarcane due to water stress was reported by Hemaprabha *et al.* (2013); Venkataramana *et al.* (1986); Singh and Reddy (1980) etc. The genotypes with superior growth rate for number of tillers per clump than the best standard during the water stress period were given in Table 4 along with the growth rate for the plant height. Similarly, after the revival from the stress, ten genotypes exhibited significantly high plant height than the best standard Taiwan 96 but in case of no. of tillers per clump only two genotypes had a significant growth than the best standard Ponape1.

Relative water content (RWC) is extensively used in drought experiments to determine the internal water status of the plants. Maintenance of leaf water status is essential for continuation of physiological and metabolic activities. RWC of the genotypes was assessed during the 8th week of the water stress at 10.81% soil moisture content and it ranged from 53.57 to 80.46%. The highest RWC was recorded by SES 121A and the lowest by IND 02-1194. Only one genotype SES 121A recorded significantly high RWC than the best standard Taiwan 96 (73.58%). The lowest RWC

Table 5: *S. spontaneum* genotypes superior for maximum number of drought tolerance traits

Accessions	Percent increase during stress in			Mean increment rate during stress for	
	Carotenoid	Chlorophyll A	RWC (%)	Plant height	No. of tillers/ plant
IND 08-1491	72.46	56.72	66.71	0.12	0.16
IND 99-848	60.72	51.83	74.29	0.28	-0.05
IND 99-847	57.23	12.69	74.34	0.60	-0.02
IND 99-863	41.88	31.69	76.43	0.58	0.03
IND 99-849	15.17	2.80	71.68	0.57	0.06
IND 99-882	12.87	18.88	66.69	0.34	-0.15
IND 02-1186	6.07	6.28	66.81	0.26	-0.06
SES 121A	-18.01	-9.01	80.46	1.32	0.12
IND 99-850	-18.98	-23.83	74.09	0.55	0.07

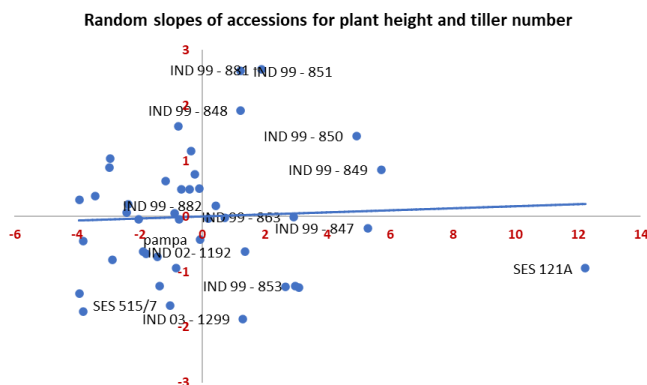


Figure 1: Biplot indicating genotypes with positive slope for both plant height (X axis) and no. of tillers/clump (Y axis)

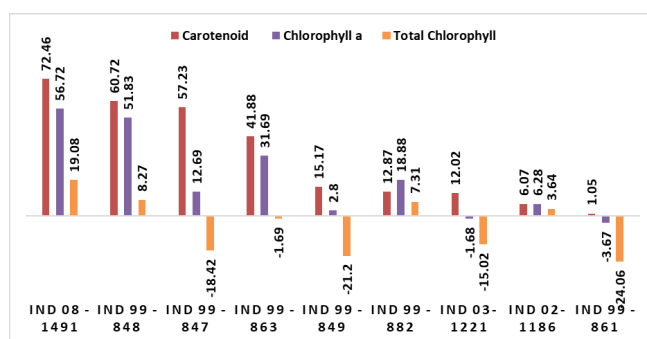


Figure 2: Genotypes with increased carotenoid and chlorophyll content during water deficit stress. Values indicate percent increase in photosynthetic pigments

of IND 02-1194 may have contributed to its lowest growth rate for no. of tillers per clump during stress period. The SES 121A with highest RWC during stress also had highest growth rate for plant height. Augustine *et al.* (2014) reported that the drought tolerant *Erianthus arundinaceus*, wild relative of sugarcane, genotype IK 76-81 recorded high relative water content during drought stress compared to the sugarcane variety Co 86032.

Chlorophyll and carotenoid contents were estimated during the 8th week of the stress (soil moisture content 10.81%) and after the recovery from the stress. The ranges of chlorophyll a, b, total chlorophyll and carotenoid contents during stress were in 0.39 to 1.89 mg/g, 0.22 to 0.62 mg/g, 0.61 to 2.52 mg/g and 0.16 to 0.75 mg/g respectively. A general reduction in chlorophyll and carotenoid contents were observed during stress period as compared to the recovery period from the stress except for few genotypes. The decrease in photosynthetic pigments under drought stress has been considered as an indication of oxidative stress and may be due to pigment photo-oxidation and chlorophyll degradation (Munawarti *et al.* 2014). Few genotypes exhibited an increased chlorophyll a, total chlorophyll and carotenoid contents during the stress period compared to the period after recovery from the

stress (Figure 2). These genotypes also exhibited superiority for early growth traits like plant height, tiller number, stalk diameter, no. of leaves on main stem as reported in the previous study (Pathy *et al.* 2022). An increased chlorophyll a/b ratio was observed during the stress compared to the period after recovery. High photosynthetic pigments during stress are an indicative of water stress tolerance. Higher amounts of chlorophyll-a and chlorophyll-b attribute to the accumulation of solutes in the cell sap through passive accumulation resulting from reduced cell size which significantly contributes to increase in osmotic potential thereby resulting in osmotic adjustment ($\Delta\psi\pi$). Energetic status of the chloroplast increases as a consequence of the drought stress which has a direct relationship to that of increased amount of total chlorophyll, chl a and chl b (Ranjbarfordoei *et al.* 2000).

The cellular membrane thermostability assay indirectly measures integrity of cellular membrane through quantifying electrolyte leakage after heat treatment. The cell membrane injury at 7.87% soil moisture content ranged from 28.24 to 71.16%. The minimum cell membrane injury was recorded in the standard Ponape 1 while the maximum was recorded by the genotype IND 99-882. Nine genotypes recorded lower membrane injury during stress period and they were on par with the best standard Ponape 1. The genotype SES 121A which exhibited higher growth rate and high RWC during stress also had a lower membrane injury (38.29%). Membrane injury was recorded in these genotypes after recovering from the stress and it is found that all the genotypes recorded a lower membrane injury percent compared to the stress period. The range of membrane injury per cent was 26.76 to 60.07% after the recovery from the stress.

Drought scoring was done in a 0 to 9 scale (Table 1) according to Ishaq *et al.* (2008) during the peak drought stress and the proportion of dryness was also calculated. Seven genotypes viz., IND 08-1491, IND 08-1492, IND 99-864, IND 03-1250, IND 03-1301 & SES 121A scored '1' indicating that they were 'tolerant' to drought. All other genotypes were scored as moderately tolerant. Being wild relative of sugarcane, *S. spontaneum* is considered as a hardy crop, which has wider adaptation to different environmental conditions. The proportion of dryness (%) was calculated by counting the number of dried and green leaves in each genotype. The proportion of dryness varied from 14.07-49.08%. The minimum dryness was observed in IND 08-1492 and the maximum was in IND 03-1220. The per cent dryness in the genotype SES 121A was 16.35%.

Total fresh and dry biomasses of the genotypes were recorded after harvesting the crop in the 11th month. The genotypes with highest fresh and dry biomasses were IND 99-850 (11.895 & 6.380 Kg), IND 99-982 (6.480 & 3.360 Kg) and IND 99-851 (6.475 & 3.365 Kg). The best standard

was Taiwan 96 with 2.645 Kg fresh biomass and 1.435 Kg dry biomass. Nine genotypes had significantly high fresh biomass than the best standard Taiwan 96 and four genotypes had significantly high dry biomass than the best standard. Nine *S. spontaneum* genotypes promising under drought condition were identified from this study. These genotypes recorded best values for maximum no. of drought tolerant traits. The details of these genotypes are given in Table 5. This is preliminary evaluation and the genotypes identified need to be evaluated in a replicated trial for multiple years or in different environments.

Pearson's correlation coefficients were worked out between the traits during and after the stress period. Plant height and no. of tillers per clump during the 8th week of the water stress had a significant positive correlation with the total fresh and dry biomass (0.570** & 0.597** and 0.650** & 0.632**, respectively). Chlorophyll 'a' (0.343*), total chlorophyll (0.326*) and carotenoid (0.320*) contents during stress exhibited a low but significant positive correlation with total dry biomass after the harvest. Relative water content had a low significant positive correlation (0.320*) with the plant height during stress. The leaf midrib thickness of the clones showed a positive relationship with plant height during stress (0.432**), fresh biomass (0.417**) and dry biomass (0.418**). The significant positive correlations of morphological traits and photosynthetic pigments with total biomass in this study suggest that these traits can be used to identify the drought tolerant *S. spontaneum* genotypes.

Conclusion

The identified nine drought tolerant genotypes will be evaluated further in replicated trials in multiple seasons/ locations and can be used in the development of drought tolerant sugarcane varieties. In the present scenario of climate change and erratic weather conditions, equipping our breeding programmes with drought/water logging tolerant pre-breeding lines is utmost important in long duration crops like sugarcane. From the correlation analysis it is concluded that photosynthetic pigment contents during drought stress can be used as selection criteria for identifying drought tolerant *S. spontaneum* lines.

Acknowledgement

The authors are grateful to Dr. G. Hemaprabha, Director, ICAR- Sugarcane Breeding Institute, Coimbatore, India and Dr. Bakshi Ram, Former Director, ICAR- Sugarcane Breeding Institute, Coimbatore, India for the support and encouragement and providing facilities to conduct this study.

References

Amalraj VA and N Balasundaram (2006) Status of sugarcane genetic resources in India, *PGR Newsletter*, 148: pp 26-31.

- Arnon DI (1949) Copper enzymes in isolated chloroplasts poly phenol oxidase in *Beta vulgaris*. *Plant Physio.* 24: 1-15.
- Augustine SM, DP Syamaladevi, MN Premachandran, V Ravichandran and N Subramonian (2014) Physiological and Molecular Insights to Drought Responsiveness in *Erianthus* spp. *Sugar Tech.* 17(2): 121-129.
- Barrs HD and PE Weatherley (1962) A re-examination of the relative turgidity technique for estimating water deficits in leaves. *Aust. J. Biol. Sci.* 15: 413-428.
- Bates D, M Mächler, B Bolker and S Walker (2015) Fitting Linear Mixed-Effects Models Using lme4. *J. Stat. Softw.* 67(1): 1-48.
- Deshmukh PS, RK Sairam and DS Shukla (1991) Measurement of ion leakage as a screening technique for drought resistance in wheat genotypes. *Indian J. Plant Physiol.* 34: 89-91.
- Govindaraj P, VA Amalraj, K Mohanraj and NV Nair (2014) Collection, Characterization and Phenotypic Diversity of *Saccharum spontaneum* L. from Arid and Semi-Arid Zones of Northwestern India. *Sugar Tech.* 16(1): 36-43.
- Hemaprabha G, S Simon, DL Lavanya, B Sajitha and S Venkataramana (2013). Evaluation of Drought Tolerance Potential of Elite Genotypes and Progenies of Sugarcane (*Saccharum* sp. hybrids). *Sugar Tech.* 15(1): 9-16.
- Hiscox JD and GF Israelstam (1979) A method for the extraction of chlorophyll from leaf tissue without maceration. *Can. J. Bot.* 57: 1332-1334.
- Ishaq MN, G Olaoye and TO Akinsanya (2008) Screening sugar-cane germplasm for drought tolerance in Nigeria. *PGR Newsletter*. 154: 48-54.
- Kandasami PA, TV Sreenivasan, K Palanichami and TC Ramana Rao (1983). Sugarcane germplasm: classification of clones. *Sugarcane*. 2: 1-3.
- Lichtenthaler HK and AR Wellburn (1983) Determinations of total carotenoids and chlorophylls a and b in leaf extracts in different solvents. *Biochem. Soc. Trans.* 11: 591-592.
- Martineau JR, JE Specht, JH Williams, and CY Sullivan (1979) Temperature tolerance in soybeans. I. Evaluation of a technique for assessing cellular membrane thermostability. *Crop Sci.* 19: 75-78.
- Munawarti A, Taryono, E Semiarti and Sismindari (2014) Morphological and Biochemical Responses of Glagah (*Saccharum spontaneum* L.) Accessions to Drought Stress. *J. Trop. Life Sci.* 4(1): 61-66.
- Pathy TL, V Vinu, SP Adhini and S Karthigeyan (2022) Constructing and comparing selection indices for early growth traits in *Saccharum spontaneum*. *Electron J. Plant Breed.* 13(1): 1-10.
- Qing ZM, LG Jing and CR Kai (2001) Photosynthesis characteristics in eleven cultivars of sugarcane and their responses to water stress during the elongation stage. *Proceedings of the XXIV Congress, Brisbane, Australia*, 24: 642-643.
- Ranjbarfordoei A, R Samson, PV Damne and R Lemeur (2000) Effects of Drought Stress Induced by Polyethylene Glycol on Pigment Content and Photosynthetic Gas Exchange of *Pistacia khinjuk* and *P. mutica*. *Photosynthetic*. 38(3): 443-447.
- Rao JT and U Vijayalakshmi (1963) World catalogue of sugarcane genetic stock. Sugarcane Breeding Institute (ICAR), Coimbatore, India, pp 1-77.
- Singh S and MS Reddy (1980) Growth, yield and juice quality performance of sugarcane varieties under different soil moisture regimes in relation to drought resistance. In: Seventeenth Congress of the International Society of Sugar Cane Technologists. Volume 1, Manila, 541-555.

- Sreenivasan TV, BS Ahloowalia and DJ Heinz (1987) Cytogenetics. In: Heinz D.J. (Ed.), *Sugarcane Improvement through Breeding*. Elsevier, New York, pp 211–253.
- Sreenivasan TV, VA Amalraj and AW Jebadhas (2001) Sugarcane genetic resources: *Saccharum spontaneum*. vol. 2. Sugarcane Breeding Institute, Coimbatore, India.
- Tollenaar M and A Aguilera (1992) Radiation use efficiency of an old and new maize hybrid. *Agron. J.* 84: 536–541.
- Venkataramana S, PNG Rao and KM Naidu (1986) The effects of water stress during the formative phase on stomatal resistance and leaf water potential and its relationship with yield in ten sugarcane varieties. *Field Crops Res.* 13: 345–353.

RESEARCH ARTICLE

Variability, Heritability, and Correlation Studies for Economic Traits in Grain Amaranth (*Amaranthus* spp.)

Ved Prakash, Gajala Ameen, Vivek K. Sandilya and Jitendra K. Tiwari*

Abstract

Grain amaranth is a potential nutri-cereal and has high demand in the market due to its nutritional status. An experiment was conducted to evaluate different agro-morphological characteristics of grain amaranth. For this purpose, 102 grain amaranth (*Amaranthus* spp.) genotypes were taken to estimate different genetic components. The characters like leaf length (cm), stem thickness (cm), petiole length (cm), seed yield (q/ha) and seed test weight (g/10 mL) showed high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values. The highest GCV and PCV were recorded with seed test weight (g/10 mL) (40.57 and 45.40%). The estimated high heritability in different characters studied ranged from 77 to 99%. Heritability was observed to be high in consequence for days to 50% flowering, petiole length (cm), stem thickness (mm), seed test weight (g/10 mL), leaf width (cm), seed yield (q/ha), leaf length (cm), plant height (cm), and inflorescence length (cm). Days to 50% flowering showed a highly significant positive correlation with days to 80% maturity ($r_g = 0.8897$, $r_p = 0.7931$) and plant height (cm) highly significant positive correlation with petiole length (cm) ($r_g = 0.3202$, $r_p = 0.2821$). Petiole length significantly correlated with leaf width ($r_g = 0.1909$, $r_p = 0.1918$). Seed yield (q/ha) had a positive but not significant correlation with inflorescence length, leaf width, and petiole length. The Euclidean distance range 0 to 8. In pair-wise comparison, the maximum distance was obtained between IC444100 and IC444105 with the Euclidean distance of 8, whereas IC340823 and IC356023 (1.7%) showed least Euclidean distance with other genotypes. This study will help the utilization of diverse amaranth germplasm in future grain amaranth breeding programs to develop desired variety.

Keywords: Cluster analysis, Correlation coefficient, Genetic variability, Genetic advance, Grain amaranth, Heritability.

Department of Genetics and Plant Breeding, RMD, College of Agriculture and Research Station, IGKV, Ambikapur, Chhattisgarh, India.

*Author for correspondence:

tiwarijk5@gmail.com

Received: 08/04/2020 Revised: 28/12/2020

Accepted: 29/09/2021

How to cite this article: Prakash V, G Ameen, VK Sandilya and JK Tiwari. (2024) Variability, Heritability, and Correlation Studies for Economic Traits in Grain Amaranth (*Amaranthus* spp.). *Indian J. Plant Genetic Resources*. 37(1): 80-89. DOI: 10.61949/0976-1926.2024.v37i01.10

Introduction

Grain amaranth is a fast-growing, dicotyledonous plant belonging to the genus *Amaranthus* and the family Amaranthaceae. The word "Amaranth" is mostly derived from the Greek word "Anthos" which means "everlasting," according to Sankaran (1943). The group amaranth is dibasic with $x = 16$ and $x = 17$ chromosomes. At the present time it is also called a 3rd millennium crop plant. The group amaranth is chiefly composed of about 70 species (Sauer, 1967). The distribution of *Amaranthus* species is based on their usage as grain, vegetable, ornamental, and weedy amaranth (Sauer, 1967). Grain amaranths are widely scattered in Asia (Pagi *et al.* 2017) and it contribute greatly to the nutritional well-being of rural and economically weak people by providing the essential nutrients required for body growth and for the prevention of diseases associated with nutritional deficiencies such as iron and vitamin A (Dua *et al.*, 2009). *Amaranthus* are adapted to different environments, as it can be cultivated in poor soils and highly elevated regions. The grain amaranth species are considered by many as the crop of the future because of the diversification purposes and superior nutritional quality of grain with high protein content in the range 13 to 18% and relatively high lysine

content is comparison with common cereals (Pandey *et al.*, 2015). Amaranth has the potential for a useful and bioactive additive in food products.

The knowledge about the nature and consequence of association of yield with various component characters is a prerequisite to bring improvement in the desired direction. Genetic variability in grain amaranth will provide the foundation for designing the breeding program. However, reports on genetic diversity and morphological variation in grain amaranth are scanty. There will be greater chances of producing a desired type with more variability. Selection based on the phenotype would be ambitious for polygenetic character. Observation of the correlation between yield and its given traits is a basic need to find plant selection guidelines. The present study was, therefore, undertaken for variability, heritability, and correlation studies for economic traits of grain amaranth's germplasm.

Materials and Methods

Plant Material

The materials for present investigation comprise of 102 germplasm lines and 5 check varieties (GA-2, BGA-2, RMA-7, SUVARNA and CG Rajgira-1) of grain amaranth from the National Bureau of Plant Genetics Resources, New Delhi for this study (Table 1).

Experimental Method

About 102 germplasm lines and 5 check varieties were grown in an augmented randomized complete block design during two rabi seasons of the year 2018 and 2019. The study was taken with four blocks, each block consisting of 25 genotypes and five check varieties. All the checks are randomly replicated in all the blocks, while the germplasm lines were unreplicated. Each genotype was sown in two rows, each with a spacing of 45 cm between the rows. Recommended agronomic practices were followed throughout the crop season during both years.

Data Recording

Observations were reported on five plants in each genotype for the 11 quantitative characters viz., leaf length (cm), leaf width (cm), days to 50% flowering, stem thickness (mm), number of branches per plant, plant height (cm), Inflorescence length (cm), days to 80% maturity, petiole length (cm), seed yield (q/ha) and seed test weight (g/10 mL) and 11 qualitative characters viz., early plant vigor, plant growth habit, leaf color, inflorescence color, inflorescence compactness, stem color, stem surface, inflorescence shape, inflorescence spininess, popping ability of seed and seed color. The data was analyzed for genotypic and phenotypic coefficients of variation and heritability (in a broad sense), and cluster analysis was done with PBT 1.4 and STAR software version 2.0.1 for Windows.

Table 1: List of grain amaranth genotypes used in this study

<i>Germplasm lines from NBPGR, New Delhi</i>	
<i>S. No.</i>	<i>Accession name</i>
1	IC 444156
2	IC 444159
3	IC 444167
4	IC 444193
5	IC 356085
6	IC 436948
7	IC 436953
8	IC 436957
9	IC 383647
10	IC 383578
11	IC 436974
12	IC 340823
13	IC 340825
14	IC 340861
15	IC 340803
16	IC 340971
17	IC 317517
18	IC 317549
19	IC 317631
20	IC 391433
21	IC 391468
22	IC 391517
23	IC 391561
24	IC 392498
25	IC 392525
26	IC 429977
27	IC 469777
28	IC 469803
29	IC 469805
30	IC 469820
31	IC 469837
32	IC 469858
33	IC 355992
34	IC 356012
35	IC 356023
36	IC 356027
37	IC 356041
38	IC 356046
39	IC 360827
40	IC 360834
41	IC 356070
42	IC 337341
43	IC 360858

44	IC 265008	90	IC 255481
45	IC 264805	91	IC 264854
46	IC 265980	92	IC 266835
47	IC 266778	93	IC 268885
48	IC 266812	94	IC 266937
49	IC 524215	95	IC 255482
50	IC 279807	96	IC 338640
51	IC 279363	97	IC 393022
52	IC 279413	98	IC 266754
53	IC 279462	99	IC 282786
54	IC 279511	100	IC 281749
55	IC 279512	101	IC 506555
56	IC 279567	102	IC 506573
57	IC 279612	CH-1	GA-2
58	IC 279631	CH-2	BGA-2
59	IC 279652	CH-3	RMA-7
60	IC 279670	CH-4	SUVARNA
61	IC 279760	CH-5	CG Rajgira-1
62	IC 279832		
63	IC 444099		
64	IC 444100		
65	IC 444105		
66	IC 317427		
67	IC 506604		
68	IC 506605		
69	IC 506611		
70	IC 506612		
71	NC 59949		
72	IC 506514		
73	IC 506519		
74	IC 506520		
75	IC 506521		
76	IC 506524		
77	IC 506528		
78	IC 506529		
79	IC 506531		
80	IC 506534		
81	IC 506535		
82	IC 506575		
83	IC 361327		
84	IC 382640		
85	IC 362257		
86	IC 341452		
87	IC 255428		
88	IC 255555		
89	IC 255419		

Results and Discussion

Genetic improvement in grain amaranth crop depends on the extent of genetic variability for yield and its components. The present investigation aims to determine the magnitude and extent of variability among genotypes for 11 different quantitative traits. The analysis of variance for grain yield and its attributing characters among blocks, treatments, checks and checks vs varieties revealed presence of significant variation in the genotypes studied. However, with respect to checks and checks vs varieties, non-significant differences were recorded for plant height and inflorescence length (Table 2).

Variability and Genetic Parameters

The nature and magnitude of variation for individual traits was assessed by range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a percentage of the mean (Table 3).

A high magnitude of GCV was recorded for trait, seed test weight (40.57), and seed yield (34.66), while high magnitude PCV was recorded for characters such as, seed test weight (45.40), seed yield (35.50) and leaf length (29.02). Moderate GCV was recorded for traits such as, petiole length (15.09), stem thickness (13.45) and leaf width (10.20), moderate PCV was recorded for traits such as, petiole length (15.14), stem thickness (13.58) and Leaf width (10.33). GCV and PCV are estimates as low (0–10%), moderate (10–20%) and high (>20%) categorized by Johnson *et al.* (1955). A high estimate of GCV and PCV indicates the high variability of characters in the germplasm. A similar result was reported for moderate GCV and PCV in petiole length and leaf blade width by

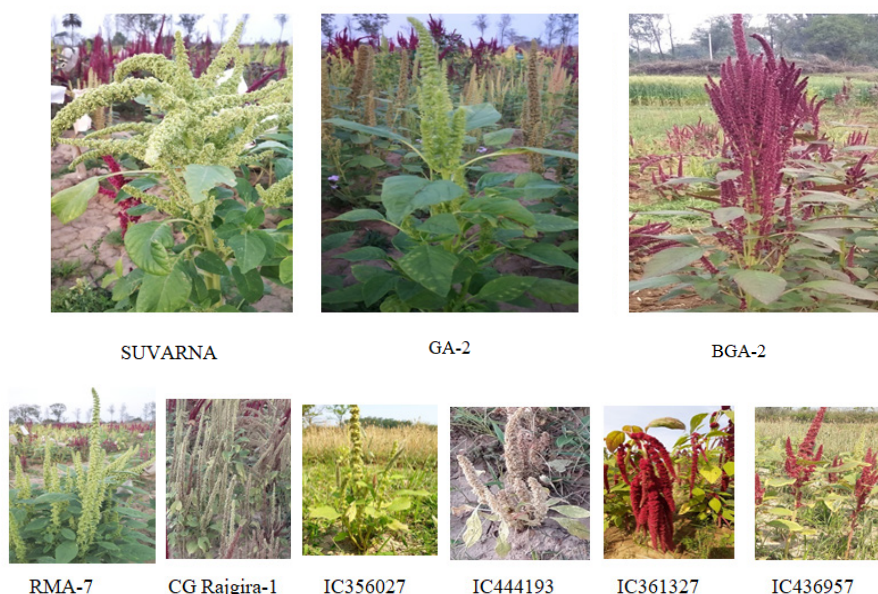
Table 2: Augmented design analysis of variance for yield and its attributing characters in grain amaranth

	DF	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Days to 50 %flowering	Stem thickness (mm)	No. of branches per plant	Plant height (cm)	Inflorescence length (cm)	Days 80% maturity	Seed yield (q/ha.)	Seed test weight (g/10 mL)
Block (ignoring treatments)	3	1.42***	0.34***	0.18***	39.43***	0.16***	2.20***	12.48**	1.51**	2.17	15.05***	0.58***
Treatment (eliminating blocks)	106	0.44***	0.21***	0.19***	23.14***	0.08***	0.99***	14.98***	1.42***	7.63**	9.57***	0.76***
Checks	4	0.33***	0.76***	0.11***	7.37***	0.15***	0.42**	7.56*	0.33	8.25*	3.10***	0.25***
Checks+Var vs. Var.	102	0.44***	0.19***	0.20***	23.76***	0.08***	1.02***	15.27***	1.46***	7.60**	9.82***	0.78***
ERROR	12	0.02	0.01	0.01	0.57	0.01	0.07	1.52	0.24	1.55	0.26	0.011
Block (eliminating Check+Var.)	3	0.13*	0.01	0.01	0.45	0.01	0.85***	4.26	0.19	2.47	0.43	0.02
Entries (ignoring Blocks)	106	0.48***	0.22***	0.20***	24.24***	0.09***	1.03***	15.21***	1.46***	7.62**	9.98***	0.78***
Checks	4	0.33***	0.76***	0.11***	7.37***	0.17***	0.42**	7.56	0.33	8.25*	3.10***	0.25***
Varieties	101	0.47***	0.15***	0.19***	23.09***	0.08***	0.59***	15.59***	1.51***	7.48**	8.57***	0.68***
Checks vs. Varieties	1	1.33***	5.06***	1.38***	207.71***	0.20***	48.25***	7.18	0.37	19.81**	180.64***	12.39***
ERROR	12	0.03	0.01	0.01	0.57	0.01	0.07	1.52	0.24	1.55	0.26	0.01
Ci - Cj	1	0.25	0.12	0.07	1.17	0.05	0.42	1.90	0.75	1.92	0.79	0.16
BiVi - BiVj	1	0.49	0.24	0.14	2.34	0.11	0.84	3.80	1.50	3.84	1.57	0.32
BiVi - BiVj	1	0.54	0.26	0.15	2.56	0.12	0.92	4.17	1.64	4.20	1.72	0.35
Ci - Vi	1	0.43	0.21	0.12	2.02	0.09	0.73	3.29	1.30	3.32	1.36	0.27

*Significant at 5% level, ** Significant at 1% level, *** Significant at 0.1% level DF- degrees of freedom.

Table 3: Genetic parameters for yield and its attributing characters in grain amaranth

Characters	General mean	Range		PCV (%)	GCV (%)	h^2 (%)	Genetic advance	GA as % of mean
		Min	Max					
Leaf length (cm)	7.05	5.60	8.54	29.02	7.48	91	3.87	54.89
Leaf width (cm)	3.67	2.92	4.88	10.33	10.20	97	0.75	20.43
Days to 50% flowering	54.27	42.00	61.00	8.47	8.41	99	9.65	17.78
Stem thickness (mm)	4.39	3.64	5.16	13.58	13.45	98	0.57	12.98
Number of branches per plant	5.73	4.00	8.60	10.44	6.26	62	0.76	13.26
Plant height (cm)	89.07	76.40	101.50	7.32	6.87	90	8.50	16.87
Inflorescence length (cm)	38.46	28.20	51.60	5.73	5.21	85	1.98	10.02
Petiole length (cm)	2.84	1.94	4.08	15.14	15.09	99	0.87	30.63
Days to 80% maturity	128.41	122.00	132.00	1.86	1.56	77	3.79	2.95
Seed yield (q/ha)	20.62	14.50	26.60	35.50	34.66	96	5.58	27.06
Seed test weight (g/10 mL)	5.70	4.10	7.58	45.40	40.57	98	5.22	91.57

**Figure 1:** Morphological variation in different genotypes in grain amaranth sequence of picture Suvarna, GA-2, BGA-2, RMA-7, IC356027, IC 444193, IC 361327, IC 436957, CG Rajgira-1

Rashmi Yadav *et al.* (2014). The characteristics that showed high GCV and PCV are of economic importance, and there is scope for improvement of these characteristics through selection.

The high heritability was reported for the character's petiole length (99%), days to 50% flowering (99%), stem thickness (98%), seed test weight (98%), leaf width (97%), seed yield (96%), leaf length (91%), plant height (90%), Inflorescence length (85%), and days to 80% maturity (77%). Moderate heritability was observed for a number of branches per plant (62%). Rabinson *et al.* (1949) categorized the heritability measure as low (0–30%), moderate (30–60%) and high (>60%). However, the heritability value provides no indication of the amount of genetic improvement that

would result from the selection of superior genotypes. Pictures of check varieties and some potential lines depicted through Figure 1.

Genetic advance as a percentage of mean was observed high seed test weight (91.57%), leaf length (54.89%), petiole length (30.63%), seed yield (27.06%) and leaf width (20.43%). The moderate GA as a percentage of mean was observed for days to 50% flowering (17.78%), plant height (16.87%), number of branches per plant (13.26%), stem thickness (12.98%), and Inflorescence length (10.02%) and low GA as a percentage of mean was observed for days to 80% maturity (2.95%). The genetic advance as % of mean was classified as below, medium or high following Johnson *et al.*, (1955) 0–10%: low, 10–20%: medium, >20% or above: high. Additive

Table 4: Estimation of genotypic (G) and phenotypic (P) correlation coefficient among various characters in grain amaranth

Character	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Days to 50% flowering	Stem thickness (mm)	Number of branches per plant	Plant height (cm)	Inflorescence length (cm)	Days to 80% maturity	Seed yield (q/ha)	Seed test weight (g/10 mL)
Leaf length (cm)	(G) 1.00	0.29**	0.06	-0.04	0.16	-0.08	-0.03	0.03	-0.07	-0.09	0.07
	(P) 1.00	0.30**	0.07	-0.05	0.16	0.01	0.01	0.07	-0.12	-0.09	0.05
Leaf width (cm)	(G) 1.00	1.00	0.19*	0.15	0.12	-0.23*	-0.06	0.10	0.18	0.09	-0.06
	(P) 1.00	1.00	0.19*	0.14	0.15	-0.10	-0.04	0.08	0.15	0.09	-0.06
Petiole length (cm)	(G) 1.00		1.00	-0.12	-0.09	-0.22*	0.32**	-0.01	-0.02	0.05	-0.01
	(P) 1.00		1.00	-0.05	-0.09	-0.16	0.28**	0.01	-0.01	0.051	-0.01
Days to 50% flowering	(G) 1.00			1.00	0.15	0.11	0.13	0.03	0.89**	-0.07	-0.01
	(P) 1.00			1.00	0.14	0.05	0.11	0.01	0.79**	-0.06	-0.02
Stem thickness (mm)	(G) 1.00				1.00	-0.01	0.02	0.06	0.04	-0.02	0.03
	(P) 1.00				1.00	-0.01	0.04	0.05	0.06	-0.02	0.02
Number of branches per plant	(G) 1.00					1.00	-0.06	-0.09	-0.11	-0.04	-0.04
	(P) 1.00					1.00	0.06	-0.08	-0.12	-0.01	-0.03
Plant height (cm)	(G) 1.00						1.00	-0.01	0.06	-0.09	0.10
	(P) 1.00						1.00	-0.02	0.06	-0.08	0.10
Inflorescence length (cm)	(G) 1.00							1.00	0.13	0.11	0.10
	(P) 1.00							1.00	0.02	0.11	0.11
Days to 80% maturity	(G) 1.00								1.00	-0.04	-0.03
	(P) 1.00								1.00	-0.05	-0.02
Seed yield (q/ha)	(P) 1.00									1.00	0.10
	(G) 1.00									1.00	0.09
Seed test weight (g/10 mL)	(P) 1.00										1.00
	(G) 1.00										1.00

*5% level of significance, ** 1% level of significance

Table 5: Sources and clustering of 102 genotypes of grain amaranth in four clusters

Clusters	Number of accessions	Name of the genotypes
I	44	IC 444156, IC 444167, IC 444193, IC 356085, IC 436948, IC 436953, IC 436974, IC 340825, IC 34086, IC 34080, IC 391517, IC 391561, IC 392498, IC 392525, IC 429977, IC 469777, IC 469803, IC 469837, IC 469858, IC 355992, IC 356046, IC 360827, IC 356070, IC 265008, IC 266778, IC 279807, IC 279413, IC 279631, IC 279670, IC 279760, IC 444100, IC 317427, IC 506611, IC 506521, IC 255481, IC 266835, IC 268885, IC 266937, IC 255482, IC 338640, IC 393022, IC 266754, IC 506555, IC 281749
II	39	IC 444159, IC 383578, IC 340823, IC 317517, IC 317549, IC 317631, IC 391468, IC 469805, IC 469820, IC 356023, IC 356041, IC 360834, IC 337341, IC 264805, IC 265980, IC 524215, IC 279462, IC 279567, IC 279612, IC 444099, IC 506605, IC 506612, IC 59949, IC 506514, IC 506520, IC 506528, IC 506529, IC 506531, IC 506534, IC 506535, IC 506575, IC 361327, IC 382640, IC 362257, IC 341452, IC 255555, IC 255419, IC 264854, IC 506573
III	7	IC 436957, IC 340971, IC 391433, IC 360858, IC 279652, IC 279832, IC 506604
IV	12	IC 383647, IC 356012, IC 356027, IC 266812, IC 279363, IC 279511, IC 279512, IC 444105, IC 506519, IC 506524, IC 255428, IC 282786

Table 6: Cluster means of different quantitative traits of grain amaranth using Gower's coefficient

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Leaf length (cm)	7.06	6.98	6.20	7.78
Leaf width (cm)	3.58	3.60	3.74	4.21
Petiole length (cm)	2.90	2.67	2.80	3.17
Days to 50% flowering	52.11	54.92	58.43	57.67
Stem thickness (mm)	4.34	4.40	4.55	4.43
Number of branches per plant	6.00	5.60	5.29	5.43
Plant height (cm)	91.84	84.77	93.99	90.34
Inflorescence length (cm)	38.97	38.93	40.03	34.14
Days to 80% maturity	127.23	128.64	131.00	130.50
Seed yield (q/ha)	20.43	18.77	24.83	21.56
Seed test weight (g/10 mL)	5.83	5.42	6.35	5.72

genes govern the high-value GA for these characters, and selection will be rewarding for the further improvement of such characters. Moderate genetic advance for the traits suggests that both the additive and nonadditive variance are operating in these traits.

Correlation Coefficient Analysis

Genotypic and phenotypic coefficients among 11 quantitative characters are presented in Table 4. A positive significance correlation of leaf length was noticed with leaf width. Days to 80% maturity showed a positive and significant correlation with days to 50% flowering. Petiole length showed a positive and significant correlation with leaf width. Leaf width showed a positive and significant correlation with leaf length. Plant height showed a positive and significant correlation with petiole length at the genotypic level only. Diwan *et al.* (2017) also reported a

similar association, who considered leaf length showed a positive correlation with leaf width. Although phenotypic variation was considered, it is likely that this variation is largely genetic and, therefore, directly usable in breeding programs.

Cluster Analysis

Agglomerative cluster analysis was performed using the STAR software version 2.0.1 to calculate from quantitative data to generate a dendrogram for 102 genotypes (Figure 2). The Euclidean distance ranges from 0 to 8. The genotypes group four major clusters (Table 5). In pair-wise comparison, the maximum distance was obtained between IC444100 and IC444105 with the Euclidean distance of 8, whereas IC340823 and IC356023 (1.7%) showed least Euclidean distance with other genotypes. The cluster means of different quantitative traits of grain amaranth are given in Table 6. Cluster I included 44 genotypes with the highest mean value for the number of branches per plant (6.00). In this group, mean values for leaf width, days to 50% flowering, stem thickness and days to 80% maturity were minimum. Cluster II included 39 genotypes with the lowest mean values for petiole length, plant height, seed yield, and seed test weight. The mean value days to 50% flowering was minimal, showing early maturity. Cluster III, comprising of 7 genotypes having the highest mean values for days to 50% flowering (58.43), stem thickness (4.55), plant height (93.99), inflorescence length (40.03), days to 80% maturity (131.00), seed yield (24.83) and seed test weight (6.35). This group has the lowest mean values for leaf length and number of branches per plant. Cluster IV comprises of 12 genotypes having the highest mean values for leaf length (7.78), leaf width (4.21) and petiole length (3.17). In this group, mean values for Inflorescence length (cm) was lowest. Cluster analysis helps in grouping accessions sharing similar characters in different clusters and identifying genetically diverse and desirable genotypes.

However, the dendrogram generated from similarity or genetic distance matrix based on morphological traits has provided an overall pattern of variation as well as

Table 7: Number of genotypes in different categories for different traits

S.N.	Traits	Category	No. of genotype
1	Early plant vigour	1 Poor	17
		2 Good	45
		3 Very good	40
2	Plant growth habit	1 Erect	59
		2 Spreading	39
		3 Drooping	4
3	Leaf color	2 Yellowish orange	1
		3 Yellowish green	2
		5 Green	53
		8 Pinkish green	20
		10 Reddish green	22
4	Inflorescence color	11 Red	4
		4 Yellowish green	16
		6 Pink	20
		7 Pinkish green	10
		8 Purple	9
5	Inflorescence compactness	9 Red	15
		10 Reddish green	2
		11 Green	28
		99 Dark red	2
6	Stem color	3 Lax	47
		5 Intermediated	46
		7 Dense	9
7	Stem surface	1 Yellow	19
		2 Yellowish green	34
		4 Pink	22
		6 Reddish green	15
		7 Reddish orange	12
8	Inflorescence shape	1 Smooth	35
		2 Ridged	67
		1 Globose	7
		2 Semi drooping	68
		3 Completely drooping	13
9	Inflorescence spininess	4 Straight	14
		99 Others	
		1 Smooth	44
		2 Glabrous	10
		3 Prickly	28
10	Popping ability of seed	4 Spiny	20
		3 Poor	36
		5 Medium	54
		7 Good	12
11	Seed color	2 Creamish	76
		3 Pale yellow	8
		7 Black	8
		8 Golden	10

the degree of relatedness among genotypes. Genotypes showing maximum dissimilarity could be used in a hybrid breeding program.

Qualitative Character

The frequency of eleven qualitative characters in one 100 two grain amaranth accessions has been shown in Table

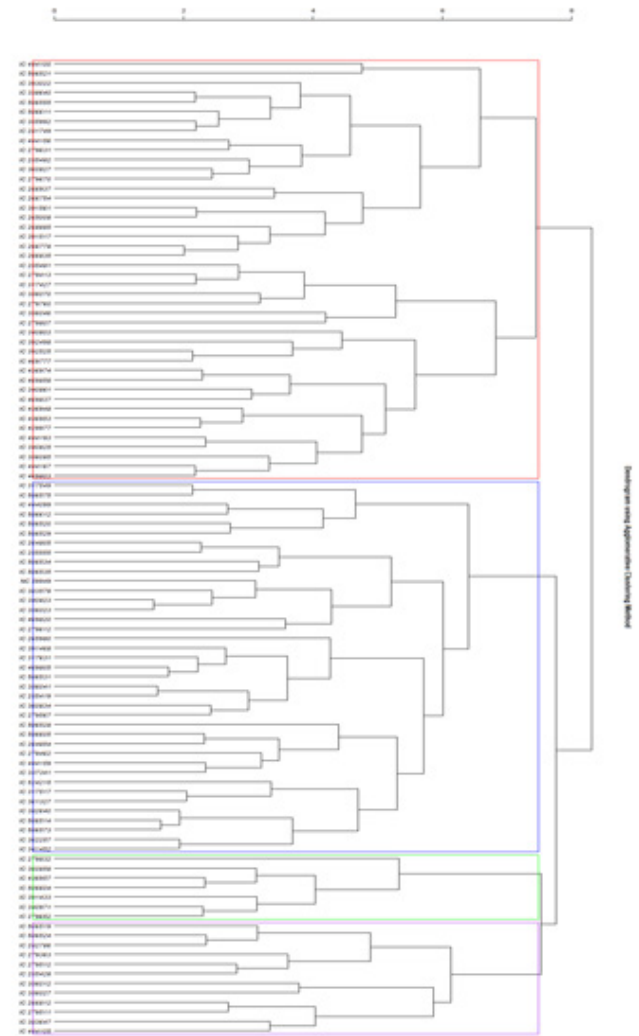
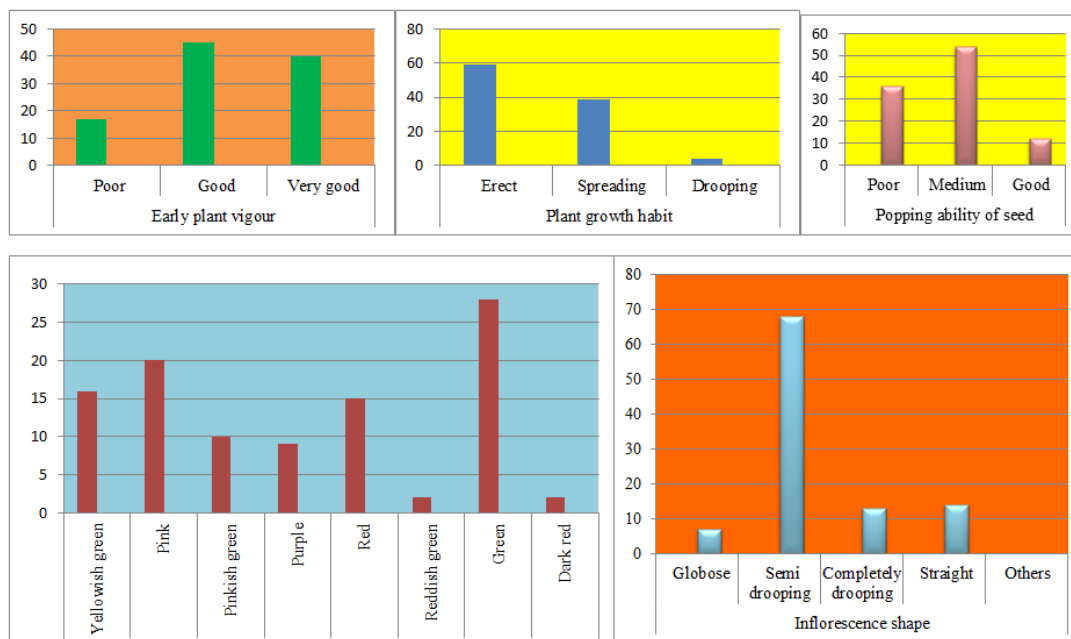


Figure 2: Dendrogram for morphological characters using Gower's Coefficient

7, which shows a variable range of characters. Early plant vigor genotypes IC436953, IC340803, IC469803, IC469805, IC469820 and IC265980 were very good. The majority of the entries were erect type with spreading type and drooping type plant habit. The inflorescence color varied from yellowish green, pink, pinkish green, purple, red, reddish green and green. Genotypes IC355992, IC356046, IC360827 were yellowish green, IC436948, IC383647, IC469858 were pink, IC356085, IC383578, IC356023 were pinkish green, IC436957, IC392525, IC360858 were purple, IC444167, IC469805, IC279760 were red, IC444156, IC444159, IC340803 were reddish green. The inflorescence shape from globose, semi-drooping, completely drooping and straight genotypes IC444159, IC436953, IC337341 were globose, IC444156, IC444193, IC356085 were semi-drooping, IC436948, IC383647, IC340803 were completely drooping, IC356023, IC356027, IC356041, IC279511 were straight. The popping ability of seed genotypes IC436957, IC317549,



Graph 1: Bar chart of different qualitative traits of grain amaranth

IC429977, IC360834, IC524215 were good. The distribution of the accessions for levels of qualitative characters showed that the growth habit of most of the genotypes was predominantly erect type (59%). Inflorescence color showed a marked variability in colors and about 28% of accessions were green, 20% pink 16% yellowish green and 15% had red color. Leaves color were of green, 53% of the accessions, reddish green, 22% of the accessions and 20% had pinkish green color, inflorescence while 47% have lax type inflorescence compactness, 46% intermediate and about 9% have dense type of inflorescence. The inflorescence spininess presented a marked variability. The seed's color presented a marked variation, although 76% were creamish with different intensities. Similar results were reported by Rashmi Yadav *et al.* (2014) for qualitative characters in grain amaranth (Graph 1).

Conclusion

Grain amaranth has extensive variation for selected traits, and high heritability and genetic advances existed among the traits of further genetic improvement in this crop. The mean performance for yield (q/ha) of IC392525, IC279832, IC340825, IC279652 and IC360858 was superior among all the genotypes. Genotypes IC469803, IC392525, IC279807, IC279760 and IC506575 were early maturity. Therefore, the enormous variation in the grain amaranth germplasm would continue to provide breeders with good opportunities for breeding and selection. Exploitation of the genetic variability available in grain amaranth germplasm for yield components will continue to be emphasized in cultivar development. These characters are effectively used in a breeding program and these important characters will

decide the future of amaranth. It may be concluded that the morphological descriptor can effectively be used for identifying and grouping of germplasm. However, morphological description also may not be sufficient for characterization criteria. Hence, some other markers/descriptors must be considered to complement the morphological descriptor.

Acknowledgment

The authors thank the IGKV, Raipur and AICRN authorities on potential crops for providing necessary facilities and support for conducting research.

References

- Ahammed AU, MM Rahman and MAK Mian (2012) Genetic Variability, Heritability and Correlation in Stem Amaranth (*Amaranthus tricolor*). *Bangladesh J. Pl. Breed. Genet.* 25(2): 25-32.
- Barrio DA and MC Anon (2010) Potential antitumor properties of a protein isolate obtained from the seeds of *Amaranthus mantegazzianus*. *Eur. J. Nutr.* 49: 73- 82.
- Chandravanshi D, PK Sharma, C Banjare and D Chandravanshi (2018) Genetic Diversity of *Amaranthus dubius* Mart. (Khedha) Used Tribal Place in Chhattisgarh, India. *Int. J. Bioresour. Stress Manag.* 9(5): 634-640.
- Diwan IS, N Shukla and V Kurrey (2017) Genetic Studies in *Amaranthus* Germplasm. *Int. J. Curr. Microbiol. Appl. Sci.* 6(8): 2459-2470.
- Dua RP, HL Raiger, BS Phogat and SK Sharma (2009) Underutilized Crops: Improved Varieties and Cultivation Practices. National Bureau of Plant Genetics Resources, New Delhi, India, p 66.
- Gelotar MJ, DT Dharajiya, SD Solanki, NN Prajapati and KK Tiwari (2019) Genetic diversity analysis and molecular characterization of grain amaranth genotypes using inter

- simple sequence repeat (ISSR) markers. *Bull. Natl. Res. Cent.* 43: 103.
- Johnson HW, HP Robinson and RE Comstock (1955) Estimate of genotypic and environmental variability in soybean. *Agron J.* 47: 314-318.
- Joshi DC, S Sood, R Hosahatti, L Kant, A Pattanayak, A Kumar, D Yadav, MG Stetter (2018) From zero to hero: the past, present and future of grain amaranth breeding. *Theor. Appl. Genet.* 131(9): 1807-1823.
- Kumar Y, R Prasad and PR Singh (2018) Studies on collection and evaluation of genetic variability available in *Amaranthus* (*Amaranthus* spp.) under Chhattisgarh plain condition. *Int. J. Curr. Microbiol. Appl. Sci.* 7(11): 3540-3547.
- Lokesh kumar BM and N Murthy (2017) Genetic Variability and Divergence Studies for Yield Component Traits in Grain Amaranth (*Amaranthus* spp.). *Int. J. Curr. Microbiol. Appl. Sci.* 6(12): 1276-1285.
- Pagi N, N Prajapati, K Pachchigar, D Dharajiya, SD Solanki, N Soni and P Patel (2017) GGE biplot analysis for yield performance of grain amaranth genotypes across different environments in western India. *J. Exp. Biol. Agric. Sci.* 5(3): 368-376.
- Pandey CD, A Kak, S Pandey and V Gupta (2015) Trait-specific Amaranth Gemplasm- Potentialities to Combat Climate Change. *Indian J. Plant Genetics Resources* 28(3): 321-328.
- Rai N and DS Yadav (2005) Advances in vegetable production. Research Co Book Centre, New Delhi, pp 530-531.
- Rastogi A and S Shukla (2013) Amaranth: A New Millennium Crop of Nutraceutical Values. *Crit. Rev. Food Sci. Nutr.* 53: 109-125.
- Robert YN, K Hiroe and K Yotaro (2008) Antioxidant activity of various extracts and fraction of *Chenopodium quinoa* and *Amaranthus* Spp. Seed, Analytical, nutritional and clinical methods. *Food Chem.* 106: 760-766.
- Robinson HF, RE Comstock and PH Harvey (1949). Estimates of heritability and degree of dominance in Corn. *Agron. J.* 41: 353-359.
- Sagar KP (2018) Genotypic Correlation Coefficients among Growth, Yield and Quality Parameters in *Amaranthus* Genotypes (*Amaranthus tricolor* L.). *Int. J. Curr. Microbiol. Appl. Sci.* 7(8): 2319-7706.
- Sankaran A (1943) Cultivation of leafy vegetables in the northern circars. *Madras Agri. J.* 31: 285-286.
- Sauer JD (1967) The grain *Amaranthus* and their relative: A revised taxonomic and geographic survey. *Ann. Mo. Bot. Gard.* 54: 103-137.
- Sood Salej, RS Pal, A Sharma, L Kant and A Pattanayak (2018) Characterization of amaranth genetic resources for agro morphological and nutritional traits in submontane Himalayan region of India. *Electron. J. Plant Breed.* 9(4): 1484-1496.
- Tiwari JK (2018) Variability and genetic parameter for different yield contributing traits in grain amaranths. *J. Res. ANGRAU.* 46(4): 11-16.
- Yada Rashmi, JC Rana and JK Ranjan (2014) Analysis of variability parameters for morphological and agronomic traits in grain amaranth (*Amaranthus* sp.) genotypes. *Bio Scan.* 9(4): 1661-1665.

RESEARCH ARTICLE

Microsatellite Markers Reveal the Genetic Integrity of Stored Accessions of Cotton (*Gossypium arboreum* L.) in the Indian National Genebank

Anto James¹, Shipra Deo², Anjali Kak² and Mukesh K. Rana^{2*}

Abstract

The regeneration of germplasm from gene banks is a critical step in conserving plant genetic resources. However, it might introduce changes in allele frequencies that can impact genetic diversity. Microsatellite markers have emerged as essential tools for tracking these changes, allowing genebank managers to make informed decisions about their conservation strategies. By using microsatellite markers, genebank managers can ensure the long-term availability and viability of plant genetic resources, contributing to the sustainability of agriculture and biodiversity conservation. The genetic integrity of six cotton accessions (*Gossypium arboreum* L.) conserved in the Indian National Genebank was investigated using microsatellite markers. These accessions were initially conserved in the genebank and subsequently regenerated during the years 2000, 2007 and 2015. The selected five microsatellite marker loci revealed the genetic integrity of these accessions with minor genetic changes at rare alleles. In three accessions, new bands at very low frequencies were observed after regeneration, whereas in two, few bands were lost after regeneration. No significant changes were observed after the regeneration of cotton accessions with respect to Nei's expected heterozygosity and Shannon's Information Index. There were no significant changes in genetic integrity and structure, indicating that the protocol being followed for regeneration was quite efficient and effective.

Keywords: Cotton, *Gossypium arboreum*, Genebank, Genetic integrity, Regeneration, SSR markers.

¹ICAR-Indian Agriculture Research Institute, Pusa Campus, New Delhi, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India

***Author for correspondence:**

mukesh.Rana@icar.gov.in

Received: 27/10/2023 **Revised:** 21/11/2023

Accepted: 21/11/2023

How to cite this article: James A, S Deo, A Kak and MK Rana. (2024) Microsatellite Markers Reveal the Genetic Integrity of Stored Accessions of Cotton (*Gossypium arboreum* L.) in the Indian National Genebank. *Indian J. Plant Genetic Resources*. 37(1): 90-96. DOI: 10.61949/0976-1926.2024.v37i01.11

Introduction

Cotton belongs to the family Malvaceae and has been known to mankind ever since human civilization started. Its economic importance as a fibre crop stands unparalleled to any other, and has been rightly called as white gold. Cotton is considered to be the backbone of the textile industry in India. The genus *Gossypium* comprises more than 50 species under eight major genome groups. Of these 50 species, four are more widely cultivated worldwide: *Gossypium arboreum* L., *G. herbaceum* L., *G. hirsutum* L., and *G. barbadense* L. India is the only country in the world where all four of these cultivated species are grown on a commercial scale.

Genebanks across the globe have amassed a total of 104780 accessions of cotton (FAO, 2019). The National Genebank at ICAR-NBPGR, New Delhi houses more than 10000 accessions of different species of cotton. A major challenge faced by the genebank curators is maintaining the genetic integrity of the conserved accessions over several years, particularly during regeneration when the viability of stored accessions starts deteriorating. Some of the factors affecting the genetic integrity of the accessions held in *ex-situ* collections include foreign contamination by pollen grains, admixtures, improper handling during regeneration, genetic drift, mislabeling, etc.

Microsatellite markers have been prominently associated with low-copy regions of plant genomes and is a powerful tool for genetic diversity analysis, population structure analysis, gene flow among populations, DNA fingerprinting, association mapping and linkage mapping in crop plants (Zalapa, J. E. *et al.* 2012, Sugita, T. *et al.* 2013, Gyawali, S. *et al.* 2016, Zhao, J. *et al.* 2017). These have been widely used in cotton also for analyzing genetic diversity (Kumar *et al.* 2022, Lu *et al.* 2022), DNA fingerprinting (Santosh *et al.* 2022), hybrid purity testing (Dongre and Parkhi 2005, Rana *et al.* 2006), QTL mapping of various economic traits like fibre quality (Shen *et al.* 2005) and population structure analysis (Tyagi *et al.* 2014, Zhu *et al.* 2019). However, microsatellite markers have not been employed much in analyzing the genetic integrity of the stored accessions except in few crops like wheat (Börner *et al.* 2000) open, pollinated species of rye (Chebotar and Börner 2002), tobacco (PAN *et al.* 2013) pearl millet (Dan *et al.* 2020) etc. To the best of our knowledge, this study is the first to report using simple sequence repeats (SSR) markers for genetic integrity in cotton.

Materials and Methods

Plant Material and DNA Preparation

The cotton database was scrutinized for accessions that had been regenerated over the years, and six accessions that were regenerated and conserved consecutively during the years 2000, 2007 and 2015 in the National Genebank at ICAR-NBPGR, New Delhi were finally selected. The seeds of these accessions from the voucher specimen were procured and sown in paper towels in the laboratory. Each accession contained a variable number of seeds and the average number of seeds varied from 35.0 to 72.7 seeds per accession (Table 1). The selected six accessions, regenerated in three cycles, gave 24 combinations of accessions x years.

The DNA from individual seeds of each accession was extracted by following the protocol given by Gupta *et al.* (2012). This modified method used an extraction buffer containing 200 mM tris-HCl, pH 8.0, 200 mM NaCl₂, 25 mM EDTA, 0.5% SDS and a CTAB solution with 2% PVP for extracting DNA from cotton seeds. The extracted DNA obtained was dissolved in 50 µL of tris-EDTA (TE) buffer. The quality of the DNA obtained was compared with standard polymerase chain reaction (PCR) products and was found enough to run the PCR. A total of 989 individual seed DNA extractions were completed from the voucher accessions and were used for analyzing the genetic integrity.

PCR Gel Electrophoresis and Data Analysis

Based on earlier studies and initial screening of over 50 microsatellite primers, a total of eight microsatellite loci (BNL3545, DPL0702, NAU2190, JESPR204, NAU1043, NAU5013, NAU6966 and NAU4926) (Table 2) that were well distributed across the various chromosomes of cotton and those having

good polymorphism information content (PIC) were used in this study. Five primers in each accession were used for integrity investigation. PCR included 1X PCR buffer, 3.0 mM MgCl₂, 0.2 mM dNTP, 0.5U *Taq* polymerase (all reagents from M/S Sigma), 0.1 µM of each forward and reverse primer and 20ng of sample DNA in a single PCR reaction.

After PCR amplification, the PCR products were separated in a gel containing 3% metaphor agarose which was stained using ethidium bromide. PCR products were mixed with loading dye for visualization of the bands. The gel electrophoresis was run in a gel chamber containing tris-acetate EDTA (TAE) buffer at 90 volts against a standard DNA ladder of 100 bp until the proper separation of the bands was obtained, usually from 2 to 3 hours. The gels were visualized under a gel documentation system using UV light and the resulting images were stored. The gel bands were converted to binary data as presence (1) or absence (0) in a scoring sheet and later fed into an Excel sheet for analysis. A number of alleles, allele frequency, gene diversity, observed heterozygosity, expected heterozygosity and fixation index values were calculated using software like Powermarker (Liu and Muse, 2005) and GenAlex (Peakall and Smouse (2012).

Results and Discussion

Germplasm stored in genebanks is subject to various risks, including genetic drift, loss of viability and contamination. To overcome these risks and maintain the genetic diversity of plant species, genebanks periodically regenerate their collections. Regeneration involves growing a subset of the germplasm, harvesting the seeds or tissues, and then restoring these new samples in the genebank. This process ensures the genetic integrity of the stored accessions and helps maintain the long-term availability of these genetic resources for research, breeding and conservation. The genetic integrity of six cotton accessions (*G. arboreum* L.) conserved in the Indian National Genebank was investigated using microsatellite markers. The number of alleles amplified by the microsatellite markers with each *G. arboreum* accession over the three years in which the accessions were regenerated is given in Table 3. Table 4

Table 1: Year wise seed number of cotton (*G. arboreum* L.) accessions used for genetic integrity analysis

S. No.	Accession	Source	2000	2007	2015
1	IC440885	Meghalaya	69	77	72
2	IC440886	Meghalaya	40	69	60
3	IC440887	Meghalaya	60	46	47
4	IC440888	Meghalaya	70	48	44
5	IC440889	Meghalaya	63	59	60
6	IC440890	Meghalaya	34	33	38
Average			56	55	53

Table 2: List of SSR primers used for the genetic integrity analysis of cotton (*G. arboreum* L.) accessions.

S. No.	Primer	Linkage group/Chromosomal Position	Forward	Reverse
1	BNL3545	Chr02	AGTCAGTTTTTTGTTAGCAATATGC	AACCATTAATTCCTATTTAACCG
2	DPL0702	Chr06	GATCTCTCTATCAACGACCAGGTT	CAACCGTCCGTCATTAGTGAATA
3	NAU2190	Chr14	CAACCAACATATTCCAAACA	TTATTTTCGGCCTTGTTTTTC
4	JESPR204	Chr13	CTCCAGGTTCAATGGTCTG	GCCATGTTGGACAAGTAGTC
5	NAU1043	AO7	GTATCCGCCCCACAAATAAAG	GCATCGTGAGAGAAAGTGAA
6	NAU5013	Chr20	GTCGGGTCATTACAAGGAAG	CTTCTGCTTTTGGTTTTGGT
7	NAU6966	Chr05.2	GTCATCATTATCGTCAAGTC	AAAGTGAGTTAAGAAAGGCT
8	NAU4926	Chr26	CGCCTCTGTATTTCGATTCTC	GCGTAAATAAAGCGAAAACC

Table 3: Alleles amplified in the cotton (*G. arboreum* L.) accessions conserved in the National Genebank after three years of regeneration using microsatellite markers

Accession identity	Year of regeneration	BNL3545	DPL0702	NAU2190	JESPR204	NAU1043	NAU5013	NAU6966	NAU4926
IC440885	2000	-	-	200	190,180	210	200,180	150,100	-
	2007	-	-	190,200	190,180	210	200,180	150,100	-
	2015	-	-	200	190,180	210	200,180	150,100	-
IC440886	2000	200,180	200,150	200	190,180	210			
	2007	200,180	200,150	200	190,180	210,180			
	2015	200,180	200,150	200	190,180	210,180			
IC440887	2000	-	200,150	200	190,	210	-	150,100	-
	2007	-	200,150	200	190,150	210	-	150,100	-
	2015	-	200,150	200	190	210	-	150,100	-
IC440888	2000	200,150	200,150	210,200	-	210	-		150
	2007	200,150	200,150	210,200	-	210	-		150
	2015	200,150	200,150	200	-	210	-		150
IC440889	2000	200	200,180	200	-	210	-		150, 80
	2007	200	200,180	200	-	210	-		150, 80
	2015	200	200,180	200	-	210	-		150, 80
IC440890	2000	200,150	200,150	210	190,180	-	-	-	150
	2007	200,150	200,150	210	190	-	-	-	150
	2015	200,150	200,150	210	190	-	-	-	150

presents a comprehensive overview of the genetic diversity indices, including the Number of alleles (N), number of effective alleles (Ne), Shannon's Information Index (I), average observed heterozygosity (Ho), average expected heterozygosity (He), Nei's Expected heterozygosity (Nei), and pairwise Fst (Fst) values calculated using GenALEx for each individual year. No major changes were observed regarding the number of bands amplified; however, some minor changes were observed which are described below accession-wise.

IC440885

The genetic integrity of the accession IC440885 was tested using five primers, namely NAU2190, JESPR204, NAU1043, NAU5013 and NAU6966 (Table 3). No major changes were observed with four primers, but with one primer, i.e., NAU

2190, in addition to amplification of a 200 bp band in all of the three regeneration years, i.e., 2000, 2007 and 2015, there was also amplification of an additional band of 190 bp which was observed during the year 2007. Possibly due to contamination, this additional band's frequency was quite low (0.029). Change in allele frequency was not found to be significant in case of the NAU2190 locus. A significant change in allele frequency was observed at the locus JESPR204 when compared for the years 2007 and 2015 and for the years 2000 and 2015. The Shannon's Information Index value decreased from 0.41 in 2000 to 0.32 in 2015; however, this difference was not found to be significant. The average gene diversity decreased from 0.29 in 2000 to 0.21 in 2015. This reduction in gene diversity might signal loss of alleles after regeneration which directly affects the genetic integrity of the accession. However, the changes in gene

Table 4: Number of alleles (N), number of effective alleles (Ne), Shannon's Information Index (I), average observed heterozygosity (Ho), average expected heterozygosity (He), Nei's Expected heterozygosity (Nei) and pairwise Fst values in comparison to original population (year 2000), values in Mean±SD in cotton (*Gossypium arboreum* L.) accessions conserved in the National Genebank

Accession identity	Year	N	N _e	I	H _o	H _e	Nei	F _{st}
IC440885	2000	1.60 ± 0.54	1.59 ± 0.54	0.41 ± 0.37	0.55 ± 0.51	0.30 ± 0.27	0.29 ± 0.27	0.000
	2007	1.80 ± 0.44	1.43 ± 0.41	0.37 ± 0.29	0.36 ± 0.38	0.25 ± 0.21	0.25 ± 0.21	0.039
	2015	1.60 ± 0.54	1.34 ± 0.36	0.32 ± 0.30	0.29 ± 0.30	0.21 ± 0.20	0.21 ± 0.20	0.066
IC440886	2000	1.60 ± 0.54	1.59 ± 0.54	0.41 ± 0.37	0.58 ± 0.53	0.30 ± 0.27	0.29 ± 0.27	0.000
	2007	1.80 ± 0.44	1.58 ± 0.51	0.43 ± 0.34	0.55 ± 0.49	0.30 ± 0.25	0.30 ± 0.25	0.005
	2015	1.80 ± 0.44	1.52 ± 0.47	0.40 ± 0.33	0.47 ± 0.43	0.28 ± 0.24	0.28 ± 0.24	0.014
IC440887	2000	1.40 ± 0.54	1.35 ± 0.49	0.26 ± 0.36	0.32 ± 0.45	0.18 ± 0.25	0.18 ± 0.25	0.000
	2007	1.60 ± 0.54	1.30 ± 0.43	0.26 ± 0.31	0.28 ± 0.42	0.17 ± 0.22	0.17 ± 0.22	0.011
	2015	1.40 ± 0.54	1.28 ± 0.42	0.23 ± 0.32	0.25 ± 0.38	0.16 ± 0.23	0.16 ± 0.22	0.011
IC440888	2000	1.60 ± 0.54	1.59 ± 0.54	0.41 ± 0.37	0.37 ± 0.51	0.30 ± 0.27	0.29 ± 0.27	0.000
	2007	1.60 ± 0.54	1.50 ± 0.49	0.38 ± 0.35	0.20 ± 0.44	0.27 ± 0.25	0.26 ± 0.25	0.024
	2015	1.40 ± 0.54	1.40 ± 0.54	0.27 ± 0.37	0.39 ± 0.54	0.20 ± 0.27	0.19 ± 0.27	0.105
IC440889	2000	1.40 ± 0.54	1.34 ± 0.47	0.26 ± 0.35	0.22 ± 0.31	0.18 ± 0.25	0.18 ± 0.25	0.000
	2007	1.40 ± 0.54	1.39 ± 0.54	0.27 ± 0.37	0.37 ± 0.51	0.20 ± 0.27	0.19 ± 0.27	0.019
	2015	1.40 ± 0.54	1.39 ± 0.54	0.27 ± 0.37	0.37 ± 0.51	0.20 ± 0.27	0.19 ± 0.27	0.017
IC440890	2000	1.60 ± 0.54	1.59 ± 0.54	0.41 ± 0.37	0.57 ± 0.52	0.30 ± 0.27	0.29 ± 0.27	0.000
	2007	1.40 ± 0.54	1.39 ± 0.54	0.27 ± 0.37	0.38 ± 0.52	0.20 ± 0.27	0.19 ± 0.27	0.107
	2015	1.40 ± 0.54	1.39 ± 0.54	0.27 ± 0.37	0.38 ± 0.53	0.20 ± 0.27	0.19 ± 0.27	0.107

diversity observed in any of the years were not found to be significant. For the sake of comparison, the individual years were assumed to be separate populations and a pairwise FST comparison was performed. The pairwise FST comparison between the various years revealed very low differentiation levels. Analysis of molecular variance (AMOVA) revealed that the total variance in the accession could be partitioned into 70% within individuals, 17% among individuals and 12% among the various regeneration years.

IC440886

The accession IC440886 was analyzed using five microsatellite markers BNL3545, DPL0702, NAU2190, JESPR204 and NAU1043. A minor change was observed in the case of NAU1043 locus. NAU1043 amplified a single band of 210 bp during all the years. However, in the years 2007 and 2015 a new band was also observed at 180 bp. The new band was present at relatively low frequencies of 0.022 and 0.017 in the year 2007 and 2015, respectively. No significant change in allele frequency was observed in any of the loci analyzed. The gene diversity values were more or less similar as these were 0.29 ± 0.27 and 0.28 during the years 2000 and 2015, respectively. Pairwise F_{ST} values revealed very low genetic differentiation among different years. AMOVA revealed that the total variance in the accession could be portioned into 96% within individuals and 4% among various years. No significant difference was observed in Shannon's information index values after the two regenerations.

IC440887

Five primers namely, DPL0702, NAU2190, JESPR204, NAU1043 and NAU6966 were used to analyze the genetic integrity of this accession. All of the primers produced same-sized fragments using PCR amplification of loci except one, i.e., JESPR204. This primer amplified a single band of the size 190 bp in all three years of regeneration. In addition, this primer produced a band of 150 bp during the year 2007 with a very low frequency of 0.025. No significant change in allele frequency was observed at all the loci analyzed. The gene diversity values were more or less similar at 0.18 and 0.16 during the years 2007 and 2015, respectively. There were no statistically significant differences in Shannon's information index after regenerations. Pairwise F_{ST} values ranged from 0.005 to 0.012, indicating low genetic differentiation after regeneration. AMOVA revealed that most of the variance in the accession was within individuals at 98% and only 2% could be attributed to among years.

IC440888

The accession was analyzed for genetic integrity changes using five microsatellite primers, namely BNL3545, DPL0702, NAU2190, NAU1043 and NAU4926. All these five primers produced consistent band across all three years except for the primer NAU2190 which produced 210 bp band during the years 2000 and 2007 while this was found missing during the year 2015. The frequency of the 210 bp band amplified

by NAU2190 steadily decreased from 0.47 in 2000 to 0.22 in 2007 and to 0 in 2015. Out of all the loci analyzed for change in allele frequency, NAU2190 showed a significant change when years 2000 and 2015 were compared. No significant change in Shannon's information Index was observed. A reduction in gene diversity was also observed in 2007, from 0.29 to 0.19 in 2015. Treating the three cycles of regeneration as three populations, pairwise F_{ST} values were found to be low indicating less genetic differentiation between the various years before and after regeneration. The AMOVA revealed that the highest share of the total variance was due to within individuals at 82% while both among individuals and among years had an equal share of 9% of the total variance.

IC440889

The five primers used for testing the genetic integrity of the accession IC440889 included BNL3545, DPL0702, NAU2190, NAU1043 and NAU4926. No changes were observed in this accession with respect to the number of bands amplified across the various regeneration cycles. No significant change in allele frequency was observed in any of the loci. The same was true for Shannon's information Index as well. The average gene diversity was 0.19 and pairwise F_{ST} values were very low indicating less differentiation between the various years after regeneration in the accession. The AMOVA revealed that 89% of the total molecular variance is from within individuals, followed by 9% from among individuals and 2% among the various years.

IC440890

Five microsatellite markers BNL3545, DPL0702, NAU2190, JESPR204 and NAU4926 were used to analyse the genetic integrity of this accession. There was no change in the bands amplified with respect to four primers, however, one primer, i.e., JESPR204 amplified two bands of the sizes 190 and 180 bp. One band of 190 bp was found consistent in all three years but an additional band of 180 bp which was there during first regeneration in the year 2000, was found to be lost during subsequent regeneration cycles during 2007 and 2015. Change in allele frequency was only found to be statistically significant in the case of JESPR204 loci, between 2000 and 2007 and between 2000 and 2015. No statistically significant changes were observed in Shannon's information index. The gene diversity also decreased from 0.29 in 2007 to 0.19 in 2015. The average gene diversity in this accession was 0.23. Pairwise F_{ST} revealed less genetic differentiation between the three cycles of regeneration in the accession when each individual year was considered as a population. AMOVA results revealed that 93% of the total variance could be attributed to within individuals and 7% due to among years.

Year-wise AMOVA analysis for the six accessions under study indicated that most of the variance was sourced from

individuals (55.8%) and within individuals (43.6%) and only 0.4% among the various years. The mean allelic pattern of the combined analysis of all the accessions year-wise are given in Figure 1.

Based on our observations, the genetic integrity of the accessions analyzed has not been altered but some minor changes have been observed. We found the appearance of additional bands, e.g. 190 bp in accession IC440885 and 150 bp in IC440887. However, these were not found to be stable as they were not observed in the subsequent regeneration cycle. Similarly, loss of bands has also been observed in one accession. In the genebank, all regeneration cycles are carried out from the base collection and not from the residual seed left from the previous cycle of regeneration. This practice is to avoid compounding negative effects, if any, on the genetic integrity of the accessions after various cycles of regeneration. These additional bands might not have been sampled from the base collection during regeneration years, where these were found to be missing and might not have been observed using microsatellite markers in the present study. Some other reasons might be that somatic mutations occurring during regeneration cycles might not be stable and revert to the original state in the next cycle of regeneration. Epigenetic modification, PCR artifacts and errors in handling the plant material could also lead to such apparent discrepancies in the presence of absence of a band. The minor fluctuations in the frequencies of bands of the rare alleles observed in the present study might be due to genetic drift. The initial representation of the accession in the gene bank might not be the representation of the entire genetic variation in the accession. Subsequent regenerations may involve different accession subsets, leading to observed frequency fluctuations.

The breeding mechanism in cotton is predominantly self-pollinating; however, cross-pollination has been reported to an extent of 10 to 50%. In the case of *G. arboreum* L., the anthers are in direct contact with the stigma, and the pollen is shed as soon as the flower opens, which makes them predominantly self-pollinated (Kottur, 1921). The natural

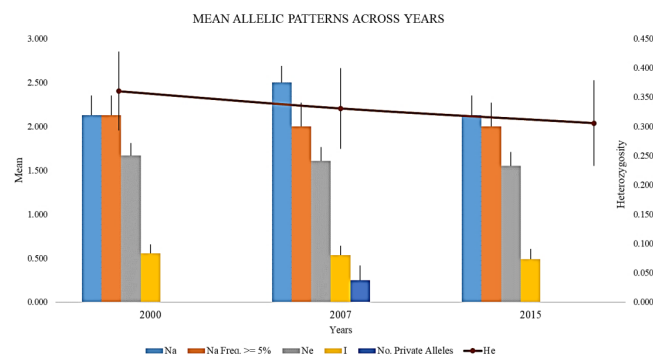


Figure 1: Mean allelic patterns across three cycles of regeneration of cotton (*G. arboreum* L.) accessions conserved in the National Genebank of India

rate of outcrossing in *G. arboreum* L. is about 2% (Afzal *et al.*, 1950). The major pollinating agents in cotton are insects; therefore, during the regeneration of cotton, bagging and insect-proofing are done to prevent inadvertent outcrossing. The accessions used in this study have been regenerated in controlled conditions in the field plot at ICAR-CICR, Nagpur. During the regeneration of these accessions, insect-proof nets are used to prevent any inadvertent introduction of foreign pollen or contamination from other accessions. Based on our observations in the genetic integrity of cotton accessions in the genebank, it can be emphasized that the regeneration protocol in place for cotton is quite efficient and effective.

In a study conducted earlier in rye, an open-pollinating species maintained in the gene bank for 45 years, significant changes in allele frequency was noted using microsatellite markers (Chebotar *et al.*, 2003). Significant allele frequency changes were also seen in landraces of barley which were analysed with isozyme markers (Parzies *et al.*, 2000). Very few studies have been carried out in the case of self-pollinated or often cross-pollinated species of plants. A genetic integrity study using eight accessions of wheat with microsatellite markers found that only a single accession showed some genetic drift, and no significant changes in genetic integrity were observed (Börner *et al.*, 2000). Allelic frequency changes in maize studied using isozyme markers revealed no major changes in allele frequency during regeneration, but minor changes due to genetic drift were observed (Reedy *et al.*, 1995).

Our study can be compared to that of Börner *et al.*, 2000, who analyzed the genetic integrity of the eight accessions of wheat accessions using microsatellite markers. They observed some minor changes due to genetic drift but no significant changes in genetic integrity after regeneration. The minor changes they observed in the genetic integrity were attributed to genetic drift, unintentional selection, pollen contamination, seed contamination, or mislabeling in self-pollinating crops. The voucher accessions used in our study have uneven sample sizes for different accessions used for genetic integrity analysis that may have hindered ascertaining the accessions' complete genetic structure. Conducting more extensive genetic and environmental tests for the material under investigation would be important. Deeper marker analysis, high-density DNP chips and DNA sequencing might clarify the underlying reasons for the observed variations. Maintaining careful records and quality control procedures like increasing area of plots for higher seed production, more stringent collection and labeling practices after regeneration, use of insect-proof cages to prevent cross-pollination and proper selection of site for regeneration and minimizing biotic and abiotic stresses may help in preserving the genetic integrity of the accessions for more period of time.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

Acknowledgments

We greatly acknowledge financial support from the Indian Council of Agricultural Research (ICAR). Director, ICAR-NBPGR and Head, Division of Genomic Resources, ICAR-NBPGR, are also acknowledged for providing laboratory facilities for carrying out this work.

References

- Abdurakhmonov IY, RJ Kohel, JZ Yu, AE Pepper, AA Abdullaev, FN Kushanov, IB Salakhutdinov, ZT Buriev, S Saha, BE Scheffler, JN Jenkins and A Abdulkarimov (2008) Molecular diversity and association mapping of fiber quality traits in exotic *G. hirsutum* L. germplasm. *Genom.* 92(6): 478-487.
- Adhikari J, S Das, Z Wang, S Khanal, R Chandnani, JD Patel, VH Goff, S Auckland, LK Rainville, D Jones and AH Paterson (2017) Targeted identification of association between cotton fiber quality traits and microsatellite markers. *Euphytica*. 213(3): 1-15.
- Afzal M and AH Khan (1950) Natural crossing in cotton in western Punjab. Natural crossing under field conditions. *Agron. J.* 42 (2): 89-93.
- Börner A, S Chebotar and V Korzun (2000) Molecular characterization of the genetic integrity of wheat (*Triticum aestivum* L.) germplasm after long-term maintenance. *Theor. Appl. Genet.* 100(3-4): 494-497.
- Brenan JPM and JB Hutchinson (1960) The application of genetics to cotton improvement. *Kew Bull.* 14(2): 249.
- Chebotar S, MS Röder, V Korzun, A Börner (2002) Genetic integrity of ex situ genebank collections. *Cell Mol. Biol. Lett.* 7(2A): 437-444.
- Chebotar S, MS Röder, V Korzun, B Saal, WE Weber and A Börner (2003) Molecular studies on genetic integrity of open-pollinating species rye (*Secale cereale* L.) after long-term genebank maintenance. *Theor. Appl. Genet.* 107(8): 1469-1476.
- Dan X, C Wang, Y Su, A Zhang, R Wang, I Khan and L Huang (2020) Evaluation of genetic integrity of pearl millet seeds during aging by genomic-SSR markers. *Mol. Biol. Rep.* 47(8): 5747-5754.
- Dongre A and V Parkhi (2005) Identification of cotton hybrid through the combination of PCR-based RAPD, ISSR and microsatellite markers. *J. Plant Biochem. Biotechnol.* 14(1): 53-55.
- Dongre AB, DM Ramteke, MR Bhandarkar, MP Raut and KJ Meshram (2011) Genetic diversity analysis of *Gossypium arboreum* (diploid cotton) cultivars revealed by PCR based molecular markers. *J. Cotton Res. Dev.* 25(1): 9-13.
- Food and Agriculture Organization (2015) *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture*. Commission on Genetic Resources for Food and Agriculture Assessments.
- Gupta R, US Chandrashekar, SK Chakrabarty and M Dadlani (2012) A simple modified method of DNA extraction from seeds for PCR amplifications. *Indian J. Agri. Sci.* 82(1): 75-77.
- Gutiérrez OA, S Basu, S Saha, JN Jenkins, DB Shoemaker, CL Cheatham and JC McCarty (2002) Genetic distance among

- selected cotton genotypes and its relationship with F2 performance. *Crop Sci.* 42(6): 1841-1847.
- Hamblin MT, ML Warburton and ES Buckler (2007) Empirical Comparison of Simple Sequence Repeats and Single Nucleotide Polymorphisms in assessment of Maize diversity and relatedness. *PLOS ONE*. 2(12): e1367.
- Liu S, RG Cantrell, JC McCarty and JM Stewart (2000) Simple Sequence Repeat-Based Assessment of Genetic Diversity in Cotton Race Stock Accessions. *Crop Sci.* 40(5): 1459-1469.
- Pan Y, Y Liu, M Ren, XW Zhang, JY Mou, XY Chen, X Cong and ZD Wang (2013) Analysis on tobacco Genetic Integrity of different populations by SSR Markers. *J. Plant Genet. Resour.* 14(5): 978-984.
- Park YH, MS Alabady, M Ulloa, B Sickler, TA Wilkins, J Yu, DM Stelly, RJ Kohel, OM El-Shihy and RG Cantrell (2005) Genetic mapping of new cotton fiber loci using EST-derived microsatellites in an interspecific recombinant inbred line cotton population. *Mol. Genet. Genom.* 274(4): 428-441.
- Parzies HK, W Spoor and RA Ennos (2000) Genetic diversity of barley landrace accessions (*Hordeum vulgare* ssp *vulgare*) conserved for different lengths of time in ex-situ genebanks. *Heredity*. 84(4): 476-486.
- Peakall R and PE Smouse (2012) GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics*. 28(19): 2537-2539.
- Rao NK, EH Roberts and RH Ellis (1988) A comparison of the quantitative effects of seed moisture content and temperature on the accumulation of chromosome damage and loss of seed viability in lettuce. *Ann Bot.* 62(3): 245-248.
- Reedy ME, AD Knapp and KR Lamkey (1995) Isozyme allelic frequency changes following maize (*Zea mays* L.) germplasm regeneration. *Maydica*. 40(3): 269-273.
- Shen X, W Guo, X Zhu, Y Yuan, JZ Yu, RJ Kohel and T Zhang (2005) Molecular mapping of QTLs for fiber qualities in three diverse lines in upland cotton using SSR markers. *Mol. Breed.* 15(2): 169-181.
- Thompson PA, RD Smith, JB Dickie, RH Sanderson and RJ Probert (1981) Collection and regeneration of populations of wild plants from seed. *Biol. Conserv.* 20(3): 229-245.
- Tyagi P, MA Gore, DT Bowman, BT Campbell, JA Udall and V Kuraparthi (2014) Genetic diversity and population structure in the US upland cotton (*Gossypium hirsutum* L.). *Theor. Appl. Genet.* 127(2): 283-295.
- Ulloa M, IY Abdurakhmonov, M Perez, R Percy and JM Stewart (2013) Genetic diversity and population structure of cotton (*Gossypium* spp) of the New World assessed by SSR markers. *Botany*. 91(4): 251-259.
- Yeh FC (1997) Population genetic analysis of co-dominant and dominant markers and quantitative traits. *Belg J. Bot.* 129: 157.
- Yu J, Z Zhang, DA Zhu C Tabanao, G Pressoir, MR Tuinstra, S Kresovich, RJ Todhunter and ES Buckler (2009) Simulation appraisal of the adequacy of number of background markers for relationship estimation in association mapping. *Plant Genom.* 2(1): 63-77.

RESEARCH ARTICLE

Studies on Traditional Melon 'Vellari' (*Cucumis melo* var. *momordica* L.) in Tamil Nadu, India

Prabhu P^{1*}, Anjula Pandey², S Rajkumar², Harish GD², Chithra Pandey² and Rakesh Bharadwaj²

Abstract

The local snapmelon landrace known as "Vellari" is an important traditional crop in southern India, specifically in the districts of Tamil Nadu. However, it has received limited attention in global studies and gene bank collections, primarily due to the lack of germplasm collections and data on its morphological traits and significant quality characteristics. This study examined seventeen germplasm accessions of "Vellari" collected from five districts representing diverse climatic zones for their fruit morphology and phenotypic variability. Organoleptic assessments based on consumer preferences were also conducted. A total of 29 quantitative and 27 qualitative descriptors were used to estimate phenotypic diversity. Principal component analysis (PCA) was performed to assess variability between the collections. The analysis identified several defining characteristics that differentiate the snap melon accessions, including leaf pubescence, flower earliness, flowering time, peduncle length, fruit shape and size, and days to maturity. The first five components explained 84.29% of the cumulative percentage of variation. A wild taxon called "Sukkangai" (*Cucumis melo* ssp. *agrestis* var. *agrestis*) was also reported for local use in the surveyed area.

Keywords: Less-known, Landraces, Tamil Nadu, Snap melon, Vellari, Sukkangai.

¹ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India

***Author for correspondence:**

pariprabhu594@gmail.com

Received: 17/07/2023 **Revised:** 20/07/2023

Accepted: 20/09/2023

How to cite this article: Prabhu P, A Pandey, S Rajkumar, GD Harish, C Pandey and R Bharadwaj. (2024) Studies on Traditional Melon 'Vellari' (*Cucumis melo* var. *momordica* L.) in Tamil Nadu, India. *Indian J. Plant Genetic Resources*. 37(1): 97-104. **DOI:** 10.61949/0976-1926.2024.v37i01.12

Introduction

Cucumis melo L. (2n = 24) (family Cucurbitaceae) is a tropical old-world species. The taxon is classified into two sub-species sub-species *melo* and ssp. *agrestis* (Jeffrey 1980; Sebastian 2010). Further, these sub-species are classified into 15 horticultural groups (Pitrat 2000; 2013). Snap melon [*C. melo* L. subsp. *agrestis* var. *momordica* (Roxb.) Duthie et Fuller] is among the important melons indigenous to India, cultivated in almost all parts of the country as a mono-crop or mixed-crop (Malik *et al.*, 2014; Muthuselvi *et al.*, 2019). During the rainy season, snap melon is grown as a sole crop in the summer and as a mixed crop, primarily with maize, bajra, and sorghum (Seshadri and More 2001). Tremendous variation exists in fruit size, shape, color, texture, flavor, and taste. Immature fruits are used as salad and for culinary purposes; mature fruits are used as a dessert. Snap melon is known as a potential resistant source for biotic stress like nematode and insect pest tolerance (Dhillon *et al.*, 2007). Indian snap melon landraces were used in various global melon breeding programs for many valuable traits (Dhillon 2015). Many of them are widely used as reference accessions and are good sources of nutrients, vitamin C, sugars, minerals and dietary fibers. Snap melons are commonly referred as *Phut* in the northern desert region of India, which means to split. Fruit can be split longitudinally or irregularly; occasionally, only the skin peels off the fruit (Dhillon *et al.*, 2007). A 100 g edible fruit with 5.6 g carbohydrates, 18.6 mg

vitamin-C, 0.3 g protein, 95.7% moisture (Peter and Hazra 2012) and 74.0 kcal energy (Goyal and Sharma 2009).

Due to the fast replacement of the vegetable melon cultivars with improved varieties of muskmelon and cucumbers, the collection and conservation of these valuable germplasm deserves a top priority (Fregany *et al.*, 2011; Koli *et al.*, 2013; Manchali *et al.*, 2019). The south Indian melons denoted with a source of resistance to cucumber mosaic virus, zucchini yellow mosaic virus, powdery mildew (races 1, 2, 3, 5), *Fusarium* wilt (races 1, 2), *Aphis gossypii* and leaf miner (Fregany *et al.*, 2011). Despite producing climacteric fruits, the poor keeping qualities of snap melon cultivars prevents widespread commercial acceptance across the country. In the Indian national collections at ICAR-National Gene Bank, New Delhi, the snap melon from Tamil Nadu is barely represented.

Keeping the importance of snap melons from south India, the study was undertaken on the less-known melons “Vellari” with aim to: 1) Exploring unrepresented areas having distinct accessions in southern Indian districts of Tamil Nadu; 2) Characterization of collected germplasm for morphological traits, and to look for associations between morphological and geographical distances; 3) Organoleptic assessment to popularize and extend its use.

Materials and Methods

Germplasm Collection

Collection sites for germplasm of “Vellari” were identified after pre-surveying in the six districts of Tamil Nadu with help of the Department of Horticulture and Plantation Crops, Government of Tamil Nadu, Tamil Nadu. The exploration was undertaken in - Dindigul, Virudhunagar, Cuddalore, Kancheepuram, Ariyalur, and Namakkal districts during February-March 2020 and a total of 156 study sites were visited. Detailed passport data were recorded as per the standard methodology for collection (Dwivedi 2010). Farmer’s fields and local markets of each district were thoroughly surveyed for variability in snap melon.

Germplasm Characterization and Data Analysis

A total of seventeen “Vellari” accessions were collected as mature fruits. The germplasm was evaluated in the field from February to May 2021. A total of 56 morphological characters were recorded, including 29 quantitative traits and 27 qualitative traits per the Cucumis melo descriptors published by IPGRI (2003) (Table 1).

Principal component analysis (PCA) was performed to determine which variable contributed more with its variance to the total variance observed in the collected accessions. Using the correlation matrix among 56 variables for 17 accessions, Eigenvalues and contribution percentages of each principal component axis were computed (Jeffers 1967). All computations were performed using SPSS 28.0.0

software, Euclidean distances were calculated across accessions, and a distance matrix was produced using DARwin 6.0.

Geo Reference Mapping and Organoleptic Assessment

Sampling sites were depicted using software (DIVA- GIS7.5) and the geo-referenced map was produced (Figure 1). The organoleptic assessment was done with the help of 36 informants. The data were recorded for edibility preferences and acceptability.

Identity Confirmation

After a study of the plants, the identity was confirmed as a snap melon. In accordance with regular herbarium procedures, herbarium specimens of chosen material with flowering and fruiting were made in the field and deposited at the National Herbarium of Cultivated Plants. (NHCP), ICAR-NBPGR, New Delhi.

Result and Discussion

Germplasm collection

During an exploration undertaken to six districts of Tamil Nadu viz., Dindigul, Virudhunagar, Cuddalore, Kancheepuram, Ariyalur and Namakkal in February-March 2020, a total of 17 accessions of distinct types of landraces of “Vellari” and two *Sukkangai* accessions were collected (Figure 2) from 156 study sites located in the farmers’ field, local market and kitchen gardens. The study area lies in a wide range between 9.6° N and 12.9° N latitude, 77.6° E to 79.8° E longitude, and altitude ranging from 5 to 325 m above mean sea level. Two *Sukkangai* accessions were collected from the Dindigul district (PP 01, PP 02). Seventeen snap melon accessions were collected from the following five districts, Virudhunagar (PP 03-04), Kancheepuram (PP

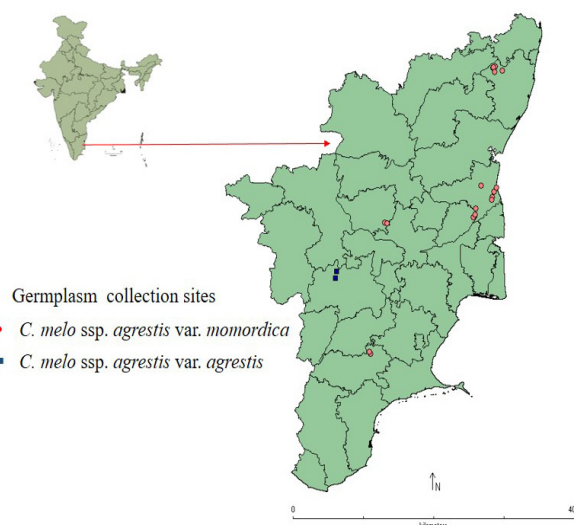


Figure 1: Area of study and collection sites

Table 1: List of descriptors used for morphological characterization

S. No	Descriptor code	Descriptor
1	PtSz	Plant size :3 (<1 m ³) 5 (1–3 m ³) 7 (>3 m ³)
2	IL	Internode length: average internode length of 10–15 th node on main vine
3	NNFF	No. of nodes to first fruit
4	STT	Stem thickness in mm
5	NPB	No of plant branches: count only flowering branches
6	LS	Leaf shape:1 (entire) 2 (trilobate) 3 (pentalobate) 4 (3- palmately lobed) 5 (5-palmately lobed) 99 other
7	LL	Leaf lobes: 3 (shallow) 5 (intermediate) 7 (deep)
8	LP	Leaf pubescence type: 3 (soft) 5 (intermediate) 7 (hard)
9	GL	Glossiness: 3 (glossy) 5 (intermediate) 7 (dull)
10	LR	Leaf ratio: Leaf length divided by leaf width. Measures leaves in the middle of the branch
11	LPL	Leaf petiole length in cm
12	EM	Earliness of male: 3 (early) 5 (intermediate) 7 (late)
13	EF	Earliness of female: 3 (early) 5 (intermediate) 7 (late)
14	DFF	Days to first flowering
15	D50	Days to 50% flowering
16	PL	Peduncle length in cm
17	FBS	Flower bud shape: 1 (globular) 2 (intermediate) 3 (long) 99 (other)
18	LSP	Mean length of standard petal in cm
19	WSP	Mean Width of standard petal in cm
20	OP	Ovary pubescence: 1 (less) 3 (medium) 3 (dense)
21	OS	Ovary shape: 1 (flat) 2 (round) 3 (long) 4 (very long)
22	FS	Fruit shape: 1 (globular) 2 (flat) 3 (oblate) 4 (elliptical) 5 (pyriform) 6 (ovate) 7 (acorn) 8 (elongate) 9 (scallop) 99 (other)
23	FSZ	Fruit size/weight in g
24	FL	Fruit length width ratio: the length from stem end to blossom end of the fruit divided by the width at the broadest point
25	TM	Time of maturity: 1 (< 70 days) 2 (70–90 days) 3 (91–110) days 4 (>110 days)
26	DFFrt	Days to first fruit
27	SC	Predominant fruit skin color: 1 (white) 2 (light yellow) 3 (cream) 4 (pale green) 5 (green) 6 (dark green) 7 (blackish green) 8 (orange) 9 (brown) 10 (grey) 99 (other)
28	SFSC	Secondary fruit skin color: 1 (white) 2 (light yellow) 3 (cream) 4 (pale green) 5 (green) 6 (dark green) 7 (blackish green) 8 (orange) 9 (brown) 10 (grey) 99 (other)
29	IMFC	Primary color of immature fruit: 1 (light green) 2 (intermediate) 3 (dark green)
30	SSCP	Secondary skin color pattern: 0 (no secondary color) 1 (light green) 2 (intermediate) 3 (dark green)
31	FSRF	Fruit surface: 1 (smooth) 2 (grainy) 3 (finely wrinkled) 4 (deeply wrinkled) 5 (shallowly wavy) 6 (rarely warts) 7 (numerous warts) 8 (lightly corked/netted) 9 (heavily corked/netted) 10 (sutures) 99 (other)
32	FSL	Fruit stem length in cm
33	CH	Fruit splitting or cracking habit 3 (low) 5 (intermediate) 7 (high)
34	MCF	Main color of flesh: 1 (white) 2 (yellow) 3 (cream) 4 (pale green) 5 (green) 6 (pale orange) 7 (salmon)
35	FT	Flesh texture: 1 (smooth-firm) 2 (grainy-firm) 3 (soft-spongy) 4 (mealy) 5 (fibrous-gelatinous) 6 (fibrous dry)
36	FF	Flesh flavor: 3 (insipid) 5 (intermediate) 7 (sweet)
37	FTH	Flesh thickness in cm
38	SDLG	Seed length in cm
39	SDW	Seed width in cm
40	SDT	Seed thickness in cm

05-07, PP18-19), Cuddalore (PP 08-12), Ariyalur (PP 13-15), and Namakkal (PP/KRR 01, PP/KRR 02). The collected germplasm was evaluated and multiplied in the Ariyalur district of Tamil Nadu from February to May 2021 and submitted to the National Gene Bank, New Delhi. Nine of 17 accessions received indigenous collection numbers (Table 2). The remaining accessions sent for multiplication. The study area includes four climatic zones of Tamil Nadu, i.e., the southern zone, Western zone, Northeastern zone, Western zone, and Cauvery delta zone (TN-ENVIS) (Figure 1).

Variability Study in “Vellari”

Genetic resources of exotic and native melons have widened our knowledge of understanding and utilization of the potential value of the melons (Sari and Solmaz 2005; Mohamed and Yousif, 2004; Laghetti *et al.*, 2008; Joseph *et al.*, 2013, 2017; Staub *et al.*, 2004; Solmaz *et al.*, 2016). Snap melons of southern India are less worked out with respect to their genetic resource potential. Accessions from south India are meagerly represented in the National Gene Bank holding compared to North Indian melons (Fregany 2011; Manchali *et al.*, 2019). Collection and utilization of such variability are essential. For 56 selected qualitative and quantitative descriptors (IPGRI 2003) were assessed in the field. About 17 accessions of snap melon collected from Tamil Nadu state, Southern India, were evaluated to estimate the genetic diversity among the snap melon accessions. Across snap melon accessions, 16 descriptors were to be uniform, which are discarded from the analysis, and the remaining 40 descriptors were used for analysis (Table 1). The snap melon accessions used in the analysis showed substantial genetic diversity (Figure 3)

Principal component analysis was used to assess the variability in snap melon accessions. The percentage of variation explained by the first five components were 34.25, 25.81, 12.30, 6.33 and 5.58, respectively; the cumulative variance of first five components was 84.6% (Tables 2 & 3 and Figure 4) and the principal characters with higher Eigenvectors delineated the accessions into separate groups in the first five components are represented (Table 3). The analysis revealed that the variations in leaf pubescence type, earliness of male and female flower, days to first flowering, days to 50% of flowering, peduncle length, flower bud shape, ovary pubescence, ovary shape, fruit shape, fruit size, fruit length-width ratio, time of maturity, days to first fruit, predominant fruit skin color, the main color of flesh and flesh flavor were contributed more to distinguish snap melon accessions evaluated in the present study, accessions showing larger variation in days to first flowering (20–34), days to 50% of flowering (24–38), ovary shape (round, long and very long) fruit shape (elongate, ovate and oblate) fruit size (450–3000 g), predominant fruit skin color (light yellow, yellow, grey, and orange) and main color of flesh (white, cream, pale orange). A total of 22 characters out of



Figure 2: Collection of germplasm: (a) *C. melo* subsp. *agrestis* var. *momordica* growing in the farmer's field; (b) *C. melo* subsp. *agrestis* var. *agrestis* in natural habitat; (c) melons sold in local market of Madurai, Tamil Nadu; (d) variability in melons

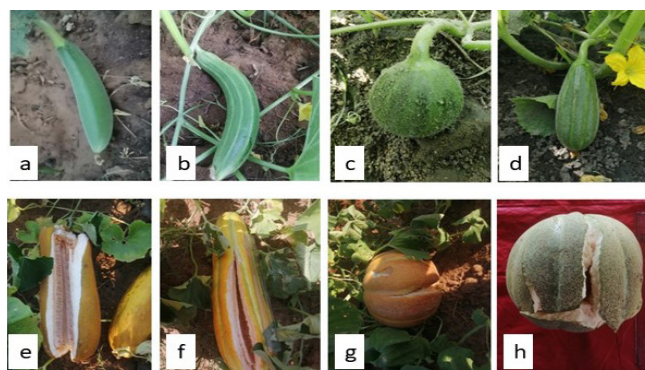


Figure 3: Variability in snap melon fruit morphology a & e - PP 04; b & f - PP/KRR 01; c & g - PP 18; d & h - PP 19

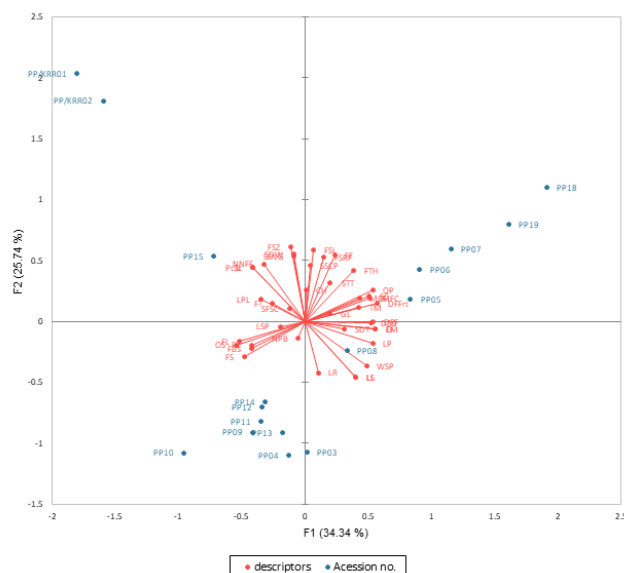


Figure 4: Principal component analysis biplot depicting the relationship of descriptors and accessions (axes F1 and F2: 60.08%)

Table 2: Indigenous collection number for collected germplasm

S. No.	Accession	Collector-No.	Crop/Species	Cultivar name/bio-status
1	IC-0647724	PP-03	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
2	IC-0647725	PP-04	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
3	IC-0647726	PP-08	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
4	IC-0647727	PP-09	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
5	IC-0647728	PP-10	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
6	IC-0647729	PP-15	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
7	IC-0647730	PP-19	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
8	IC-0647731	PP/KRR-01	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace
9	IC-0647732	PP/KRR-02	Snapmelon/ <i>Cucumis melo</i> var. <i>momordica</i>	Vellari/landrace

40 showed significant variance, and these characters were used to generate a dendrogram (Figure 5). The Euclidean distances were calculated across landraces and a distance matrix was produced using DARwin 6.0 software. The 17 accessions were separated into three clusters: the first cluster had eight accessions, the second cluster had seven accessions, and the third cluster had two accessions. These clusters were mainly separated by fruit shape and size. Accessions collected from each district have significant fruit size and shape variations, so most accessions from the same district were clustered together. According to the dissimilarity matrix, PP 10 and PP 15 are extremely distant accessions with a dissimilarity index of 33.9, while PP/KRR 01 and PP/KRR 02 are extremely similar with a dissimilarity index of 1.59.

The present collection included landraces producing fruits mostly appropriate for local trading and self-consumption since seeds were exchanged between local farmers who grew snap melon for such purposes. So these snap melon cultivations are restricted to particular geographical areas based on local people's preferences because they are not suitable for distant markets due to their poor quality of keeping. We found that each district in our study area has distinct fruit types.

Germplasm collected from the Kancheepuram district was preferred in the same way as the muskmelon due to fruit taste, shape and skin type, showing intermediate characters between the muskmelon and snapmelon. Detailed morphological study coupled with the molecular study will better understand its identity and relation with other materials. A recent study (Pandey *et al.*, 2021) observed that a landrace called 'Arya' in Rajasthan has some intermediate characteristics of snake melon and snap melon; a molecular study confirmed that 'Arya' is a separate taxon. Crossability studies with other taxa of *melo* will enrich the gene pool and help to assign a distinct taxonomic status based on the outcome of the hybridization (Joseph *et al.*, 2013).

Organoleptic Assessment

The comparison was made based on an organoleptic assessment that included 36 people, mostly women folks

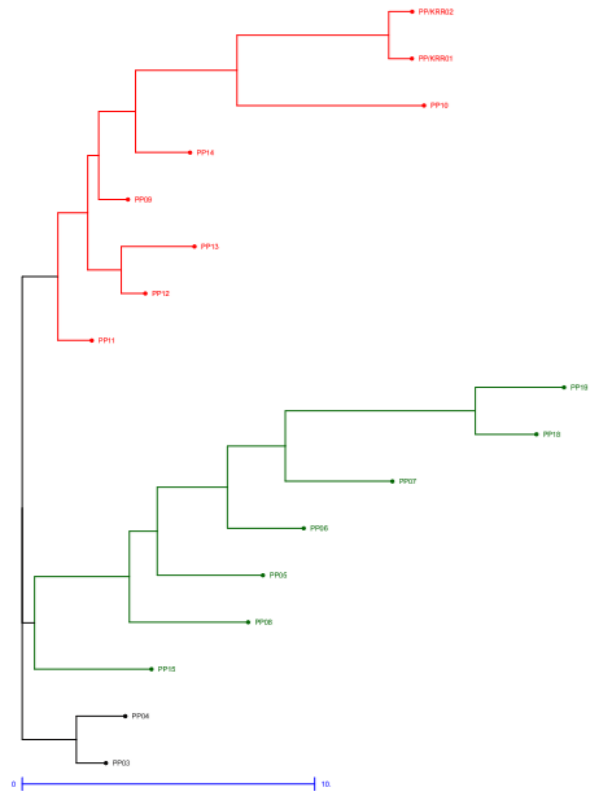


Figure 5: Euclidean distance clustering of 17 snap melon accessions based on 22 morphological descriptors

between the ages of 30 and 60. It was carried out to determine consumer preferences, and three fruit characteristics were evaluated: 1) Salad preference, 2) Dessert preference, 3) The aroma of ripened fruit. For a salad, the majority of participants preferred PP15 (40%), while none preferred the following accessions: PP05, PP06, PP07, PP18 and PP19. On the other hand, 72% of people highly preferred the above-mentioned accessories for dessert purposes because of their sweet flesh and aroma. These six accessions were collected from the Kancheepuram district, where they were primarily cultivated and used for desserts because of their sweet flesh and pleasant aroma. However, due to their rough skin, they were not suitable for salads. The remaining eleven

Table 3: Eigen value and percent of total variation and component matrix for the principal component axes

Principal component	F1	F2	F3	F4	F5
Eigenvalue	13.735	10.296	4.925	2.564	2.228
Variability (%)	34.337	25.739	12.311	6.409	5.569
Cumulative (%)	34.337	60.076	72.388	78.796	84.365
Descriptor code					
PtSz	-0.171	0.211	0.142	-0.078	0.058
IL	-0.171	0.211	0.142	-0.078	0.058
NNFF	-0.135	0.227	-0.001	-0.136	0.16
STT	0.084	0.153	0.293	0.022	0.1
NPB	-0.022	-0.066	-0.109	0.143	-0.196
LS	0.167	-0.219	0.137	0.081	-0.004
LL	0.167	-0.219	0.137	0.081	-0.004
LP	0.225	-0.085	-0.132	0.078	0.105
GL	0.083	0.031	-0.307	-0.142	0.215
LR	0.046	-0.201	0.165	-0.037	-0.114
LPL	-0.143	0.088	-0.243	-0.041	0.159
EM	0.232	-0.03	0.049	-0.02	0.31
EF	0.232	-0.03	0.049	-0.02	0.31
DFF	0.223	0	-0.01	0.062	0.321
D50	0.215	-0.005	0.019	0.042	0.367
PL	-0.174	-0.092	0.161	0.039	-0.03
FBS	-0.173	-0.106	0.068	-0.069	-0.042
LSP	-0.079	-0.019	0.374	0.007	0.116
WSP	0.204	-0.175	-0.086	0.01	0.089
OP	0.224	0.125	-0.006	0.01	-0.163
OS	-0.225	-0.092	0.019	0.068	0.181
FS	-0.197	-0.137	-0.127	0.003	0.117
FSZ	-0.044	0.292	0.086	0.099	0.013
FL	-0.213	-0.079	-0.149	-0.006	0.138
TM	0.178	0.054	0.156	-0.342	-0.124
DFFrt	0.236	0.07	0.086	-0.157	0.083
SC	0.211	0.099	-0.007	0.099	-0.231
SFSC	-0.049	0.052	0.414	-0.017	0.095
IMFC	0.212	0.091	-0.021	0.157	-0.285
SSCP	0.017	0.22	-0.242	-0.026	0.152
FSRF	0.062	0.251	-0.132	0.052	-0.112
FSL	0.028	0.281	-0.079	-0.013	0.021
CH	0.005	0.124	0.055	0.532	0.026
MCF	0.179	0.09	-0.082	0.169	0.047
FT	-0.105	0.07	0.149	0.49	0.116
FF	0.098	0.259	-0.095	-0.044	-0.148
FTH	0.159	0.201	0.108	0.102	-0.101
SDLG	-0.035	0.257	0.158	-0.03	0.149
SDW	-0.036	0.266	-0.002	-0.143	0.007
SDT	0.13	-0.028	0.184	-0.336	-0.074

accessions were cultivated for immature and mature fruits with delicate skin and excellent palatability, making them ideal for salads. In this study, two snapmelon accessions from Tamil Nadu were used for comparison in the National Gene Bank, i.e., IC597018 and IC597021.

Ethnobotany and Uses

Snap melon is used in a variety of ways in Tamil Nadu, including immature fruits as salad, mature fruits as dessert and summer drinks with jaggery or sugar that provide a soothing sensation during summer. The young fruits are often confused with cucumber (*Cucumis sativus* L.) fruit due to their similar utility and common name, 'Vellari'. In some parts of the Cuddalore district, farmers get a good price for the seeds used to garnish sweets and savory dishes in the same way as other cucurbit seeds. In the same area, the immature fruits of "Sukkangai" (*Cucumis melo* ssp *agrestis* var *agrestis*) have a strong bitter taste. Local people were reported to process them for processed vegetables. The fruits are sliced into small pieces and soaked in buttermilk for a few days, then sun-dried and stored for future use. They are also used to cure stomach worm problems in children.

Focus needs to be placed on the following: fine grid survey, collection and conservation of germplasm from areas of availability (other districts and states in south India), diversity analysis, and comparative study with North Indian melons. South Indian snap melons, "Vellari," have been rapidly dwindling due to the improved cultivars of the common cucumber over the past two decades, and their significant traits can be used in crop improvement for better adaptability to drought conditions and other biotic stress tolerant traits.

References

- Dhillon NPS, R Ranjana, K Singh, I Eduardo, AJ Monforte, M Pitrat, NK Dhillon and PP Singh (2007) Diversity among landraces of Indian snap melon (*Cucumis melo* var. *momordica*). *Genet. Resour. Crop Evol.* 54: 1267–1283.
- Dhillon NPS, H Singh, M Pitrat, AJ Monforte and JD McCreight (2015) Snap melon (*Cucumis melo* L. *Momordica* group), an indigenous cucurbit from India with immense value for melon breeding. *Acta Hort.* 1102: 99–10.
- Dwivedi NK, OP Dhariwal, S Gopala Krishnan and DC Bhandari (2010) Distribution and extent of diversity in *Cucumis* species in the Aravalli ranges of India. *Genet. Resour. Crop Evol.* 57: 443–452.
- Fregany M, K Balvir, AJ Monforte, M Pitrat, C Rys, H Lecoq, NPS Dhillon and SS Dhaliwal (2011) Variation in melon (*Cucumis melo*) landraces adapted to the humid tropics of southern India. *Genet. Resour. Crop Evol.* 58: 227–243.
- Goyal M and SK Sharma. (2009) Traditional Wisdom and value addition prospects of arid foods of desert of North-West India. *Indian J. Tradit. Knowl.* 8: 581–585.
- IPGRI (2003) Descriptors for melon (*Cucumis melo* L.). International Plant Genetic Resources Institute, Rome, Italy, X+ 64p.
- Jeffers JNR (1967) Two case studies in the application principal component analysis. *Appl. Stat.* 16: 225–236.
- Jeffrey C (1980) A review of the Cucurbitaceae. *Bot. J. Linn. Soc.* 81: 233–247.
- Joseph JK, YC Roy, MV Krishnaraj, VAM Nissar, M Latha and KV Bhat (2017) Ecological and morphological characterization of two rare and endemic wild edible *Cucumis* species (Cucurbitaceae) of Western Ghats of India. *Genet. Resour. Crop Evol.* 64: 149–158.
- Joseph JK, S Scariah, VAM Nissar, M Latha, S Gopalakrishnan, SR Yadav and KV Bhat (2013) On the occurrence, distribution, taxonomy and gene pool relationship of *Cucumis callosus* (Rottler) Cogn. & Harms, the wild progenitor of *Cucumis melo* from India. *Genet. Resour. Crop Evol.* 60: 1037–1046.
- Koli SP and HN Murthy (2013) Estimation of phenotypic divergence in a collection of *Cucumis melo* from Kerala State Southern India. *Agri. Sci.* 4: 21–31.
- Laghetta G, R Accogli and K Hammer (2008) Different cucumber melon (*Cucumis melo* L.) races cultivated in Salento (Italy). *Genet. Resour. Crop Evol.* 55: 619–623.
- Malik AA, VK Vashisht, K Singh, A Sharma, DK Singh, H Singh, AJ Monforte, JD McCreight and NPS Dhillon (2014) Diversity among melon (*Cucumis melo* L.) landraces from the Indo-Gangetic plains of India and their genetic relationship with USA melon cultivars. *Genet. Resour. Crop Evol.* 61: 1189–1208.
- Manchali S, K Kavya, T Sudhakara (2019) Diversity in Melon (*Cucumis melo* L.) landraces of Karnataka state of Southern India for downy and powdery mildew disease resistance. *Indian J. Plant Genetics Resources.* 32(2): 158–165.
- Mohamed ETI and MT Yousif (2004) Indigenous melons (*Cucumis melo* L.) in Sudan: a review of their genetic resources and prospects for use as sources of disease and insect resistance. *Plant Genet. Resour. Newsl.* 138: 36–42.
- Muthuselvi R, S Praneetha, ZJ Kennedy and D Uma (2019) Assessment of variability in snap melon (*Cucumis melo* var. *momordica* duth. & full) genotypes. *J. Pharmacog. Phytochem.* 8(4): 654–657.
- Pandey A and S Rajkumar (2021) A new potential variety of cultivated melon (*Cucumis melo* L.) from north-western India. *Genet. Resour. Crop Evol.* 68: 785–794.
- Peter and Hazra (2012) *Handbook of Vegetables*. Thomson Press Limited, New Delhi, 359p.
- Pitrat M (2013) Phenotypic diversity in wild and cultivated melons (*Cucumis melo*). *Plant Biotechnol.* 30(3): 273–278.
- Pitrat M, P Hanelt and K Hammer (2000) Some comments on infraspecific classification of cultivars of melon. In: Katzir N, Paris HS (Ed.) *Proceedings of Cucurbitaceae, 7th Eucarpia Meeting on Cucurbit Genetics and Breeding. Acta Horti.* 510: 29–36.
- Sari N and I Solmaz (2005) Fruit characterization of some Turkish melon genotypes. III International Symposium on Cucurbits 731, September 2005, pp 103–109.
- Sebastian P, H Schaefer and SS Renner (2010) Cucumber and melon have wild progenitors in India, and the sister species of *Cucumis melo* is from Australia. *Proceedings of the National Academy of Sciences.* 107(32): 14269–14273.
- Seshadri VS and TA More (2001) Indian landraces in *Cucumis melo*. II International Symposium on Cucurbits, 28 September 2001, pp 187–193.
- Solmaz I, YA Kacar, O Simsek and N Sari, (2016). Genetic Characterization of Turkish Snake Melon (*Cucumis melo* L.

subsp. *melo flexuosus* group) Accessions Revealed by SSR Markers. *Biochem.Genet.* 54: 534-543.
Staub JE, Al Lopez-Sesé and N Fanourakis (2004) Diversity among

melon landraces (*Cucumis melo* L.) from Greece and their genetic relationships with other melon germplasm of diverse origins. *Euphytica.* 136: 151-166.

RESEARCH ARTICLE

Acclimatization Pattern of Cultivated *Capsicum* spp. in an Agro-Ecologically Diverse Habitat, Kerala, India

Asish I. Edakkalathur^{1*}, Presannakumari K.T.¹, Latha M², Minimol J.S.¹, Manju P.¹, Pradeepkumar T.¹, Krishnan S.¹ and Sivaraj N.³

Abstract

About 135 chili accessions belonging to *Capsicum annuum*, *C. chinense* and *C. frutescens* and representing various horticultural types as well as various agro-ecological zones (AEZs) of Kerala ranging from hill to coastal zone were analyzed using 18 qualitative descriptor states. Across AEZs, the distribution of species expressed variation, whereas most of the uneconomic characters did not exhibit any difference. Species-specific desirable features, secondary introduction and adaptability to environmental factors might be the possible factors behind the species-level distribution differences across AEZs. However, the absence of an association between uneconomic characters and fitness might have contributed to the lack of differences of these character states across AEZs. Selection and spread of accessions across AEZs was predominantly based on the size and weight of fruits as well as the adaptability of species. The association of climatological data with the distribution of species, horticultural types and characters worked out to elucidate possible climatic features that influenced the acclimatization. The extent of wild features retained in each species varied, which may depend on ancestor species and the intensity of selection in the domestication process. Geographical diversity analysis revealed the extent of diversity and locations of high diversity.

Keywords: Chili, Domestication, Agro-ecological zone, Secondary introduction, DIVA-GIS.

¹Kerala Agricultural University, Thrissur, Kerala, India.

²ICAR-NBPGR Regional Station, Thrissur, Kerala, India.

³ICAR-NBPGR Regional Station, Rajaendra Nagar, Hyderabad, Telangana, India.

***Author for correspondence:**

asish.ei@kau.in

Received: 05/12/2021 **Revised:** 01/08/2023

Accepted: 06/02/2024

How to cite this article: Edakkalathur AI, KT Presannakumari, M Latha, JS Minimol, P Manju, T Pradeepkumar, S Krishnan and N Sivaraj. (2024) Acclimatization Pattern of Cultivated *Capsicum* spp. in an Agro-Ecologically Diverse Habitat, Kerala, India. *Indian J. Plant Genetic Resources*. 37(1): 105-117.
DOI: 10.61949/0976-1926.2024.v37i01.13

Introduction

Chili is grown worldwide as a spice, condiment, vegetable, medicine, and ornamental plant. It belongs to the genus *Capsicum* which comprises of nearly 40 species out of which *Capsicum annuum* L., *C. chinense* Jacq and *C. frutescens* L. form the major part of chili cultivation and trade around the world (Zonneveld *et al.*, 2015).

Chili is believed to have been introduced to India by Portuguese sailors. It has acclimatized well to Indian conditions, making the country the largest producer and exporter of dried chili (Anonymous, 2023). Adaptation to the diverse climatic conditions of India further proved the presence of secondary centers of diversity for cultivated species and recognition of locally adapted types. Low pungent and highly colored *C. annuum* type in Jammu and Kashmir, hot chili types in the Guntur region of Andhra Pradesh, Bhut jolokia of North East India, Byadgi chili of Karnataka and Edayur chili of Kerala are examples for successful adaptations of the crop with unique characteristics supporting trade. Kerala has been identified as a secondary center of diversity for *C. chinense* and *C. frutescens* (Singh and Upadhyay, 2017).

Kerala, the state situated at the Southern end of peninsular India, has unique geographical features as a narrow strip of land between the Western ghats and the Arabian sea. Western ghats is acknowledged as one of the world's eight 'hottest hotspots of

biodiversity' (UNESCO, 2020). Based on altitude, rainfall pattern, soil type and topography, Kerala can be broadly classified into three main agro-ecological zones (AEZ): eastern hill zone, midland and western coastal plain. Western coastal plain (AEZ1) lies adjacent to the Arabian sea with an elevation of less than 30 m from mean sea level. Midland laterite zone (AEZ2) is situated between hill zone and the coastal plain with an elevation of 30 to 300 m. Eastern hill zone (AEZ3) comprises a hilly region more than 300 m above mean sea level (Rajasekharan *et al.*, 2015; KAU, 2020). Foot hills, high hills and parts of Palakkad plains with an elevation of more than 300 m are included in the Eastern hill zone (AEZ3).

Huge diversity of chili cultivars imposes a confusing task to taxonomists. To meet the needs of pepper processing industry in the United States, cultivars were classified based on fruit shape, size, texture, pungency, thickness of fruit wall, color and flavor so that similar horticultural types could be grouped together (Greenleaf, 1986; Smith *et al.*, 1987). Major horticultural types include Cayenne, Anaheim, Red chili, Serrano, Cherry, Cuban, Ancho, Waxy, Tabasco, Bell, Pimento, Squash and Jalapeno. The Cayenne group includes highly pungent chili with long, slender fruits and thin as well as wrinkled fruit surface. Anaheim chili has long fruits with medium-thick flesh and smooth fruit surfaces. They are moderate to less pungent. Red chili and Serrano are members of small hot group. As the group name indicates, it has slender fruits with high pungency. The Cherry group comprises small spherical fruits with thick flesh. Fruits of Cuban group have irregular shapes with yellowish green intermediate color. They are mildly pungent and thin-walled. Large, heart-shaped fruits with smooth surface and thin fruit walls characterize the Ancho group. The Waxy group has waxy yellow intermediate fruit color with a medium to thick fruit wall. The Tabasco group comprises slender fruits with high pungency. Other groups like Bell type, Pimento, Squash and Jalapeno have characteristic block, heart, round and cylindrical shapes, respectively.

DIVA-GIS is an updated technology that supports the exploration and analysis of gene banks and herbarium databases to elucidate genetic, ecological, and geographic patterns in the distribution of crops and wild species (Hijmans *et al.*, 2001). Not many studies have been carried out to analyze the variability of chili germplasm in Kerala based on the species level, horticultural group and agroecological zone perspectives. An attempt has been made to use the DIVA-GIS for the diversity analysis of *Capsicum* species collected from Kerala. This study evaluated the variability expressed by landraces belonging to *C. annum*, *C. chinense*, and *C. frutescens* species from three distinct agroecological zones. The inferences based on qualitative descriptors were extrapolated to analyze introduction pattern, secondary domestication features and adaptability with help of climatological data. This study is also helpful in

understanding the acclimatization pattern of an introduced crop to a rich biodiversity area.

Material and Methods

Chili accessions collected from different AEZs of Kerala *viz.*, coastal plain, laterite midland and hill zone were evaluated at Regional Station of the National Bureau of Plant Genetic Resources, Thrissur. The evaluation was carried out on 135 accessions (Table 1) belonging to three major cultivated species and representing various horticultural types. Eighteen unit characters (Table 2) per capsicum descriptor (IPGRI, 1995) representing the stages from seedling to seed were evaluated.

The latitude and longitude of collection sites were collected and mapped (Figure 1) using ArcGIS software. The distribution pattern of different species and horticultural types across the three AEZs, association of different species with unit characters and distribution pattern of different unit characters across AEZs were assessed by Chi-square analysis using SPSS 15.0. Climatological data at collection sites for a period of 30 years from 1984 was collected using NASA POWER and the relationship of various climatological features (Table 3) with the distribution of species, horticultural groups and unit characters was analyzed. DIVA-GIS version 7.5.0, free downloadable software (www.diva-gis.org), was used

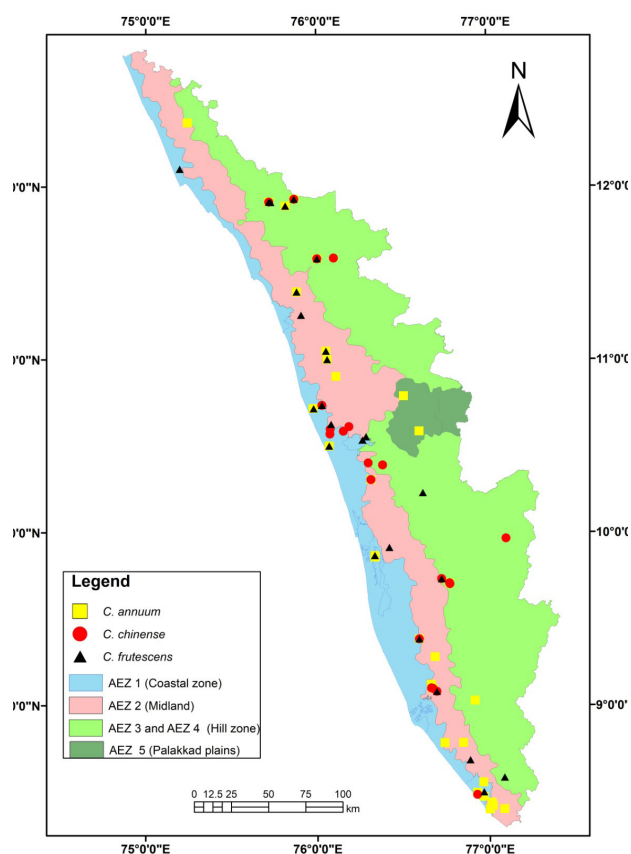


Figure 1: Geographic distribution map of chili accessions using ArcGIS

Table 1: Species, AEZ and horticultural type particulars of accessions used in the study

Species	AEZ	Horticultural group													
		Anaheim	Tabasco	Squash	Red chili	Cherry	Wax group	Jalapeno	Santaka	Cuban	Serrano	Ancho	Cayenne	Pimento	Bell
C. annuum (54)	AEZ-1 Coastal plane (21)	10, 116 (2)	9 (1)		22, 36G (2)	23, 109, 36P (3)	111, 111-I, 111-II (3)		35, 112, 113 (3)	226 (1)		71, 110, 149, 217, 231, 235 (6)			
	AEZ-2 Midland (22)	24, 27, 28, 33, 198, 200, 242 (7)			179, 180 (2)	222 (1)	25 (1)	26, 161 (2)	30 (1)	196, 234, 236 (3)		162, 197, 199 (3)		158, 178 (2)	
	AEZ-3 Hill zone (11)	84 (1)	41 (1)		173, 243 (2)	86, 92 (2)	91 (1)			46 (1)		90, 210 (2)	104 (1)		
	AEZ-1 Coastal plane (12)			17, 144, 152 (3)			145, 147, 150, 244 (4)			39 (1)	137, 148, 153, 238 (4)				
C. chinense (47)	AEZ-2 Midland (6)									190, 191, 195 (3)	119, 194 (2)			182 (1)	
	AEZ-3 Hill zone (29)			61, 64 (2)		53, 85 (2)	59, 140, 141, 142, 143, 140G, 140P (7)			60, 63, 65, 66, 80, 99, 176, 245, 246, 253, 254 (11)	51, 54, 138, 139, 156, 177 (6)			188 (1)	
C. frutescens (34)	AEZ-1 Coastal plane (10)		11, 13, 14, 15, 20, 21, 114, 219, 225, 260 (10)												
	AEZ-2 Midland (11)		1, 2, 31, 32, 40, 181, 184, 207, 211, 215, 216 (11)												
	AEZ-3 Hill zone (13)		43, 56, 76, 97, 101, 103, 120, 131, 187, 221, 230, 252 (12)			87 (1)									

*Number of accessions assigned in each group is furnished in brackets

Table 2: Species-wise descriptor state frequencies of unit characters and Chi-square analysis of distribution of unit characters and species

S. No.	Character	Descriptor state	Frequency			Chi-square value	Asymp. sig. (2-sided)
			<i>C. annuum</i>	<i>C. chinense</i>	<i>C. frutescens</i>		
1	Shape of primary leaf	Elong-deltoid	0.030	0.022	0.030	10.148	0.038
		Ovate	0.200	0.259	0.178		
		Lanceolate	0.170	0.067	0.044		
2	Plant growth habit	Intermediate	0.305	0.331	0.212	4.235	0.120
		Erect	0.059	0.025	0.068		
3	Branching habit	Sparse	0.096	0.037	0.030	11.443	0.022
		Intermediate	0.281	0.296	0.170		
		Dense	0.022	0.015	0.052		
4	Number of flowers per axil	One	0.326	0.015	0.052	69.49	0
		Two	0.074	0.333	0.200		
5	Flower position	Pendant	0.104	0.052	0.000	49.887	0
		Intermediate	0.178	0.178	0.000		
		Erect	0.119	0.119	0.252		
6	Margin of calyx	Entire	0.067	0.126	0.111	12.787	0.012
		Intermediate	0.252	0.207	0.119		
		Dentate	0.081	0.015	0.022		
7	Stigma exertion	Inserted or same level	0.030	0.089	0.007	11.346	0.003
		Exerted	0.370	0.259	0.244		
8	Annular constriction at pedicel end	Absent	0.363	0.022	0.244	99.338	0
		Present	0.037	0.326	0.007		
9	Immature fruit position	Pendant	0.267	0.170	0.000	82.023	0
		Intermediate	0.015	0.141	0.015		
		Erect	0.119	0.037	0.237		
10	Mature fruit position	Pendant	0.274	0.200	0.000	80.448	0
		Intermediate	0.022	0.133	0.030		
		Erect	0.104	0.015	0.222		
11	Neck at the base of fruit	Absent	0.363	0.215	0.052	44.08	0
		Present	0.037	0.133	0.200		
12	Fruit shape at blossom end	Pointed	0.333	0.185	0.244	23.456	0
		Blunt or sunken	0.067	0.163	0.007		
13	Fruit blossom end appendage	Absent	0.400	0.230	0.252	33.985	0
		Present	0.000	0.119	0.000		
14	Fruit cross-sectional corrugation	Slightly corrugated	0.363	0.052	0.207	73.852	0
		Intermediate	0.037	0.185	0.044		
		Corrugated	0.000	0.111	0.000		
		Smooth	0.296	0.007	0.015		
15	Fruit surface	Semi-wrinkled	0.089	0.215	0.237	96.395	0
		Wrinkled	0.015	0.126	0.000		
16	Persistence of ripe fruit (pedicel with stem)	Slight	0.052	0.244	0.015	52.791	0
		Intermediate	0.274	0.096	0.193		
		Persistent	0.074	0.007	0.044		

17	Persistence of ripe fruit (pedicel with fruit)	Intermediate	0.148	0.156	0.074	1.978	0.372
		Persistent	0.252	0.193	0.178		
18	Seed color	Straw	0.385	0.230	0.230	19.176	0
		Brown	0.015	0.119	0.022		

to map diversity and analyze selected qualitative traits. The collection sites mapped with geographical coordinates were analyzed with the software in an effort to know the spatial distribution and assessment of variability for each of the aforementioned plant traits recorded. Inferences on distribution patterns and diversity were made based on the Shannon diversity index.

Characters with distinct states that could clearly distinguish wild and cultivated types such as plant growth habit, the position of pedicel at anthesis, the position of immature as well as mature fruit and the persistence of ripe fruit with pedicel, were used to construct species-wise phenograms demarcating wild and cultivated types (NTSYS 2.10z).

Results

Distribution Pattern of Various Species and Horticultural Groups Across AEZs

The distribution patterns of different species and horticultural groups are estimated, and the results are furnished in Table 1. The calculated Chi-square value for the distribution of species across AEZs was 19.435 with an asymptotic significance (2-sided) value of 0.001. *C. annuum* types were the predominant species in the coastal plane (AEZ1) and midlands (AEZ2), contributing 48.84 and 56.41% of accessions in the above two zones. A predominance of *C. chinense* was noticed in the hilly zone (AEZ3), which constituted 54.72% of accessions in that zone. Among the three cultivated species, *C. annuum* was the least represented type in the hilly zone with a representation of 20.76% only of total accessions in that zone. However, *C. frutescens* showed a more or less even distribution in the three AEZs, ranging from 38.24% in the hilly zone to 29.41% in coastal plains.

Major share of *C. annuum* accessions belonged to the Cayenne group (22.22%), followed by Anaheim (18.52%), Red chili (11.11%), and Cherry (11.11%) groups. Among *C. chinense* accessions, Cuban group was predominant (31.92%) followed by Ancho (25.53%) and Waxy groups (23.40%). Majority of *C. frutescens* accessions (97.06%) fell into the Tabasco group.

Across three AEZs, Tabasco type was the major horticultural group with 25.58, 28.21 and 24.53% representation in AEZ1, AEZ2 and AEZ3, respectively. In AEZ1, waxy type (16.28%) and Cayenne type (13.95%) were predominant after Tabasco type. Anaheim (17.95%) and Cuban (15.39%) constituted second and third positions,

respectively in distribution percentage in AEZ2. In AEZ3, Cuban (20.76%) and Waxy type (16.98%) constituted the second and third positions, respectively. The least represented groups were Pimento and Serrano types (0.74% each), which were present in AEZ3.

Distribution of Unit Characters Across Species

Distribution of unit characters and Chi-square values depicting relationships of different unit characters with cultivated species are depicted in Table 2. The distribution and relationship of each character across species are described below. Among the accessions with lanceolate shaped cotyledon, 60.53% belonged to *C. annuum*. Accessions having lanceolate cotyledon was only 19.15 and 17.65% among *C. chinense* and *C. frutescens*, respectively. A dense branching pattern was exhibited by 20.59% accessions belonging to *C. frutescens*. However, it was limited to 5.56 and 4.26% in *C. annuum* and *C. chinense*, respectively. Among the three species, accessions with sparse branching pattern were more frequent in *C. annuum* (24.07%). However, such types represented only 10.64 and 11.77% of *C. chinense* and *C. frutescens*, respectively.

Most of the *C. annuum* accessions (81.48%) were characterized by the presence of only a single flower per axil. Two or more flowers per axil were present in 95.75 and 79.41% of *C. chinense* and *C. frutescens* accessions, respectively. Among the accessions possessing two or more flowers per axil, 87.81% belonged to either *C. chinense* or *C. frutescens*. All the *C. frutescens* accessions expressed erect flower position. Among *C. annuum* and *C. chinense* species, accessions with erect pedicel were 29.63 and 34.04%, respectively. Majority of accessions belonging to *C. annuum* (44.44%) and *C. chinense* (51.06%) expressed intermediate flower position. Irrespective of species alignment, exerted stigma was prevalent in 87.41% of accessions. Among the *C. chinense* accessions, 25.53% expressed stigma at the same level of the anther lobe. This feature was limited to 7.41 and 2.94% in *C. annuum* and *C. frutescens* species, respectively. Irrespective of species type, intermediate margin was predominant in calyx. An association between *C. annuum* and dentate margin of calyx was suggested as 68.75% of accessions with dentate calyx margin belonged to the above species. Among *C. chinense* and *C. frutescens* species, it was limited to only 4.26 and 8.82%, respectively.

The presence of annular constriction could identify accessions belonging to *C. chinense*. Pseudo-annular constriction was observed among 9.26 and 2.94% of accessions belonging to *C. annuum* and *C. frutescens*,

Table 3: Chi-square analysis of climatological data with species, horticultural type and characters

Sl. No.	Character	Earth skin temperature		Canopy temperature		Relative humidity		Soil wetness		Maximum canopy temperature		Precipitation		Photosynthetically active radiation (PAR)	
		Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)	Chi square value	Asymp. Sig. (2-sided)
1	Species	11.73	0.02	11.42	0.02	3.05	0.55	10.07	0.04	12.21	0.02	13.42	0.01	5.35	0.25
2	Horticultural group	41.42	0.03	36.22	0.09	54.48	0.00	21.14	0.73	42.34	0.02	40.78	0.03	22.02	0.69
3	Shape of primary leaf	3.34	0.50	6.24	0.18	4.84	0.30	15.84	0.00	7.57	0.11	10.78	0.03	2.97	0.56
4	Plant growth habit	2.60	0.63	1.00	0.91	13.13	0.01	2.33	0.68	3.66	0.46	7.49	0.11	0.86	0.93
5	Branching habit	5.58	0.23	7.20	0.13	0.52	0.97	15.33	0.00	3.33	0.50	3.90	0.42	3.99	0.41
6	No of flowers per axil	10.77	0.10	11.23	0.08	2.61	0.86	17.76	0.01	24.60	0.00	21.76	0.00	11.79	0.07
7	Flower position	3.07	0.55	1.13	0.75	5.58	0.23	5.60	0.23	6.42	0.17	11.70	0.02	3.03	0.55
8	Margin of calyx	5.17	0.08	5.60	0.66	1.11	0.57	0.34	0.85	0.93	0.63	0.40	0.98	4.97	0.08
9	Stigma exertion	0.07	0.97	1.76	0.41	1.00	0.61	3.38	0.18	4.21	0.12	2.72	0.26	2.07	0.36
10	Annular constriction at pedicel end	4.43	0.11	2.56	0.28	2.25	0.32	5.46	0.07	10.67	0.00	16.44	0.00	5.37	0.07
11	Immature fruit position	8.83	0.07	5.83	0.21	5.99	0.20	2.02	0.73	2.33	0.68	6.12	0.19	1.19	0.88
12	Mature fruit position	12.38	0.02	7.06	0.13	4.06	0.40	0.89	0.93	2.64	0.62	7.33	0.12	3.40	0.49
13	Neck at the base of fruit	0.73	0.69	0.93	0.82	3.90	0.14	0.78	0.68	8.12	0.02	0.02	0.99	0.62	0.73
14	Fruit shape at blossom end	9.44	0.01	7.48	0.00	1.98	0.37	3.18	0.20	4.74	0.09	0.78	0.68	2.12	0.35
15	Blossom end appendage	5.07	0.08	2.51	0.28	4.75	0.09	3.16	0.21	33.26	0.00	6.35	0.04	1.93	0.38

16	Fruit cross sectional corrugation	5.03	0.28	7.72	0.10	2.09	0.72	2.24	0.69	7.58	0.11	6.05	0.20	1.24	0.87
17	Fruit surface	16.79	0.00	13.44	0.01	1.12	0.89	7.24	0.12	22.08	0.00	11.73	0.02	5.46	0.24
18	Persistence of ripe fruit (pedicel with stem)	4.15	0.39	5.21	0.27	7.23	0.12	7.90	0.10	7.15	0.13	11.50	0.02	3.17	0.53
19	Persistence of ripe fruit (pedicel with fruit)	0.10	0.95	0.44	0.80	0.93	0.63	0.92	0.63	1.88	0.39	1.89	0.39	3.31	0.19
20	Seed color	3.04	0.22	2.46	0.29	1.29	0.53	2.25	0.33	1.59	0.45	0.94	0.63	0.78	0.68

respectively. Fruit neck was absent in majority of accessions (90.74%) coming under *C. annuum*. However, fruit neck was present in 79.41% of accessions under *C. frutescens*. Among the *C. chinense* accessions, 38.30% had fruit neck. Majority of accessions across species exhibited pointed shape at the blossom end of fruit. Among *C. chinense* accessions, 46.81% had blunt fruit end. Among *C. annuum* and *C. frutescens*, 16.67 and 2.94% of accessions had blunt fruit end. Blossom end appendage on fruit was entirely absent in *C. annuum* and *C. frutescens* accessions. However, 51.61% of *C. chinense* accessions exhibited appendages on blossom end of fruit.

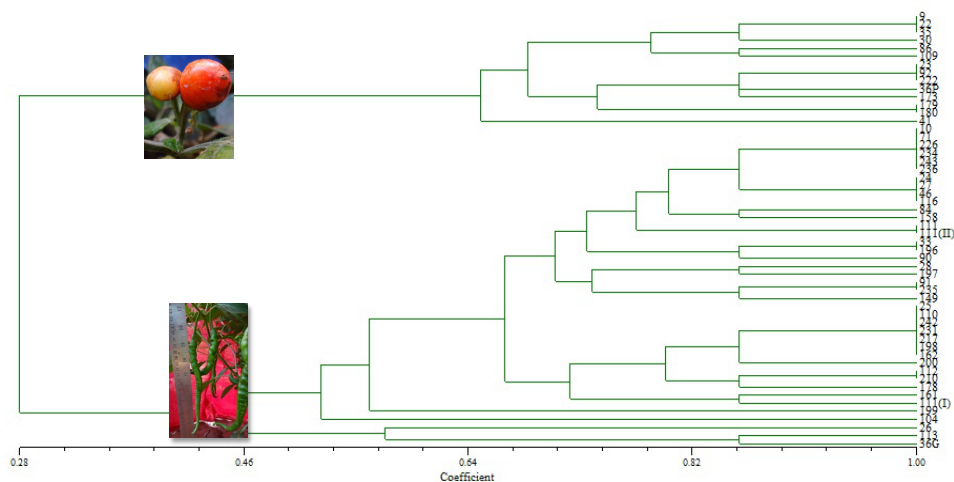
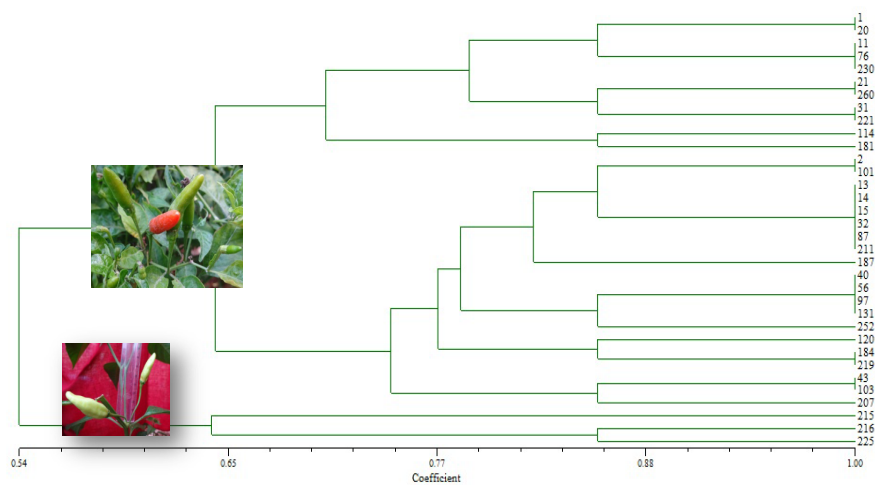
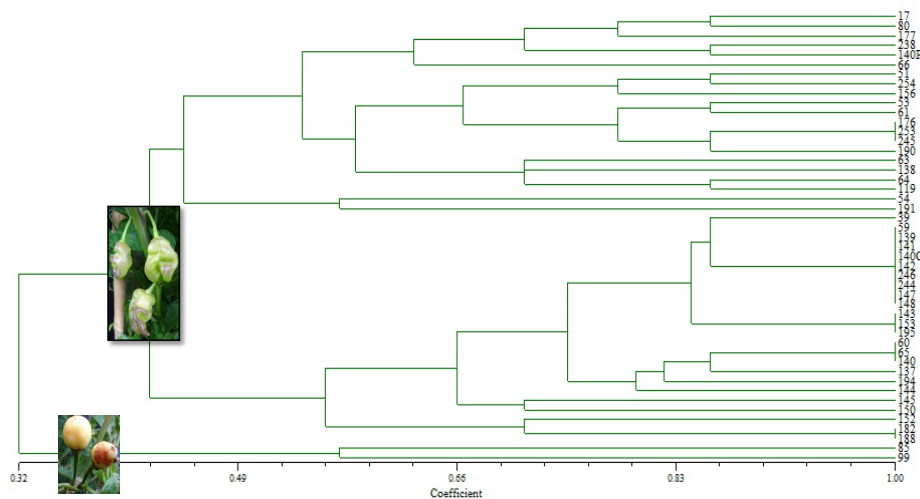
About 68.52% of *C. annuum* accessions, expressed pendant fruit position at mature stage. However, 25.93% of *C. annuum* accessions had erect pedicel at mature stage. Among *C. frutescens* accessions, 88.24% were erect and the rest were semi-pendant types. Only 4.26% of *C. chinense* accessions had erect fruits. Persistence of fruit pedicel with stem was slight in most *C. chinense* accessions (70.21%); hence, the fruits were easily detachable from the plant. Easily detachable fruits were present only in 5.88 and 12.96% of *C. frutescens* and *C. annuum* accessions, respectively.

Irrespective of species alignment, most of the accessions recorded straw (yellow) seed color. The predominance of yellow seed color was evident in *C. annuum* and *C. frutescens*. Nearly 96.30 and 91.18% of accessions of the above two species exhibited this trait. The majority of the accessions (76.19%) with brown seeds, belonged to *C. chinense*. This accounted for about 34.04% of the accessions belonging to that species. Plant growth habit and ripe fruit persistence with pedicel did not express any significant variation across the species.

Distribution of Unit Characters Across AEZs

Most of the characters did not express any significant variation across different AEZs. Features that expressed significant variation across AEZs include plant growth habit, number of flowers per axil, immature fruit position, fruit shape at the blossom end, fruit blossom end appendages, and cross-sectional corrugation of fruit and fruit surface. Accessions with compact growth habit were prevalent in all the three zones. Accessions with two or more flowers per axil was predominant in AEZ1 (58.14%) and AEZ3 (75.47%).

The occurrence of accessions with blunt fruit increased progressively from AEZ1 to AEZ3 with 16.28 and 35.85%, respectively, through an intermediate 15.39% occurrence in AEZ2. Accessions from AEZ2 were characterized with the total absence of blossom fruit end appendage. In AEZ1 and AEZ3, blossom end appendage was present among 16.28 and 16.98% of accessions, respectively. AEZ1 and AEZ2, together, contributed 86.05% of accessions with smooth fruit surfaces. Among the accessions in AEZ3, 88.68% had either semi-wrinkled or wrinkled fruit surfaces. Accessions with slightly corrugated fruits amounted to 65.12 and 79.49% in AEZ1 and AEZ2, respectively whereas such types were

Figure 2a: *C. annuum* accessionsFigure 2b: *C. frutescens* accessionsFigure 2c: *C. chinense* accessions

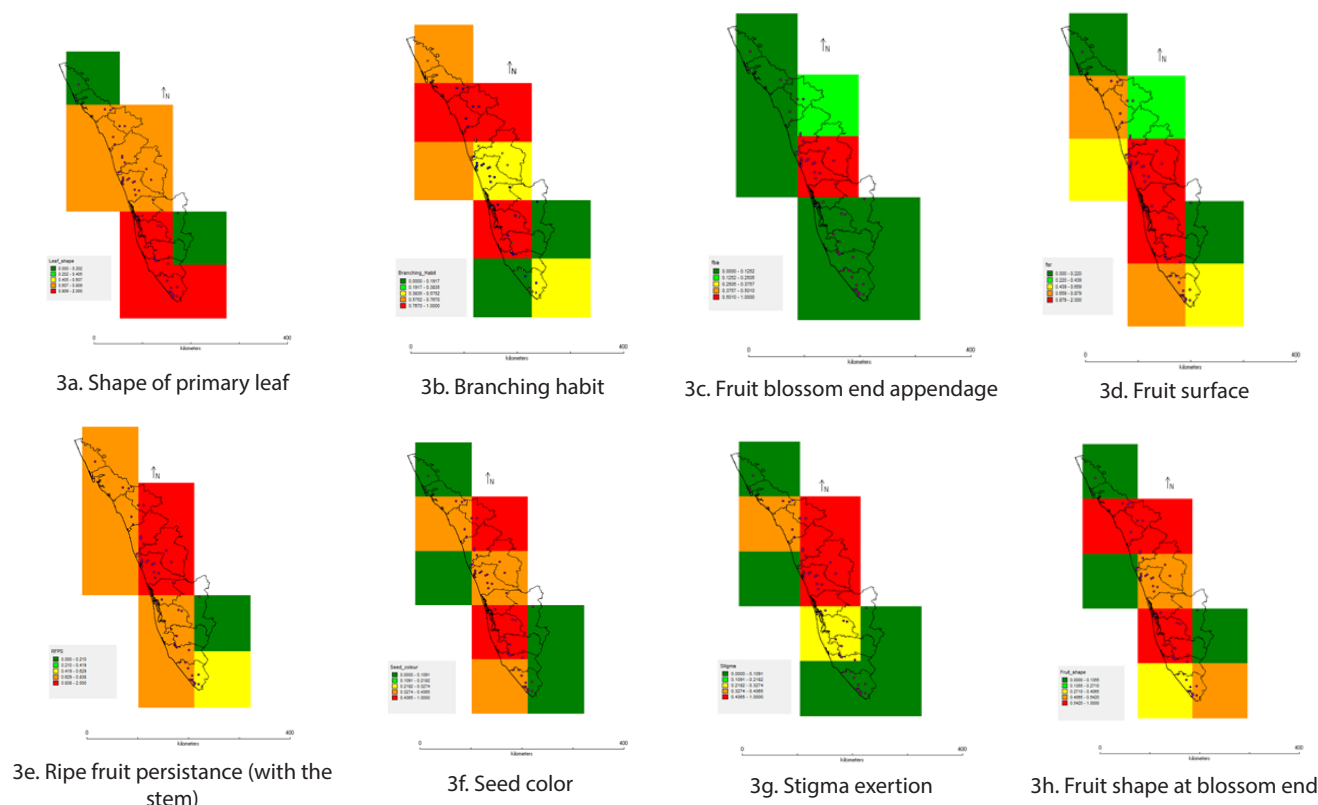


Figure 3: Diversity grid maps generated with DIVA-GIS. Grids are filled with dark green, light green, yellow, orange and red colors according to increase in Shannon diversity index

47.17% in AEZ3. AEZ3 was found to be characterized with a higher representation of accessions with intermediate to highly corrugated fruits.

Influence of Climatological Data on Species, Horticultural Type and Unit Characters

The association of climatological data with species, horticultural type and unit characters are presented in Table 3. All analyzed climatological features, except relative humidity and photosynthetically active radiation (PAR), have influenced species distribution. Among the recorded climatological features, precipitation and maximum canopy temperature had a profound role in deciding fitness of accessions with various unit characters, whereas PAR had no marked role in the same.

Species-wise Domestication Features

Species-wise dendrograms constructed based on characteristics differentiating between wild and domesticated types are presented in Figures 2a, b and c. The dendrograms demarcated wild types from domesticated in each species. Accessions that retained wild-type features accounted for 25.93 and 91.18% among *C. annuum* and *C. frutescens*, respectively. Accessions with wild features were limited to nearly 4.26% only in *C. chinense*.

Diversity Analysis using DIVA-GIS

Grid maps generated for diversity analysis of the selected traits are presented in Figures 3a to 3h. As the Shannon diversity index expresses an ascending trend, grids are filled with dark green, light green, yellow, orange and red colors.

Discussion

Acclimatization Pattern and Distribution of Species and Horticultural Types Across AEZs

A predominance of *C. annuum* was observed in the coastal zone and midlands whereas the hilly zone had higher representation of *C. chinense*. In the hilly region, *C. annuum* was the least represented species of *Capsicum*. Proportion of *C. frutescens* decreased progressively from hilly region to coastal plane. Coastal plains (AEZ1) comprise almost level to less sloping land with sandy and coastal laterite soils. Midland laterite zone (AEZ2) includes undulating lands scattered with valleys. AEZ3 comprises small hills, narrow valleys and steep slopes. The prevalence of *C. annuum* accessions in the coastal zone and midlands, as well as the increased representation of numerous horticultural types within *C. annuum*, points to the consumer and trade interests that are prevalent for that species. Similar to the

world trend, major part of the chili trade in Kerala is limited to *C. annuum* and it is the most utilized chili species (Patel *et al.*, 2011; Dhaliwal *et al.*, 2014). Marketability, early maturity, high-yielding nature and consumer preferences associated with *C. annuum* types might have led to the prevalence of that species in coastal and midland zones. Due to the steep slope, intensive and repeated agronomic operations are difficult in the hilly region. In these situations, the seasonal and annual nature of *C. annuum* makes its cultivation unattractive. Further, commercial types of *C. annuum* may not be adapted to the humid climate in hills. These factors might have contributed to widespread perennial or biennial types of *C. chinense* and *C. frutescens* in hilly zones (Smith and Heiser, 1951; Bosland and Votava, 2012). The erect and bright red colored fruits and their easy detachment from pedicel enables the birds to play a significant role in the seed dispersal of *C. frutescens* (Carvalho *et al.*, 2014). These natural seed dispersing mechanisms are well operated in less populated and ecologically undisturbed areas as in hilly zones. Further, the undisturbed ecosystem in hilly zone also confirms the maintenance of this perennial species. Extensive root system of *C. frutescens* (Singh and Upadhyay, 2017) might have also helped its adaptation to the hill slope. Increased representation of *C. frutescens* in hilly zone may be the effect of above features. Eco-geographical zone based differential distribution of species in the present study is in well agreement with origin and domestication of cultivated species of chili in South and Central America. *C. annuum* has centre of origin and centre of domestication as Mexico. *C. chinense* and *C. frutescens* originated in Amazon's river basins and domesticated at South American Plains and South-Central America, respectively. *C. baccatum* and *C. pubescens* originated in Peru-Bolivia and domesticated in low lands and high lands of Bolivia, respectively (Eshbaugh, 1970; Pickersgill, 1971; Greenleaf, 1986; Eshbaugh, 1983; Pickersgill, 1997; Bosland and Votava, 2012; Eshbaugh, 2012 and Carvalho *et al.*, 2014). Albrecht *et al.* (2012) reported significant influence of eco-geography in the genetic diversity of *C. baccatum* accessions in South America.

C. annuum accessions are grouped into 12 horticultural types. However, all except one of the *C. frutescens* belonged to the Tabasco type. The presence of different kinds of horticultural types belonging to *C. annuum* suggests the possibility of secondary introductions in that species promoted by trade and consumer interests. Bell, Pimento, Serrano and Jalapeno types belonging to *C. annuum* have only meager representation, indicating either recent introduction or hindrances in acclimatization of the above types or lack of economic advantage in farming. The occurrence of such secondary introductions are not evident in case of *C. frutescens*, represented by Tabasco type, with a prominent share across AEZs. Another reason for low variability among *C. frutescens* may be due to relatively

lower genetic variability inherent to this species than other cultivated *Capsicum* species (Carvalho *et al.*, 2015). Despite of this, *C. frutescens* exhibited variability in the present study for fruit-related features like color of immature fruits, type of fruit surface and number of fruits per axil. Present study identified six horticultural types in *C. chinense*. Bosland and Votava (2012) reported high diversity among *C. annuum* and *C. chinense* accessions and very low variability among *C. frutescens* for fruit shape. Manju and Sreelathakumary (2002) observed pronounced variability in fruit shape among *C. chinense* accessions collected from Kerala.

Prevalence of Cuban, Waxy, Cayenne, Ancho and Anaheim types points to the fact that size and weight of fruit have played a major role in deciding the selection of types for cultivation and their spread. Prevalence of pendent fruit types, irrespective of AEZs, also indicates the selection for increased fruit weight. Higher representation of *C. chinense* over *C. frutescens* in hill zone might be due to a preference for higher fruit dimensions. As the population in the three AEZs does not differ much in their consumption pattern, the adaptability of each species and horticultural type might also have a major role in deciding the cultivable area. Hence, it may be suggested that selection for yield as well as factors promoting acclimatization, might have played a prominent role in deciding the distribution of the species and horticultural types across the zones.

Species-related Unit Characters

In accordance with earlier studies, key characters and associated characters attributed to each species had expressed significant association with that species. This include lanceolate shaped cotyledon and single flower per axil in *C. annuum*; presence of annular constriction and two or more flowers per axil in *C. chinense* and one or two flowers per axil and erect flowers and fruits in *C. frutescens* (Smith and Heiser Jr. 1951; Smith and Heiser Jr. 1957; Greenleaf, 1986; Bosland and Votava, 2012 and Carvalho *et al.*, 2014). The present study indicated that majority of *C. annuum* germplasm had comparatively dentate calyx margin and *C. chinense* had easily detachable fruits from plant.

Distribution of Unit Characters Across AEZs

Most of the uneconomic characters did not exhibit any significant difference across AEZs. As the chance for artificial selection for above characters is very limited, forces that are operating to make variations among populations include mutation, migration and natural selection. These forces also seem to have failed to bring out significant differences in the phenotypic frequency of the above traits across the zones. As the fixation of alleles controlling these uneconomic characters occurred in a similar pattern in all the AEZs, it may be inferred that these characters are not associated with fitness. The minimal role of natural selection leading to the formation of distinct populations differing

in phenotypic frequency according to microclimatic environments may be due to lack of initial genetic variability as chili is an introduced crop. Pickersgill (1997) reported reduced variation in less noticeable characters in chili due to founder effects associated with domestication. Characters that expressed differentiation across AEZs were mostly secondary taxonomic characters whose association with AEZ was due to differential species distribution across AEZs.

Influence of Climatic Features on AEZ-wise Expression Pattern

We may now discuss the climatic features that influenced the AEZ-wise differential distribution of species, horticultural types and other traits. As evidenced from Table 3, canopy temperature, maximum canopy temperature, earth skin temperature, soil wetness and precipitation had role in influencing species distribution patterns. Climatological features deciding AEZ-wise distribution of horticultural groups include relative humidity, precipitation, earth skin temperature and maximum canopy temperature. Among the climatic features analyzed, only relative humidity significantly influenced growth habits with an AEZ-specific expression pattern. Rather than individual climatological features, species-specific distribution may lead to AEZ-wise differential expression of number of flowers per axil, fruit position, fruit shape at blossom end, and cross-sectional corrugation of fruit and fruit surface as these are mostly species-associated features. This was evident from Chi-square analysis as flower position, immature fruit position, and fruit cross-sectional corrugation did not express any significant association with any of the analyzed climatological features. The same pattern was expressed by the calyx margin of fruit, ripe fruit persistence with fruit, seed color and stigma exertion. The difference in morphological characters in chili according to climatic features of place of origin is in agreement with a previous report (Albrecht *et al.*, 2012).

Species-wise Domestication Features

As the weight of fruit increases, the pedicel becomes pendant to accommodate the increased weight. Human selection for increased fruit size and weight might have resulted in pendant fruits in cultivated varieties. However, the wild types have brightly colored fruits with erect pedicels which are clearly visible from above the canopy help in their dispersal by birds. Easy detachment of fruits from pedicel also aids in the dispersal (Carvalho *et al.*, 2014). Present study revealed the preference for increased size and weight of fruit across AEZs from the preponderance of accessions with pendant fruits.

Majority of accessions belonging to *C. frutescens* have expressed wild characteristics. Among the *C. frutescens* accessions, only 8.82% expressed domesticated traits and are found to be characterized with bending down of pedicel upon fruit maturity due to larger fruit size. These accessions

might have evolved due to the selection for size and weight of fruits. Carvalho *et al.* (2014) reported that *C. frutescens* is the most preserved species among the domesticated forms of *Capsicum* as the shape, size and color of fruits were conserved across wild and domesticated forms of that species.

Compared to other species, the domestication trend was intense among *C. chinense*. Among the *C. chinense* accessions, 95.75% belonged to domesticated groups with intermediate or pendant fruit pedicel. This throws light on the intense selection practiced for fruit weight in these types. Further, the fruits of most of the *C. chinense* accessions were easily detachable from the plant, making harvesting less cumbersome. The proportion of accessions with inserted stigma were also higher in *C. chinense*, resulting in higher fruit set than other species. Comparatively less exertion of style and stigma in *C. chinense* was also reported by Eshbaugh (2012). Eshbaugh (1970) and Pickersgill (1971) postulated that *C. chinense* originated from *C. frutescens* gene pool. The intense level of domestication observed may be the result of evolution from an already domesticated species and the introduction of such domesticated materials.

C. annuum accessions also exhibited a high degree of wild nature. Nearly 25.93% of *C. annuum* accessions expressed erect fruit position. The higher degree of wild nature may be due to presence of ornamental type chilies with erect fruit pedicel included in the present study. Another reason for the increased presence of wild types among *C. annuum* germplasm may be selection for bushy, early flowering and compact plant types, resulting in fasciculate flowering types and erect fruit bunch types (Elitzure *et al.*, 2009).

Diversity Analysis on a Geographical Scale

Geographical information systems has been a valuable tool in natural resources management in India viz., watershed management, land use planning etc. DIVA-GIS is a geographic information system (GIS) designed to assist the plant genetic resource explorers and biodiversity communities to map the range of distribution of species they are interested in (Hijmans *et al.*, 2000). However, it is less used for plant genetic resources management in India. DIVA-GIS enable us to understand and comprehend the distribution of diversity on a geographical scale and also help in identifying gaps in germplasm collection.

Traits viz., plant growth habit, flower position, neck at base of fruit, fruit cross-sectional corrugation, smoothness of fruit surface, calyx margin of fruit, mature fruit position, ripe fruit persistence with pedicel, number of flowers per axil and fruit shape at blossom end had high Shannon diversity index indicating presence of diverse accessions for the above traits throughout the state. Most of the above traits do not have primary economic importance like yield. It could be assumed that economically important traits may not be associated with above traits and so the cultivated germplasm preserves diverse accessions for such traits.

Another reason is species association of above traits and presence of multiple species in each location. For example, *C. annuum* had almost round cross-sections, whereas *C. chinense* has corrugated cross-sections. Similarly, *C. chinense* mostly had pendant or intermediate fruit position whereas *C. frutescens* had an erect fruit position. On the contrary, traits viz., fruit blossom end appendage and stigma exertion have low Shannon diversity index throughout state. This low diversity index may be due to genetic bottleneck as the introduced material has low diversity for these traits. Some traits have localized centers of diversity. For example, ripe fruit persistence with stem has diverse genotypes in Malappuram, Thrissur and Palakkad. Seed color has diverse accessions in Wayanad, Kozhikkode, Kottayam, and parts of Pathanamthitta. Similarly, Kottayam, Alleppy, Pathanamthitta and parts of Ernakulam and Kollam had diverse accessions with respect to branching habits. For fruit shape at the blossom end, diverse accessions were present in Kannur, Kozhikkode, Wayanad, Malappuram, Ernakulam, Kottayam, Alleppy and Pathanamthitta. Immature fruit position, primary leaf shape and flower position have higher diversity in Southern Kerala, whereas ripe fruit persistence with stem and branching habit had higher diversity towards Northern Kerala. This information could be used to decide exploration sites for the above traits. DIVA-GIS mapping may be effectively used for diversity analysis, identifying gaps in collection and distribution patterns and developing new conservation strategies, particularly in the wake of recent international developments related to food and nutritional security. GIS mapping has been successfully used in assessing biodiversity (Varaprasad *et al.*, 2008) and in identifying areas of high diversity in black gram (Abraham *et al.*, 2010); *Phaseolus* bean (Jones *et al.*, 1997); wild potatoes (Hijmans *et al.*, 2003); horse gram (Sunil *et al.*, 2008); *Jatropha curcas* (Sunil *et al.*, 2009); linseed (Sivaraj *et al.*, 2009; 2012); *Canavalia* (Sivaraj *et al.*, 2010); onion (Kamala *et al.*, 2011); and medicinal plants (Varaprasad *et al.*, 2007).

Conclusion

The distribution pattern of *Capsicum* species across AEZs was found to be based on superiority for economic traits and adaptability to environmental factors. Selection in favor of increased fruit size and weight was evident across AEZs. The extent of domestication was intense in *C. chinense*, whereas it was the lowest in *C. frutescens*. This reveals the role of ancestor relationships and selection pressure. The present study elucidated the AEZ-wise differential distribution of species and horticultural types. Integration of omics information with edaphic-climatic conditions prevailing in the AEZs could reveal genomic and molecular basis of acclimatization. This could be further utilized to develop AEZ-specialized cultivars with beneficial GxE interaction.

Diversity analysis on the geographical scale could be used to decide future study exploration sites.

Acknowledgment

We acknowledge funding received from the University Grants Commission, India in the form of Junior Research Fellowship and assistance of Mr. Ayyoob KC and Dr Divya Vijayan, Assistant Professors, KAU in statistical analysis.

References

- Abraham BV, N Kamala, N Sivaraj, N Sunil, SR Pandravada, M Vanaja and KS Varaprasad (2010) DIVA-GIS approaches for diversity assessment of pod characteristics in black gram (*Vigna mungo* L. Hepper). *Curr. Sci.* 98(5): 616-619.
- Albrecht E, D Zhang, AD Mays, RA Saftner, and JR Stommel (2012) Genetic diversity in *Capsicum baccatum* is significantly influenced by its ecogeographical distribution. *BMC Genet.* 13(68): 1-15.
- Anonymous (2023) <https://www.tridge.com/intelligences/other-chili-pepper/production>. and <https://www.volza.com/p/dried-chili/export/>. Accessed on 26 July 2023
- Bosland PW and EJ Votava (2012) *Peppers: Vegetable and Spice Capsicums*. CABI Publishing, New York, 198p.
- Carvalho SIC, CF Ragassi, LB Bianchetti, FJB Reifschneider, GSC Buso and FG Faleiro (2014) Morphological and genetical relationships between wild and domesticated forms of peppers (*Capsicum frutescens* L. and *C. chinense* jacquin). *Genet. Mol. Res.* 13(3): 7447-7464.
- Carvalho SIC, CF Ragassi, IB Oliveira, ZPS Amaral, FJB Reifschneider, FG Faleiro and GSC Buso (2015) Transferability of microsatellite markers of *Capsicum annuum* L. to *C. frutescens* L. and *C. chinense* Jacq. *Genet. Mol. Res.* 14(3): 7937-7946.
- Dhaliwal MS, A Yadav and SK Jindal (2014) Molecular characterization and diversity analysis in chili pepper using simple sequence repeats (SSR) markers. *Afric. J. Biotechnol.* 13(31): 3137-3143.
- Elitzur T, H Nahum, Y Borovsky, I Pekker, Y Eshed and I Paran (2009) Coordinated regulation of flowering time, plant architecture and growth by FASCICULATE: The pepper orthologue of SELF PRUNING. *J. Expt. Bot.* 60: 869-880.
- Eshbaugh WH (1970) A biosystematic and evolutionary study of *Capsicum baccatum* (Solanaceae). *Brittonia* 22: 31-43.
- Eshbaugh WH (1983) The genus *Capsicum* (Solanaceae) in Africa. *Bothalia* 14(3&4): 845-848.
- Eshbaugh WH (2012) The taxonomy of the genus *Capsicum*. In: Russo VM (Ed.) *Peppers: Botany, Production and Uses*. CAB International, New York, pp 14-28.
- Greenleaf WH (1986) Pepper Breeding. In: Bassett, M. J. (Ed.), *Breeding of Vegetable Crops*. Avi Publishing Company, Connecticut, pp 69-134.
- Hijmans RJ, KA Garret, Z Huaman, DP Zhang, M Schreuder and M Bonierbale (2000) Assessing the geographic representatives of genebank collections: the case of Bolivian wild potatoes. *Conservation Biol.* 14: 1755-1765.
- Hijmans RJ, I Guarino, M Cruz and E Rojas (2001) Computer tools for spatial analysis of plant genetic resources data. *Plant Genet. Resour. Newsletter.* 127: 15-19.
- Hijmans RJ, J Mirjam, B John, Bamberg and MS David (2003) Frost tolerance in wild potato species: Assessing the predictivity of taxonomic, geographic, and ecological factors. *Euphytica*.

- 130: 47–59.
- IPGRI (International Plant Genetic Resources Institute) (1995) *Descriptors for Capsicum (Capsicum spp.)*. International Plant Genetic Resources Institute, Rome, 48p.
- Jones PG, SE Beebe, J Tohme and NW Galway (1997) The use of geographical information systems in biodiversity exploration and conservation. *Biodiversity and conserve*. 6: 947-958.
- Kamala V, AJ Gupta, N Sivaraj, SR Pandravada, N Sunil, KS Varaprasad and KE Lawande (2011) Diversity analysis of onion germplasm collections from north Telangana region of Andhra Pradesh. *Indian J. Plant Genet. Resour.* 24(2): 163-171.
- KAU (2020) New Approach for Agricultural Development in Kerala – Delineation of Agro-Ecological Zones and Recommended Cropping Pattern. Kerala Agricultural University, Thrissur, 140p.
- Manju PR and I Sreelathakumari (2002) Genetic cataloging of hot chili (*C. chinense* Jacq.) types of Kerala. *J. Trop. Agric.* 40: 42-44.
- Patel AS, N Sasidharan, AG Vala and V Kumar (2011) Genetic relation in *Capsicum annuum* (L.) cultivars through microsatellite markers: SSR and ISSR. *Electr. J. Plant Breed.* 2(1): 67-76.
- Pickersgill B (1971) Relationships between weedy and cultivated forms in some species of chili peppers (Genus *Capsicum*). *Evol.* 25(4): 683-691.
- Pickersgill B (1997) Genetic resources and breeding of *Capsicum* spp. *Euphytica* 96: 129-133.
- Rajasekharan P, KM Nair and VK Venugopal (2015) Agro Ecological Management Units of Kerala – Towards a New Development Approach in Agriculture. Kerala State Planning Board, Thiruvananthapuram, 11p.
- Singh B and DK Upadhyay (2017) Biodiversity in Vegetables in India. In: Peter KV (Ed.) *Biodiversity in Horticultural Crops*. Vol 5, Daya Publishing House, New Delhi, pp 81-87.
- Sivaraj N, N Sunil, SR Pandravada, V Kamala, BVSK Rao, RBN Prasad, ER Nayar, JK Joseph, Z Abraham and KS Varaprasad (2010) Fatty acid composition in seeds of Jack bean [*Canavalia ensiformis* (L.) DC] and Sword bean [*Canavalia gladiata* Jacq.] DC germplasm from South India: A DIVA-GIS analysis. *Seed Technol.* 32(1): 46-53.
- Sivaraj N, N Sunil, SR Pandravada, V Kamala, K Vinod, BVSK Rao, RBN Prasad and KS Varaprasad (2009) DIVA-GIS approaches for diversity assessment of fatty acid composition in linseed (*Linum usitatissimum* L.) germplasm collections from peninsular India. *J. Oilseeds Res.* 26(Special issue): 13-15.
- Sivaraj N, N Sunil, SR Pandravada, V Kamala, K Vinod, A Babu, BVSK Rao, RBN Prasad and KS Varaprasad (2012) Variability in linseed (*Linum usitatissimum*) germplasm collections from peninsular India with special reference to seed traits and fatty acid composition. *Indian J. Agric. Sci.* 82(2): 102-105.
- Smith GP, CB Jr Heiser (1951) Taxonomic and genetic studies on the cultivated peppers, *Capsicum annuum* L. and *Capsicum frutescens* L. *Am. J. Bot.* 38(5): 362-368.
- Smith GP and CB Jr Heiser (1957) Taxonomy of *Capsicum sinense* Jacq. and the geographic distribution of the cultivated *Capsicum* species. *Bull. Torrey Bot. Club.* 84(6): 413-420.
- Smith PG, B Villalon, PL Villa (1987) Horticultural classification of peppers grown in the United States. *Hort. Sci.* 22(1): 11-13.
- Sunil N, N Sivaraj, K Anitha, B Abraham, KE Vinod, M Sudhir, Vanaja and KS Varaprasad (2009) Analysis of diversity and distribution of *Jatropha curcas* L. germplasm using Geographic Information System (DIVA-GIS). *Genet. Resour. Crop Evol.* 56: 115-119.
- Sunil N, N Sivaraj, SR Pandravada, V Kamala, RP Raghuram and KS Varaprasad (2008) Genetic and geographical divergence in horsegram germplasm from Andhra Pradesh, India. *Plant Genet. Resour.: Characterization and Utilis.* 7(1): 84-87.
- UNESCO (2020) World Heritage Site - Western Ghats. <https://whc.unesco.org/en/list/1342/> Accessed 17 November 2020.
- Varaprasad KS, N Sivaraj, I Mohd and SK Pareek (2007) GIS mapping of selected medicinal plants diversity in the Southeast Coastal Zone for effective collection and conservation. In: K Janardhan R, B Bahadur B, Bhadrachiah and MLN Rao (Ed.) *Advances in Medicinal Plants*. Universities Press (India) Private Ltd., India, pp 69-78.
- Varaprasad KS, N Sivaraj, SR Pandravada, V Kamala and N Sunil (2008) *GIS mapping of Agrobiodiversity in Andhra Pradesh*. Proceedings of Andhra Pradesh Academy of Sciences. Special Issue on Plant Wealth of Andhra Pradesh, pp 24-33.
- Zonneveld MV, M Ramirez, DE Williams, M Petz, S Meckelmann, T Avila, C Bejarano, L Rios, K Pena, M Jager, D Libreros, K Amaya and X Scheldeman (2015) Screening genetic resources of *Capsicum* peppers in their primary center of diversity in Bolivia and Peru. *PLoS ONE* 10(9): e0134663.

RESEARCH ARTICLE

Genetic Diversity, Variability, and Correlation Studies in South Indian Culinary Melon (*Cucumis melo* ssp. *agrestis* var. *acidulus*) Accessions

Ratnakar M. Shet^{1*}, Virupakshi Hiremata¹, Raghavendra Gunnaiah² and Santosha Rathod³

Abstract

Genetic diversity, parameters and correlation among 15 quantitative traits were studied in 80 diverse culinary melon accessions from South India during the summer 2019 and 2020 at the College of Horticulture, Sirsi. The ward's clustering revealed the presence of five clusters, which are differentiated based on geographical regions. The phenotypic coefficient of variance (PCV) estimate is higher than the genotypic coefficient of variance (GCV) in all the characters studied, indicating the influence of the environment on the expression of characters. Among the traits, except for vine length, seed cavity width, seed length and seed diameter, all other quantitative traits exhibited the highest estimate of PCV and GCV. High heritability and high genetic advance as percent mean were recorded for all the characters except vine length and seed cavity width. The correlation study revealed that peduncle length (0.524), average fruit weight (0.588), fruit length (0.551), seed cavity length (0.496), flesh thickness (0.415), and fruit number per vine (0.386) had a highly significant correlation with fruit yield per vine. The high genetic variability and nature of correlations among the fifteen traits in the collected accessions would serve as a basis for deploying specific accessions and formulating strategies for further improvement of culinary melon.

Keywords: Genetic diversity, Variability, Heritability, Correlation, Culinary melon and Mangalore melon.

¹College of Horticulture, Sirsi, UHS Bagalkot, Karnataka, India

²College of Horticulture, Bagalkot, UHS Bagalkot, Karnataka, India

³ICAR- Indian Institute of Rice Research, Hyderabad, Telangana, India

***Author for correspondence:**

ratnakar.shet@uhsbagalkot.edu.in

Received: 28/06/2022 **Revised:** 24/02/2023

Accepted: 07/02/2024

How to cite this article: Shet RM, V Hiremata, R Gunnaiah and S Rathod. (2024) Genetic Diversity, Variability, and Correlation Studies in South Indian Culinary Melon (*Cucumis melo* ssp. *agrestis* var. *acidulus*) Accessions. *Indian J. Plant Genetic Resources*. 37(1): 118-124. DOI: 10.61949/0976-1926.2024.v37i01.14

Introduction

Culinary melons (*Cucumis melo* subsp. *agrestis* var. *acidulus*) of South India, locally referred as Mangalore melon or Sambar Southe, belong to the family Cucurbitaceae with a somatic chromosome number $2n = 2x = 24$ (Pitrat *et al.*, 2000). In Karnataka, it is called by local names as Mogge kayi or Mangalore southe. In Kerala, it is known as Vellari, Kanivellari and Dosakaya in Andhra Pradesh (Shet *et al.*, 2022). Previously, culinary melon/Mangalore melons were classified under var. *conomon* rather than under var. *acidulus* (Gondi *et al.*, 2016; Lakshmi *et al.*, 2017; Mukunda *et al.*, 2017; Swamy, 2017; Vinutha *et al.*, 2017). The majority of the morphological traits, including sex type (monoecious) of culinary melons, are similar to the traits of *C. melo* ssp. *agrestis* var. *acidulus* (Pitrat, *et al.*, 2000) and classified under var. *acidulus*. Culinary melon is a cross-pollinated crop that performs better in warm weather compared to rainy, humid conditions and is traditionally cultivated in paddy fallow using residual soil moisture mainly grown for fresh vegetables as well as for pickling and cooking purposes (Gondi *et al.*, 2016, Kamgaoud *et al.*, 2018, Shet *et al.*, 2022).

An improvement in yield and quality of cross-pollinated crops like culinary melon is affected mainly by selecting genotypes with desirable characters from the germplasm or by developing hybrids. The basic requirement for adopting a suitable breeding method is

sound knowledge of the genetic makeup of the characters and their expression in different genetic backgrounds. The assessment of diversity present among the collected genetic stock and further clustering will help the breeders for the selection of desirable genotypes for the trait-based hybridization program.

In general, genetic variability is the basic material and pre-requisite for any crop improvement program and knowledge of certain genetic parameters is essential for proper understanding followed by their manipulation during plant breeding. Genetic parameters such as genotypic coefficients of variation (GCV), phenotypic coefficient of variation (PCV), heritability and GA are useful biometric tools for the determination of genetic variability. Information on the nature and extent of genetic variability and the degree of character transmission is paramount in enhancing the efficiency of selection. The fruit yield is a complex quantitative trait, and an integrated function of a number of component characters. Therefore, selection for yield *per se* may not be very rewarding unless other yield-attributing traits are taken into consideration. A correlation study provides a measure of association between characters and helps identify important characters to be considered while selecting. The knowledge of correlations between various characters and their relative contribution to yield is useful for the selection of multiple characters and suitable plant type (Nayana and Fakrudin, 2020). The present study was aimed at understanding the magnitude of genetic variability and the nature of correlations among a set of 15 traits, including fruit yield.

Materials and Methods

The experimental material for the study consisted of 80 diverse culinary melon germplasm accessions collected from South Indian states *viz.*, Karnataka, Kerala, Andhra Pradesh, Tamil Nadu, Telangana and Goa. These diverse lines were evaluated for different growth and yield parameters at the College of Horticulture, Sirsi, Karnataka, following the recommended package of practice of melon during March-May 2019 and 2020. The experiment was laid out in augmented block design with Mudicode Local and Soubhagya as check varieties. The seeds of 80 accessions and two checks were soaked in water for overnight. The next morning, soaked seeds were sown in the main field, laid out by mulch sheet and drip irrigation system. The spacing of 0.60 m between vine to vine and 2 m between rows was followed with a row containing 10 seedlings. After every ten accessions one check variety was repeated and each block consisted of 20 accessions. Four equal such blocks were maintained. Recommended cultural operations and plant protection measures were taken to ensure uniform and healthy crop stand per the package of practices. The observations were recorded for five plants in each accession

on 15 yield-related traits *viz.*, number of female flowers at peak flowering stage, vine length (cm), peduncle length (cm), average fruit weight (g), number of fruits per vine, fruit length (cm), fruit breadth (cm), seed cavity length (cm), seed cavity width (cm), flesh thickness (cm), 100 seed weight (g), seed diameter (mm), seed length (mm), total soluble sugar (TSS %brix) and fruit yield per vine (kg) and pooled mean values over two years data were used for analysis. The data obtained were subjected to analysis of variance (ANOVA) by using SAS software version 9.2 (SAS, 2008). The hierarchical cluster analysis of Ward's minimum variance method (Ward, 1963) was adopted. The phenotypic and genotypic coefficients of variability were computed using Burton and De Vane's (1953) methods. The method of (Johnson *et al.*, 1955) was followed to estimate broad sense heritability and record the genetic advance for all the traits. The correlation coefficient among all possible character combinations were estimated using SAS software employing Pearson's correlation coefficient formula.

Results and Discussion

The analysis of variance indicated significant differences among the accessions for all the studied traits (Table 1). The significant range observed among the accessions for sex ratio (7.7–20.0%), average fruit weight (196–2400 g), fruit length (10.4–29.4 cm), fruit width (4.5–14.8 cm), seed cavity length (6–26.2 cm), flesh thickness (0.50–4.40 cm), TSS (1.5–5.80% brix) and fruit yield per vine (0.60–8.10 Kg) indicating maximum variability present in these traits (Table 2). It showed the existence of high degree of genetic variability among the accessions and enough scope for bringing about improvement in the desirable direction (Kamgoud *et al.* 2018). Apart from these inherent traits, culinary melon fruits are attracted by its wide range of color, shape and size. Most of the Karnataka accession fruits are oblate to ovate in shape, with colors varying from light green to dark green and a combination of patchy green with white to yellow stripes. Whereas, the Kerala accessions produced oblate to elongated yellow color fruits on maturity with or without prominent stripes. However, the Andhra and Telangana accessions fruits were round or globular in shape and yellow color with plain or scattered patches on the skin (Figure 1). This indicated availability of wide in fruit shapes and colors for breeding consumer preferable size and color fruits varieties/hybrids in the future (Shet *et al.*, 2022).

The diversity among the accessions using cluster analysis revealed five distinct major clusters at the level of 14 Euclidean distances (Figure 2). Among these five clusters, four major clusters, namely cluster I, cluster II, cluster III and cluster V, constituted of 15, 28, 18 and 17 accessions, respectively. The accessions collected from Karnataka, Kerala and Andhra Pradesh states formed the major clusters and exhibited a reasonable level of locational grouping.

Table 1: Analysis of variance for quantitative traits in germplasm accessions of culinary melon

Traits	Mean square values				
	Block	Genotype	check	che+ check vs var	error
	df = 3	df = 81	df = 1	df = 80	df = 3
No female flower	0.99	0.3421*	0.05	0.3458*	0.05
Sex ratio	14.68	6.63*	3.93	6.66*	3.97
Vine length (cm)	588.00	233.6**	343.2**	232.2**	42.40
Peduncle length (cm)	3.23	1.62*	3.72	7.66*	0.22
Fruit weight (g)	153259	55833*	180901**	54270*	2941
Number of fruits /vine	3.95	0.60*	0.32	0.60	0.20
Fruit width (cm)	2.56	3.425*	9.418*	3.351*	1.70
Fruit length (cm)	37.06	15.97*	11.04*	16.04*	1.81
Seed cavity length (cm)	24.04	13.18**	349.8***	8.97**	0.03
Seed cavity width (cm)	2.76	0.455**	0.165*	0.459**	0.01
Flesh thickness (cm)	3.64	0.624*	0.98*	0.62*	0.04
100 seed weight (g)	0.43	0.11*	0.00	0.11	0.03
Seed diameter (mm)	0.42	0.824**	1.638***	0.814**	0.01
Seed length (mm)	3.36	1.072*	2.916*	1.049*	0.11
TSS (%brix)	6.07	0.809**	0.361**	0.815**	0.01
Fruit yield/vine (kg)	0.29	0.3357*	0.6845**	0.3313*	0.01

* & ** indicates significant at 5 and 1% probability level

Table 2: Estimates of mean, range and genetic parameters for 15 quantitative traits in culinary melon accessions

Traits	Mean $\pm$ SE	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GAM (%)
		Min	Max				
Number of female flower at peak flowering stage	3.75 $\pm$ 0.14	1.50	9.00	32.21	29.11	81.68	54.28
Vine length (cm)	152.59 $\pm$ 3.31	101.8	233.69	20.13	13.9	47.71	19.81
Peduncle length (cm)	3.12 $\pm$ 0.14	1.07	6.2	29.00	24.68	72.41	43.26
Average fruit weight (g)	810.61 $\pm$ 56.7	88.12	2209	55.03	49.79	87.29	59.37
Number of fruits/vine	3.37 $\pm$ 0.26	1.25	16.25	32.82	26.80	66.67	45.08
Fruit length (cm)	15.33 $\pm$ 0.47	6.31	25.12	29.19	26.06	79.14	48.00
Fruit breadth (cm)	10.09 $\pm$ 0.37	4.57	27.53	34.23	33.54	95.99	67.78
Seed cavity length (cm)	11.46 $\pm$ 0.40	4.50	22.00	31.40	29.81	90.11	58.39
Seed cavity width (cm)	4.81 $\pm$ 0.12	2.49	7.64	20.70	11.34	30.01	12.82
Flesh thickness (cm)	2.55 $\pm$ 0.098	0.50	4.50	35.14	29.97	72.73	52.73
100 seed weight (g)	2.25 $\pm$ 0.062	0.67	3.66	24.44	24.08	97.13	48.98
Seed diameter (mm)	3.39 $\pm$ 0.076	0.562	4.47	20.05	19.31	92.73	38.37
Seed length (mm)	8.18 $\pm$ 0.13	4.6	10.06	14.77	14.68	98.91	30.13
TSS (%brix)	2.72 $\pm$ 0.11	0.63	5.38	36.14	35.35	95.51	71.26
Fruit yield/vine (kg)	2.53 $\pm$ 0.17	0.57	8.83	57.18	45.46	63.22	74.58

GCV-Genotypic coefficient of variation, PCV- Phenotypic Coefficient of variation, h^2 (bs) –Heritability in broad sense, GAM- Genetic advance as mean

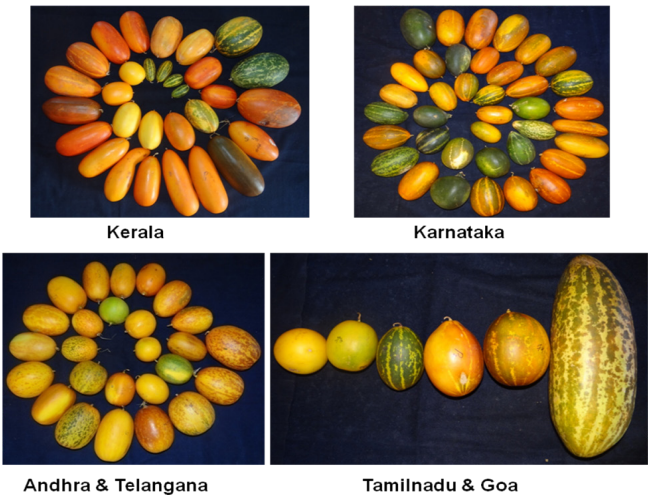


Figure 1: The diversity observed among accessions collected from different south Indian states for fruit color, size and shape

The majority of the accessions collected from Karnataka were accommodated in clusters I and II, while accessions from Kerala were grouped in cluster V. However, cluster III accommodated the Andhra and Telangana accessions. This could be due to the fact that quantitative clustering obtained from each state is related to similarity in adaptation (Van Hintum 1995). Cluster IV has only four accessions and is characterized by more fruits per vine and small fruits, of which two accessions belong to *agrestis*, the progenitor for culinary melon. Similar results were obtained by Raja *et al.* (2009) in a bitter melon diversity analysis study from tribal belts of India. A relationship between clusters and geographical region could exist due to the restricted movement of planting material from one state to another. The estimates of genetic parameters, *viz.*, genotypic and

phenotypic coefficients of variation, heritability in a broad sense, genetic advance, and mean and range of different characters, are presented in Table 2. A considerable range of variation was observed for all the characters under study. Generally, the PCV revealed relatively high values in comparison to the corresponding GCV for all the characters, indicating the effects of environment in the expression of traits. The range of PCV was observed from 14.77 to 57.18% for the traits under study, which provides a picture of the extent of phenotypic variability in the population. The PCV was noted high for characters like fruit yield per vine (57.18%), average fruit weight (55.03%), TSS (36.14%), flesh thickness (35.14%), fruit length (34.23%) number of fruit per vine (32.82%), number of female flowers at peak flowering stage (32.21%), fruit breadth (29.19%) and peduncle length (29%). The rest of the characters showed moderate values of PCV. The genotypic coefficient of variation, which expresses the picture of the extent of genetic variability in the population, ranged from 13.9 to 49.79%. The GCV was noted high for the characters like average fruit weight (49.79%), fruit yield per vine (45.46%), TSS (35.35%), fruit length (33.54%), flesh thickness (29.97%), number of female flowers at peak flowering stage (29.11%), number of fruit per vine (26.80%), fruit breadth (26.06%) and peduncle length (24.68%). Moderate GCV values were observed for seed diameter (19.31%) seed length (14.68%), vine length (13.90%) and seed cavity width (11.34%). These findings are in agreement with Rakhi and Rajamony (2005) and Silpa *et al.* (2020). Thus, these traits further provided an opportunity for genetic improvement. The phenotypic and genotypic coefficient of variation indicated that fruit yield per vine (kg), average fruit weight (g), flesh thickness (cm), fruit length (cm), number of fruit per vine, number of female flowers

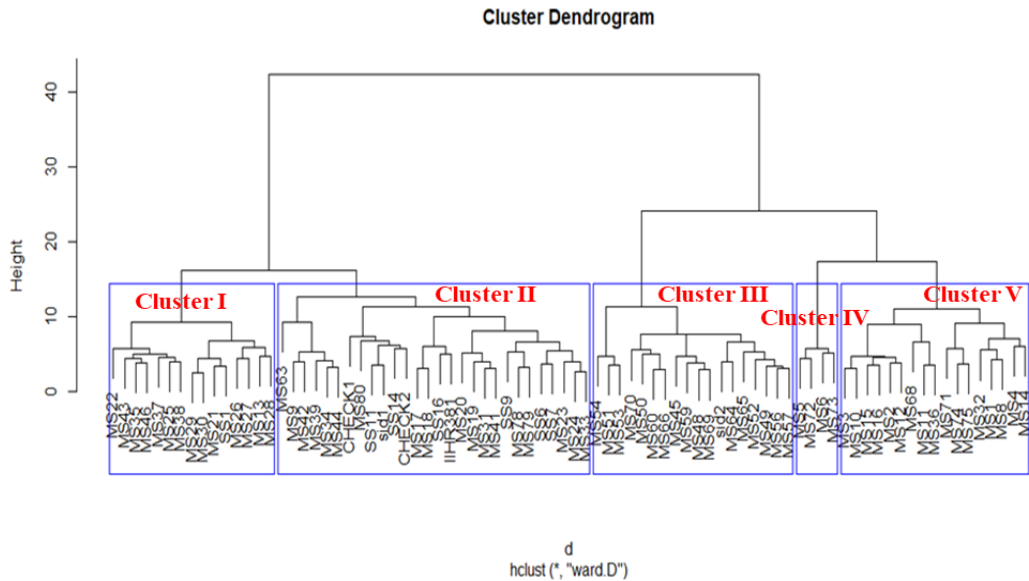


Figure 2: Dendrogram generated by ward's method of cluster analysis of morphological data of culinary melon accessions

Table 3: Pearson's correlation coefficients among 15 quantitative traits for accessions of culinary melon ($N = 82, Prob > |r|$ under $H_0: Rho = 0$)

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15
X1	1.000	0.118	-0.301	-0.283	0.437	-0.331	-0.327	-0.278	-0.163	-0.379	-0.182	-0.042	-0.337	0.032	-0.048
X2		0.292	0.006	0.010	<0.001	0.002	0.003	0.012	0.144	0.001	0.102	0.708	0.002	0.772	0.670
X3		1.000	-0.133	0.002	0.206	-0.170	0.130	-0.171	0.026	-0.317	-0.214	0.063	-0.250	-0.071	0.097
X4			0.233	0.989	0.063	0.128	0.245	0.125	0.819	0.004	0.054	0.571	0.023	0.525	0.384
X5			1.000	0.685	-0.132	0.630	0.424	0.487	0.295	0.416	0.338	0.182	0.632	0.177	0.524
X6				<0.001	0.238	<0.001	<0.001	<0.001	0.007	<0.001	0.002	0.101	<0.001	0.112	<0.001
X7				1.000	-0.311	0.832	0.727	0.616	0.410	0.410	0.380	0.219	0.751	0.169	0.588
X8					0.005	<0.001	<0.001	<0.001	0.000	0.000	0.000	0.048	<0.001	0.130	<0.001
X9					1.000	-0.278	-0.291	-0.142	-0.129	-0.206	-0.127	-0.080	-0.377	0.210	0.386
X10						0.011	0.008	0.202	0.250	0.064	0.254	0.477	0.001	0.058	0.000
X11						1.000	0.478	0.693	0.303	0.401	0.357	0.062	0.687	0.239	0.551
X12							<0.001	<0.001	0.006	0.000	0.001	0.579	<0.001	0.030	<0.001
X13							1.000	0.439	0.379	0.339	0.287	0.214	0.485	0.095	0.329
X14								<0.001	0.001	0.002	0.009	0.054	<0.001	0.394	0.003
X15								1.000	0.463	0.513	0.361	0.080	0.697	0.262	0.496
									<0.001	<0.001	0.001	0.474	<0.001	0.017	<0.001
									1.000	0.303	0.238	0.248	0.411	-0.095	0.386
										0.006	0.031	0.025	0.000	0.396	0.000
										1.000	0.572	0.444	0.503	0.118	0.270
											<0.001	<0.001	<0.001	0.292	0.014
											1.000	0.697	0.314	0.117	0.333
												<0.001	0.004	0.293	0.002
												1.000	0.123	-0.049	0.176
													0.271	0.662	0.113
													1.000	0.256	0.415
														0.020	0.000
														1.000	0.157
															0.159

X1- Number of female flowers at peak flowering, X2- vine length(cm), X3- Peduncle length (cm) X4- Avg fruit wt (g) X5- Number of fruits /plant X6- fruit length(cm), X7- fruit width (cm) X8- seed cavity length (cm), X9- seed cavity width (cm), X10- 100 seed wt (g), X11- Seed length (mm), X12- Seed width (mm), X13- Flesh Thickness (cm) X14- TSS % brix, X15- Fruit yield per plant (kg)

at peak flowering stage, fruit breadth (cm) and peduncle length (cm) were found to be important characters. The difference between PCV and GCV values was low for most of the characters studied, suggesting minimal influence of environment on the expression of the character.

Genetic coefficient of variation, along with heritability estimates, would provide a clear picture on the efficiency of the selection (Burton, 1952). The estimate of broad sense heritability was the highest for all the characters studied except vine length (47.71%) and seed cavity width (30.01%) (Table 2). The values were especially high for seed length (98.91%), 100 seed weight (97.13%), fruit breadth (95.99%), TSS (95.51%), seed diameter (92.73%), seed cavity length (90.11%) and average fruit weight (87.29%). Similarly, high heritability values for average fruit weight, TSS, fruit yield/vine, fruit breadth and flesh thickness was reported by Kamgoud *et al.* (2018). In the present investigation, almost all the traits under the study showed a high magnitude of heritability in broad sense (>60%), suggesting that the highly heritable characters were least affected by environmental variations and selection for these characters based on phenotypic performance may be more effective for culinary melon improvement.

Heritability alone does not provide clues for genetic gain from the best-selected individuals. Burton (1952) suggested that heritability, in combination with genetic advance (GA), was more reliable in predicting the effect of selection. The estimates of genetic advance (as percent of mean) ranged from 12.82 for seed cavity width to 74.58 for fruit yield/vine (Table 2). The estimates of GA (as percent mean) were high (>20%) for all the traits studied except for seed cavity width (12.82%) and vine length (19.81%), which showed moderate estimates of GA (Table 2).

The results in the experiment revealed that higher heritability (>60%) estimates coupled with high genetic advance (>20%) for all the characters except vine length and seed cavity width. High heritability with high genetic advance indicated additive gene action in the control of making these characters to respond better for selection (Johnson *et al.*, 1955). The characters with high genotypic variance and high heritability coupled with high genetic gain would be effective for selection in the improvement of the crop. The traits namely number of female flower at peak flowering stage (81.68; 54.28%), peduncle length (72.41; 43.26%), average fruit weight (87.29; 59.37%), fruit length (79.14; 48.00%), fruit breadth (95.99; 67.78%), seed cavity length (90.11; 58.39%), flesh thickness (72.73; 52.73%), number of fruits per vine (66.67; 45.08%) and fruit yield/vine (63.22; 74.58%) showed high heritability coupled with high genetic advance as percent mean, respectively. Similar findings were also reported by Shivadatt *et al.* (2021), Kamgoud *et al.* (2018), Shet *et al.* (2019), Ramesh Babu and Hariprasad Rao (2018) in oriental pickling melon.

The present findings corroborated that the existing variability among the genotypes with respect to these traits is mainly due to additive types of genes (Panse 1957). However, the vine length and seed cavity breadth reported moderate to low heritability with moderate genetic advance, indicating the role of non-additive gene action, which can be exploited for heterosis breeding (Bhimappa and Choudhary, 2017). Thus, the traits with high heritability coupled with high genetic advance can be considered for the improvement of culinary melon accessions.

Yield is a complex quantitative character, and direct selection for yield may not result in successful improvement. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement of an associated complex quantitative character like yield. The correlation study revealed that peduncle length (0.524), average fruit weight (0.588), fruit length (0.551), seed cavity length (0.496), flesh thickness (0.415), and fruit number per vine (0.386) had highly significant positive correlation with fruit yield per vine (Table 3). It indicates that the selection in any of these yield-attributing traits will increase the other traits, thereby enhancing the fruit yield. Similar results were reported by Shivadatt *et al.* (2021), Shet *et al.* (2018), and Hossain *et al.* (2010) in cucumber. However, the number of female flowers at the peak flowering stage showed a significant positive association with the number of fruits per vine (0.437) but a negative correlation with other traits, including fruit yield per vine (-0.048), indicating that all the female flowers at peak flowering stage may not be contributes to the fruit yield. In conclusion, high genetic variability and the nature of correlations among the fifteen traits in the collected accessions would serve as a basis in deploying specific accessions and formulation of strategies for further improvement of culinary melon. The selection for average fruit weight, fruit length, fruit breadth, flesh thickness, seed cavity length, number of fruits per vine and peduncle length can enhance the productivity of culinary melon.

Conclusion

Evaluation of collected accessions is an important aspect of the breeding program. The grouping and further classification of accessions into different clusters help to select diverse accessions as a parent in a trait-based hybrid development program. The high genetic variability and nature of correlations among the 15 traits in the collected accessions would serve as a basis for deploying specific accessions and formulating strategies for further improvement of culinary melon. Molecular characterization and further molecular diversity study of collected accessions will provide the precise grouping of accessions for further improvement of culinary melon.

Acknowledgment

The author expresses sincere thanks to Dr. Prem Nath Agriculture Science Foundation, Bangalore (Project No. 132/PNASF- UHSB/2018-19) for encouragement and financial assistance.

References

- Bhimappa BB and H Choudhary (2017) Genetic variability, heritability and genetic advance in muskmelon (*Cucumis melo* L.). *Ann. Agric. Res. New Series*. 38(2): 212-217
- Burton GW and EM De Vane (1952) Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.* 51: 515-518.
- Shruti PG, VM Ganiger, G Bhuvaneshwari, MB Madalageri, YK Kotikal and G Manjunatha (2016) Evaluation of oriental pickling melon (*Cucumis melo* L. var. *conomon*) genotypes for pest and disease reaction under northern dry zone of Karnataka. *J. I Environ. Ecol.* 7(1): 29-36.
- Hossain F, MG Rabban, MA Hakim, ASM Amanullah and ASM Ahsanullah (2010) Study on variability character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh. Res. Publ. J.* 4: 297-311.
- Johnson HW, JF Robinson and RE Comstock (1955) Estimation of genetic and environmental variability in soya bean. *Agron. J.* 7: 314-318.
- Kamagoud S, MS Ratnakar, N Sandhyarani, H Shivanand, CN Hanchinmani and A Prashanta (2018) Assessment of genetic variability among oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes. *Int. J. Chem. Studies*. 6(4): 2630-2633.
- Lakshmi LM, H Lingaiah, AM Rao, T Raju, M Pitchaimuthu and D Gowda (2017) Variability and genetic divergence studies for economic traits in indigenous oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes. *Electronic J. Pl. Breed.* 8: 365-370.
- Mukunda LL, H Lingaiah, AM Rao and S Ramesh (2017) AFLP analysis of genetic relationships and diversity of some oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes in Karnataka. *Intl. J. Agril. Sci.* 13: 242-248.
- Nayana RS and B Fakrudin (2020) Genetic variability, heritability and correlation studies in soybean (*Glycine max*). *Indian. J. Agril. Sci.* 90(4): 704-707.
- Pitrat M, P Hanelt and K Hammer (2000) Some comments on infraspecific classification of cultivars of melon. *Acta Hort.* 510: 29-36.
- Raja Shankar, GB Balakrishna and AM Tukaram (2009) Diversity analysis of bitter gourd (*Momordica charantia* L) germplasm from tribal belt of India. *Asian Austr. J. Pl. Sci Biotech.* 3(1): 21-25.
- Rakhi R and L Rajamony (2005) Variability, heritability and genetic advance in landraces culinary melon (*Cucumis melo* L.). *J. Tropical Agril.* 43(1/2): 79-82.
- Ramesh Babu R and N Hariprasad Rao (2018) Studies on genetic variability, heritability and genetic advance in oriental pickling melon (*Cucumis melo* L. var. *conomon*) genotypes. *Int. J. Pure App. Biosci.* 6(5): 1042-1047.
- SAS institute. 1999. SAS/SAT user guide. Version 8.0 (1st Edn) SAS Institute, Cary, NC, USA.
- Silpa R, ST George, P Anitha, T Pradeepkumar, VS Sujatha, B Dijee, P Berin and C Laly John (2020) Genetic divergence analysis in oriental pickling melon (*Cucumis melo* var. *conomon* Mak.). *Res. J. Agril. Sci.* 11(1): 115-119.
- Shivadatta Kumbar, T Shantappa, MS Ratnakar, D Satish, RC Jagadeesha, VD Gasti and Raghavendra Gunnaiah (2021) Genetic variability and correlation studies in intervarietal hybrids of Mangalore melon (*Cucumis melo* var. *acidulous*) for productivity traits. *Pharma Innovation J.* 10(7): 448-451.
- Shet RM, T Shantappa, Ashok and SB Gurumurthy (2018) Genetic variability and correlation studies for productivity traits in cucumber (*Cucumis sativus* L.). *Int. J. Chem. Studies*. 6(5): 236-238.
- Shet RM, S Kamagoud, Shivanand Hongal and N Sandhyarani (2019) Assessment of genetic diversity in culinary Melon (*Cucumis melo* var *conomon*) under rainfed condition. *Int. J. Curr. Microbiol. App. Sci.* 8(12): 2786-2791.
- Shet RM, Shivanand Hongal, T Shantappa, SM Veeresha and RC Jagadeesha (2022) Survey, collection and preliminary observation of culinary melon germplasm from southern India. *Indian J. Plant Genet. Resour.* 35(1): 85-93.
- Swamy KRM (2017) Origin, distribution and systematics of culinary cucumber (*Cucumis melo* subsp. *Agrestis* var. *conomon*). *J. Hort. Sci.* 12: 1-22.
- Van Hintum TJL (1995) Hierarchical approaches to the analysis of genetic diversity in crop plants. In: Hodgkin T, Brown AHD, Van Hintum TJL and Moracles EAU (Eds.) *Core collections of Plant genetic resources*. John Wiley & Sons, New York, pp 23-34.
- Vinutha B, YK Kotikal, V Venkateshalu V, G Manjunath and S Patil (2017) Insect-pests composition and natural enemies association on oriental pickling melon (*Cucumis melo* var. *conomon*). *J. Entomol. Zoology Stud.* 5: 1838-1840.
- Ward JH (1963) Hierarchical grouping to optimize an object function. *J. Amer. Statistical Assoc.* 58: 236.

RESEARCH ARTICLE

Performance of Exotic and Indigenous Coconut Genotypes for Growth, Fruit Yield, Fruit and Nut Characters under Assam Conditions of North East Region of India

Leichombam S Singh¹, Niral Vittal², Gobinda C Acharya³ and Manju Chaithra¹

Abstract

Coconut is an important plantation crop grown in India. Considering the value of this crop which provides food, drink, medicine, shelter and a variety of raw materials, besides sustaining the livelihood of many small and marginal farmers of North East region of the country, it is essential to improve the productivity of coconut in North East region to ensure higher income and profitability to growers. A lot of research has been carried out to improve coconut in many of India's major coconut-growing states. However, systematic work on coconut improvement in the Northeast region has been limited. A few varieties are grown in Northeast India, especially Assam, but not much work has been done on the suitability of different coconut varieties. Therefore, the present study was undertaken to evaluate four exotic and eleven indigenous coconut genotypes, including released varieties for their growth, nut yield and fruit characters under Assam conditions. The data on growth characters were recorded for five years, from 2015 to 2019, and nut yield (number of nuts per palm) was recorded for seven years (2016–2022), while observations on, fruit component characters were recorded four years from 2017–2020 and the mean data was used for analysis. Significant differences were observed between the genotypes for most of the characters recorded. Nut yield varied from 35.34 (Malayan Yellow Dwarf) to 109.32 (Kera Sankara). The hybrid variety Kera Sankara recorded a higher nut yield (109.32) than other varieties. Fruit weight among the varieties varied from 605.04 to 1173.47 g. Variety Assam Green Tall recorded higher fruit weight (1173.47 g), husked fruit weight (832.04 g) and endosperm weight (379.50 g). Maximum husk thickness (2.87 cm) and husk-to-fruit percentage was observed in Fiji tall variety (45.97%). Considering the nut yield, the hybrid Kera Sankara can be recommended for cultivation in the northeastern region of India. Therefore, The present study indicates the importance of characterization and evaluation of coconut germplasm suited for the northeastern region of India.

Keywords: Coconut, fruit yield, fruit, growth, nut characters

¹ICAR-Central Plantation Crops Research Institute, Research Centre, Kahikuchi, Guwahati, Assam, India.

²ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala, India.

³Central Horticultural Experiment Station, ICAR-Indian Institute of Horticultural Research, Bhubaneswar, Odisha, India.

***Author for correspondence:**

singhleichombam@gmail.com

Received: 20/12/2023 **Revised:** 13/03/2024

Accepted: 18/03/2024

How to cite this article: Singh LS, N Vittal², GC Acharya and M Chaithra. (2024) Performance of Exotic and Indigenous Coconut Genotypes for Growth, Fruit Yield, Fruit and Nut Characters under Assam Conditions of North East Region of India. *Indian J. Plant Genetic Resources*. 37(1), 125-130. DOI: 10.61949/0976-1926.2024.v37i01.15

Introduction

Coconut (*Cocos nucifera* L.) is an important plantation crop grown in Assam, cultivated in an area of 20.80 thousand hectares with a production of 148.51 million nuts and productivity of 7,140 nuts/ha (Thamban *et al.*, 2023). It is mainly grown for its nutritious endosperm (kernel), which provides food, drink, medicine and a variety of products of commercial importance. Coconut is grown in all 33 districts, covering the upper, middle and lower parts of Assam: Nagaon, Barpeta, Kamrup, Sonitpur, Nalbari, Golaghat, Cachar, Karimganj, Morigaon, Udalguri, Darang, Bongaigaon, Baksa and Shivasagar are the leading coconut growing and producing districts in Assam (Gopalakrishnan, 2013). However, most of the coconuts grown are of the local type, and there is scope for increasing production and productivity in the state by planting more productive varieties. Assam Green Tall is the most common cultivar of coconut grown in this region. A higher average yield of about 105 nuts per palm per year has been reported in an Assam Green Tall selection. This indicates the potential for improving

coconut productivity in the state and the need to identify more improved varieties for cultivation in Assam. Towards developing improved varieties for specific agro-climatic zones, it is necessary to characterize and evaluate the coconut genetic resources to identify their yield potential and adaptive features for utilization in the coconut improvement programme. Characterization of coconut populations/cultivars/germplasm has been undertaken based on fruit traits (Whitehead, 1968; Harries, 1978; Niral *et al.*, 2009), botanical and agronomic traits (Sugimura *et al.*, 1997; Niral *et al.*, 2008). Using the coconut descriptor traits, morphological characterization was undertaken and descriptors have been published, not only in India (Ratnambal *et al.*, 1995, 2000) but also internationally for conserved coconut germplasm (Bourdeix *et al.*, 2010) as well as farmer's varieties (Bourdeix and Batugal, 2005). Research on crop improvement work is in progress in southern parts of India, where coconut is grown commercially. However, in North East region of India, limited work has been conducted to study the suitability of coconut varieties in this region. So far, Assam Green Tall and Kalpa Samrudhi are the only coconut varieties/hybrid which were found to be suitable for the region. Therefore, the present investigation was undertaken to study the performance of fifteen coconut varieties for growth, nut yield, and fruit and nut characteristics to enhance the coconut germplasm suitable for Assam.

Material and Methods

Study was conducted for five years from 2015 to 2022 at ICAR-Central Plantation Crops Research Institute, Research Centre, Kahikuchi, Guwahati, Assam, situated at 20° 18' N latitude and 91° 78' E longitude with an altitude of 50 m above the mean sea level (MSL). The mean maximum temperature varies from 15 to 3°C and the mean minimum temperature ranges between 8 and 22°C. The station enjoys a sub-tropical climate with an annual rainfall of about 1,500 mm. The soil of the experimental site was alluvial clay loam, with a pH range of 4.8 to 5.5. The study involved 15 coconut genotypes, including released varieties/hybrids planted during May 2004 at a spacing of 7.5 x 7.5 m (Table 1). The experiment was laid out in Randomized Blocks Design (RBD) with three replications. Six palms per replication were taken for observations. Vegetative growth parameters and fruit and nut characters viz., palm height, stem circumference (measured at the height of 1.0 m from ground level), number of leaves, number of leaf scars per meter (measured at the height of 1 to 2 m from ground level), fruit weight, fruit length, fruit circumference, nut weight (husked fruit weight), nut length (husked fruit length), nut circumference (husked fruit circumference), husk thickness, shell thickness, shell weight, endosperm (fresh kernel) thickness and endosperm weight were recorded. The fruit length and nut length (husked fruit length) were measured at the polar zone,

while the fruit circumference and nut circumference (husked nut circumference) were measured at the equatorial zone of the fruit. The husked weight was divided by the whole fruit weight to calculate the husk percentage. The annual nut yield per palm was recorded during each harvest and used to compute the annual nut yield (number of nuts per palm per year). Individual fruit component characters were recorded in thirty fruits from each variety harvested during the September harvest and data were statistically analyzed using MSTAT software.

Results and Discussion

Vegetative growth characters

Vegetative growth characters of 15 coconut genotypes recorded during the course of the present investigation have been presented in Table 2. Vegetative growth characters viz., palm height, number of leaves, circumference, number

Table 1: Place of origin of 15 coconut genotypes investigated during the present study

Name	Abbreviation	Description/origin
Assam Green Tall	AGT	Local tall from Assam
West Coast Tall	WCT	Indigenous tall from Kerala
Lakshadweep Ordinary Tall	LCT	Indigenous tall from the Lakshadweep Islands
Fiji Tall	FJT	Indigenous tall from Fiji
Malayan Green Dwarf	MGD	Exotic dwarf from Malaysia
Chowghat Orange Dwarf	COD	Indigenous dwarf from Kerala
Malayan Orange Dwarf	MOD	Exotic dwarf from Malaysia
Malayan Yellow Dwarf	MYD	Exotic dwarf from Malaysia
Gangabondam Green Dwarf	GBGD	Indigenous dwarf from Kerala
Kera Sankara	HKS	WCT x COD - Hybrid variety from ICAR-CPCRI
Chandra Sankara	HCS	COD x WCT - Hybrid variety from ICAR-CPCRI
Chandra Laksha	HCL	LCT x COD - Hybrid variety from KAU
Kera Ganga	HKG	WCT x GBGD - Hybrid variety from KAU
Laksha Ganga	HLG	LCT x GBGD - Hybrid variety from KAU
Kera Sree	HKS	WCT x MYD - Hybrid variety from KAU

Table 2: Vegetative growth characters of 15 coconut genotypes evaluated under Assam condition

Varieties/ Hybrid	Palm height (m)	No. of leaves	Circumference (cm)	No. of leaf scar/m	Leaf stalk length (cm)	Length of leaflets bearing portion (cm)	No. of leaflets (L)	No. of leaflets (R)	Leaflet length (cm)	Leaflet breadth (cm)
AGT	3.96	23.25	85.25	16.42	104.95	3.16	102.16	103.04	122.41	4.36
MGD	4.30	24.16	92.16	13.00	111.58	3.18	103.58	104.08	95.91	5.40
COD	2.21	22.41	60.67	27.74	92.51	2.11	96.85	96.96	93.52	4.05
HCS	4.63	27.16	77.49	22.97	125.73	3.10	107.65	108.31	138.09	5.02
MOD	2.79	22.76	60.12	26.80	120.11	2.69	86.64	87.44	87.92	4.96
HCL	4.64	21.06	80.60	18.67	110.88	3.04	102.46	102.93	94.42	5.54
WCT	5.17	24.72	85.73	15.28	112.24	3.31	111.21	112.40	100.60	5.61
FJT	5.71	22.18	95.16	13.85	119.81	3.23	107.41	107.81	94.50	5.89
MYD	3.21	22.43	66.10	28.32	98.27	2.85	85.38	85.99	86.70	4.69
HLG	4.23	25.67	94.16	19.67	122.27	3.73	118.66	118.88	111.54	5.79
HKS	5.31	27.32	95.15	18.33	116.41	3.74	103.00	103.83	114.91	5.65
HKG	5.53	23.50	93.00	15.50	119.75	3.59	106.50	107.50	130.49	5.66
LCT	5.86	22.50	107.50	12.67	136.08	3.67	111.50	109.99	128.41	5.60
HKS	4.67	24.67	101.00	14.33	119.83	3.26	106.00	106.16	109.65	5.18
GBGD	2.43	22.67	70.00	19.50	104.49	2.76	90.16	91.25	99.49	4.11
SEm (+/-)	0.48	0.69	3.49	0.67	6.49	0.11	3.56	3.71	5.32	0.24
CD (0.05%)	1.40	2.01	10.11	1.96	18.81	0.32	10.33	10.76	15.43	0.70

of leaf scar per meter, leaf stalk length, length of leaflets bearing portion, number of leaflets and leaflet length and breadth showed significant differences among the genotypes studied. Palm height among the tall types and hybrid varied from 3.96 to 5.86 m. Greater palm height was observed in the Lakshadweep Ordinary (5.86 m) variety, which was statistically at par with most of the varieties except for Assam Green Tall and Hybrid Laksha Ganga. Among dwarf types, the Malayan Green Dwarf recorded higher palm height (4.30 m) followed by Malayan Yellow Dwarf (3.21 m). Regarding the number of leaves produced, hybrid Kera Sankara was found to produce more (27.32) on the crown. The Present study shows that although higher palm height was observed in Lakshadweep Ordinary variety, a significantly higher number of functional leaves were observed in hybrid Kera Sankara. Nath *et al.* (2017) also reported production of 28.8 numbers of leaves in hybrid Kera Sankara in an experiment conducted at Horticultural Research Station, Assam Agricultural University, Kahikuchi, Guwahati, Assam. In an adult palm, the presence of about 25 to 35 opened leaves have also been reported by Niral and Jerard (2017). Stem circumference showed significant differences among the varieties studied. Lakshadweep Ordinary produce higher stem circumference as compared to other varieties. Tall types and hybrids were found to produce higher stem circumference than the dwarf types, except in Malayan Green Dwarf variety, showing high variability as compared to other dwarf types. Sudha *et al.* (2019), Sudha *et al.* (2021), Zhang *et al.* (2021) and Sudha *et al.* (2023) also reported significant variability among the genotypes for stem circumference. Higher stem circumference might be varietal characters. A recent study has also reported variation in trunk girth among varieties, with higher trunk girth in tall types like Andaman Giant and Zanzibar Tall coconut types in an experiment conducted at Coconut Research Station, TNAU, Aliyarnagar (Tripura *et al.*, 2018). In the current study, dwarf types were found to produce more leaf scar per meter than tall and hybrid coconut types. Ratnambal *et al.* (1995) and Kumaran *et al.* (2006) have also reported more leaf scar in dwarf coconut types than tall coconut varieties. Regarding the length of the leaflet bearing portion, number of leaflets and leaflet size, shorter length of leaflet bearing portion and fewer leaflets were seen in most of the dwarf types except Malayan Green Dwarf. Niral and Jerard (2017) also reported variations in leaf length, number of leaflets and leaflet size in coconut palms depending on variety, growing condition and age of the palm.

Fruit and Nut Characters

Fruit and nut characters of 15 coconut genotypes recorded during the course of present investigation have been presented in Table 3. Significant differences were observed for the fruit weight, fruit length, fruit circumference, husked nut weight, husked nut length, husked nut

circumference, husk thickness, shell thickness, shell weight, fresh endosperm (kernel) thickness and fresh endosperm weight. Fruit weight among the genotypes varied from 605.04 to 1173.47 g. Assam Green Tall produced greater fruit weight (1173.47 g) followed by Fiji Tall (1079.71 g) compared to other varieties. The lowest fruit weight was recorded in Malayan Yellow Dwarf (605.04 g). The present study has revealed that the fruit weight of coconut varieties was lower under Assam conditions than in other South Indian states. In an experiment conducted at the East Coast region of Andhra Pradesh, fruit weight of hybrid and varieties varied from 971 to 1464.7 g. Hybrid Chandra Laksha (1464.7 g) recorded higher fruit weight (Ramanandam *et al.*, 2018). Similarly, in another experiment conducted at Coconut Research Station, TNAU, Aliyarnagar, higher fruit weight (1064.50 g) was observed in Malayan Green Dwarf (Tripura *et al.*, 2018). Significant fruit weight variation among coconut varieties was also reported (Ramanandam *et al.*, 2018). Though Assam Green Tall recorded the maximum fruit weight among the varieties, higher fruit length and fruit circumference was observed in Fiji Tall. With regards to husked fruit weight, variety Assam Green Tall was found to produce greater husked fruit weight (832.04 g), which was found to be statistically at par with hybrid Kerasree (711.54 g). Husked fruit weight is an important trait required for the recovery of the kernel. In the present study, the husked fruit weight among the varieties varied from 359.78 to 832.04 g. Interestingly, though the fruit weight is less compared to South Indian conditions, the husked fruit weight was found to be on higher side. The dehusked nut weight of promising hybrids and varieties of coconut in East Coast region of Andhra Pradesh showed a varying range from 357.85 to 607.84 g (Ramanandam *et al.*, 2018). Chandra Sankara produce nut weight of 569.20 g. However, at the Research Centre, Kahikuchi, nut weight (665.75 g) was found to be higher in hybrid Chandra Sankara. The percentage of husk to fruit ratio among the varieties varied from 31.70 to 45.97%. Fiji Tall variety was found to produced a higher husk-to-fruit ratio percentage (45.97%) followed by hybrid Laksha Ganga (44.09%). Lesser husk to fruit ratio percentage was found in Malayan Orange Dwarf (29.38%). This might be attributed to thicker husk in Fiji tall variety as compared to other varieties. With respect to husked fruit length and circumference, maximum husked fruit length was observed in Fiji Tall variety (17.19 cm) followed by Assam Green Tall (17.06 cm). Whereas maximum husked fruit circumference was observed in the Assam Green Tall variety (35.22 cm). Husk thickness among the varieties was found to vary from 1.11 to 2.87 cm. Fiji tall variety recorded the maximum husk thickness (2.87 cm). Shell thickness and shell weight were also found to vary across the variety. Higher shell thickness was observed in hybrid Kera Ganga (0.35 cm). In terms of shell weight, Assam Green Tall was higher (182.79 g) followed

by hybrid Kera Ganga (162.90 g). Fresh endosperm weight showed that variety Assam Green Tall was found to produce significantly higher endosperm weight (379.50 g), followed by hybrid Chandra Sankara (317.48 g) and Kera Sree (316.56 g). Genetic variability in fruit size, husked fruit weight, husk thickness, endosperm thickness and endosperm weight among coconut genotypes were also reported by Natarajan *et al.* (2010).

Fruit Yield

The yield of 15 coconut genotypes recorded in terms of the number of nuts during the present investigation is presented in Table 3. The mean value showed that coconut varieties' yield varies from 35.34 to 109.32 nuts per plant per year. Significant differences were observed among the genotypes for the number of nuts recorded per palm per year. Hybrid Kera Sankara recorded the maximum yield per palm per year (109.32) followed by hybrid Chandra Sankara (75.48). The lowest mean yield was recorded in Malayan Yellow Dwarf (35.34). The yield data revealed that coconut hybrids gave higher nut yields as compared to other genotypes, which could be attributed to their hybrid vigor and higher yield potential (Ramanandam *et al.*, 2018). Better performance of hybrid *viz.*, Kalpa Samrudhi over Assam tall variety was also reported by Nath *et al.*, (2017) in an experiment conducted at Horticultural Research Station (AICRPP), Assam Agricultural University, Kahikuchi, Guwahati. Though Assam Green Tall variety is recommended for cultivation under Assam conditions, in the present study, hybrid Kera Sankara was also found to produce more nuts with an average nut yield of 109.32 nuts per palm per year. This may be due to better morphological growth, such as a higher number of functional leaves per palm. Tripura *et al.* (2018) have earlier reported the importance of more leaves as an important trait in increasing yield of coconut since it increases the photosynthetic efficiency of the palm. Variation in fruit yield among different coconut genotypes was also reported in the Coconut Research Station, Aliyarnagar, Tamil Nadu (Subramanian *et al.*, 2019).

Correlation among fruit and nut characters

Correlation among fruit and nut characters of 15 coconut genotypes recorded during the course of present investigation has been presented in Table 4. Fruit weight exhibited a significant positive correlation with most of the fruit parameters *viz.*, fruit length, fruit circumference, nut weight, nut length, nut circumference, husk thickness, shell thickness, shell weight, fresh kernel thickness and fresh kernel weight. Similar results were obtained by Baudouin *et al.* (2006), indicating that such a positive correlation was due to the interdependence between the different fruit parts. Shell thickness was not correlated with fresh kernel thickness and fresh kernel weight. Geethanjali *et al.* (2014) also reported that kernel thickness and shell thickness were

Table 3: Fruit yield and nut characters of 15 coconut genotypes evaluated under Assam conditionz

Varieties/ Hybrid	Yield (Nuts/ palm/year)	Fruit weight (g)	Fruit length (cm)	Fruit circumference (cm)	Husked fruit weight (g)	Fruit:Husk ratio	Husked fruit length (cm)	Husked fruit circumference (cm)	Husk thickness (cm)	Shell thickness (cm)	Shell weight (g)	Endosperm thickness (cm)	Endosperm weight (g)
AGT	37.79	1173.47	26.57	48.15	832.04	33.49	17.06	35.22	1.62	0.32	182.79	1.16	379.50
MGD	41.60	857.44	24.75	46.74	561.72	35.75	15.31	32.34	1.52	0.28	135.67	1.17	271.46
COD	43.86	665.52	20.84	39.69	446.17	31.78	14.82	29.67	1.24	0.24	116.17	1.00	227.50
HCS	75.48	976.34	25.22	44.98	665.75	31.70	16.78	32.40	1.44	0.30	162.40	1.18	317.48
MOD	43.22	650.04	21.00	39.67	433.68	29.38	15.71	29.17	1.11	0.23	117.11	1.02	230.01
HCL	65.49	937.11	26.10	42.84	595.69	35.16	16.30	31.91	1.76	0.34	138.81	1.16	284.02
WCT	58.37	781.75	22.92	43.91	475.02	39.24	15.24	28.92	2.14	0.27	113.15	1.19	248.57
FJT	48.42	1079.71	29.23	52.15	522.71	45.97	17.19	29.03	2.87	0.31	152.14	1.20	261.07
MYD	35.34	605.04	22.20	38.90	359.78	40.38	14.21	29.15	1.15	0.25	104.03	0.93	183.92
HLG	62.84	765.18	23.49	41.44	426.10	44.09	15.08	29.48	1.59	0.29	118.02	1.01	223.38
HKS	109.32	836.30	24.71	44.35	508.54	36.20	15.26	30.68	1.82	0.33	131.50	1.09	249.96
HKG	71.63	955.90	24.54	44.48	659.30	33.61	16.44	32.33	1.65	0.35	162.90	1.15	309.35
LCT	44.69	806.15	23.10	41.40	521.21	36.03	15.36	30.96	1.38	0.32	134.84	1.12	274.39
HKS	50.05	937.24	23.91	39.13	711.54	32.13	16.08	32.02	1.30	0.34	143.52	1.01	316.56
GBGD	53.85	944.84	25.26	42.25	612.03	40.81	16.92	32.44	1.23	0.24	123.75	1.11	314.05
SEm (+/-)	6.22	64.59	0.54	1.16	52.01	2.71	0.45	1.14	0.12	0.02	9.83	0.03	21.82
CD (0.05%)	18.01	187.11	1.58	3.36	150.68	7.85	1.32	3.31	0.35	0.06	28.48	NS	63.22

Table 4: Correlation among fruit traits recorded in 15 coconut genotypes evaluated under Assam condition

Traits	FW	FL	FC	HFW	HFL	HFC	HT	ST	SW	ET	EW
FW	1										
FL	0.898**	1									
FC	0.880**	0.844**	1								
HFW	0.714**	0.553*	0.467 ^{NS}	1							
HFL	0.805**	0.766**	0.612**	0.760**	1						
HFC	0.511*	0.420 ^{NS}	0.279 ^{NS}	0.928**	0.577*	1					
HT	0.551*	0.674**	0.746**	-0.038 ^{NS}	0.346 ^{NS}	-0.236 ^{NS}	1				
ST	0.552*	0.546*	0.354 ^{NS}	0.474 ^{NS}	0.376 ^{NS}	0.453 ^{NS}	0.256 ^{NS}	1			
SW	0.823**	0.675**	0.638**	0.874**	0.774**	0.765**	0.198 ^{NS}	0.676**	1		
ET	0.807**	0.690**	0.801**	0.584*	0.643**	0.393 ^{NS}	0.567*	0.413 ^{NS}	0.603*	1	
EW	0.706**	0.556*	0.477 ^{NS}	0.976**	0.783**	0.896**	-0.004 ^{NS}	0.357 ^{NS}	0.816**	0.568*	1

FW- Fruit weight (g), FL-Fruit length (cm), FC-Fruit circumference (cm), HFW- Husked fruit weight (g), HFL- Husked fruit length (cm), HFC- Husked fruit circumference (cm), HT- Husk thickness (cm), ST- Shell thickness (cm), SW- Shell weight (g), ET- Endosperm thickness (cm), EW- Endosperm weight (g)

not correlated with any of the fruit components. A negative correlation was observed with nut length, shell thickness, fresh kernel thickness, fruit circumference, and nut length. No correlation was seen for fruit length with nut weight, nut length, nut circumference, shell thickness and shell weight. Fresh kernel thickness and fresh kernel weight were found to be significantly and positively correlated with each other.

Conclusion

Coconut, a vital plantation crop in India, supports the livelihood of many small and marginal farmers in the North East region. Despite its importance, there has been limited systematic effort to boost coconut productivity in this area. This study evaluated fifteen coconut genotypes, both exotic and indigenous, to understand their growth, nut yield, and fruit characteristics in Assam conditions from 2015 to 2022. Significant variations were found, particularly in nut yield and fruit attributes. The hybrid variety Kera Sankara showed promising nut yield, indicating its suitability for cultivation in the North East. Additionally, Assam Green Tall displayed superior fruit characteristics. This research underscores the need for more focused coconut improvement studies in the Northeast and emphasizes the importance of tailoring coconut germplasm to the region's unique conditions. The insights gained from this study can guide local farmers, extension services, and policymakers toward improved coconut cultivation practices, ultimately contributing to increased income and profitability for coconut growers in the region.

References

- Baudouin L, P Lebrun, JL Konan, E Ritter, A Berger and N Billotte (2006) QTL analysis of fruit components in the progeny of a Rennell Island Tall coconut individual. *Thor. Appl. Genet.* 112: 258-268.
- Geethanjali S, D Rajkumar and N Sobha (2014) Correlation and path coefficient analysis in coconut. *Electron. J. Plant Breed.* 5: 702-707
- Gopalakrishnan R (2013) Global coconut scenario-India Forges Ahead. *Ind. Coconut J.* 10: 2-12.
- Harries HC. (1978) The evolution, dissemination and classification of coconut. *Bot. Rev.* 44: 265-319.
- Natarajan CK, Ganesamurthy and M Kavitha (2010) Genetic variability in coconut (*Cocos nucifera* L.). *Electron. J. Plant Breed.* 1: 1367-1370.
- Niral V and BA Jerard (2017) Botany, Growth and Development. In: Chowdappa P, V Niral, BA Jerard and K Samsudeen (Eds.) *Coconut*. Daya Publishing House, a division of Astral International Pvt. Ltd., New Delhi.
- Niral V, BA Jerard, KV Kavitha, K Samsudeen and RV Nair (2008) Variability and association among floral traits and pollen recovery in coconut (*Cocos nucifera* L.). *J. Plant. Crops.* 36: 186-191.
- Niral V, RV Nair, BA Jerard, K Samsudeen and MJ Ratnambal (2009) Evaluation of coconut germplasm for fruit component traits and oil yield. *J. Oilseeds Res.* 26: 668-670.
- Ramanandam G, E Padma, M Kalpana, K Ravindra Kumar, NBVC Rao and HP Maheswarappa (2018) Evaluation of promising hybrids and varieties of coconut in East Coast region of Andhra Pradesh. *Int. J. Pure Appl. Biosci.* 6: 207-211.
- Subramanian A, R Nirmal Raj, HP Maheswarappa and N Shoba (2019) Genetic variability and multivariate analysis in tall coconut germplasm. *J. Pharmacogn. Phytochem.* 8: 1949-1953.
- Sudha R, MK Rajesh, V Niral, K Samsudeen, S Shil, S Ramchander and Y Diwakar (2023) Analysis of genetic diversity and population structure in worldwide coconut germplasm (*Cocos nucifera* L.) using microsatellite markers. *Sci. Horti.* 309: 111681.
- Thamban C, Alpana Das, LS Singh and Anok Uchoi (2023) Challenges and prospects of coconut cultivation in North East India. *Ind. Coconut J.* pp 5-9.
- Tripura U, P Paramaguru, J Suresh, N Kumaravadivel, A Subramanian and N Sobha (2018) Performance of indigenous and exotic coconut germplasm for yield and nut quality under Aliyarnagar condition. *Int. J. Curr. Microbiol. Appl. Sci.* 7: 2611-2617.
- Zhang R, H Cao, C Sun and JJJ Martin (2021) Characterization of morphological and fruit quality traits of coconut (*Cocos nucifera* L.) germplasm. *Hort. Sci.* 56: 961-969.

Plant Germplasm Registration Notice®

The Plant Germplasm Registration Committee (PGRC) of ICAR held its XXXXVIth meeting on December 24, 2021 in virtual mode. 131 proposals were received and examined at ICAR-NBPGR out of which 74 proposals complete in all respects and reviewed by experts were considered for registration. 67 proposals with unique/novel features belonging to 27 species were finally recommended for registration. The information on registered germplasm is published with the purpose to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes.

1. **RP 5690-20-6-3-2-1 (IC0641981; INGR21176), a rice (*Oryza sativa*) germplasm with resistance to brown planthopper and whitebacked plant hopper. Possessing *bph4*, *Bph 9*, *Bph 17* and *Bph 32* genes for BPH resistance; and *wbph 9* & *wbph 10* genes for WBPH resistance**

G Padmavathi*, V. Jhansi Lakshmi, M Sheshu Madhav, P Senguttuvel, Ch Suvarna Rani, LV Subba Rao and RM Sundaram
ICAR-Indian Institute of Rice Research, Hyderabad-500030, Telangana, India

*Email: padmaguntupalli6@gmail.com

Considering the enormous yield losses caused in rice by two dreaded insect pests of rice namely brown planthopper (BPH) and white backed planthopper and (WBPH) for which limited donors are available, a focussed research program is being carried out at ICAR-IIRR, Hyderabad to develop elite lines conferring resistance to both the plant hoppers. An inbred line, RP 5690-20-6-3-2-1 developed from Sona mahsuri/SR 26-B following pedigree method was identified as resistant to planthoppers during seedling stage under controlled conditions against BPH and WBPH population of Hyderabad. It is a medium duration culture (128 days) with tall plant stature (139 cm) possessing long bold grains.

It was evaluated in multi-location testing trial viz. Planthopper Screening (PHS) trial for two years in 2017 and 2018 against BPH and WBPH populations at 13 hot spots as well as controlled greenhouse conditions in AICRIP entomology program. It exhibited stable and durable reproductive stage resistance against planthoppers at 4 locations continuously for 2 years (Table 1) in 3 locations (IIRR- Hyderabad, Ludhiana and Pantnagar with a mean DS: 3.2 against BPH; at one location (IIRR, Hyderabad) resistance reaction against WBPH (DS: 3.1) and moderate resistance reaction (DS: 4) at another single location (Maruteru) against mixed population of planthoppers. The resistant checks PTB 33 and MO1

Table 1: Glass house and field reaction of RP 5690-20-6-3-2-1 to BPH, WBPH and mixed population of planthoppers during 2017-2018

S. No.	Designation	Year of testing	DS of BPH (Green house reaction)				DS of WBPH (Green house reaction)	DS of Planthoppers (Field reaction)
	Screening locations		IIRR	LDN	PNT	Mean DS	IIRR	MTU
1	RP 5690-20-6-3-2-1	2017	4.8	2.3	1.7	2.9	2.3	5
		2018	2.8	3.6	4.5	3.6	3.9	3
		Mean	3.8	2.95	3.1	3.2	3.1	4
2	PTB 33 (R check for BPH)	2017	0.5	1.7	2.1	1.4		5
		2018	1.3	1.6	7.6	3.5		1
		Mean	0.9	1.65	4.85	2.4		3
3	MO1 (R check for WBPH)	2017					1.6	9
		2018					4.2	7
		Mean					2.9	8

IIRR: Indian Institute of Rice Research, Hyderabad; LDN: Ludhiana, PNT: Pantnagar, MTU: Maruteru

*Edited by: **Anju Mahendru Singh** and **Anjali Kak**, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India.

Acknowledgement is due to **Mr. Arup Das, YP** for providing technical assistance in compilation

recorded mean damage scores ranging from 0.9 to 4.85 and 1.6 to 4.2 respectively (Padmavathi *et al.* 2019; ICAR-IIRR, 2018. Progress Report 2017, Vol 2; ICAR-IIRR, 2019. Progress Report 2018, Vol 2).

Molecular characterization using linked and designed markers reported earlier revealed the presence of a synergistic combination of 4 known BPH Resistance genes (*bph4*, *Bph 9*, *Bph 17* and *Bph 32*) and 2 WBPH resistance genes (*wbph 9* & *wbph 10*) imparting stable resistance to the prevailing populations of planthoppers. This line could be exploited as a vital genetic source for imparting durable resistance to BPH and WBPH in recombination breeding

programs along with good grain quality and high grain yield.

References

- Padmavathi G, V Jhansilakshmi, MS Madhav, Md Tahseen and GS Prasad (2019) IET 26826: A rice dual donor conferring resistance to planthoppers and tolerance to alkalinity. *ICAR-IIRR Newslett.* 18(3): 3.
- ICAR-Indian Institute of Rice Research (2018) Progress report, 2017. Vol 2, Crop Protection (Entomology and Plant Pathology) 2.5p.
- ICAR- Indian Institute of Rice Research (2019) Progress Report 2018, Vol 2, Crop Protection (Entomology and Plant Pathology) p2.5.

2. CRR 363-36 (IET19251) (IC640650; INGR21177), a rice (*Oryza sativa*) germplasm with aroma, early maturity (85-90 days) and long slender grain for rainfed uplands

NP Mandal*, Somnath Roy and Amrita Banerjee

Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India

*Email: npmandal@hotmail.com

The rice elite line CRR 363-36 (IET 19251) was developed through pedigree breeding from a cross between Gaurav and Kalinga III at CRURRS (ICAR-NRRI), Hazaribagh. Among the parents Gaurav is a Basmati 370 mutant with excellent grain quality and aroma, and Kalinga III (AC540/Ratna) is an upland variety released for Orissa and Bihar. The CRR 363-36 was developed with an objective to produce a high yielding early maturing variety having excellent grain quality and aroma for rainfed uplands in eastern India because most of the developed upland rice varieties are poor in terms of grain quality and none of them is having aroma. Good grain quality can fetch better premium at the market and partially compensate upland rice farmers for low yield. The line was evaluated as IET 19251 in AICRIP - very early group

in 2005 and subsequently tested under Orissa state adaptive trials during 2007-2010. Agro-morphologically, CRR 363-36 is intermediately tall, it flowers in 55-60 days and has excellent long slender grains with good elongation ratio, considerable aroma and acceptable amylose content (Table 1). It is resistant to brown spot and moderately resistant to blast diseases which are the major diseases of uplands, based on National Screening nursey – 2005 data of AICRIP. CRR 363-36 is also resistant to gall midge-1, stem borer and moderately resistant to gall midge-4 & -5 and leaf folder. Due to its very early nature, CRR 363-36 usually escape drought stress under rainfed uplands. This improved elite line can be used as a donor for superior grain quality in upland rice breeding programmes.

Table 1: Salient agro-morphological features of rice elite line CRR 363-36

Characteristics	CRR 363-36	Characteristics	CRR 363-36
Plant type	Intermediate	Kernel breadth(mm)	1.85
Coleoptile colour	Green	Grain L/B ratio	3.45
Early plant vigour	Vigorous	Kernel appearance	LS
Basal leaf sheath colour	Green	1,000 grain weight (g.)	23.55
Leaf blade colour	Green	Threshability	Easy
Leaf pubescence	Pubescent	Husk colour	Straw
Leaf length (cm)	27.74	Hulling recovery (%)	77
Leaf width (cm)	1.24	Milling recovery (%)	65
Leaf angel	Horizontal	Head rice recovery - HRR(%)	52
Days to 50% flowering	55-60	Chalkiness	OC
Panicle exertion	Full	Kernel length after cooking(mm)	9.9
Stigma colour	White	Elongation ratio	1.54

Apiculus colour	Straw	Alkali value	4
No. of effective tillers/plant	14	Amylose content (%)	18.75
No. of panicles/sq.mt	238	Aroma	Present
Plant height (cm)	96		
Plant height (cm)	96		
Panicle length (cm)	23.86		
Panicle type	Compact		
Awning	Absent		
Days to maturity	85-90		
Seed coat(kernel) colour	White		
Kernel length(mm)	6.39		

3. RR 433-2-1 (IET 19252) (IC0560851; INGR21178), a rice (*Oryza sativa*) germplasm tolerant to drought and high yielding for rainfed direct seeded upland conditions

NP Mandal*, Somnath Roy and Amrita Banerjee

Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India

*Email: npmandal@hotmail.com

The rice elite line RR 433-2-1 (IRAT112/Annada) is a derivative of a *tropical japonica* × *indica* cross, of intermediate stature with the better lodging resistance of the *japonica* parent and more responsive to moderate-input management than traditional varieties. This line was developed at CRURRS (ICAR-NRRI), Hazaribag through pedigree breeding. The line (IET19252) was tested under All India Coordinated Rice Improvement Project (AICRIP) trials during 2005-2007, and based on overall performance it was identified as promising for release in the states of Orissa, Gujarat and Maharashtra (irrigated ecology). RR 433-2-1 recorded superior yield potential and stability under drought affected direct seeded conditions in AICRIP trials. Drought tolerance of this elite culture is well documented (Mandal *et al.*, 2010). Under normal conditions, RR433-2-1 recorded average grain yield of 3.0-3.5 t ha⁻¹. Under managed drought experiments across environments, it recorded grain yield of 2.10 t ha⁻¹ and 0.60 t ha⁻¹ under moderate and severe drought conditions, respectively which is considerably higher than Vandana (1.7 t ha⁻¹ and 0.60 t ha⁻¹, respectively) (Verulkar *et al.*, 2010). A study with RR433 showed that it has deeper roots (17.37 cm), higher root volume (20.6) and thicker roots (1.20 mm) than check varieties such as Vandana, Kalinga III and Brown gora (Pushpam *et al.*, 2018). RR 433-2-1 is moderately

resistant to Brown spot, Sheath rot and Leaf blast. It is resistant gall midge biotype 4 and moderately resistant to gall midge biotype 1, and moderately resistant to stem borer and leaf folder. Agro-morphologically, RR433-2-1 has intermediate plant height (90-100 cm), very early maturity (95-100 days), non-shattering panicles, long-bold grains (L/B ratio: 2.79), straw hulls and white kernels (Table 1). It possesses good cooking quality (amylose content 23.01% and Gel consistency 25-33 mm) with acceptable physical grain quality (Long bold grains, very occasional chalkiness, kernel length 6.1 mm and kernel breadth 2.18).

References

- Mandal NP, PK Sinha, M Variar, VD Shukla, P Perraju and A Mehta (2010) Implications of genotype × input interactions in breeding superior genotypes for favorable and unfavorable rainfed upland environments. *Field Crops Res.* 118: 135-144.
- Pushpam R, S Manonmani, NV Varthini and S Robin (2018) Studies on yield, root characters related to drought tolerance and their association in upland rice genotypes. *Electron. J. Pl. Breed.* 9: 856-862.
- Verulkar SB, NP Mandal, JL Dwivedi, BN Singh, PK Sinha and RN Mahato (2010) Breeding resilient and productive genotypes adapted to drought-prone rainfed ecosystem of India. *Field Crops Res.* 117: 197-208.

Table 1: Salient agro-morphological features of RR 433-2-1

Characteristics	RR433-2-1	Characteristics	RR433-2-1	Characteristics	RR433-2-1
Seedling vigour	Good	Maturity group	Early (95-100 days)	Kernel length	6.10 mm
Tillering ability	Medium	Panicle type	Compact	Kernel breadth	2.18 mm
Leaf blade pubescence	Intermediate pubescent	Panicle exertion	Well exerted	Length/ Breadth ratio)	2.79
Leaf blade colour	Pale green	Panicle length	20.5-24.2 cm	Grain type	LB
Leaf angle	Erect	Spikelet fertility	Highly fertile	Kernel colour	White
Ligule colour	White	Threshability	Intermediate	Endosperm type	Non-glutinous
Leaf senescence	Intermediate	Hull colour	Straw	Chalkiness of Endosperm	Present
Ligule shape	2-cleft	Awning	Absent	Head rice recovery	70.8%
Collar colour	Light green	Apiculus colour	Purple	Drought reaction	Tolerant
Culm angle	Erect	Stigma colour	White	Brown spot reaction	MR
Culm strength	Intermediate	Lemma & palea pubescence	Hairy	Leaf blast reaction	MR
Culm number	6 - 10	Grain length	7.50 mm	Leaf folder reaction	MR
Plant height	Intermediate tall (90-100 cm)	Grain width	3.45 mm	Stem borer reaction	MR
Days to 50% flowering	68-72 days	1000-grain weight	24.24 g	Gall midge biotype 1 & 4	MR & R, respectively

4. Kalakeri (IC0640883; INGR21179), a rice (*Oryza sativa*) germplasm tolerant to drought and phosphorus starvation with weed competitiveness

Somnath Roy¹, NP Mandal¹, P Swain², Amrita Banerjee¹ and BC Patra^{2*}

¹Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India

²ICAR-National Rice Research Institute, Cuttack- 753006, Odisha, India

*Email: bcpatracrri@yahoo.com

Kalakeri is a highly drought tolerant *aus* rice landrace originally from Odisha. The drought tolerant rice variety Vandana (RR 167-982) was developed by using Kalakeri as a tolerant donor (Kalakeri/C22) (Sinha *et al.* 1994). It possesses both vegetative and reproductive stage drought tolerance. In a recent study, several *DTY* QTLs for grain yield under reproductive stage stress such as *qDTY_{1.2}*, *qDTY_{1.3}*, *qDTY_{2.2}*, *qDTY_{2.3}*, *qDTY_{3.2}* and *qDTY_{6.1}* were recorded in Kalakeri using QTL-linked SSR markers (Roy *et al.*, 2021). Over the multi-environments trials Kalakeri exhibited leaf rolling and leaf drying scores of 3.0-4.3, indicative of a tolerant genotype. It showed lower spikelet sterility (36.4%) and a higher grain yield than Vandana under reproductive stage drought (ICAR-NRRI Annual Report 2013-14). Kalakeri is a good weed competitive genotype in terms of early emergence of plumule and initial higher leaf area index, tiller number, number of roots/plant and root depth. Under normal conditions, Kalakeri is found to be extra-vigorous

(very fast growing, plants at 5-6 leaf stage have 2 or more tillers). It has considerable tolerance to low phosphorus conditions in terms of higher biomass production under low P, and it possess the tolerant (Kasalath type) haplotype in *Phosphorus uptake 1 (Pup1)* locus, including the *Phosphorus starvation tolerance 1 (PSTOL1)* gene (Roy *et al.*, 2021). Agro-morphologically, Kalakeri has intermediate plant type (105 cm), maturity 90-95 days, and low tillering ability. It has medium-bold kernel type, and intermediate amylose content (20.7-25.2%) (Table 1)

References

- Sinha PK, M Variar, CV Singh, K Prasad and RK Singh (1994) Upland rice variety Vandana is suitable for Bihar plateau. *Ind. Farm.* 44: 3-4.
- Roy S, BC Verma, A Banerjee, J Kumar, US Ray and NP Mandal (2021) Genetic diversity for drought and low-phosphorus tolerance in rice (*Oryza sativa* L.) varieties and donors adapted to rainfed drought-prone ecologies. *Sci. Rep.* 11: 13671.

Table 1: Agro-morphological characteristics of Kalakeri (IC0640883)

Characteristic	Kalakeri	Characteristic	Kalakeri	Characteristic	Kalakeri
Early plant vigour	Extra vigorous	Leaf width (cm)	1.15	Brown rice length (mm)	6.13
Tillering ability	Low (9 tillers/plant)	Days to 50% flowering (days)	59	Brown rice width (mm)	2.81
Plant height	Intermediate (105 cm)	Panicle length (cm)	25.2	Brown rice length	Medium
Panicle exertion	Well exerted	Panicle axis	Straight	Brown rice shape	Bold
Leaf blade pubescence	Glabrous	Awning	Absent	100-grain weight (g)	2.33
Leaf blade colour	Light green	Apiculus colour	Purple	Grain yield (g)	2.08-3.25 t/ha
Basal leaf sheath colour	Light purple	Stigma colour	White	Aroma	No
Leaf angle	Erect	Lemma and palea colour	Black	Biotic stress susceptibility	Moderately resistant to blast and brown spot (SES score = 4.0)
Flag leaf angle	Erect	Sterile lemma colour	Gold		
Leaf length (cm)	43.0	Seed coat colour	Speckled brown		

5. Hango-2 (IC0640652; INGR21180), a wheat (*Triticum aestivum*) germplasm with novel leaf rust resistance gene *Lr80*. Confers broad spectrum leaf rust resistance.

Subodh Kumar¹, SC Bhardwaj^{1*}, OP Gangwar¹, VK Vikas², Hanif Khan³, Pramod Prasad¹ and GP Singh³

¹ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India

²IARI Regional Station, Wellington-643231, Tamil Nadu, India

³ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: Subhash.Bhardwaj@icar.gov.in

Leaf rust, caused by *Puccinia triticina* inflicts more losses on wheat than any other rust Bhardwaj *et al.* 2021). Deployment of rust resistance is an economic, effective and ecologically friendly approach to control this disease. Therefore, identifying new and effective rust resistance sources is always a priority in breeding wheat varieties. Common wheat landraces are valuable sources of genetic diversity for resistance to biotic and abiotic stress resistance (Bansal *et al.* 2013).

Wheat landrace Hango-2 (*LWH2*) collected from the Himalayan area of Hango, District Kinnaur, in Himachal Pradesh in 2006 exhibited a very low infection type (IT_i) at the seedling stage to all Indian leaf rust pathotypes (*Puccinia triticina*) pathotypes, except the pathotype 5R9-7 (16-1 old Indian notation) or DBBGB (North American designation) which produced IT 3+ (Table 1).

Genetic analysis based on Agra Local/Hango-2-derived F3 families indicated monogenic control of leaf rust resistance, and the underlying locus was temporarily named *LrH2*. Bulk segregant analysis using 303 simple sequence repeat (SSR) markers located *LrH2* in the short arm of chromosome 2D. An additional set of 10 chromosome

2DS-specific markers showed polymorphism between the parents and these were mapped on the entire Agra Local/Hango-2 F3 population. *LrH2* was flanked by markers cau96 (distally) and barc124 (proximally). The 90 K Infinium SNP array was used to identify SNP markers linked with *LrH2*. Markers KASP_17425 and KASP_17148 showed association with *LrH2*. Comparison of seedling leaf rust response data and marker locations across different maps demonstrated the uniqueness of *LrH2* and it was formally named *Lr80*. The *Lr80* linked markers KASP_17425, KASP_17148 and barc124 were developed for its utilization in marker assisted selection.

Most of the resistance genes identified in the past have minor effect or adult plant resistance. Contrarily *Lr80* is a major gene and can be identified in seedling stage as well as through the linked markers. Identification of *Lr80* from a local wheat is again a testimony that landraces are effective sources of biotic and abiotic resistance. This is the sixth rust resistance gene designated from India in 75 years of rust resistance gene cataloguing in wheat world over. Other *Lr* genes reported from India are *Lr10* (based on the work in Canada), *Lr48*, *Lr49*, *Lr57* and *Lr58*. Since this gene

Table 1: Response of *Lr* genes located on 2DS to different virulent and predominant pathotypes of *Puccinia tritricina* in India

Pathotypes		<i>Lr</i> genes on 2DS chromosome								Parental lines
Indian Designation	Common name	<i>Lr2a</i> (TC)	<i>Lr2b</i> (TC)	<i>Lr2c</i> (TC)	<i>Lr11</i> (Tc)	<i>Lr15</i> (TC)	<i>Lr22a</i> (TC)	<i>Lr22b</i> (TC)	<i>Lr39</i> (KS92WRGC15)	Hango 2 (Lr80)
29R45	12-5	;1	;12	3+	3+	0;	3+	3+	0;	;-
5R9-7	16-1	;1	;	3+	;	0;	33+	33+	0;	3+
109R63	77-1	3+	3+	3+	3+	3+	3+	3+	0;	;-
109R31-1	77-2	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R63-1	77-5	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R55-1	77-6	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R127	77-7	3+	3+	3+	3+	3+	3+	3+	0;	;-
253R31	77-8	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R60-1	77-9	;	;	;	3+	3+	3+	3+	0;	;-
377R60-1	77-10	;	;	;	3+	3+	3+	3+	0;	;-
21R55	104-2	;12	;12	3+	3+	0;	3+	3+	0;	;-
21R63	104-3	;12	;12	3+	3+	0;	3+	3+	0;	;-

confers resistance to leaf rust, therefore, it is being used to pyramiding of resistance and breeding wheat varieties.

References

Bhardwaj SC, S Kumar, OP Gangwar, P Prasad, PL Kashyap, H Khan, S Savadi, GP Singh, N Gupta and R Thakur (2021) Physiologic

specialization and genetic differentiation of *Puccinia tritricina* causing leaf rust of wheat in the Indian subcontinent during 2016-2019. *Pl. Disease*. 105(7): 1992-2002.

Bansal UK, VN Arief, IH DeLacy and H Bariana (2013) Exploring wheat landraces for rust resistance using a single marker scan. *Euphytica* 194: 219–233.

6. HS661 (IC0638606; INGR21181), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm resistant to all pathotypes of yellow (stripe) rust. Possessing rust resistance genes *Yr15* and *Sr25/Lr19*

Dharam Pal^{1*}, SC Bhardwaj², Madhu Patial¹, Subodh Kumar², OP Gangwar², Pratima Sharma³ and KV Prabhu⁴

¹ICAR-IARI, Regional Station [CHC], Shimla-171004, Himachal Pradesh, India

²ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India

³Green Glen Layout, Palm Avenue, Bengaluru-560103, Karnataka, India

⁴PPVFRA, NASC Complex, New Delhi-110012, Delhi, India

*E-mail: dpwalia@rediffmail.com

Stripe rust or yellow rust caused by fungus *Puccinia striiformis* f. sp. *tritici*, has its impact on the wheat crop grown in 10-12 million hectares (mha) of Northern India (Bhardwaj and Singh 2019). Grain yield loss due to stripe rust ranged from 10-70% (Chen, 2005; Ashmawy and Ragab, 2016). It can cause 100% yield loss if infection occurs at an early stage of growth and the disease continues to develop during the growing season (Afzal *et al.*, 2007). Rust resistance breeding program against a multi-racial pathogen is always faced with the problems of complexities of race composition and the evolution of new pathotypes. It is imperative to have choice of parents possessing diverse rust resistance genes for developing and deployment of wheat cultivars with durable resistance for increasing their longevity. In this direction,

a rust resistant wheat germplasm HS661, was developed from a cross HS295*2/FLW20(*Lr19*)/HS295*2/FLW13(*Yr15*) through back crossing followed by Bulk-Pedigree method of breeding at Indian Agricultural Research Institute, Regional Station, Shimla. HS661 has been found resistant against all the pathotypes of yellow rust under seedling resistance test at IIWBR, RS, Shimla. Besides, it has shown seedling resistance to all pathotypes of brown rust and stem rust (Table1) (AICRPW&B Progress Report, Crop Protection, 2018). HS661 was found to possess adult plant resistance (APR) to yellow rust at four locations viz., Bajaura, Dhaulakuan, Malan and Una. It was also resistant to all the three rusts including yellow rust in Plant Protection Screening Nursery (AICRPW&B Progress Report, Crop Protection, 2018). HS661

Table1: All stage resistance in HS661 against wide array of rust pathotypes

Yellow Rust Pathotypes																					
Genotype	46S119	110S119	78S84	110S84	238S119	110S247	T	P	111S68	79S68	79S4	750	K	650	20A	L	N	38A	Gene		
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R		
FLW20	S	S	S	S	S	S	S	S	S	S	S	R	S	S	S	S	S	S	S		
FLW13	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R		
HS295	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S		
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S		

Brown Rust Pathotypes																									
Genotype	11	12-2	12-5	12-7	12-8	16-1	77	77-1	77-2	77-5	77-6	77-7	77-8	77-9	77A-1	77-10	104-2	104-3	104B	106	108-1	162-1	162A	162-3	
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
FLW20	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
FLW13	R	R	S	S	R	R	R	R	S	R	S	R	S	R	S	S	S	S	R	R	R	R	R	R	
HS295	R	R	S	S	R	R	R	R	S	R	S	R	S	R	S	S	S	S	R	R	R	R	R	R	
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	
Black Rust Pathotypes																									
Genotype	11	11A	14	15-1	21	21-1	21A-2	24A	34-1	40	40A	40-1	40-2	40-3	42B	117A	117A-1	117-1	117-2	117-3	117-4	117-5	117-6	184	295
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
FLW20	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
FLW13	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
HS295	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	R	R	R	R	R	R	R	R	R	R
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S

was confirmed to possess *Yr15* using molecular marker *gwm11* (Pal *et al.*, 2019), also confirmed for presence of *Sr25/Lr19* using STS marker *Gb*.

HS661 possesses good agronomic features viz., semi-erect growth habit, waxy flag leaf sheath, tapering ear shape, 88cm of plant height, white ear with white awns, attitude of awns is spreading, the grains are semi-hard and ovate shaped, amber in colour with thousand grain weight of 39g. The rust resistance genes *Yr15* and *Sr25/Lr19* rendering broad spectrum resistance against wide array of pathotypes of all the three rusts along with good agronomic features present in HS661 could be a desirable choice for breeding rust resistant wheat varieties in India.

References

- Afzal SN, MI Haque, MS Ahmedani, S Basir and AR Rattu (2007) Assessment of yield losses caused by *Puccinia striiformis* triggering stripe rust in the most common wheat varieties. *Pakistan J. Bot.* 39: 2127-2134.
- Ashmawy MA and KE Ragab (2016) Grain yield of some wheat genotypes to stripe rust in Egypt. *Menoufia J. Pl. Protect.* 1: 9-18.
- Bhardwaj SC and GP Singh (2019) Tackling wheat rusts through resistance- success, challenges and preparedness. *Curr. Sci.* 116: 1953-1954.
- Chen XM (2005) Epidemiology and control of stripe rust (*Puccinia striiformis* f. sp. *tritici*) on wheat. *Canadian J. Pl. Pathol.* 27: 314-337.
- ICAR-IIWBR (2018) Progress Report of AICRP on Wheat and Barley 2017-18, Crop Protection (Eds. D.P. Singh, Sudheer Kumar, Poonam Jasrotia, P.L. Kashyap and GP Singh) ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p259.
- ICAR-IIWBR (2018) Progress Report of AICRP on Wheat and Barley 2017-18, Crop Improvement (Eds. Chatrath R, V Tiwari, G Singh, R Tiwari, BS Tyagi, A Gupta, R Kumar, SK Singh, L Kumar, AK Sharma, H Khan, S Kumar, C Singh, CN Mishra, K Venkatesh, HM Mamrutha, V Gupta, Rinki, K Gopalareddy, A Verma and GP Singh) ICAR- Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p206.
- Pal D, SC Bhardwaj, M Patial, S Kumar, OP Gangwar, P Sharma and KV Prabhu (2019) Transfer of leaf rust and stripe rust resistance genes *Lr19* and *Yr15* into a susceptible wheat cultivar HS295. *Indian J. Genet.* 79: 618-621.

7. QBP18-8 (IC0640679; INGR21182), a Wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high hectoliter weight (80.6Kg/hl)

Anju Mahendru Singh^{1*}, SV Sai Prasad², Arvind K Ahlawat¹ and Ram Bihari Shukla¹

¹Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

²ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India

*Email: Anju.Singh@icar.gov.in

Flour recovery is a much sought after trait by the Indian millers as it increases their profit margins. It is also a highly desirable trait for superior chapati quality. Flour recovery is affected by several genetically controlled traits and soil characteristics. Among the genetically controlled traits, hectoliter or test weight is the most important. Test weight determinants are grain shape, diameter, weight and grain density. Genotypes combining all four criteria are less common in Indian wheat varieties. Major wheat varieties have mean test weight between 75-77 Kg/hl. A genotype QBP 18-8 was developed as a pure line from selection of the entry from the HarvestPlus Yield trial and possesses much

higher test weight than the prevalent check varieties.

The mean values of test weight in the four agroclimatic zones for wheat viz., North Western Plains Zone, the North Eastern Plains Zone, the Central Zone and the Penninsular Zone of India were 81 Kg/hl, 80.6 Kg/hl, 81.3 Kg/hl and 79.7 Kg/hl respectively. Thus, QBP 18-8 recorded significantly higher mean value of 80.6 Kg/hl against the mean value of 75.9 Kg/hl of the popular wheat variety HD3086 and showed a high stability over all the locations. Thus, QBP18-8 is a stable donor for high test weight across varied environments and therefore, can be used in breeding programmes to increase the flour recovery of the new lines.

8. QBI20-14 (IC0640680; INGR21183), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high grain zinc concentration (57mg/kg)

Anju Mahendru Singh*, Shailendra K Jha, Arvind K Ahlawat and Ram Bihari Shukla

¹Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

*Email: Anju.Singh@icar.gov.in

Development of Bio fortified wheat is an important goal for wheat plant breeders today. In the initial phase, a number of crosses were made with wild species many of which had been reported to have high grain iron and zinc

concentration. However, it was soon realized that not only do the wild relatives bring in a lot of linkage drag but in many cases, the high content observed is mainly due to the "concentration effect" in the grain. Therefore, more

efforts are now being made to search for high grain iron and zinc in the adapted germplasm and involving wild relatives or progenitors at the most only once in the cross. With such efforts, a number of genotypes responding to soils with even moderate content of available zinc have been developed.

QBI20-14 is one such genotype and it has shown higher

levels of grain zinc concentration over five locations as compared to the varietal check GW322 and micronutrient check WB02. The genotype QBI20-14 is also higher in yield as compared to both the checks. Thus, coupled with high grain yield and protein content (13.6%), QBI20-14 is a stable donor of grain zinc for breeding programmes to improve nutritional quality of wheat.

9. QBP18-10 (IC0640681; INGR21184), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high hectoliter (test) weight (80.4 kg/hl) and superior grain appearance

Anju Mahendru Singh^{1*}, Divya Ambati², Arvind K Ahlawat¹ and Ram Bihari Shukla¹

¹Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

²ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India

*Email: Anju.Singh@icar.gov.in

Major wheat varieties have mean test weight between 75-77 Kg/hl. The genotype QBP 18-10 has a much higher test weight. The mean value of test weight in the four locations of NWPZ was 79.6 Kg/hl, in the NEPZ was 79.4 Kg/hl, in the CZ was 80.4 Kg/hl and in the PZ, it was 82.4 Kg/hl. Overall, QBP 18-10 recorded a very high mean value of 80.4 Kg/hl against the mean value of 75.9 of the check variety HD 3086. Thus, along with QBP18-8 (IC640679; INGR21182), QBP18-10 (mentioned at S No. 7 above) is an elite donor for High Test weight.

Moreover, the grain of genotype QBP18-10 is very much

like the hard, vitreous and lustrous sharbati grain which gets a better premium in the market. It has recorded very high grain Appearance score (7.1). The grain protein of QBP18-10 is also high (mean value of 12.3%). These traits are invaluable to the milling industry and fetch a better price to the farmer and the miller. Thus, QBP18-10 shows stability for high test weight across varied environments, has a very appealing grain appearance and also has a good protein content above 12% and this genotype can be involved as one of the parents in breeding programmes to increase the flour recovery and market value of the new lines.

10. QBP17-7 (IC0640682; INGR21185), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high grain iron concentration (48.1 mg/Kg)

Anju Mahendru Singh^{1*}, Pradeep K Singh¹, Arvind K Ahlawat¹ and Ram Bihari Shukla¹

¹Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

*Email: Anju.Singh@icar.gov.in

Iron is a major component of plant and human enzymes and biomolecules. Wheat grain has higher level of grain zinc and iron concentration as compared to rice and maize kernels. However, the current levels of grain micronutrients in wheat are not sufficient to provide even 50% of the RDA for adults. Since wheat is the staple food in India especially in the Northern and Central parts of the country, iron is an important nutritional trait to be improved by plant breeding efforts called bio-fortification. QBP17-7 is a germplasm developed by intermating of high iron source and high yielding lines.

QBP17-7 showed 43.2 mg/Kg (ppm) in NWPZ as against 41.3 ppm of the check WB02, 45.2 ppm in NEPZ as against 44.6 ppm in WB02 and 55.8 ppm in CZ against WB02 with 47.9 ppm. Thus, it has recorded higher mean value zone wise as well overall higher mean (48.1 ppm) of grain iron concentration over the bio-fortified variety WB02 having an overall mean of 44.8 ppm in the AIW&BRP. This line has maintained the protein content of 13.1% similar to WB02 (13.3%). Thus, with its good yielding background, higher iron concentration and high protein content QBP 17-7 is a valuable resource and donor for biofortification.

11. HD3241 (IC0640684; INGR21186), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high sedimentation value (73-75 ml) for greater gluten strength

Anju Mahendru Singh¹, Jang Bahadur Singh² and Arvind Kumar Ahlawat¹

¹Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

²ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India

*Email: Anju.Singh@icar.gov.in

India has seen an upsurge in the value based industry in the recent past. The milling and baking industry of India is rapidly expanding and is valued at ~Rs 73 billion. The industrial handling of wheat flour has been a subject of concern in the baking industry of India. The bread and pizza flour requires strong gluten for retaining the carbon dioxide gas released during fermentation of the dough. However, Indian wheat varieties have moderately strong gluten with sedimentation values in the range of 40-50 ml. Therefore, the use of conditioners such as potassium bromate, ascorbic acid etc. is rampant in Indian baking industry which is not advisable for consumers' health. Hence, varieties with greater gluten strength for industrial handling and better baking are sought. India could see an upsurge in its export if such varieties are developed using the high trait donors. Sedimentation test is an indicator of gluten content and gluten strength.

HD 3241 was identified during the screening of germplasm received from CIMMYT as an entry in the trials for quality traits. It is an elite germplasm with high yield, resistance to all the three rusts and has height of 110-113cm & 160 tillers/meter. HD3241 was analysed for quality traits also and was promoted to Quality Component and Wheat Biofortification Nursery (QCWBN) planted at 12 locations during 2018-19 under the AIW&BRIP. HD3241 was found to be excellent in its SDS-Sedimentation Value (SV) in all the four zones. It showed SV of 70ml and 77ml in NWPZ and NEPZ respectively and 76ml across CZ and PZ. Thus, the mean value of HD3241 over all the four zones was found to be 75 ml which is the highest reported for any of the genotypes tested so far in the AIW&BRIP. HD3241 also has a Protein content of 12.6% and Hectoliter (Test) weight of 78.4 kg/hl and also has hard and lustrous grains. Therefore, HD3241 is a highly stable donor of very high sedimentation value for use in wheat breeding programmes for bread making quality.

12. IC290156 (IC290156; INGR21187), a wheat (*Triticum aestivum*) germplasm with resistant to stripe rust pathotypes 46S119 and 47S103

Sundeep Kumar^{1*}, Anjan Kumar Pradhan¹, Amit Kumar Singh¹, Neeraj Budhlakoti¹, Dwijesh Chandra Mishra¹, Divya Chauhan¹, Suneel Kumar Meena¹, Subodh Kumar², SC Bhardwaj², Anil Rai³ and Kuldeep Singh³

¹ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

²ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India

³ICAR-Indian Agricultural Statistics Research Institute, Pusa Campus-110012, New Delhi, India

*Email: sundeepksharma77@rediffmail.com

Stripe rust is the most damaging and widely prevalent disease which caused by *Puccinia striiformis* f. sp. *tritici* (Pst) in wheat. It causes significant yield losses in almost every part of the world where cool and humid conditions persist during crop season. Yield losses due to this disease vary from 10 to 40% which depends upon various factors like severity level, susceptibility of cultivars, stage of infection, rate of disease development, and duration of disease. In India, stripe (yellow) rust is the major disease in North West Plain Zones (NWPZ) especially sub-mountainous parts of Punjab, Haryana, and Western Uttar Pradesh, the major wheat growing regions of India. Occurrence of stripe rust has also been observed frequently in Jammu & Kashmir, Punjab, Himachal Pradesh, *tarai* regions of Uttarakhand and western Uttar Pradesh. However, a major outbreak of stripe rust was observed in the North Western Plain Zone (NWPZ) and the Northern Hills Zone (NHZ) of India in 2006 and 2012–13 which caused heavy yield losses. Keeping in consideration an experiment was conducted on a set of 391 wheat germplasm lines comprised of Indian landraces,

Indigenous germplasm collection and some exotic lines and breeding stocks. These germplasm lines were evaluated separately against four pathotypes 46S119, 238S119, 47S103 and 110S119 for two consecutive years 2018 and 2019 winter season (8 environments). In addition, a genome wide association study (GWAS) was also preferred to identify QTLs/genes associated with stripe rust resistance.

The germplasm line IC290156 which showed the presence of resistance-associated favourable alleles and therefore showed high disease severity index for stripe rust. This germplasm line was found resistant against two pathotypes i.e., 46S119 and 47S103. It is also associated with a candidate gene TraesCS6D02G384800, that functions as leucine-rich repeat receptor-like protein kinases (LRR) which play key role in pathogen recognition and disease resistance. The study also revealed 20 novel QTLs, which 11 QTLs for 46S119 and 47S103(T) pathotypes distributed on 2DL, 3AL, 3B, 3DS, 4DL, 5BS and 6DL which are linked with IC290156 line. This line is a potential genetic resource for stripe rust resistance, which can be further used in wheat improvement programme.

13. IC321906 (IC321906; INGR21188), a wheat (*Triticum aestivum*) germplasm with terminal heat tolerance

Sundeep Kumar^{1*}, Jyoti Kumari¹, Nabin Bhusal², Anjan Kumar Pradhan¹, Neeraj Budhlakoti³, Dwijesh Chandra Mishra³, BK Meena⁴, Divya Chauhan¹, Suneel Kumar¹, Amit Kumar Singh¹, Gyanendra Pratap Singh⁴, Kuldeep Singh¹ and Sindhu Sareen⁴

¹ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

²Agriculture and Forestry University, Bharatpur 44200, Nepal

³ICAR-Indian Agricultural Statistics Research Institute, Pusa Campus-110012, New Delhi, India

⁴ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: sundeepksharma77@rediffmail.com

A comprehensive study was conducted to identify heat tolerant wheat lines from an association mapping panel of 205 wheat accessions, evaluated under late sown conditions in India at three different locations (Delhi, Hisar and Karnal) for 3 consecutive years (2015-2017). Planting was done in three replications on each location. In the field screening, data was recorded for 16 agronomic traits such as days to heading (DH), days to anthesis (DA), days to physiological maturity (DM), chlorophyll fluorescence (CFL), cell membrane stability (CMS), grain filling duration (GFD), grain weight/spike (GW, g), grain numbers/spike (GN), grain numbers/m (GNM), productive tillers/m (PTL), plant height (PHT, cm), 1,000 grain weight (TGW, g), biomass (BM, gm–2), grain yield (GY, gm–2), grain filling rate (GFR), and harvest index (HI, %) to find out the variation among studied wheat accessions. Stability analysis and AMMI biplot was also performed to analyze the stable performance of genotypes across the environment and years.

Genotyping using a high density 35 K array, revealed a large number of SNPs that could be used for the GWAS analysis. In total, 69 QTLs were identified for the ten agronomic traits.

The favourable alleles for each QTL region were identified by comparing the extreme phenotypic values in association mapping panel. The analysis revealed heat tolerant germplasm lines based on presence of favourable alleles for few accessions viz. HD2888, IC611071, IC611273, IC75240, IC321906, IC416188 and J31-170. Among these germplasm lines, co-localized QTLs were found for IC321906 accession showing favourable alleles for 3 different traits viz. GY (1), GFR (7) and BM (2). This accession is a variant of C306 (a popular drought tolerant wheat cultivar released in 1960's) as its parent from Jharkhand is being proposed to be registered as genetic stock for heat tolerance. This is a potential genetic resources for heat tolerance, which can be further used in wheat improvement programmed.

14. BNSR6 (IC0641982; INGR21189), a wheat (*Triticum aestivum*) germplasm having high Fe (43.8 ppm), Zn (48.6 ppm) and protein (14.3 %)

Sewa Ram^{1*}, OP Gupta¹, Vanita Pandey¹, Sunil Kumar¹, BS Tyagi¹, Gopalareddy K¹, VS Sohu² and GP Singh¹

¹ICAR-Indian Institute of Wheat and Barley Research, Karnal 132001, Haryana

²Punjab Agricultural University, Ludhiana -141004, Punjab

*Email: sewa.ram@icar.gov.in

Worldwide over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children under the age of 5-10 years have zinc/iron or some other micronutrient deficiency. Zinc is one of the important micronutrient for normal growth and development. BNSR 6 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing DPW 621-50 // GLUPRO*3 / PBW 568. The hand threshed grains of 10 centres in QCWBN comprising all the major wheat growing zones of the country has been analysed for grain iron and zinc concentration and 11 centres for grain protein concentration. BNSR 6 was found to be superior for grain zinc concentration

(48.6 ppm), grain iron concentration (43.8 ppm), and grain protein concentration (14.3 %) over the locations to all the check varieties (Table 1 and 2). Thus, BNSR 6 would be a potential source to be utilized in future breeding programs to develop high yielding bread wheat varieties with enhanced grain zinc, iron, and protein concentration.

Reference

Progress Report of All India Coordinated Research Project on Wheat and Barley (2020-21) Wheat Quality. (Eds: Sewa Ram, Sunil Kumar, O.P. Gupta, Vanita Pandey and G.P. Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. p151.

Table 1: Grain iron and zinc concentration of BNSR 6 and check varieties at 10 locations during 2020-21

Zone	Location	Genotype							
		BNSR 6		WB02		HD3226		GW322	
		Zn	Fe	Zn	Fe	Zn	Zn	Fe	Zn
NWPZ	Karnal	39.8	38.7	35.1	36.9	31.0	32.5	35.0	33.6
	Hisar	47.1	48.6	44.4	42.8	35.8	42.1	40.5	40.1
	Delhi	61.9	42.3	59.1	39.9	48.7	53.3	40.0	52.4
	Ludhiana	41.4	48.5	37.4	41.6	33.7	34.4	37.5	35.5
NEPZ	Kanpur	39.4	33.1	38.0	34.0	32.3	40.6	35.2	38.4
	Varanasi	35.0	38.9	34.6	38.0	29.2	33.2	37.9	34.2
CZ	Indore	53.7	44.5	51.1	40.2	42.8	50.7	42.7	47.4
	Vijapur	55.0	43.2	56.1	46.5	44.1	49.6	45.5	49.5
PZ	Pune	58.4	44.8	50.0	44.2	42.4	46.7	40.6	47.8
	Dharwad	54.0	51.8	37.6	43.1	29.9	31.2	39.8	34.9
Mean (National)		48.6	43.4	44.3	40.7	37.0	41.3	39.5	41.4

Table 2: Grain protein concentration of BNSR 6 and check varieties at 11 locations during 2020-21

Zone	Location	Genotype			
		BNSR 6	WB02	HD3226	GW322
NWPZ	Karnal	14.7	13.8	12.8	11.1
	Hisar	12.8	12.8	11.2	10.5
	Delhi	16.1	15.7	14.5	12.5
	Ludhiana	14.4	13.2	12.8	11.2
NEPZ	Kanpur	11.5	11.6	11.1	9.2
	Varanasi	12.9	12	11.9	10.1
CZ	Indore	14	14.5	13.7	10.8
	Vijapur	14	14.6	13.5	11
PZ	Pune	15.3	15.1	14	11.1
	Dharwad	17.3	16	13.5	10.9
	Niphad	14.7	13.8	13.1	10.9
Mean		14.3	13.9	12.9	10.9

15. HI 8807 (IC0641983; INGR21190), a wheat (*Triticum durum*) germplasm with resistance to stem, leaf, stripe rusts and Karnal bunt.

Divya Ambati, Rahul M Phuke, SV Sai Prasad, Jang Bahadur Singh, Prakasha TL* and Dilip Kumar Verma

ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India

*Email: prakash7385@gmail.com

Durum wheat (*Triticum turgidum* subsp. *durum* (Desf.) Husnot) is the second most important cultivated wheat species. Globally, it is cultivated in 17 million ha, with a production of 38.1 million tonnes. Rainfall, biotic (pests and diseases) and abiotic (drought, sunlight, cold, and salinity) stresses found to affect durum wheat productivity (Xynias *et al.*, 2019). Central and peninsular zones comprising of Madhya Pradesh, Gujarat, Maharashtra and Karnataka states are the major durum wheat growing regions in India. Among diseases, stem and leaf rusts are major diseases in these zones. Managing diseases through host plant resistance is the most economical and viable strategy to manage diseases. Diverse genetic base is required to minimize crop losses caused by these ever-evolving pathogens. Identifying and utilizing multiple disease resistant along with high yielding genotypes is important in durum wheat improvement.

HI 8807 (HI 8695/ HI 8663// HI 8663), a semi erect durum wheat genotype with strong waxiness on leaf sheath and spike, white, dense tapering spike and without glume pubescence. It was identified to be resistant to stem, leaf and stripe rusts in multi-location testing viz., Plant

Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2017 to 2021 (Table 1). It showed resistance to Karnal bunt disease (Table 2) over two years of testing at different locations. HI 8807 showed superiority in mean weighted grain yield superiority of 0.4 to 4.3% in NIVT and AVT-I in comparison to bread wheat check varieties. As the availability of multiple disease resistant high yielding genotypes is rare, HI 8807 can be used as potential resistance donor to breed varieties against these multiple pathogens and also a source of high grain yield.

References

- Xynias IN, I Mylonas, EG Korpetis, E Ninou, A Tsaballa, ID Avdikos and AG Mavromatis (2020) Durum Wheat Breeding in the Mediterranean Region: Current Status and Future Prospects. *Agronomy* 10: 432.
- Progress report of the All India Coordinated Wheat and Barley Improvement Project (2018-21) Crop Protection. ICAR-IIWBR, Karnal, India.
- Progress report of the All India Coordinated Wheat and Barley Improvement Project (2018-19), Crop Improvement. ICAR-IIWBR, Karnal, India.

Table 1: Disease data of HI 8807 in comparison with check varieties over years

Year of testing	Trial		Stem rust		Leaf rust				Stripe rust	
			South		South		North		North	
			HS	ACI	HS	ACI	HS	ACI	HS	ACI
2017-18	NIVT 3B	HI 8807	10MS	2.5	10MS	1.5	TR	0.0	10S	3.4
		HD 2864 (c)	5MR	0.9	5MS	1.3	30S	4.9	80S	59.0
		HD 2932 (c)	30MR	6.3	80S	15.1	70S	21.0	90S	58.0
2018-19	AVT I	HI 8807	20MS	3.3	5MS	0.6	20S	2.8	20MS	3.4
		HD 2864 (c)	10S	2.8	40S	6.5	20S	6.0	100S	61.8
		HD 2932 (c)	20MS	8.4	40S	19.4	90S	34.6	80S	55.0
2019-20	EPPSN	HI 8807	10MS	2.2	TMS	0.3	20S	7.6	20MS	4.9
2020-21	MDSN	HI 8807	10S	2.7	20MS	2.7	0	0	5S	1.7

(HS-Highest score, ACI-Average Coefficient of Infection)

Source: AICW&BIP – Crop Protection Report (2017-21)

Table 2: Disease score of Karnal bunt

Year of testing	Trial		Karnal bunt (%)						HS	Avg
			Jammu	Hisar	Delhi	Ludhiana	Pantnagar	Dhaulakuan		
2018-19	AVT I	HI 8807	2.7	1.6	8.8	1.0	-	-	8.8	3.5
		HD 2864 (C)	12.2	5.6	3.3	8.0	-	-	12.2	7.3
2019-20	EPPSN	HI 8807	2.4	6.7	0.0	0.0	2.5	1.3	2.2	6.7
2020-21	MDSN	HI 8807	-	-	-	-	-	-	7.4	1.9
		HD 2967	-	-	-	-	-	-	12.5	6.0

16. HI 8812 (IC0641984; INGR21191), a wheat (*Triticum durum*) germplasm with resistance to stem, leaf, stripe rusts and flag Smut. High yielding.

Rahul M Phuke, Divya Ambati, SV Sai Prasad, Jang Bahadur Singh, Prakasha TL* and Dilip Kumar Verma

ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India

*Email: prakash7385@gmail.com

Global wheat production is affected by many biotrophic fungi like *Puccinia* (causing rust diseases) and *Urocystis Agropyri* (causing flag smut). The flag smut inoculum can survive in soil for 7-10 years. Therefore, breeding varieties which are resistant to these pathogens is extremely important in managing these diseases. Durum wheat is cultivated in central and peninsular parts of India. Developing resistant varieties with broader genetic base is the need of the hour owing to rapid evolution of these pathogens.

HI 8812 (HI 8680/ HI 8663), is a erect durum wheat genotype with strong waxiness on was identified to be resistant to stem, leaf and stripe rusts and flag smut in multi-location testing viz., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2017 to 2021 (Table 1). It showed resistance to flag smut disease (Table 2) over two years of testing at different locations. HI 8812 showed superiority in mean

weighted grain yield superiority of 2.1 to 3.2% in NIVT and AVT-I in comparison to check varieties. As the availability of multiple disease resistant high yielding genotypes is rare, HI 8812 can be used as potential resistance donor to breed varieties against these multiple pathogens and also a source of high grain yield.

References

- Progress report of the All India Coordinated Wheat and Barley Improvement Project (2018-2021) Crop Protection. ICAR-IIWBR, Karnal, India,
- Progress report of the All India Coordinated Wheat and Barley Improvement Project (2018-2020). Crop Improvement. ICAR-IIWBR, Karnal, India,
- Kashyap PL, S Kumar, RS Kumar, A Sharma, P Jasrotia, DP Singh and GP Singh (2020) Molecular Diagnostic Assay for Rapid Detection of Flag Smut Fungus (*Urocystis agropyri*) in Wheat Plants and Field Soil. *Front. Pl. Sci.*, 11, p554213.

Table 1: Disease data of HI 8812 in comparison with check varieties over years

Year of testing	Trial		Stem rust		Leaf rust		Stripe rust			
			South		South		North		North	
			HS	ACI	HS	ACI	HS	ACI	HS	ACI
2017-18	NIVT 4	HI 8812	TMS	0.2	20MS	3.0	5MR	0.3	10MS	3.8
		HI 8713 (c)	30S	14.3	30S	3.9	20S	2.9	10S	3.3
		HI 8737 (c)	30S	13.7	20S	2.7	10MS	1.7	20MS	3.3
2018-19	AVT I	HI 8812	5MS	2.0	20MS	2.6	20S	2.6	10S	3.4
		HI 8713 (c)	10MS	1.6	5MR	0.3	10S	3.4	20S	3.9
		HI 8737 (c)	40S	11.0	20MS	3.0	20S	3.3	15S	3.0
2019-20	EPPSN	HI 8812	10MS	4.4	TMR	0.1	15S	8.0	40S	6.2
2020-21	MDSN	HI 8812	10S	2.7	15MR	2.1	5S	1.0	5S	1.7

(HS-Highest score, ACI-Average Coefficient of Infection)

Source: AICW&BIP – Crop Protection Report (2017-21).

Table 2: Disease score of Flag smut

Year of testing	Trial		Flag smut (%)					Average
			Ludhiana	Hisar	Durgapura	Karnal	Highest Score	
2018-19	AVT I	HI 8812	0.0	0.0	0.0	4.9	4.9	1.2
		HI 8737(C)	0.0	8.5	0.0	1.3	8.5	2.1
		HI 8713 (C)	0.0	9.6	0.0	2.3	9.6	3.0
2020-21	MDSN	HI 8812	-	-	-	-	0	0

17. RWP-2018-32 (IC0641985; INGR21192), a wheat (*Triticum aestivum*) germplasm tolerant to heat stress with lower grain yield reduction. Higher grain number and higher grain weight under heat stress

Mamrutha HM*, Hanif Khan, Om Parkash Tuteja, Rinki, Gopalareddy K, Sonu Singh Yadav, Satish Kumar, CN Mishra, SK Singh, Gyanendra Singh and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: mamrutha.M@icar.gov.in

The wheat genotypes RWP-2018-32 (HD3131/DBW90) was developed at ICAR-IIWBR, Karnal. This entry was evaluated in national multi-location heat tolerance trial (MLHT1) during the year 2018-19 and 2019-20 crop seasons and was evaluated at Durgapura, Hisar, Karnal, Ludhiana, Kanpur, Pusa, Ranchi, and Sabour centres which are hot spot locations for heat stress. RWP-2018-32 (0.90) has showed Heat Susceptibility Index (HSI) values lower than checks, DBW150 (0.94), Raj3765 (0.93) and HD2932 (1.22). RWP-2018-

32 recorded lower yield reduction (27%) compared to checks (Table 1) except WH730. Lower yield reduction (YR) under heat stress is the important character of a heat tolerant genotype. This genotype was found to be promising for other traits like biomass plot⁻¹ (BM), grain number spike⁻¹ (GNS), grain weight spike⁻¹ (GWS) and grain yield⁻¹ plot (GY) under late sown condition (Table 2). Thus, RWP-2018-32 can serve as a potential source to be utilized in future breeding programs to develop heat tolerant wheat varieties.

Table 1: The HSI and yield reduction (%) of wheat genotypes over years (2018-19 & 2019-20)

Genotype	HSI			Yield Reduction (%)		
	2018-19	2019-20	Mean	2018-19	2019-20	Mean
RWP-2018-32	0.87	0.94	0.90	31.5	23.3	27.4
DBW150(C)	1.06	0.82	0.94	38.4	20.3	29.4
HD2932(C)	1.22	1.19	1.22	44.1	29.6	36.9
Raj3765(C)	1.06	0.79	0.93	38.4	19.7	29.1
WH730(C)	0.89	0.91	0.88	30.8	22.6	26.7

Table 2: Pooled data of agro-morphological traits of wheat genotype under MLHT1 2018-19 & 2019-20 under late sown condition

Genotype	DH	DM	PT/3mt	BM(g)	PH(cm)	GNS	GWS(g)	GY(g)
RWP-2018-32	81	109	293.59	4597.13	89.44	56.64	2.18	1325
DBW150 (C)	78	106	275.88	4750.63	95.53	50.88	1.96	1248
HD2932 (C)	80	108	285.06	4289.38	89.97	48.34	1.80	1270
RAJ3765 (C)	76	106	293.53	4318.75	89.15	49.26	1.96	1270
WH730 (C)	79	104	296.12	4512.24	98.7	51.6	2.01	1302

18. DBW302 (IC0641986; INGR21193), a wheat (*Triticum aestivum*) germplasm with resistance to black and brown rusts. Resistant to Karnal bunt and flag smut.

Hanif Khan^{1*}, Ravish Chatrath¹, Om Parkash¹, CN Mishra¹, Gopalareddy K¹, OP Gangwar², Raj Kumar¹, Satish Kumar¹, Mam-rutha HM¹, Poonam Jasrotia¹, SC Bhardwaj², Sudheer Kumar¹, Sunil Kumar¹, Gyanendra Singh¹ and GP Singh¹

¹ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India

²ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India.

*Email: Hanif.Khan@icar.gov.in

Combining resistance genes in wheat breeding to facilitate the development of more durable resistances is a well-known procedure in wheat breeding (Bhardwaj, 2013; Khan et al. 2021). Wheat breeder's strategy has been to utilize germplasm sources that are as diverse as possible for rust resistance. Availability of resistance against multiple diseases of wheat will speed up the breeding process and ensure such targeted resistance combinations are present in the breeding lines.

DBW302 has been developed from cross between DBW112/HD3108 through pedigree method of breeding. Its multi-location testing for yield traits was done at six locations in the Special High Yield Potential Trial (SPL-HYPT 2018-19) under all India Coordinated Wheat Improvement trials. The proposed genotype was found resistant against black/stem and brown/leaf rusts and moderately resistant against yellow/stripe rust of wheat under multi-location Plant Pathological Nursery. Based on its resistance to three rusts the entry was selected for evaluation in Multiple Disease Screening Nursery (MDSN).

During 2020-21, MDSN was conducted at the centres: for stem rust: Mahabaleshwar, Indore, Dharwar, Niphad and Wellington; for stripe rust: Ludhiana, Pantnagar, Hisar, Dhaulakaun, Malan, Almora and Karnal; for leaf rust (N): Delhi, Ludhiana, Hisar and Karnal; for leaf rust (S): Mahabaleshwar, Indore, Dharwar, Niphad and Wellington; for Karnal bunt: Delhi, Dhaulakaun, Pantnagar, and Ludhiana; for flag smut: Hisar, Ludhiana and Durgapura; for powdery mildew: Dhaulakaun, Malan, Jammu, Pantnagar, and Malan; for foliar aphid: Nphad, Ludhiana, Karnal and Shillongani.

Table 1: Average disease scores under multi-location testing in MDSN (2020-21)

Genotype	Average coefficient of infection (ACI) of rust				Karnal %	Flag Smut %
	Stem	Leaf(South)	Leaf(North)	Stripe		
DBW302	2.7	5.4	3.0	6.2	2.7	2

Based on multilocation testing DBW302 was found to be resistant to wheat rusts as indicated by low ACI; stem rust 2.7, leaf rust (South) 5.4 and leaf rust (North) 3.0, Karnal bunt (2.7%) and flag smut (2%) (Table1) following disease score 0-100 scale (Loegering, 1959). It was found to be moderately resistant to and stripe rust (ACI 6.2) powdery mildew (4) and foliar aphids (grade 3). Plants of DBW302 medium tall statured with average height of 107 cm and has maturity duration of 155 days in NWPZ under timely sown conditions. Grains are hard textured with amber colour and has 1000 gain weight of 42g. Overall DBW302 has multiple disease resistance in good agronomic background.

References

- Bhardwaj SC (2013) Puccinia -Triticum interaction: an update. *Indian Phytopathol.* 66(1): 14–19.
- Khan H, OP Gangwar, SC Bhardwaj, P Prasad, O Parkash, CN Mishra, R Kumar, K Gopalareddy, S Kumar, SS Yadav and PL Kashyap (2021) Identification of multiple rust resistant bread wheat genotypes. *J. Cereal Res.* 13(1): 89-93.
- Loegering WQ (1959). Methods for recording cereal rust data. USDA, International spring wheat nursery (IRN). Washington, DC: USDA.

19. IIWBR DN 502 (IC0640669; INGR21194), a wheat (*Triticum aestivum*) germplasm having Glu-D1 double null with lowest sedimentation volume in the background of PBW 502 and suitable for biscuit making.

Sewa Ram^{1*}, Sneh Narwal², BS Tyagi¹ and GP Singh¹

¹ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India

²ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India.

*Email: sewa.ram@icar.gov.in

There are limited numbers of varieties having characteristics suitable for biscuit making in India. This is primarily because of more emphasis has been given for improving hard wheat with medium strong gluten suitable for chapati. However, soft wheat with weak and extensible gluten is required for biscuit making. Breeding for soft wheat products can be expedited by using molecular markers for soft grain texture and weak gluten. In this investigation *Glu-D1* double null trait of NAP HAL has been transferred into high yielding backgrounds of PBW502 using molecular marker assisted selection and microlevel tests.

The crossing was initiated during 2005-06 using PBW502 as recurrent parents and Nap Hal as donor and subsequently advanced into higher generations using molecular markers and microlevel tests for sedimentation volume. Advanced lines of the crosses between PBW502 and Nap Hal were evaluated for grain hardness, sedimentation volume and biscuit making quality during 2015-2016; 2016-17 and 2017-18 and 2018-19 and low sedimentation lines stable across years with high biscuit spread factor (>11.0) and high yield potential were identified.

The sedimentation value of advanced lines of the cross between PBW 502 and Nap Hal exhibited sedimentation value in low range (1.8 to 3.9). Mixograph analysis also showed significant reduction in Mixograph Peak Time (MPT) in advanced generations as compared to varieties indicating potential for better biscuit making quality. There was significant reduction in time to peak parameter (from 2.50 minute in PBW 502 to 0.90 minute in advanced line) indicating very weak nature of the gluten caused by *Glu-D1* double null and thus suitable for biscuit making.

Table 1: Sedimentation volume of PBW 502 and *Glu-D1* double null line (IIWBR DN 502) measured across the years (2016-2019). Now the advanced line is at BC₂ F₉ stage (2020-21).

Cultivars and Cross combinations	Sedimentation volume in cc (1 g test)				
	2016	2017	2018	2019	Mean
PBW 502	7.5	7.2	7.4	7.3	7.4
NAP HAL	3.6	3.6	3.4	3.5	3.5
IIWBR DN 502 (PBW502/*2/NAP HAL)	2.7	2.6	2.3	2.5	2.5

20. DBW308 (IC0640675; INGR21195), a wheat (*Triticum aestivum*) germplasm highly resistant to blast, brown rust as well as black and yellow rust diseases of wheat

Hanif Khan^{1*}, Om Parkash², CN Mishra¹, Gopalareddy K¹, OP Gangwar², Raj Kumar¹, Satish Kumar¹, Mamrutha HM¹, Poonam Jasrotia¹, SC Bhardwaj², Sudheer Kumar¹, Sonu Singh Yadav¹, Gyanendra Singh¹, Ravish Chatrath¹ and GP Singh¹

¹ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

²ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India

*Email: Hanif.Khan@icar.gov.in

Wheat blast (WB) disease reported first time from Brazil in 1985 has recently emerged as in Bangladesh in the year 2016, thereby putting a threat to wheat in the entire South Asia. A very high propensity of WB becoming pandemic to a particular geographical localization takes the threat to the next level. Therefore, it is imperative to develop resistant varieties/genetic stock efforts in collaboration with national and international partners. Also, wheat rusts are widely distributed across all the major wheat-growing regions in the world. Regular shifts in virulences pose a major challenge to achieving durable rust resistance. Wheat breeder's strategy has been to utilize germplasm sources that are as diverse as possible for rust resistance.

DBW308 has been developed from cross between HD3108/HD2967 through pedigree method of breeding. Its multi-location testing for yield traits was done at 20 locations in the National Initial Varietal Trial 1A (NIVT-1A) under all India Coordinated Wheat Improvement trials (2019-20). The proposed genotype was found highly resistant (score 0, 0) against wheat blast during at International WB screening facility of CIMMYT, Jassore, Bangladesh screened in two different dates of sowing, at three locations i.e. US, Okinawa and Quirusillas (Bolivia) during 2019-20 and at two locations i.e. Jassore, and Quirassallis at two different dates of sowing during 2020-21 (Table 1).

Table 1: Data testing under PPSN (22 locations) and International WB screening facility of CIMMYT (three locations two years)

Genotype	Average coefficient of infection (ACI) of rust				Av. WB score 2019-20	Av. WB score 2020-21
	Stem	Leaf (South)	Leaf North)	Stripe		
DBW308	2.6	2.1	2.6	10.2	0	0
Susc. Check	77.5	77.5	70.0	72.5	100	100

Besides, screening for various wheat diseases Plant Pathological Screening Nursery (PPSN 2019-20) at 23 locations viz. Bajaura, Malan, Dhaulakuan, Gurdaspur, Ludhiana, Jammu, Hisar, Karnal, Durgapura, Delhi, Pantnagar, Faizabad, Kanpur, Indore, Powarkheda, Vijapur, Junagadh, Pune, Niphad, Mahabalseshwar, Dharwad, Wellington. Based on multilocation testing DBW308 was found to be resistant

to all the three rusts of wheat as indicated by low ACI (stem rust 2.6, leaf rust 2.1 south, 2.6 north and stripe rust 10.2) (Table 1). It is thus highly resistant to brown (leaf) and black (stem) rusts and moderately resistant to yellow(stripe) rust based on 23 locations data. It would provide genetic variability for developing wheat blast and rust resistant wheat varieties for all the zones.

21. HW5073 (IC0640676; INGR21196), a wheat (*Triticum aestivum*) germplasm with adult plant minor stem rust resistance gene *Sr2* with pleiotropic effect on leaf rust (*Lr27*) and stripe rust (*Yr30*) resistance

Vikas VK¹, Aravindh R², Sivasamy M¹, Ganesamurthy K², Jayaprakash P¹, Gopalakrishnan C², Sundeep Kumar³, Geetha M¹, Nisha R¹, Shajitha P¹, John P¹, Sindhu PA¹ and GP Singh⁴

¹ICAR-IARI Regional Station, Wellington-643231, Tamil Nadu, India

²Tamilnadu Agricultural University, Coimbatore -641003, Tamil Nadu, India

³ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

⁴ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: vikaswtn21@gmail.com

Wheat is one of the most widely consumed cereal crops worldwide that provides 20% of dietary calories and protein. In India, wheat is the most important cereal crop after rice with a production of 107.18 MT during 2019-20. But with the rapidly increasing population, India will need more than 140 million tons of wheat by 2050. Among many factors, intensified agricultural practices and climate change have increased the incidence of pathogens in wheat in the recent years. Stem and leaf rust diseases continually pose threat to wheat production. In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Most of the rust resistance genes are all stage resistance (ASR)/major gene and therefore succumb to new variants of the respective pathogen soon after their deployment, whereas adult plant resistance (APR)/minor genes have small to intermediate effects when present alone. High and durable rust resistance can be achieved by combining the ASR and APR genes together.

Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew

resistance genes, *Sr2/Lr27/Yr30*, *Sr24/Lr24* and *Sr36/Pm6* were pyramided in the background of HD2833 cultivar through marker assisted backcross approach. Presence of the resistance genes were carried out using molecular markers, *gwm533* (*Sr2+*) (Spielmeyer *et al.*, 2003), *Sr24#12* (*Sr24/Lr24*) (Mago *et al.*, 2005) and *stm773-2* (*Sr36/Pm6*) (Tsilo *et al.*, 2008), in the pyramided lines. Stable and high yielding line (HW5073) was selected at BC4F7 generation and further evaluated for four seasons in two years. Adult plant reaction of pyramided lines showed resistance to the stem rust, leaf rust and powdery mildew pathotypes prevailing in India. Using gene pyramids of minor (*Sr2/Lr27/Yr30*) and major resistance genes (*Sr24/Lr24* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment. Genetic stock can diversify the rust resistance genes among the wheat germplasm and provide a vital source for imparting durable rust resistance in wheat.

References

Mago R, HS Bariana, IS Dundas, W Spielmeyer, GJ Lawrence, AJ Pryor and JG Ellis (2005) Development of PCR markers for the selection of wheat stem rust resistance genes *Sr24* and *Sr26* in diverse wheat germplasm. *Theo. and Appl. Genet.* 111: 496-504.

Spielmeyer W, P Sharp and E Lagudah (2003) Identification and validation of markers linked to broad-spectrum stem rust resistance gene in wheat. *Crop Sci.* 43(1): 333-336.

Tsilo TJ, Y Jin and JA Anderson (2008) Diagnostic microsatellite markers for the detection of stem rust resistance gene *Sr36* in diverse genetic backgrounds of wheat. *Crop Sci.* 48: 253-261.

22. DCMS 22A & DCMS 22B (IC0640654 & IC0640655; INGR21197), a new cytoplasmic genetic male sterile wheat (*Triticum aestivum*) in DBW 16 background with CMS source MTSA 2A

SK Singh*, Pradeep Sharma, Satish Kumar, Suresh Kumar, RP Gangwar, Snehanishu Singh and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: sksingh.dwr@gmail.com

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields.

The proposed genetic stock DCMS 22A was developed using MTSA 2A based CMS 2A (MTSA 2A/8*RAYON) as female parent in first cross with Indian advanced variety DBW 16 as male parent. After initial cross, 8 generations of backcrosses were made with the variety DBW 16 used as recurrent parent. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results

indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 22A (Table 1).

The heading period in DCMS 22A ranged from 95-109 days with mean of 100 days whereas average plant height was 95 cm with range of 92-100 cm. Compared to this, the maintainer line DCMS 22B showed similar average days to heading of 100 days with plant height of 98 cm. These features are helpful in synchronised flowering and better pollen movement for maximum seed set.

It may be concluded that the proposed genetic stock DCMS 22A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS22A and its maintainer for quantitative traits

Year	DCMS22A (CMS- A line)			DCMS 22B (DBW 16: B line)	
	Male sterility(%)	Days to heading	Plant height(cm)	Days to heading	Plant height(cm)
2015-16	100	98	94	98	98
2016-17	100	95	92	95	98
2017-18	100	97	92	97	98
2018-19	100	109	100	110	97
Mean	100	100	95	100	98

23. DCMS 23A & DCMS 23B (IC0640656 & IC0640657; INGR21198), a New cytoplasmic genetic male sterile line of wheat (*Triticum aestivum* subsp. *aestivum*) in DBW 16 background with CMS source Chuan 13A

SK Singh*, Satish Kumar, Pradeep Sharma, Suresh Kumar, RP Gangwar, Snehanishu Singh and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: sksingh.dwr@gmail.com

The proposed genetic stock DCMS 23A was developed using CHUAN 13A based CMS 8A (CHUAN13A/5/7*ATTILA/3/HUI/CARC//CHEN/CHTO/4/ATTILA) as female parent in first cross with Indian advanced variety DBW 16 as male parent. After initial cross, 8 generations of backcrosses were made with DBW 16 as

recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 23A (Table 1).

The heading period in DCMS 23A ranged from 95-108 days with mean of 100 days whereas average plant height was 97 cm with range of 96-98 cm. Compared to this, the

maintainer line DCMS 23B showed similar average days to heading of 100 days with plant height of 98 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

It may be concluded that the proposed genetic stock DCMS 23A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS23A and its maintainer for quantitative traits

Year	DCMS23A (CMS- A line)			DCMS 23B (DBW 16: B line)	
	Male sterility(%)	Days to heading	Plant height(cm)	Days to heading	Plant height(cm)
2015-16	100	98	96	98	92
2016-17	100	95	96	95	104
2017-18	100	97	98	97	99
2018-19	100	108	98	109	97
Mean	100	100	97	100	98

24. WAPD 1508 (IC0640666; INGR21199), a wheat (*Triticum aestivum*) germplasm with triple gene dwarf genotype possessing bold seeds and longer spikes

SK Singh, Satish Kumar, Pradeep Sharma, OP Gupta, Suresh Kumar and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: sksingh.dwr@gmail.com

The wheat growing areas in the country are experiencing a kind of stagnation in yield levels. The agronomic manipulations for fertiliser dose and schedule are being done for developing high yielding genotypes for irrigated timely sown conditions. Such manipulations sometimes lead to increased biomass that result in lodging during crop stages. Research efforts at IIWBR resulted in selection of dwarf transgressive segregants that resulted in development of 38 short statured genotypes.

The proposed germplasm line WAPD 1508 was developed from the cross 35IBWSN 159/34IBWSN 24//23ESWYT 43 following modified pedigree method. The first cross was made between 35IBWSN 159 [Croc_1/Ae. *Squarrosa* (205)//Kauz/3/Attila] and 34IBWSN 24 [Altar 84/Ae. *squarrosa* (219)//Seri] and the resultant F1 was again crossed with pollen parent 23ESWYT 43 [Munia/CHTO/3/PFAU/ BOW//VEE#9/4/Chen/ Ae. *squarrosa* (Taus) //BCN]. The dwarf plants from the segregating populations of this three-way cross were selected and fixed. The proposed entry WAPD 1508 is characterised for presence of dwarfing genes through molecular markers for genes *Rht B1b* (237bp), *Rht D1b* (254 bp) and *Rht 8* (192 bp) alongwith check varieties DBW 93, DM 6 and DM 7. WAPD 1508, DM 6 and DM7 were confirmed as triple gene dwarf genotypes whereas DBW 93 has two

dwarfing genes. Initially WAPD 1508 was evaluated for agro-morphological traits alongwith check DBW 93 during 2016-17 in PYT at Karnal. Thereafter, two triple gene dwarf checks DM6 and DM7 were included for comparison of agro-morphological traits. After its better performance for various agro-morphological traits, WAPD 1508 was evaluated in multi-locational National Genetic Stock Nursery (NGSN) at 32 locations during 2019-20 and 31 locations during 2020-21.

The entry WAPD 1508 showed promising performance during three years of evaluation at Karnal location under timely sown irrigated conditions (Table.1). On mean basis of three years' data (2016-17 to 2018-19), it showed mean yield of 64.4q/ha which was 24.3% higher than the best check variety DBW 93 (51.8q/ha). The short statured nature with plant height 70 cm was comparable to other dwarf checks DM 6 and DM 7 that indicated its suitability for non-lodging. It was earliest in heading (93 days) and possessed bolder grains (42.0g TGW) longer spike (13.0cm), high harvest index (39.2%). It but has more grain filling period of 47 days that supported proper grain development. During 2019-20 and 2020-21, it was evaluated in NGSN at 32 and 31 locations, respectively across the country representing all 5 wheat growing zones. In NGSN, WAPD 1508 showed higher yield than the other triple gene dwarf checks DM 6 & DM 7 and

was at par to the DBW 93. It also showed longer spikes and bolder seeds than the checks and comparable performance for heading, maturity and plant height.

Based on above results, it may be concluded that the germplasm line WAPD 1508, a triple gene dwarf statured genotype is suitable for high potential areas where more

yield can be harvested by manipulating agronomic package of practices. Increased fertiliser dose may be supported by its dwarf stature leading to non-lodging conditions. It may also be suitable for mechanised farming system. In view of its traits, it can be further utilised as potential donor in developing dwarf high yielding genotypes suitable to mechanised farming.

Table 1: Performance of WAPD 1508 for yield and component traits during 2016-17 to 2018-19

Genotypes	DH (days)	DM (days)	PH (cm)	TPM	SPL (cm)	GPS	TGW (g)	GY (q/ha)	HI (%)	Dwarfing genes		
										Rht B1b	Rht D1b	Rht 8
WAPD 1508	93	140	70	157	13.0	59	42.0	64.4	39.2	+	+	+
DM 6 ©	96	138	65	163	11.5	77	23.5	30.0	26.7	+	+	+
DM 7 ©	95	138	64	165	12.0	78	23.0	35.0	27.0	+	+	+
DBW 93©	94	136	90	129	9.0	56	40.7	51.8	36.1	-	+	+

DH-Day to heading, DM-Days to maturity, PH-Plant ht., TPM- Tillers per meter length, SPL-Spike length, GPS- Grains per spike, TGW- 1000 grains wt., GY-Gr yield, , HI- harvest index

25. DWAP 18-07 (IC0640667; INGR21200), a wheat (*Triticum aestivum*) germplasm with highly tolerant to water stress conditions of warmer areas and Low yield reduction under stress

SK Singh, Pradeep Sharma, OP Gupta, Suresh Kumar, Rinki and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: sksingh.dwr@gmail.com

The wheat growing areas in the country are experiencing warmer climatic conditions in present climatic scenario. The high temperature conditions coupled with water scarcity conditions becomes more crucial for harvesting good wheat yields. In such areas, AICRP on wheat & barley has advocated restricted irrigation condition in which one pre-sowing irrigation and another irrigation at 45 DAS is given. The wheat improvement for warmer areas programme of the ICAR-IIWBR has developed number of elite lines for such conditions using shuttle breeding approach for target oriented wheat improvement.

The germplasm line DWAP 18-07 was developed from the cross HW 1080/DBW 17 following modified pedigree method. The segregating generations were evaluated at Karnal and 8 shuttle breeding centres in CZ and PZ for target oriented selection. It was evaluated at 10 locations in all four zones i.e., Karnal in NWPZ, Ayodhya in NEPZ, Jabalpur, Junagadh, Vijapur and Bilaspur in CZ and Akola, Niphad and Dharwad in PZ under timely sown irrigated condition and timely sown restricted irrigation condition in replicated

trials. The check varieties are the latest commercial cultivars of all the zones for various production conditions. The yield data was analysed location wise to estimate the stress susceptibility index (Fischer & Maurer, 1978) and percent reduction of yield under stress conditions (Choukan *et al.*, 2006). The pooled analysis of SSI and Red (%) indicated wide range of variability among the genotypes in the experiment. In general, the genotypes having SSI <1.0 is considered as stress tolerant genotypes.

The proposed genotype DWAP 18-07 showed least SSI of 0.14 (Table 1) alongwith least reduction in yield under stress conditions (3.54) which reflects its high tolerance nature to water scarcity conditions.

References

- Choukan R, T Taherkhani, MR Ghanadha and M Khodarahmi (2006) Evaluation of drought tolerance in grain maize inbred lines using drought tolerance indices. *Iranian J. of Crop Sci.* 8(1): 79-89.
- Fischer RA and R Maurer (1978) Drought Resistance in spring wheat cultivars. I. Grain Yield Responses. *Aust. J. Agric. Res.*, 29: 897-912

Table 1: Stress susceptibility index of selected entries of wheat in multilocations

S. No.	Entry	Stress susceptibility index (SSI)											Reduction in yield under stress (%)
		Akola	Ayodhya	Jabalpur	Niphad	Dharwad	Junagadh	Powarkheda	Vijapur	Bilaspur	Karnal	Pooled	
1	DWAP 18-07	0.50	0.91	0.12	0.71	0.60	1.21	2.59	0.85	-0.70	-4.89	0.14	3.54
2	DBW 110 ©	-0.13	0.66	4.43	1.16	0.80	1.16	4.97	1.13	1.04	-3.62	0.66	17.04
3	DBW 93 ©	1.25	0.59	-24.67	0.79	0.90	0.83	2.68	1.52	1.23	0.53	0.70	18.05
4	HD 2967 ©	-3.13	1.42	-6.52	1.06	1.30	0.89	-1.30	-0.13	1.10	1.06	1.04	26.59
5	HD 2932 ©	1.84	0.59	8.84	0.91	0.98	0.86	0.74	1.00	0.73	1.31	1.12	28.79
6	GW 322 ©	0.84	2.15	3.58	1.01	1.07	1.11	3.46	1.77	1.11	2.65	1.25	31.99
7	MACS 6222 ©	1.57	0.68	1.72	1.09	1.05	1.15	-0.93	0.79	0.89	-0.44	1.28	32.78
8	DBW 222 ©	0.05	2.23	3.61	1.18	1.01	1.43	1.27	1.18	0.77	2.02	1.29	33.05

26. TAW 33 (IC0631397; INGR21201), a wheat (*Triticum aestivum*) germplasm with high grain hardness index

BK Das¹, Abhijit Shitre¹, Gautam Vishvakarma¹, Sudhakar Mali¹, SG Bhagwat¹, Potdukhe N R², Swati Bharad³, BD Gite⁴, Gadekar DA⁵, Suresh Dodke⁶ and UG Kachole⁶

¹Nuclear Agriculture & Bio-Technology Division, BARC-400094, Maharashtra, India

²Cotton research unit, Dr. PDKV, Akola 444104, Maharashtra, India

³Wheat research unit, Dr. PDKV, Akola 444104, Maharashtra, India

⁴ARS, Washim-444505, Maharashtra, India

⁵College of Agriculture, Muktainagar-426306, Maharashtra, India

⁶ARS, Niphad, Dist Nasik-422303, Maharashtra, India

*Email: bkdas@barc.gov.in

Wheat is second largest staple food for the world after rice and consumed in different types of end products like breads, biscuits, cakes, noodles, pasta, chapati etc. One of the fundamental means of classifying wheat as hard or soft wheat is through its endosperm texture. It impacts significantly on the milling process affecting flour particle size and milling yield (1). The quality of the end product ultimately depends on the viscoelastic properties of gluten proteins and physical properties of the wheat flour being used for the preparation of dough. These physiochemical parameters include grain hardness index, colour of the flour, quantity and quality of gluten proteins, starch content, size and packing of starch and protein granules in wheat kernel. Among these, grain hardness index is most important physical quality parameter which determines starch damage and particle size during milling of wheat grains. Soft grain with low protein content are required for cake and biscuits making where as hard grain and high protein content are suitable for bakery products (2). High grain hardness index is correlated with more damaged starch causing more water absorption and keeping the end-product soft for longer duration.

Taw 33 is a stable *T. aestivum* genotype developed through conventional breeding and recurrent selection. The parents used in the crossing were HD2385/FLW2. TAW33 was

tested for grain hardness and other morphological traits over a period of two years from 2016-17 to 2017-18 in ICAR trials. This genotype has consistently exhibited the highest grain hardness index among the 52 *T. aestivum* genotypes tested in AICRP during the years 2017-18. TAW 33 recorded grain hardness index as high as 102 against that of the check varieties which ranged from 32.8 to The genotype TAW33 also possessed the 5+10 subunits of glutenin which impart strength to dough resulting in strong dough that is suitable for bread making. Thus, TAW 33 having highest grain hardness index with 12% protein content and 5+10 glutenin subunits will be a very valuable genotype as a potential donor in wheat quality improvement programme. TAW33 also has very good agronomical traits like long panicle, bold lustrous grain and very sturdy stem which resist the crop lodging at the time of maturity.

The other Agronomical and quality traits of TAW33 and check varieties are given in Table 1.

References

- Famera O, M Hruskova and D Novatna (2004) Evaluation of methods for wheat grain hardness determination. *Pl. Soil Environ.* 50(11): 489-493.
- Turnbull KM and S Rahman (2002) Endosperm texture in wheat. *J. Cereal Sci.* 36: 327-337.

Table 1: Agronomical and quality traits of TAW33 and check varieties

	UP2672	C306	NIAW1415	HS490	DDW42	TAW33
Protein content	13	11.6	11.5	11.2	11.9	12
Sedimentation value	62.2	46.8	48.8	43.4	44.7	52.3
Tiller No	92	89	84	89	86	103
TGW	41	38	39	39	40	40
Yield (gm/m ²)	415	340	399	337	376	393
Grain appearance score	5.8	6.6	5.2	4.7	5.5	6.1
Hectoliter weight	77.1	80.4	76.1	73.8	78.4	77.8

27. BHS 478 (BBM 800) (IC0640686; INGR21202), a barley (*Hordeum vulgare*) germplasm with seedling resistance against all races of leaf and stripe rust and Adult plant resistance to yellow rust and leaf rust

Madhu Patial, Dharam Pal, SC Bhardwaj, KK Pramanick and OP Gangwar

¹ICAR-IARI Regional Station, Shimla 171004, Himachal Pradesh, India

²ICAR-IIWBR, Regional Station, Shimla-171002, Himachal Pradesh, India

*Email: mcaquarian@gmail.com

BHS 478 (BBM 800) is a barley (*Hordeum vulgare* L.) line resistant against stripe, leaf and stem rust. It has shown highest degree of resistance against all the prevailing pathotypes of stripe and leaf rust at seedling stage and is resistant to both the rust at adult plant stage. BHS 478 (BBM 800) also showed resistance or moderately resistance response against all the pathotype of stem rust (except for pathotype 11 showing moderately susceptible response) at seedling stage and also resistant response (5S) at adult plant stage (Table 1). This line is developed following pedigree method of breeding involving crosses between barley breeding material BHS 385 and registered barley genetic stock BHS 369 at ICAR- IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.).

BHS 478 (BBM 800) has semi spreading growth habit with medium maturity (169 days) under Northern Hill condition. The average yield is 3.23 t/ha under rainfed condition of Northern Hill Zone of All India Co-ordinated trials 2019-20.

The distinguish features of BHS 478 (BBM 800) are six-rowed; hulled; semi-spreading growth habit; semi-erect flag leaf attitude; green leaves; white colour of ear at maturity and thousand grain weight of 45 grams.

References

- ICAR-IIWBR (2019) Progress Report of AICRP on Wheat & Barley 2018-19, Barley Improvement. (Eds. AS Kharub, Chuni Lal, Dinesh Kumar, Jogendra Singh, Vishnu Kumar, Amit Kumar Sharma, Anil Khippal, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. p215.
- ICAR-IIWBR (2020) Progress Report of AICRP on Wheat & Barley 2019-20, Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. p230.

Table 1: Reaction to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 478 (BBM 800)	Page No.
Stripe Rust (Resistant to yellow rust)	IBDSN (APR)	2018-19	ACI= 0.0 HS= 0	3.7 of Reference (i)
	NBDSN (APR)	2019-20	ACI=8.6	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant to all races)	3.28 of Reference (ii)
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2019-20	HS= 5S	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant to all races)	3.28 of Reference (ii)
Stem Rust (Resistant to black rust)	NBDSN (APR)	2019-20	HS=5S	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant) to moderately resistant (MR) response to all races (Except for race 11 showing moderately susceptible response)	3.28 of Reference (ii)

ACI= Average Coefficient of incidence HS= Highest Score IBDSN= Initial Barley Disease Screening Nursery NBDSN= National Barley Disease Screening Nursery

28. DWRBG4 (IC0641987; INGR21203), a barley (*Hordeum vulgare* subsp. *vulgare*) germplasm with combination of high beta-glucan (7.5% dwb) and high protein (13.2%)

Rekha Malik*, Dinesh Kumar, RPS Verma, Ajit Singh Kharub, Lokendra Kumar, Jogendra Singh, Chuni Lal, Poonam Jasrotia, Surendra Singh, Rajendra Kumar and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: rekha.malik@icar.gov.in

DWRBG-4 (Tested as RMB11) is a two-row hulled barley genotype derived from a cross DWR30/Shebac and further advanced through pedigree selection of plant breeding approach. RMB11 was evaluated in Barley Quality Screening Nursery in AICRIP trials during 2020-21 along with checks at five locations and as expected, gave high score of protein and beta glucan percentage which is a rare found combination in two row hulled barley. DWRBG-4 has shown higher level of beta glucan content (7.5% dwb) which is higher than the malt varieties (4.2 to 6.2 % dwb) and DWR 30 (6.9% dwb), the previously registered germplasm for this trait (Table 1). Also, this genotype has higher level of protein content (13.2% dwb) which is higher than registered varieties (11.5 to 12.3 % dwb) and comparable to previously registered genetic stock BK1127 (13.8% dwb) (Table 2). This unique combination of high protein and high beta glucan is very much desirable for health food industry and is not yet

reported or registered till date in Indian barley germplasm. DWRBG-4 is the outcome of institute barley breeding programme and can serve as potential candidate genotype across AICWBIP for introgression of quality traits in barley. Average values for agro-morphological traits were observed as 50% flowering in 92 days and matured in 138 days. Plant height was measured 114 cm and foliage colour was light green. The genotype other traits calculated are 1000 grain weight (55.1g), test weight (61.8) and starch content (59.4).

Reference

Anonymous (2021) Progress report of AICRP on Wheat and Barley. 2020-21. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. pp 5.28-5.43.

Table 1: Beta glucan content (% dwb) from different locations in AICWBIP BQSN 2020-21

Code	Genotype	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
R-11	DWRBG-4 (RMB -11)	7.7	5.5	6.9	8.8	7.6	8.3	7.5
M-17	DWRUB52 (c)	5.4	4.2	4.4	5.2	5.1	5.3	4.9
M-18	DWRB101 (c)	5.4	4.4	5.9	5.0	5.1	5.0	5.1
M-23	DWRB182 (c)	4.2	4.2	4.4	4.7	4.0	4.0	4.2
M-27	BK 306	3.8	4.3	4.4	4.7	4.5	4.5	4.4
M-33	DWRB 197	6.3	6.4	6.6	6.4	6.5	5.9	6.4

Table 2: Protein content (% dwb) from different locations in AICWBIP BQSN 2020-21

Code	Genotype	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	Average
R-11	DWRBG-4 (RMB -11)	12.0	15.5	13.0	12.7	12.6	13.1	13.2
M-17	DWRUB52 (c)	12.0	11.6	14.5	12.0	9.7	12.5	12.1
M-18	DWRB101 (c)	12.1	11.7	12.8	11.7	9.6	11.1	11.5
M-23	DWRB182 (c)	12.2	11.6	14.2	13.2	12.1	10.4	12.3
M-2	BK1127	13.0	15.1	15.4	15.1	10.4	13.6	13.8
M-27	BK 306	12.5	13.7	13.8	11.5	11.5	11.4	12.4

#Predicted values through NIR

29. DWRBG1 (IC0641988; INGR21204), a barley (*Hordeum vulgare*) germplasm with combination of low grain beta-glucan (3.8%) and higher grain protein content (13%)

Dinesh Kumar*, RPS Verma, Sneh Narwal, Rekha Malik, Ram Pal Saini and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: Dinesh.Kumar3@icar.gov.in

DWRBG 1 (tested as ICARDA 5) is a two-row hulled barley genotype, selected from PYT- 2014-15 entry number-41 of ICARDA. It has been identified for lower grain beta glucans content coupled with desirable protein content. Grain beta glucan (β 1-3, 1-4 glucan) content is a very important component in determining the malting quality of any malt barley genotype. In case of malt barley, the beta glucan content should be as low as possible and not higher than 4%. Higher content of beta glucans poses a problem in proper modification of endosperm as after the dissolution of cell wall (where major component is beta glucan), the starch hydrolysing agents can only gain entry to the starch molecules. Genotype is the major determinant of grain beta glucan content and is also influenced by environment. Barley is grown in short days in India with a limited grain filling window and getting low grain beta glucans content is a challenge. The identified genotype DWRBG1 has low grain beta glucans content of 3.67% (Table 1). Further, protein content is a very important quality trait influencing malting and brewing quality of barley grain. Very high protein content (> 14%) in the grain impacts adversely the malt extract yield. Very low content of protein (<9.0%) is also not desirable since in brewing process yeasts need optimum quantity of amino acids for growth. In case of malt-based food products,

good quantity and quality of protein is required. Nowadays brewing industry also requires higher protein content (12-13%), especially to get higher diastatic power and free amino nitrogen especially in cases wherever adjuncts are being used or higher protein derived components are required in the end product. The genotype DWRBG1 has average protein content of 12.81% (Table 2) and is very unique in the sense that it has low grain beta glucans content also. Thus, DWRBG1 is a potential genotype which can be used as donor parent for improving the quality in malt barley.

References

- Anonymous (2020) Progress Report of AICRP on Wheat & Barley 2019-20, Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India.
- Anonymous (2021) Progress report of AICRP on Wheat and Barley. 2020-21. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India.

Table 1: Grain beta glucan (%dwb) in ICARDA-5 at different locations during 2019-21

Genotype	2019-20		2020-21					Mean
	Karnal	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	
ICARDA 5	2.9	3.6	3.9	4.3	4.1	3.3	3.8	3.7
DWRUB 52 (c)	4.9	5.4	4.2	4.4	5.2	5.1	5.3	4.9
DWRB 101 (c)	4.7	5.4	4.4	5.9	5.0	5.1	5.0	5.1
DWRB-182 (c)	3.3	4.2	4.2	4.4	4.7	4.0	4.0	4.1
DWR 37 (c)*	-	4.8	4.4	4.8	5.0	5.4	4.8	4.9
DWR 39 (c)*	-	4.6	2.9	NA	NA	4.4	4.2	4.0

*Registered stocks for the trait

Table 2: Grain protein content in ICARDA-5 at different locations during 2019-21

Genotype	2019-20		2020-21							Mean
	Karnal	Hisar	Pantnagar	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	
ICARDA 5	11.1	13.5	10.6	13.9	12.9	13.9	14.0	12.0	11.4	12.6
DWRUB 52 (c)	10.6	13.4	9.8	12.0	11.6	14.5	12.0	9.7	12.5	11.8
DWRB 101 (c)	11.1	13.0	10.2	12.1	11.7	12.8	11.7	9.6	11.1	11.5
DWRB-182 (c)	11.7	12.8	11.5	12.2	11.6	14.2	13.2	12.1	10.4	12.2
DWR 37 (c)*	-	-	-	14.6	16.3	12.9	12.8	15.5	13.2	14.2
DWR 39 (c)*	-	-	-	15.8	16.6	NA	NA	NA	NA	16.2

*Registered stocks for the trait

30. DWRBG 3 (IC0641990; INGR21205), a barley (*Hordeum vulgare*) germplasm with combination of low grain beta-glucan content (3.88%) and desirable thousand grain weight (45g)

Dinesh Kumar*, RPS Verma, Sneha Narwal, Rekha Malik, Ram Pal Saini and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: Dinesh.Kumar3@icar.gov.in

DWRBG-3 (tested as ICARDA-9) is a two-row hulled barley genotype, selected from PYT-2014- 15 entry number-93 of ICARDA. It has been identified for lower grain beta glucans content coupled with desirable thousand grain weight (44-46 g). Grain beta glucan (β 1-3, 1-4 glucan) content is a very important component in determining the malting quality of any malt barley genotype. In case of malt barley, the beta glucan content should be as low as possible and *not higher than 4%*. Higher content of beta glucans poses a problem in proper modification of endosperm as after the dissolution of cell wall (where major component is beta glucan), the starch hydrolysing agents can only gain entry to the starch molecules. Genotype is the major determinant of grain beta glucan content and is also influenced by environment. Barley is grown in short days in India with a limited grain filling window and getting low grain beta glucans content is a challenge. The identified genotype DWRBG-3 has low grain beta glucans content of 3.87% Table 1). Further, thousand grain weight (TGW) is an important contributor of grain yield and quality. For malt purpose barley, thousand grain weight of 44-46 g is desirable for two row barley variety. The genotype DWRBG-3 has TGW of 45 grams (Table 2), which is well in required/ desirable range. Usually, two rowed barleys have higher thousand grain weight as compared to six rowed barleys. Lower thousand grain weight may result in lower yields and lower

values of malt extract. Very high thousand grain weight (> 48 g) lead to under modification of grains during malting (conversion of endosperm starch in to sugars), as during steeping stage water may not reach to core of grain and poor ignition of aleurone layer for secretion of amylases, leading to undigested starch in some parts of endosperm. Genotype or variety is the major determinant of thousand grain weight, but is also affected by environment, cultural practices and biotic/abiotic stresses. Thus, DWRBG-3 is a potential genotype which can be used as donor parent for improving the quality in malt barley.

References

- Anonymous (2020) Progress Report of AICRP on Wheat & Barley 2019-20, Barley Improvement. Eds: RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India.
- Anonymous (2021) Progress report of AICRP on Wheat and Barley. 2020-21. Barley Improvement. Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India.

Table 1: Grain beta glucan (%db) in DWRBG-3 (ICARDA-9) at different locations during 2019 - 2021

Genotype	2019-20		2020-21					Mean
	Karnal	Hisar	Karnal	Ludhiana	Durgapura	Pantnagar	Kanpur	
ICARDA-9	3.8	3.7	3.0	4.2	4.3	3.7	4.4	3.87
DWRUB 52 (c)	4.9	5.4	4.2	4.4	5.2	5.1	5.3	4.93
DWRB 101 (c)	4.7	5.4	4.4	5.9	5.0	5.1	5.0	5.07
DWRB-182 (c)	3.3	4.2	4.2	4.4	4.7	4.0	4.0	4.11
DWR 37*	NT	4.8	4.4	4.8	5.0	5.4	4.8	4.87
DWR 39*	NT	4.6	2.9	NA	NA	4.4	4.2	4.03

*Registered stocks for the trait

Table 2: Thousand grain weight in DWRBG-3 (ICARDA-9) at different locations during 2019 - 21

Genotype	2019-20		2020-21					Mean	
	Hisar	Karnal	Pantnagar	Karnal	Ludhiana	Durgapura	Pantnagar		Kanpur
ICARDA-9	50.7	43.5	45.9	45.9	46.4	41	42.7	50.2	45.8
DWRUB 52 (c)	56.1	40.5	47.1	47.1	49.3	48.4	33.8	51.4	46.7

DWRB 101 (c)	52.9	47.9	50.1	50.1	49	55.5	49.6	51.3	50.8
DWRB-182 (c)	43	41.2	43.0	39.9	43.9	44.2	41.1	49.9	43.3
DWR 37*	NT	NT	41.2	NT	47.7	50.7	52.9	52.8	49.1
DWR 39*	NT	NT	39.9	NT	24.6	44.7	NA	NA	36.4

*Registered stocks for the trait

31. DWRBG5 (IC0641991; INGR21206), a huskless barley (*Hordeum vulgare*) germplasm with high thousand grain (43.5g) weight, bold grain percentage (63.2%) and protein content (14.7%)

Jogendra Singh*, RPS Verma, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Rekha Malik, Charan Singh, Ajit Singh Kharub and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: jogendra.singh2@icar.gov.in

DWRBG-6 (DWRB217) is a six-row hulless barley genotype, selected from exotic (INBYT-(2013)- HI-2, ICARDA) breeding material (PETUNIA2/M112). DWRBG-6 was screened for stripe rust at 7 locations in National Barley Disease Screening Nursery (NBDN) during 2019-20. DWRBG-6 exhibited resistance to stripe rust with ACI= 4.0 and HS=10S, while the huskless checks Karan16, NDB943, PL891 and infector were highly susceptible (Table 1).

This genotype was also screened in Seedling Resistance Tests (SRT) against 7 pathotypes for infection response during 2019-20. DWRBG-6 exhibited resistance against five currently prevailing pathotype (M, G, Q, 6S0 and 7S0) including the two new pathotypes (Table 2). This also supports the field screening results with the currently prevailing pathotypes. The check varieties showed susceptible reaction against all 7 pathotypes except PL 891 having resistant response to pathotype 24.

The starch content was registered 63.7%, which is 1.3% higher than better checks (Table 3). The genotype also had 72.3 kg/hl test weight and protein content 13.6%.

Agro-morphological and quality traits: DWRBG-6 flowers in 92 days and matures in 135 days. Its average plant height is 106 cm and has 117 tillers/meter. The average spike length is 6.9 cm with 73 grains and thousand grain weight of 38.2g.

References

- Anonymous (2020) Progress report of AICRP on Wheat and Barley. 2019-20. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India pp 3.14-3.16.
- Anonymous (2021) Progress report of AICRP on Wheat and Barley. 2020-21. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India p5.34.

Table 1: Stripe rust reaction of DWRBG-6 (DWRB-217) at adult plant stage during 2019-20

Genotype	Durgapura	Ludhiana	Bajaura	Jammu	Karnal	Hisar	Almora	ACI	HS
DWRBG-6	5MR	10S	0	10MS	5MS	0	NG	4.0	10S
Karan16 ©	60S	40S	20S	40S	5MS	0	10S	24.9	60S
NDB943©	100S	80S	80S	60S	0	0	NG	53.3	100S
PL891©	10MR	0	30S	0	60S	60S	0	22.0	60S
Infector	100S	60S	100S	80S	100S	84.00	100S	88.6	100S

Table 2: Stripe rust reaction of DWRBG-6 (DWRB-217) at seedling resistance during 2019-20

Genotype	Pathotypes						
	57	24	M	G	Q	6S0	7S0
DWRBG-6	S	MS	R	R	R	R	R
Karan16 ©	S	S	S	MS	S	S	S
NDB943©	S	S	S	NG	S	S	S
PL891©	NG	R	NG	NG	S	NG	S

Table 3: Starch content of DWRBG-6 (DWRB-217) at different locations during 2019-20

Genotype	Starch content (% db)						Mean
	Durgapura	Pantnagar	Kanpur	Hisar	Karnal	Ludhiana	
DWRBG-6	65.6	64.5	65.0	61.5	64.3	61.0	63.7
Karan16 ©	65.8	60.2	63.8	60.1	63.4	61.3	62.4
NDB943©	65.1	NA	62.8	59.8	63.6	60.9	62.4
PL891©	63.0	59.8	61.7	60.0	61.4	62.0	61.3

32. DWRBG6 (IC0641992; INGR21207), a huskless barley (*Hordeum vulgare*) germplasm with adult plant resistance to stripe rust, seedling resistance to new pathotypes 6S0 and 7S0 and high starch content (63.7%).

Jogendra Singh^{1*}, RPS Verma¹, Sudheer Kumar¹, OP Gangwar², Dinesh Kumar¹, Chuni Lal¹, Lokendra Kumar¹, Rekha Malik¹, Charan Singh¹, AS Kharub¹ and GP Singh¹

¹ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India

²ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India

*Email: jogendra.singh2@icar.gov.in

DWRBG-6 (DWRB217) is a six-row hulless barley genotype, selected from exotic (INBYT-(2013)- HI-2, ICARDA) breeding material (PETUNIA2/M112). DWRBG-6 was screened for stripe rust at 7 locations in National Barley Disease Screening Nursery (NBDSN) during 2019-20. DWRBG-6 exhibited resistance to stripe rust with ACI= 4.0 and HS=10S, while the huskless checks Karan16, NDB943, PL891 and infector were highly susceptible (Table 1).

This genotype was also screened in Seedling Resistance Tests (SRT) against 7 pathotypes for infection response during 2019-20. DWRBG-6 exhibited resistance against five currently prevailing pathotype (M, G, Q, 6S0 and 7S0) including the two new pathotypes (Table 2). This also supports the field screening results with the currently prevailing pathotypes. The check varieties showed susceptible reaction against all 7 pathotypes except PL 891 having resistant response to pathotype 24. The starch content was registered 63.7%, which is 1.3% higher than better checks (Table 3). The genotype also had 72.3 kg/hl

test weight and protein content 13.6%.DWRBG-6 flowers in 92 days and matures in 135 days. Its average plant height is 106 cm and has 117 tillers/meter. The average spike length is 6.9 cm with 73 grains and thousand grain weight of 38.2g.

References

- Anonymous (2020) Progress report of AICRP on Wheat and Barley. 2019-20. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. pp 3.14-3.16.
- Anonymous (2021) Progress report of AICRP on Wheat and Barley. 2020-21. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. pp 5.34.

Table1: Stripe rust reaction of DWRBG-6 (DWRB-217) at adult plant stage during 2019-20

Genotype	Durgapura	Ludhiana	Bajaura	Jammu	Karnal	Hisar	Almora	ACI	HS
DWRBG-6	5MR	10S	0	10MS	5MS	0	NG	4.0	10S
Karan16 ©	60S	40S	20S	40S	5MS	0	10S	24.9	60S
NDB943©	100S	80S	80S	60S	0	0	NG	53.3	100S
PL891©	10MR	0	30S	0	60S	60S	0	22.0	60S
Infector	100S	60S	100S	80S	100S	84.00	100S	88.6	100S

Table 2: Stripe rust reaction of DWRBG-6 (DWRB-217) at seedling resistance during 2019-20

Genotype	Pathotypes						
	57	24	M	G	Q	6S0	7S0
DWRBG-6	S	MS	R	R	R	R	R
Karan16 ©	S	S	S	MS	S	S	S

NDB943©	S	S	S	NG	S	S	S
PL891©	NG	R	NG	NG	S	NG	S

Table 3: Starch content of DWRBG-6 (DWRB-217) at different locations during 2019-20

Genotype	Starch content (% db)						
	Durgapura	Pantnagar	Kanpur	Hisar	Karnal	Ludhiana	Mean
DWRBG-6	65.6	64.5	65.0	61.5	64.3	61.0	63.7
Karan16 ©	65.8	60.2	63.8	60.1	63.4	61.3	62.4
NDB943©	65.1	NA	62.8	59.8	63.6	60.9	62.4
PL891©	63.0	59.8	61.7	60.0	61.4	62.0	61.3

33. IML 21 (IC0640688; INGR21208), a maize (*Zea mays*) germplasm resistant to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh^{1*}, SI Harlapur², N Mallikarjuna³, R Devlash⁴, H Rajashekara⁵, KS Hooda⁶, Chikkappa GK⁷, Bhupender Kumar⁶, Ramesh Kumar⁶, Santosh Kumar¹, Parveen Bagaria⁶, RK Kasana¹, Sushil Kumar¹, SS Gangoliya⁷, N Sunil⁸, Yatish KR⁸, BS Jat⁶, Krishan Kumar⁶ and Sujay Rakshit⁶

¹Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India

²University of Agricultural Sciences, Dharwad-580005, Karnataka, India

³Zonal Agricultural Research Station, V.C. Farm, Mandya-571405, Karnataka, India

⁴CSKHPKV, HAREC, Bajaura, Distt. Kullu-175125, Himachal Pradesh, India

⁵ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India

⁶ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India

⁷ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India

⁸WNC (ICAR-IIMR), Hyderabad-500030, Telangana, India

*Email: singhsb1971@rediffmail.com

Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses. Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Helminthosporium turcicum* Pass.) is of worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al.* 2013; De-Rossi *et al.*, 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech *et al.* 2015; Hooda *et al.* 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using commercial maize hybrids as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 21 (IMLSB 343-2) displayed a mean disease score of 2.6 at par with the resistant check i.e. 2.6 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated

against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, viz., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation. The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al.* (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1-5.0 as moderately resistant (MR), 5.1- 7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1-5.0 and 15 inbred lines were moderately susceptible

with TLB score 5.1 to 7.0 (Singh *et al.* 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration.

IML 21 is a late maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.6 on the scale of 1-9), medium height, medium ear placement, straight attitude of lateral tassel branches, sparse spikelets of tassel, yellow round shaped and semi-dent/semi-flint kernels. It is derived from normal maize segregating progeny by continuous selfing following pedigree breeding method. IML 21 is high yielding maize inbred line with yield potential of 33.1 q/ha. This inbred is also suitable for cultivation during rabi season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and semi-dent or semi flint kernels.

Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

References

- De-Rossi RL, ML Reis and R Brustalin (2015) Fungal baseline for mycelia sensitivity of *Exserohilum turcicum*, causal agent of northern corn leaf blight. *Summa Phytopathol.* 41(1): 25-30.
- Hooda KS, PK Bagaria, M Khokhar, H Kaur and S Rakshit (2018) Mass screening techniques for resistance to maize diseases. ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana- 141004, 93p.
- Reddy TR, PN Reddy, and RR Reddy (2013) Pathogenic variability of isolates of *Exserohilum turcicum*, incitant of leaf blight of maize. *Indian J. Pl. Protect.* 41(1): 72-75.
- Singh SB, CG Karjagi, KS Hooda, N Mallikarjuna, SI Harlapur, H Rajashekara, R Devlash, S Kumar, RK Kasana, S Kumar, SS Gangoliya and S Rakshit (2018) Identification of resistant sources against turcicum leaf blight of maize (*Zea mays* L.) *Maize J.* 7(2): 64-71.
- Wathaneeyawech S, P Sirithunya, and P Smitamana (2015) Collections, isolations, morphological study of *Exserohilum turcicum* and screening resistant varieties of corn to Northern Corn Leaf Blight disease. *Int.J. Agri. Techn.* 11(4): 937-952.

Table 1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

S.No.	Name of inbred	Another name	TLB score	Reaction	Days to 50% anthesis (rabi)	Days to 75 % dry husk maturity (rabi)	Grain yield (q/ha)	Maturity group
1	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
2	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
3	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
4	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
		Resistant Check (CL 4/ NAH 1137	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

34. IML 12 (IC0640689; INGR21209), a maize (*Zea mays*) germplasm with resistance to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh^{1*}, KS Hooda², Chikkappa GK³, Bhupender Kumar², Ramesh Kumar², Santosh Kumar¹, Parveen Bagaria², SI Harlapur⁴, N Mallikarjuna⁵, R Devlash⁶, H Rajashekara⁷, RK Kasana¹, Sushil Kumar¹, SS Gangoliya³, N Sunil⁸, Yatish KR⁸, BS Jat², Krishan Kumar² and Sujay Rakshit²

¹Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India

²ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India

³ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India

⁴University of Agricultural Sciences, Dharwad-580005, Karnataka, India

⁵Zonal Agricultural Research Station, V.C. Farm, Mandya-571405, Karnataka, India

⁶CSKHPKV, HAREC, Bajaura, Distt. Kullu-175125, Himachal Pradesh, India

⁷ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India

⁸WNC (ICAR-IIMR), Hyderabad-500030, Telangana, India

*Email: singhsb1971@rediffmail.com

Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses.

Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Helminthosporium turcicum* Pass.) is of

worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al.* 2013; De-Rossi *et al.*, 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech *et al.*, 2015; Hooda *et al.*, 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using commercial maize hybrids as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 12 (IMLSB 446-2) displayed a mean disease score of 2.5 at par with the resistant check i.e. 2.4 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, viz., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation. The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al.* (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1–5.0 as moderately resistant (MR), 5.1–7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and

susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1–5.0 and 15 inbred lines were moderately susceptible with TLB score 5.1 to 7.0 (Singh *et al.* 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration. IML 12 is a medium maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.5 on the scale of 1–9), medium height, medium ear placement, straight attitude of lateral tassel branches, sparse spikelets of tassel, yellow round shaped and flint kernels. It is derived from normal maize test cross progeny by continuous selfing following pedigree breeding method.

IML 12 is high yielding maize inbred line with yield potential of 31.9 q/ha. This inbred is also suitable for cultivation during rabi season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and semi-dent or semi flint kernels.

References

- De-Rossi RL, ML Reis and R Brustalin (2015) Fungal baseline for mycelia sensitivity of *Exserohilum turcicum*, causal agent of northern corn leaf blight. *Summa Phytopath.* 41(1): 25–30.
- Hooda KS, PK Bagaria, M Khokhar, H Kaur and S Rakshit (2018) Mass screening techniques for resistance to maize diseases. ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana- 141004, 93p.
- Reddy TR, PN Reddy, and RR Reddy (2013) Pathogenic variability of isolates of *Exserohilum turcicum*, incitant of leaf blight of maize. *Indian J. Pl. Prot.* 41(1): 72–75.
- Singh SB, CG Karjagi, KS Hooda, N Mallikarjuna, SI Harlapur, H Rajashekara, R Devlash, S Kumar, RK Kasana, S Kumar, SS Gangoliya and S Rakshit (2018) Identification of resistant sources against turcicum leaf blight of maize (*Zea mays* L.). *Maize J.* 7(2): 64–71.
- Wathaneeyawech S, P Sirithunya, and P Smitamana (2015) Collections, isolations, morphological study of *Exserohilum turcicum* and screening resistant varieties of corn to Northern Corn Leaf Blight disease. *Int. J. Agri. Techno.* 11(4): 937–952.

Table1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

S.No	Name of inbred	Another name	TLB score	Reaction	Days to 50% anthesis (rabi)	Days to 75 % dry husk maturity (rabi)	Grain yield (q/ha)	Maturity group
1	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
2	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
3	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
4	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
		Resistant Check (CL 4/ NAH 1137)	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

35. IML 13 (IC0640690; INGR21210), a maize (*Zea mays*) germplasm resistant to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh^{1*}, KS Hooda², Chikkappa GK³, Bhupender Kumar², Santosh Kumar¹, Ramesh Kumar², N Sunil⁴, Yatish KR⁴, Krishan Kumar², BS Jat², SI Harlapur⁵, N Mallikarjuna⁶, H Rajashekara⁷, R Devlash⁸, Parveen Bagaria², RK Kasana¹, Sushil Kumar¹, SS Gangoliya³ and Sujay Rakshit²

¹Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India

²ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India

³ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India

⁴WNC (ICAR-IIMR), Hyderabad-500030, Telangana, India

⁵University of Agricultural Sciences, Dharwad-580005, Karnataka, India

⁶Zonal Agricultural Research Station, V.C. Farm, Mandya-571405, Karnataka, India

⁷ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India

⁸CSKHPKV, HAREC, Bajaura, Distt. Kullu-175125, Himachal Pradesh, India

*Email: singhsb1971@rediffmail.com

Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses. Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Helminthosporium turcicum* Pass.) is of worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al.* 2013; De-Rossi *et al.*, 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech *et al.*, 2015; Hooda *et al.*, 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using Non QPM pool as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 13 (IMLSB 1041-4-1-1) displayed a mean disease score of 2.4 at par with the resistant check i.e. 2.4 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, viz., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation.

The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al.* (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1–5.0 as moderately resistant (MR), 5.1–7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1–5.0 and 15 inbred lines were moderately susceptible with TLB score 5.1 to 7.0 (Singh *et al.* 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration. IML 13 is a medium maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.4 on the scale of 1-9), medium height, low ear placement, curved attitude of lateral tassel branches, dense spikelets of tassel, yellow round shaped and flint kernels. It has low ASI (3days). It is derived from non-QPM pool, (a normal maize population) following pedigree breeding method.

IML 13 is high yielding maize inbred line with yield potential of 36.4 q/ha. This inbred is also suitable for cultivation during rabi season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and flint kernels. It is also moderately tolerant to waterlogging.

Table 1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

S. No.	Name of inbred	Another name	TLB score	Reaction	Days to 50% anthesis (rabi)	Days to 75 % dry husk maturity (rabi)	Grain yield (q/ha)	Maturity group
1	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
2	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
3	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
4	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
		Resistant Check (CL 4/ NAH 1137	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

References

- De-Rossi RL, ML Reis and R Brustalin (2015) Fungal baseline for mycelia sensitivity of *Exserohilum turcicum*, causal agent of northern corn leaf blight. *Summa Phytopath.* 41(1): 25-30.
- Hooda KS, PK Bagaria, M Khokhar, H Kaur and S Rakshit (2018) Mass screening techniques for resistance to maize diseases. ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana- 141004, 93p.
- Reddy TR, PN Reddy and RR Reddy (2013) Pathogenic variability of isolates of *Exserohilum turcicum*, incitant of leaf blight of maize. *Indian J. Pl. Protect.* 41(1): 72-75.
- Singh SB, CG Karjagi, KS Hooda, N Mallikarjuna, SI Harlapur, H Rajashekara, R Devlash, S Kumar, RK Kasana, S Kumar, SS Gangoliya and S Rakshit (2018) Identification of resistant sources against turcicum leaf blight of maize (*Zea mays* L.). *Maize J.* 7(2): 64-71.
- Wathaneeyawech S, P Sirithunya and P Smitamana (2015) Collections, isolations, morphological study of *Exserohilum turcicum* and screening resistant varieties of corn to Northern Corn Leaf Blight disease. *Int. J. Agri. Technol.* 11(4): 937-952.

36. WN 585 (IC0624599; INGR21211), a finger millet (*Eleusine coracana*) germplasm with early flowering & early maturity (100-110 days), red grain & high yield

Harshal Eknath Patil¹, Gopal D Vadodariya¹, Brijeshkumar K Patel¹ and M Elangovan²

¹Hill Millet Research Station, Navsari Agricultural University, Waghai-394730, Gujarat, India

²ICAR-Indian Institute of Millets Research, Hyderabad, Telangana 500030, India

*Email: harshalpatil@nau.in

The proposed culture, WN-585 is early flowering, early maturing and high yielding red grain genotype have been developed through selection from local germplasm collected from the Dangs district by Hill Millet Research Station, NAU, Waghai, Dangs, Gujarat. The WN-585 was tested under various categories of station trials at Waghai, Varanasi and Dahod centers as well as tested in 20 AICRP small millets locations across seven states at national level from 2017-18, 2018-19 to 2019-20.

The early maturing (100-110 days) culture WN-585 (3065 kg/ha) performed well with 21.3 % and 13.7 % grain yield superiority over national check 'VL-149' and 'VL-352', respectively in Gujarat. At national level, it showed 19.6 % grain yield improvement over national check 'VL-352'. The genotype 'WN-585' yields on an average 2607 kg/ha of grain yield which was 15.3, 19.6, 5.4 and 4.2 per cent higher than national checks GPU-47, VL-352, PR-202 and VL-376, respectively in 20 locations across the All India Coordinated

trials conducted during 2017-18, 2018-19, 2019-20 at Gujarat, Maharashtra, Odisha, Tamilnadu and Telangana under rainfed conditions. (Annexure - I & II). Also, WN-585 yielded 6369 kg/ha of fodder yield with 14.5 per cent increased yield over national check VL-352 in All India Coordinated trials conducted during 2017-18, 2018-19, 2019-20 at Gujarat, Maharashtra, Odisha, Tamilnadu and Telangana under rainfed conditions. (Annexure - III).

With respect to pest and diseases, it was found superior to checks and moderately resistant for the same. Considering the increasing demand of red grain culture 'WN-585' with early maturing, high yield potential culture, desirable grain quality and moderately resistant to foot rot and blast disease. It is proposed to best culture for early maturing finger millet growing dry lands, hill and tribal areas of India. Hence it can be used directly in recombination breeding for induction of earliness with red grain colour and high grain yield.

37. CCB 12 (IC0641999; INGR21212), a cotton (*Gossypium barbadense*) germplasm with cleistogamous flower and three locule bolls

KPM Dhamayanthi*, A Manivannan and K Rathinavel

ICAR-CICR Regional Station, Coimbatore-641003, Tamil Nadu, India

*Email: dhamayanthikpm@gmail.com

Cleistogamy, a breeding system in which plants produce unopened flowers, and this feature facilitates self-pollination, this phenomenon has received increasing attention in recent years. It is present in 693 angiosperm species, distributed over 228 genera and 50 families. Recent investigations have indicated that evolution of cleistogamy in these taxa may be influenced by the occurrence of heterogeneous environments, inbreeding depression and geitonogamy. Cleistogamy mechanism helps in ensuring the self-pollination by which genetic purity is reserved.

Gossypium barbadense grows indeterminately and flowers; flower buds are denoted as squares. The flower bud is surrounded by three bracts and forms a pyramid-like shape. The first square is typically appearing on node 5 or 6 in about 37 to 39 days after sowing. Anthesis takes place approximately 24 days after the formation of first square. The bloom process takes several days, and bloom age can be estimated by the bloom characteristics. On the day a flower opening, it appears yellow in color. Pollination in a flower usually occurs within a few hours of flower opening.

A three way cross (SN (SN x ICB 75) 7-1-6-2) was made during 2012-2013 crop season. Among the F₃ population a single plant bearing flowers (cleistogamous) in different nature from that of the parents was isolated. The identified plant is semi spreading type with an average height of 133 cm, with sympodia ranging from 6 to 7 per plant. The cultivar

exhibited solitary bolls, ovate in shape with pointed tip. At present, this cultivar is in F₈ generation. It was evaluated for three years to study the flowering pattern during the phenology, seed cotton production and fiber quality, at ICAR-CICR Regional Station, Coimbatore and subsequently, confirmative trials were conducted at ICAR-CICR, Nagpur, MPKV, Rahuri and ICAR- CICR Regional Station, Sirsa, under diverse agro climatic zones. The morphological observations recorded in all the locations have confirmed that the cultivar is true to type with cleistogamous flowers. Average seed cotton yield of 7.5 q/ha was recorded. This cultivar is rated under ELS category as per the fibre quality parameters with the staple length of 35 mm, strength of 34 g/tex and micronaire of 2.5 µ/inch.

Occurrence of cleistogamous flowers in *G. barbadense* is very rare phenomenon. The identified cultivar was from an intra barbadense cross (Suvin x (Suvin x ICB-75) and found stable for cleistogamous flower production. The trait is controlled by two recessive genes (cg1 and cg2) and can be transferred in populations through breeding methods, like haploidisation or backcrosses. Digenic inheritance of 15:1 is reported for this trait. The petals are locked each other as to prevent the opening of the flower, thereby excluding the possibility of cross-pollination. This character in breeding lines would be of great importance for maintaining genetic purity in often-cross pollinated crops like cotton.

38. CNH 204710 (IC0641997; INGR21213), a cotton (*Gossypium hirsutum*) germplasm with ginning outturn percentage of 43.9%

SM Palve* and Nita Kate

ICAR-Central Institute for Cotton Research, Nagpur-440010, Maharashtra, India

*Email: smpalve@gmail.com

Ginning outturn (GOT) is an important component of fibre yield in cotton as it is directly associated with lint. The amount of lint borne on a single seed is a matter of considerable economic importance. It is commonly represented as the ginning percent. GOT is the ratio of weight of lint to the weight of seed-cotton (lint and seed) expressed as percentage. It is much used measurement in cotton production, marketing and ginning. Ginning out-turn is a useful indicator of the performance of a genotype. Since, cotton lint is considered to be the most economic and valued from textile industries and fabrics manufacturing point of view. The measurement of lint as an index or in terms of

percentage helps to identify varieties/ genotypes producing more lint. Genotypes with high ginning out-turn values are thus preferable, because they yield more lint.

CNH 204710 was developed from an interspecific cross involving *G. barbadense* (Gb) and *G. hirsutum* (Gh) species. A backcross inbred population was developed involving *G. hirsutum* cv. Suraj as a recurrent parent and *G. barbadense* cv. Suvin as a donor. Crosses were made between Suraj as female parent and Suvin as the male parent during 2013- 14 at ICAR-Central Institute for Cotton Research, Nagpur. The F₁ (Suraj x Suvin) was then backcrossed to Suraj to produce BC₁F₁ population during 2014. In 2015, BC₁F₁ population was grown

and extensively self-pollinated. In subsequent generations up to BC₁F₆, continued self-pollination of selected single plant progenies was done. The field experiment was conducted during 2018-19, 2019-20, and 2020-21 at ICAR-Central Institute for Cotton Research, Nagpur with 19 BC₁ families of 4-14 plants per family and tested for yield components and fibre properties.

CNH 204710 is morphologically typical of upland cotton with hairy leaves and stem. It has normal leaf shape, higher internode length, long duration of 170-190 days maturity and growth habit similar to the varieties Suraj and NH 615. The introgression line CNH 204710 was selected on the basis of

the results of 3-year field trials for superior ginning outturn percentage of 43.9 % than those of the released check varieties Suraj and NH 615. NH 615 is regularly being used as zonal check for Central zone had ginning outturn of 36.9 % and quality check Suraj had 36.2 %. The donor parent Suvin had ginning outturn of 31.6 %. The identified introgression line CNH 204710 had upper half mean length of 29.1 mm, fibre strength of 26.5 g/tex and boll weight of 4.8 g. Fibre length of CNH 204710 was comparable to NH 615 (28.6 mm). Overall, CNH 204710 a high GOT (43.9 %) introgression line is an excellent source for cotton breeding programs.

39. DPB-1 (IC0632628; INGR21214), a broccoli (*Brassica oleracea* var. *italica*) germplasm with purple heading

Pritam Kalia, Shrawan Singh* and BS Tomar

Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India

*Email: singhshrawan@rediffmail.com

Nutritionally, broccoli is a very important vegetable crop because it is rich source of health benefiting anticancer glucosinolates and dietary minerals and vitamins. Broccoli is rich source of health beneficial glucosinolates such as glucoraphanin and glucoiberin. It has diverse variants for attractive colours such as green, purple and light yellow. The green is most common but purple colour is most attractive with added value of anthocyanin. Although, a purple heading variety 'Palam Vichitra' is developed for Indian condition but it takes long period (110-120 days after transplanting) and have dull shade of purple colour. While, the major demand arises near metro cities particularly in north Indian condition, hence it was essential to develop genotype having short harvest period (85-95 days) and attractive purple heads to fulfil the rising demand.

A new purple heading genotype with purple head was derived by recurrent selection from a segregating exotic material. The new genotype 'Delhi Purple Broccoli-1' was developed by recurrent selection. For this, the plant with purple colour head was selected and selfed by bud-pollination. From its progeny the selection and selfing process was continued for two more generation and each time, plants were selected with desirable traits such as medium head size, fine to medium size buds, partial to compact, medium to intense purple heads, early maturity,

seed production capacity etc. The fixed genotype was designated as 'Delhi Purple Broccoli-1'. It is distinct from the only purple heading broccoli 'Palam Vichitra' in India. Palam Vichitra takes 120 days after transplanting for maturity and produce seeds only in hills. While, the Delhi Purple Broccoli takes around 85-95 days after transplanting and produce seeds profusely in plains of north India during winter season. The distinguishing features between heads of both can be seen from. Its average head width is 17.6 cm, head length 15.6 cm and weight ranges from 600-750 g. It is rich in anthocyanin (30.31±0.68 mg/100g fw), higher than Palam Vichitra (17.8 mg/100 g fw). It is suitable for staggered sowing/planting from September to October, hence, has a longer harvest window, a desirable trait for market.

Delhi Purple Broccoli-1 is a medium stature variety and suitable to accommodate a greater number of plants per unit area. Unlike Palam Samridhi, it doesn't produce side spears which attract farmers for single harvest. Similar to other broccoli, it needs to be harvested with stalk when heads are compact, buds are well grown but still unopened and looks attractive. Yield potential of Delhi Purple Broccoli-1 is 21.8 t/ha, higher than Palam Samridhi (14.1 t/ha) and Pusa KTS-1 (15.60 t/ha). Important plant and yield traits are given in Table 1 and year-wise yield comparison in Table 2.

Table 1: Horticultural traits of Delhi Purple Broccoli-1 alongwith checks in Delhi condition

Character	Days to harvest (after transplating)	Spacing (cm)	Plant height (cm)	Plant spread (cm)	Gross plant weight (g)	Seed yield (g/plant)	Marketable head weight (g)	Net head weight (g)	Marketable yield (t/ha)
Delhi Purple Broccoli-1	85-95	45 × 45	52.5	48.3	1350		570	450	21.5
Palam Vichitra	120	60 × 45	63.2	60.0	1870		730	720	23.9

Table 2: Year-wise marketable yield of Delhi Purple Broccoli-1 genotype at IARI, New Delhi

Entry	Marketable head yield (tonnes/ha)					Avg. marketable yield (tonnes/ha)	Maturity*
	2015-16	2016-17	2017-18	2018-19	2019-20		
Delhi Purple Broccoli-1	27.0	20.8	21.5	19.5	20.3	21.8	December – January
Palam Vichitrai	-	22.8	23.9	25.0	26.5	26.4	February - March

*Due to temperature requirement for head initiation and development.

40. 635414 (IC0635414; INGR21215), a bottle gourd (*Lagenaria siceraria*) germplasm resistant to powdery mildew

Dhananjaya MV*, Sandeep Kumar GM, Varalakshmi B and Mahesh B

ICAR-Indian Institute of Horticultural Research, Bengaluru-560089, Karnataka, India

*Email: Dhananjaya.MV@icar.gov.in

Introduction

Bottle gourd [*Lagenaria siceraria* (Mol) Standley; 2n = 22] commonly known as ‘white flowered gourd’ or ‘calabash gourd’ belongs to the family Cucurbitaceae. Its fruits are known for good nutritive value. It is rich source of vitamins, minerals and also possess diuretic, antioxidant, cardio protective properties (Barot *et al.* 2015). Acceptability for fruit shape varies with the region and segment. The Southern parts of the country prefer cylindrical shape, whereas North and north eastern regions prefer round to oblong shaped fruits. For achieving quick cultivar development in the desired shape, presence and utilization of resistance source in the desired fruit shape is well appreciated by the breeders in the development of varieties/hybrids with resistance. Keeping in view, ICAR-IIHR, Bengaluru has come out with genetic stocks having resistance to major biotic stress *i.e* powdery mildew which is confronting the farmers. A promising genetic stock BG-8-1 with elongated straight shape fruits with green stripes was developed through individual plant selection from an open pollinated population collected and maintained in the germplasm. It was found to be resistant for powdery mildew disease reaction. Plants are monoecious, annual vine with soft pubescence and produces white solitary flowers during evening hours. It takes an average of 54.18 days for first female flower appearance at 17.33 node. Fruits are elongated straight shape with green stripes with a length of 35.05 cm and circumference 25.66 cm. It also produces 4.88 number of fruits per plant with a marketable yield of 32.20 t/ha (Table 1).

Fruits are medium, elongated straight with stripes on the surface of the fruits and shows resistant reaction for powdery mildew disease. It is a typical warm season vegetable, it cannot withstand frost and usually prefers hot and moist climate for cultivation. Seeds are sown from January to February for summer crop, June to July for rainy season crop and October - November for Rabi season. Land should be prepared well before planting by repeated ploughing and harrowing, 20-25 tonnes of farm yard

Table 1: Morphological, quality traits and disease reaction of BG-8-1

Sl. No	Character	BG-8-1
<i>Morphological Traits</i>		
1.	Days to first female flower appearance	54.18
2.	Node on which first female flower appeared	17.33
3.	Number of female flower	10.15
4.	Number of fruits per plant	4.88
5.	Yield /ha	32.20
<i>Fruit quality traits</i>		
6.	Fruit length(cm)	35.05
7.	Fruit circumference (cm)	24.25
8.	Fruit weight(kg)	1.10
9.	Fruit shape	Elongated straight with green stripes
<i>Disease reaction</i>		
10.	Powdery Mildew	13.58 (PDI) 300.00 (AUDPC)

manure/ha should be broadcasted after the first ploughing. Apply the recommended fertilizer mixture of 75 kg N, 100 kg P₂O₅ and 35-70 K₂O/ha in two to three splits. Seeds are sown on raised beds of 15- 30cm height, 1-1.5 m width during rainy season by maintaining a spacing of 1.6 m between the rows and 1 m between the plants. Two to three seeds were sown per hill and covered with soil and light irrigation was given. Thinning of seedling should be done 25-30 days after sowing, retaining one healthy seedling per hill. Plants should be properly trained on the supporting structure to facilitate intercultural operations, thereby it reduces the incidence of pest and disease.

References

Dhananjaya MV (2018) Production technology of vegetable crops (Bottle gourd)- A hand book (Ed: Sadashiva AT, Hebbar SS, Nair AK, and Senthil Kumar M), IIHR, Bengaluru

(INDIA), pp 26-28.

Amit B, P Suneeta, B Smitha and JP Prajapati (2015) Composition,

Functional Properties and Application of Bottle Gourd in Food Products. *J. Dairy Sci. Technol.* 4(1): 15–27.

41. VRT4-55-20 (HCP/YSR-6/) (IC0637253; INGR21216), a tomato (*Solanum lycopersicum*) germplasm with broad spectrum resistance to tomato leaf curl virus (ToL CV) with *Ty-2* and *Ty-3* genes

Prasanna HC¹, Yerasu Suresh Reddy^{1*} and Major Singh²¹ICAR-Indian Institute of Vegetable Research, Varanasi-221305, Uttar Pradesh, India²ICAR-Directorate of Onion and Garlic Research, Pune-410505, Maharashtra, India

*Email: yerasusureshreddy@gmail.com

Wild relatives of crops are good source of allelic variation that can boost the genetic improvement of agriculturally important crops. Resistance breeding against Tomato (yellow) leaf curl disease (TYLCD/ToLCD) got benefited from wild relatives of tomato (*Solanum lycopersicum* L.). Resistance to tomato-infecting begomoviruses has been successfully introgressed from different wild species of tomato like *Solanum pimpinellifolium*, *Solanum peruvianum*, *Solanum chilense* and *Solanum habrochaites* (Ji *et al.*, 2007b). From these sources, a few resistance genes have been introgressed into cultivated tomatoes. Among them *Ty2* and *Ty3* genes are well characterized and fine mapped using molecular markers.

Tomato line VRT4-55-20 with *Ty2* and *Ty3* genes pyramided was developed at ICAR-Indian Institute of Vegetable research, Varanasi. It has good resistance against ToLCV. VRT4-55-20 was developed through marker assisted selection from F₂ populations of a cross between FLA478-6-1-11 × CLN2498C and FLA478-6-1-11 × CLN1621E. The lines CLN2498C and CLN1621E carry *Ty-2* gene. The line FLA478-6-1-11 carries *Ty-3* gene (Prasanna *et al.*, 2015). VRT4-55-20 showed a higher level of resistance in agro inoculation test with two bipartite Tomato leaf curl New Delhi virus (ToLCNDV) and Tomato leaf curl Palampur virus (ToLCPaV), and a monopartite Tomato leaf curl Bangalore virus (ToLCBV). VRT4-55-20 showed high level of resistance under natural epiphytotic conditions also. Cultivars Kashi Vishesh

and Punjab Chhuhara were used as susceptible checks and they showed disease symptoms in all the experiments (Prasanna *et al.*, 2015).

The pyramided line VRT4-55-20 recorded an average fruit yield of 1.28 kg per plant. The fruits of the line plum shaped with a per carp thickness of 0.5 cm with an average locule number of 2 per fruit. TSS of 3.6 Brix was recorded. Fruit have distinctive thick green shoulder.

VRT4-55-20 can be used in different future tomato ToLCV resistance breeding programmes like the line can be tried as a parent in hybrid development programmes and the line can be used as source of *Ty-2* and *Ty-3* genes in gene pyramiding programmes with other economically important genes. Importantly, the line can be used in developing resistant cultivars for green fruit shoulder tomato market segment.

References

- Prasanna HC, DP Sinha, GK Rai, R Krishna, SP Kashyap, NK Singh, M Singh and VG Malathi (2015) Pyramiding *Ty-2* and *Ty-3* genes for resistance to monopartite and bipartite tomato leaf curl viruses of India. *Pl. Pathology*. 64 (2): 256- 264.
- Ji Y, JW Scott, P Hanson, E Graham and DP Maxwell (2007b) Sources of resistance, inheritance, and location of genetic loci conferring resistance to members of the tomato-infecting begomoviruses. In: (Ed. Czosnek H), Tomato Yellow Leaf Curl Virus Disease: Management, Molecular Biology, Breeding for Resistance. Dordrecht, The Netherlands: Springer, pp 343–62.

42. BR-207 (IC0642000; INGR21217), a cauliflower (*Brassica oleracea* var. *botrytis*) germplasm single dominant resistant gene to black rot disease caused by *Xanthomonas campestris* pv. *campestris* race 1

Pritam Kalia¹, Partha Saha, SR Sharma, Shrawan Singh and Dinesh Singh¹Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India²ICAR-IARI Regional Station, Katrain, Himachal Pradesh-175129, India³ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi-110012, India

*Email: partha.saha@icar.gov.in

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the most important winter vegetable grown widely in India. Among the various diseases, black rot caused by

Xanthomonas campestris pv. *campestris* (Xcc) (Pammel) Dowson is the most devastating disease of cauliflower worldwide including India (Singh and Dhar, 2011; Saha et

al., 2014; Saha et al., 2015; Saha et al., 2021). The line 'BR-207' is resistant to black rot disease caused by *Xcc* race 1. It was developed from progeny selection of a cross of S. No. 15 (susceptible genotype) and MGS-2-3 (resistant) by Division of Vegetable Science, ICAR-IARI, New Delhi, India. The line carries a single dominant resistant gene (Saha et al., 2015).

The resistant line BR 207 belongs to mid-late maturity group with semi erect growth habit and medium in height (45–50 cm). The leaves are light green, medium in size with medium puckering habit. The curds are medium, compact and creamy white with an average weight of 350 g. The reaction of the plant at adult stage showed resistant reaction with mean disease score of 1.2 and 100 % plants were resistant (Table 1) (Saha et al., 2012).

The curd matures in the month of mid-January requiring 16–20°C temperature for curd initiation and development. The crop gets ready to harvest in 75 days after transplanting in its normal growing season. The flowers of 'BR-207' are yellow and stalk length is medium and flowering occurs during March. The line can be a useful source for transferring the resistant gene in commercially susceptible variety (s) or to develop hybrid (s).

For each inoculated leaf, disease scores were taken at 21 days post inoculation. The severity of symptoms was assessed on a six-point scale of 0–9 based on the relative lesion size as 0 = no symptoms, 1 = small necrosis or chlorosis surrounding the infection point, 3 = typical small V-shaped lesion with black veins, 5 = typical lesion half way to the middle vein, 7 = typical lesion progressing to the middle vein, and 9 = lesion reaching the middle vein (Vicente et al. 2002).

References

- Saha P, P Kalia, M Sharma and D Singh (2016) New source of black rot disease resistance in *Brassica oleracea* and genetic analysis of resistance. *Euphytica*. 207:35–48.
- Singh D and S Dhar (2011) Bio-PCR based diagnosis of *Xanthomonas campestris* pv. *campestris* in black rot infected leaves of crucifers. *Indian Phytopath.* 64: 7–11.
- Thakur BS, BN Korla and K Khosla (2003) Inheritance of black rot resistance in late cauliflower. *Annl. Agric. Res.* 24:244–248.
- Vicente JG, JD Taylor, AG Sharpe, IAP Parkin, DJ Lydiate and GJ King (2002) Inheritance of race-specific resistance to *Xanthomonas campestris* pv. *campestris* in *Brassica* genomes. *Phytopathology*. 92:1134–1141

Table 1: Response of BR-207 and commercial cauliflower varieties to black rot disease in four different season/environment after artificial inoculation with black rot pathogen (*Xcc* race 1)

Genotype/lines	Mean disease score 21 days' post inoculation Environment 1/ season 1 (a)	PDI at 60 days after inoculation Environment 2/ season 2 (b)	PDI at 60 days after inoculation Environment 3/ season 3 (c)	PDI at 60 days after inoculation Environment 4/ season 4 (d)	Disease reaction*
BR-207	1.2	0.2	0.80	1.0	Resistant
Pusa Himjyoti	9.0	8.2	9	8.6	Highly susceptible
Pusa Sharad	9.0	7.4	8.6	8.2	Highly susceptible

43. PC-1 (IC0642001; INGR21218), a cauliflower (*Brassica oleracea* var. *botrytis*) germplasm rich in anthocyanin (40.6±2.74 mg/100g FW)

Shrawan Singh* and Pritam Kalia

Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India

*Email: singhshrawan@rediffmail.com

Speciality foods are major attraction of premier high-end market. In cauliflower, colourful curds orange, purple and green are gaining popularity in global and Indian markets. Anthocyanins have strong free radical scavenging activity and, thereby, good for health. These compounds help in neutralizing reactive oxygen species (ROS) and reactive nitrogen species (RNS), thereby reducing the oxidative stress (Ozcan and Ogun, 2015).

The 'PC-1' is a new purple curding genotype of Indian cauliflower which is developed by recurrent selection from a segregating material of 'Sicilian Purple' type. The 'Sicilian purple' is botanically an intermediate of broccoli and cauliflower and appears closer to broccoli. It forms

curd-like heads at a temperature range of 16 to 25°C and does not require vernalisation but needs cold temperature for bolting and flowering. Hence, it produces attractive full-size cauliflower-like curds during December–March months, set seeds profusely, and is easily crossable with Indian cauliflower. Unlike 'Graffiti', it accumulates anthocyanin only in 'pre-floral rudimentary buds' demonstrating the difference in genetic regulation of anthocyanin content between the two varieties.

Anthocyanin content in 'PC-1' was observed to increase up to 21st day of curd formation when it was recorded to be 41.2 mg/100 g fw. However, it declines afterward to 34.2 mg/100 g fw on 24th day of curd initiation. Hence, the ideal

stage of harvesting is 21 – 24 days after curd initiation. This may slightly vary from planting time, growing region and nutrition status. This has no deformity in curd portion in homozygous or heterozygous state, hence, can be used for heterosis breeding by developing CMS lines or self-incompatible lines in purple background.

44. DCA-295 (IC0642004; INGR21219), a chilli (*Capsicum annuum*) germplasm resistant to chilli veinal mottle virus disease and a good general combiner for yield and quality traits

Prabhudeva Ajjappalavara^{1*}, Megharaj KC², TB Allolli², HB Patil², Revanappa³, Abdul Kareem M⁴, MH Tataga⁴ and Ratnakar Shet⁴

¹UHS, Horticultural Research & Extension Center, Haveri-581110, Karnataka, India

²College of Horticulture, Bagalkot-587104, Karnataka, India

³Horticulture Extension Education Unit, Yadgir-585201, Karnataka

⁴College of Horticulture, Sirsi, Uttara Kannada - 581 401, Karnataka, India

*Email: prabhudev.ajjappalavar@uhsbagalkot.edu.in

As chilli is an economically important crop due to its significant value in regional as well as export market, the chilli production is taken up throughout the year mainly by the small farmers both in high and lowlands under rain-fed as well as irrigated conditions. In India, chilli veinal mottle virus (ChiVMV) is an economically important viruses causing yield loss to an extent of 50 per cent when the crop becomes infected at early stage. The predominance of ChiVMV during *Kharif* season is dominant because of favoured micro climatic condition. Hence, Identification of superior resistant lines for ChiVMV is very essential for the improvement of yield as well as the national productivity and also the national economy.

Forty-nine chilli genotypes were evaluated for virus complex in the open field under unsprayed condition during *Kharif* 2015 and the results obtained that virus infection was ranged from 16.36% to 89.72%. The lowest per cent incidence was found in DCA-295 (16.36%), DCA- 107 (17.36%) and DCA-154 (17.86%). The selected accessions evaluated

References

- Ozcan A and M Ogun (2015) Biochemistry of reactive oxygen and nitrogen species. In: S.J.T. Gowder (ed.) Basic Principles and Clinical Significance of Oxidative Stress. IntechOpen, London, U. K. doi: 10.5772/61193.
- Yuan Y, Chiu, LW, L Li (2009) Transcriptional regulation of anthocyanin biosynthesis in red cabbage. *Planta*, 230: 1141–1153.

against chilli veinal mottle virus through mechanical inoculation under shade net condition during *Kharif* season indicated that three genotypes (DCA-295, DCA-154 and DCA-107) were found to be immune showing no symptoms at both 30 and 45 days after mechanical inoculation for four consecutive *kharif* (2016, 2017, 2018 and 20219) season.

In order to understand the genetics of the resistance against Chilli veinal mottle virus, the F₂, BC₁ and BC₂ generations were developed by using immune germplasm to develop the population (Byadgi Dabbi x DCA-295, Byadgi Kaddi x DCA-295) and these populations were screened for the resistance through artificial inoculation to study the genetic inheritance pattern in the DCA-295 germplasm. The inheritance studies in the Byadgi Dabbi x DCA-295, Byadgi Kaddi x DCA-295 derived advanced populations showed that it is governed by single recessive gene. The tester DCA-295 was identified as a good general combiner for plant height, canopy spread (N-S), canopy spread (E-W), green chilli average fruit weight, ascorbic acid and total chlorophyll.

45. VRRAD-12 (A line) & VRRAD-204 (B line) (IC0642005 & IC0642006; INGR21220), Cytoplasmic Male Sterile and maintainer lines of radish (*Raphanus sativus*) with lyrate leaf shape and blunt root: Good combiner for yield (12.5-33.6%), root length (6.5-32.4%) and root weight (17.2-30.0%)

BK Singh* and PM Singh

ICAR-Indian Institute of Vegetable Research, Varanasi-221305, Uttar Pradesh, India

*Email: bksinghkushinagar@yahoo.co.in

Radish (*Raphanus sativus* L.) is a most important salad crop belongs to Brassicaceae family which is grown round the year for fleshy roots and soft leaves. Heterosis (hybrid vigour) is of

commercial importance for commercialization of F₁ hybrids in various vegetable crops, and is being facilitated by use of cytoplasmic male sterility (CMS) and self-incompatibility (SI)

in radish. Nonetheless, the SI system in most of the radish genotypes is very weak; hence, there is always chance to get undesirable sibs in hybrid seeds. Therefore, in radish, CMS system is mostly preferred genetic emasculation technique for triggering the F_1 hybrid development, and cost-effective and easy hybrid seed production commercially.

First hybrid radish was developed by Frost (1923); moreover, CMS was first identified in a cultivar of Japanese radish by Ogura (1968) popularly known as Ogura-CMS; and thereafter, it has been transferred into different *Brassica* vegetables. Although radish is the most important salad crop in India because of availability and uses of roots round-the-year, yet only ICAR-IIVR, Varanasi, UP among Public Sector Institutes in India priorities its research on development of CMS lines and CMS-based hybrids. Realizing the importance and advantage of CMS lines especially in easy maintenance of female parent, harnessing heterotic vigour for economic traits (root length, root weight, marketable yield, earliness, uniformity produce, heat tolerance), and cheaper & quality seed production of F_1 hybrids; ICAR-IIVR, Varanasi, UP has developed CMS lines by backcross method and identified better hybrids (Singh et al. 2018, Singh and Singh 2020, Singh et al. 2021). The Ogura-CMS line 'VRRAD-12 or A Line', was developed by crossing CMS plants from open population with an elite line 'VRRAD-204 or B Line or Maintainer Line' which is having better combining ability, higher heterosis for economic traits (12.5-33.6% for marketable root) and suitable for winter season cultivation (Singh and Singh 2020). Significant heterotic hybrids for yield, longer roots, earliness, vigour consistency and uniformity have also been reported previously by many researchers (Kutty and Sirohi 2003, Singh et al. 2018, Kochetov and Sinyavina 2019).

CMS line VRRAD-12 is having lyrate type of leaf morphology (leaf division incision), develops white root with blunt-end (non-tapering) during winter season, bears white flower and ready to seed harvest in about 4.5 months after transplanting of seedlings. The quantitative traits of VRRAD-12 for consecutively three years (2017-18, 2018-19 and 2019-20) were observed as 45.7, 42.2 & 38.5 days to first root harvest; 273.5, 261.3 & 246.5 g gross plant weight; 190.3, 172.4 & 152.6 g root weight; 24.8, 23.1 & 22.4 cm root

length; 37.5, 39.1 & 44.8 cm shoot length; 3.6, 3.7 & 3.4 cm root diameter; 11.3, 11.0 & 10.5 number of leaf; 60.2, 59.5 and 56.4 t/ha marketable yield; 41.6, 37.8 & 43.1 days to 50% flowering; 410.3, 391.6 & 426.8 pods/plant; 3.7, 3.8 & 3.8 seed/pod; and 12.9, 13.5 & 13.9 g of 1000 seed weight. Moreover, the economic parameters of its maintainer VRRAD-204 during 2017-20 were observed as 42.8, 42.3 & 36.5 days to first root harvest; 258.9, 251.6 & 238.3 g gross plant weight; 184.5, 170.4 & 151.8 g root weight; 24.1, 23.2 & 22.6 cm root length; 35.9, 37.1 & 42.7 cm shoot length; 3.6, 3.5 & 3.3 cm root diameter; 11.5, 11.1 & 10.6 number of leaf; 58.8, 56.4 and 53.7 t/ha marketable yield; 41.0, 38.1 & 42.5 days to 50% flowering; 400.5, 385.4 & 419.8 pods/plant; 3.8, 3.6 & 3.6 seed/pod; and 13.2, 12.4 & 13.3 g of 1000 seed weight. In conclusion, newly developed CMS line VRRAD-12 would be very effective in harnessing heterotic potential, developing CMS-based F_1 hybrids suitable for winter season, and cost-effective commercial hybrid seed production in radish.

References

- Kochetov AA and NG Sinyavina (2019) The strategy of creating highly productive forms of radish, adapted for cultivation under artificial light conditions. *Russian Agri. Sci.* 1: 29–33.
- Kutty CN and PS Sirohi (2003) Exploitation of hybrid vigour in radish (*Raphanus sativus* L.). *Indian J. Hort.* 60(1): 64–68.
- Ogura H (1968) Studies of male sterility in Japanese radish with special reference to the utilization of this sterility towards the practical raising of hybrid seeds. *Meun. Fac. Agri. Kagoshima Univ.* 6: 39–78.
- Singh BK and PM Singh (2020) Unleashing the genetic potential of CMS-based F_1 hybrids of radish (*Raphanus sativus* L.) to winter and summer temperature. *Veg. Sci.* 47(1): 16–22.
- Singh BK, TK Koley, P Karmakar, A Tripathi, B Singh and M Singh (2017) Pigmented radish (*Raphanus sativus* L.) Genetic variability, heritability and inter-relationships of total phenolics, anthocyanins and antioxidant activity. *Indian J. Agric. Sci.* 87(12): 1600–1606.
- Singh BK, PM Singh and B Singh (2018) Heterosis for economic traits in single cross-hybrids of radish (*Raphanus sativus* L.). *Veg. Sci.* 45(1): 45–49.
- Singh BK, PM Singh and B Singh (2021) VRRAD-201 (IC 0625064; INGR20032)- A cytoplasmic male sterile (CMS) line of radish. *Indian J. Plant Genet. Resour.* 34(2): 333–334.

46. DPPMR-09-1 (IC0642003; INGR21221), a pea (*Pisum sativum* subsp. *hortense*) germplasm resistant to powdery mildew disease

Akhilesh Sharma* and DK Banyal

Dept. of Vegetable Science & Floriculture, CSKHPKV, Palampur-176062, Himachal Pradesh, India

*Email: assharmaakhil1@gmail.com

Garden pea (*Pisum sativum* L; $2n=2x=14$), belonging to family Leguminosae is an important cool season vegetable crop grown throughout the world for its tender green pods, seeds and foliage. Garden pea is quite palatable and

excellent food for human consumption, which is eaten as fresh, canned, frozen and in dehydrated forms. Green peas are rich in health promoting phytonutrients, minerals, vitamins and antioxidants. Powdery mildew in garden pea

caused by *Erysiphe pisi* DC. is a serious disease that can cause 25-50 per cent yield losses (Fondevilla and Rubiales 2012). Genetic resistance is quite effective as it is more cost-effective and environment friendly than fungicide applications. In this perspective, hybridization programme was initiated involving diverse parents to isolate powdery mildew resistant progenies with superior attributes during 2004. Line DPPMR-09-1 was isolated in BC1F5 generation from the cross '(VRPMR-10 × Sugar Giant) × VRPMR-10' during 2010 (Sharma *et al.* 2013). The line was further screened for powdery mildew reaction over the years in different

locations and showed resistant reaction both under field (Table 1) and *in vitro* (Table 2) conditions. The line is a good resistant source for powdery mildew disease and can be utilized for developing powdery mildew resistant varieties.

References

- Fondevilla S and D Rubiales (2012) Powdery mildew control in pea: a review. *Agronomy Sustainable Developmen.* 32: 401–409.
Sharma A, P Kapur, V Katoch, Y Singh and JD Sharma (2013) Development of powdery mildew resistant genotypes in garden pea (*Pisum sativum* L.) through generation mean analysis approach. *Indian J. Genet.* 73 (4): 371-377.

Table 1: Reaction of garden pea genotypes to Powdery mildew disease under field conditions

Genotypes	2014	2017	2018-19	2019-20	2020-21	Overall	
	Kukumseri		Palampur			Infection type	Reaction type
DPPM-65	3	3	3	3	3	3	MS
DPPM-74	3	3	3	3	3	3	MS
DPPMFWR-27	4	4	3	3	3	4	S
DPPMFWR-30	2	2	2	1	2	2	MR
DPPMR-09-1	1	1	1	1	1	1	R
Lincoln	4	4	4	4	4	4	S
Palam Priya	3	4	3	3	3	4	S
Azad P-1	4	4	4	4	4	4	S
Pb-89	3	2	2	2	2	3	MS

Where, R-Resistant; MR-Moderately resistant; MS-Moderately Susceptible; S-Susceptible

Table 2: Reaction of garden pea genotypes to Powdery mildew disease under in-vitro conditions

Genotypes	Naturally ventilated polyhouse				Detached leaf assay		Overall	
	Infection type			Disease reaction	Infection type	Disease reaction	Infection type	Disease reaction
	2018-19	2019-20	2020-21					
DPPMFWR-30	2	2	2	MR	2	MR	2	MR
DPPMR-09-1	1	1	1	R	1	R	1	R
Lincoln	4	4	4	S	4	S	4	S
Palam Priya	4	4	3	S	4	S	4	S
Azad P-1	4	4	4	S	4	S	4	S
Pb-89	2	2	2	MR	2	MR	2	MR

Where, R-Resistant; MR-Moderately resistant; MS-Moderately Susceptible; S-Susceptible

47. EC762384 (EC762384; INGR21222), a cowpea (*Vigna unguiculata*) germplasm with dense pubescence

Kuldeep Tripathi^{1*}, AK Parihar², Niranjana Murthy³, Revanasidda², DP Wankhede¹, Neeta Singh¹, SK Deshpande⁴, Gayachara¹ and Ashok Kumar¹

¹ICAR-National Bureau of Plant Genetic Resources, Pusa Campus—110012, New Delhi, India

²ICAR-ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India

³University of Agricultural Sciences, Bengaluru-560065, Karnataka, India

⁴University of Agricultural Sciences, Dharwad-580005, Karnataka, India

*Email: kuldeep.tripathi@icar.gov.in

Cowpea is a climate resilient multipurpose leguminous crop cultivated in tropics. Identification of trait specific

germplasm is prerequisite to meet the present and future needs of cowpea breeding programme. After characterizing

more than 5,000 accessions at the ICAR-NBPGR, New Delhi, a rare and unique cowpea accession, namely EC762384, was identified with very high pubescence. This unique accession had very prominent trichomes on the entire plant that was visible to the naked eye. Pubescence is measured by counting number of trichomes on leaf. Younger leaves exhibited higher pubescence (185.3 ± 35.39 and 137.5 ± 38.18 , respectively) compared to mid-age (163.7 ± 36.94 and 132.4 ± 38.91 , respectively) and older leaves (112.4 ± 25.79 and 97.5 ± 27.75 , respectively). It is a unique and stable character consistently observed over the years (*khariif*, 2019-2020 and 2020-2021) and locations (NBPGR, Issapur farm, IIPR, Kanpur, UAS Dharwad

and UAS Bengaluru). The identified accession can be used in the hybridization programme for various genetical studies and development of cowpea varieties with high pubescence. In addition, further studies on this genetic resource may provide insights in insect tolerance and defence mechanism through phenotyping under controlled conditions.

Reference

Tripathi K, AK Parihar, N Murthy, DP Wankhede, N Singh, SK Deshpande and A Kumar (2020) Identification of a unique accession in cowpea with dense pubescence. *J. Food Legumes*. 33(4):278-9.

48. IC241473 (IC241473; INGR21223), a lentil (*Lens culinaris*) germplasm with multiflowering and multipodding with fasciated stem.

Kuldeep Tripathi^{*1}, Gyan P Mishra², Gayacharan¹, HK Dikshit², Padmavati G Gore¹, Dileep Tripathi, Reena Mehra³, Neeta Singh¹, Ashok Kumar¹, Ashutosh Sarker³ and Kuldeep Singh⁴

¹ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India

²ICAR-Indian Agricultural Research Institute, New Delhi-110012, India

³International Center for Agricultural Research in the Dry Areas, Amalaha-466 113, Madhya Pradesh India

⁴International Crops Research Institute for the Semi-Arid Tropics, Patancheru-502324, Telangana, India

*Email: kuldeep.tripathi@icar.gov.in

The inflorescence in lentil is racemose, with usually one to three flowers per peduncle. Multi-flowering (MF) accessions can be identified with an expression of three or more flowers at one or multiple flowering nodes. Multi-flowering clusters have been documented for a few flowering nodes in *Pisum sativum* (up to five FPP), chickpea (upto nine FPP), lentil (up to seven FPP) (Mishra *et al.*, 2020). The phenotypic characterization of entire lentil accessions (2,324) of Indian genebank, ICAR-NBPGR, New Delhi lead to the identification of a unique multi-flowering germplasm accession, IC241473, in cultivated lentil (*Lens culinaris* Medik.), forming up to 16 flowers per peduncle at multiple flowering node. Besides, this accession was also having a fasciation of the main stem. The multi-flowering expression was observed under field conditions at ICAR-NBPGR, New Delhi, India, consecutively during the winter seasons of year 2017-18, 2018-19, 2019-20 and was validated at NBPGR, New Delhi, NBPGR, RS, Ranchi and ICARDA, Amlaha (Madhya Pradesh) during 2020-2021.

Unlike earlier reported fasciated accessions in legumes, this fasciated accession showed stable multi-flowering expression over the years and locations and was also found fertile with fully developed reproductive organs. This unique and novel germplasm accession can be utilized for genetic studies to identify the locus regulating the multi-flowering trait in lentil and its association with environmental factors.

References

Mishra GP, HK Dikshit, J Kumari, K Tripathi, J Devi, M Aski, R Mehra, A Sarker and S Kumar (2020) Identification and characterization of novel penta-podded genotypes in the cultivated lentil. *Crop Sci*. 60(4): 1974-1985.

Tripathi K, GP Mishra, Gayacharan, D Tripathi, HK Dikshit, R Mehra, A Kumar, A Sarker and K Singh (2021) First Report of a Novel Multi-flowering Germplasm with Fasciated Stem in Lentil (*Lens culinaris* Medik.). *Indian J. Plant Genetic Resources*. 34(1):1-4.

49. EC398949 (EC398949; INGR21224), a mung bean (*Vigna radiata*) germplasm with ability to maintain a cool canopy even under moisture stress

SK Raina^{1*}, Jagadish Rane², Nikhil Raskar², AK Singh², V Govindasamy³, Mahesh Kumar², SC Ekatpure⁴, PS Minhas² and SM Sultan¹

¹ICAR-NBPGR Regional Station, Srinagar-190019, Jammu & Kashmir, India

²ICAR-National Institute of Abiotic Stress Management, Pune-413115, Maharashtra, India

³ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

⁴Kerala Agricultural University, Thrissur-680656, Kerala, India

*Email: Susheel.Raina@icar.gov.in

Mungbean [*Vigna radiata* (L.) Wilczek] is an important warm season contributing to nutritional security of vegetarian population of South-east Asia. It is a rich source of carbohydrates, protein (27%), folate and iron (Noble *et al.*, 2017). Drought stress during vegetative stage reduces plant size, root growth, leaf area, pod number and harvest index which ultimately lead to reduced grain yields (Raina *et al.*, 2016). Canopy temperature is an important physiological trait associated with drought tolerance. Under limited soil moisture conditions, cooler canopy genotypes maintain relatively higher transpiration rates compared to genotypes with higher canopy temperature. Cooler canopy was positively associated with grain yield in rice, sugarcane, chickpeas, pearl millet and soybean under water deficit conditions (Bazzer and Purcell, 2020). Deviation of temperature of plant canopy from air temperature known as Canopy temperature depression (CTD) is an indicator of overall plant water status. Based on evaluation in field conditions in year 2014 and 2015, a landrace accession VC-6173-C (EC-0398949) imported from Thailand was found to have significantly ($p<0.01$) cooler canopy compared to the local check Vaibhav under drought conditions. The canopy temperature depression (CTD) of this accession under drought stress conditions varied from 5.18 - 8.0°C. Since CTD is an effective surrogate trait for screening drought tolerant genotypes, the identified accession has potential utility in breeding drought-tolerant mungbeans. VC-6173-C can also

serve as a valuable genetic stock to decipher role of canopy temperature in contributing to drought tolerance in this fast growing legume crop.

The data on associated agro-morphological traits is given in Table 1.

References

- Raina SK, V Govindasamy, M Kumar, AK Singh, J Rane and PS Minhas (2016) Genetic variation in physiological responses of mungbeans (*Vigna radiata* (L.)Wilczek) to drought. *Acta Physiol Pl.* 38: 268.
- Noble TJ, Y Tao, ES Mace, B Williams, DR Jordan, CA Douglas and SG Mundree (2018) Characterization of linkage disequilibrium and population structure in a mungbean diversity panel. *Front Plant Sci.* 8: 2102.
- Bazzer SK and LC Purcell (2020) Identification of quantitative trait loci associated with canopy temperature in soybean. *Sci Rep.* 10: 17604.

Table 1: Associated agro-morphological traits in VC-6173-C

Agro-morphological trait	VC-6173-C
Days to 50% flowering (days)	38
Plant height (cm)	27.25
Pods/plant	18.2
Pod length (cm)	5.72
Seeds/pod	5.47
Yield under drought(gm/plant)	1.8-4.55

50. EC414478 (INGR21225), a unique seed morphotype of pea (*Pisum sativum*) germplasm with extended funiculus.

Kuldeep Tripathi^{1*}, Padmavati G Gore¹, Ruchi Bansal¹, Gayacharan¹, Vinod Kumar¹, Neeta Singh¹, Chithra Devi Pandey¹, BB Sharma², SB Choudhary³, AK Parihar⁴ and, Ashok Kumar¹

¹ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

²ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

³ICAR-National Bureau of Plant Genetic Resources, Ranchi, Jharkhand- 834003, India

⁴ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India

*Email: kuldeep.tripathi@icar.gov.in

A unique seed morphotype of pea (*Pisum sativum* L.) with extended funiculus was identified during mega germplasm characterization programme at ICAR-NBPGR, New Delhi undertaken during Rabi 2019–2020. Based on comparative study with selected accessions (seven) for seed morphology, imbibition and physiological behaviour, this accession was identified with very distinct and intact funiculus at maturity and higher rate of water uptake. It was a novel report of seed morphotype in pea with extended funiculus. All the accessions selected for imbibition behaviour study were of the same moisture content. Imbibition curves clearly indicated that water absorption and weight gain of the seeds were highest in atypical accession as compared to normal cultivars used in the study. All the accessions

selected for this study were of the same moisture content (~10.5%). Imbibition curves indicated that the seeds' water absorption and weight gain were highest in EC0414478 accession compared to checks and the accessions used in the study. The highest water uptake was observed in seeds with completely intact funiculus compared with completely varnished hilum and completely removed funiculus. When the reading was taken on the 4th day, germination speed was also fast in the EC0414478 compared to all other accession used in the study. Funicle was remain intact with seed in 1-month old seedlings that indicate uniqueness of atypical accession in holding funicle as fixed character. In the present study, we observed the physiological response and growth of different pea accessions by measuring

chlorophyll, RWC and biomass at the early vegetative stage. Our results indicated that EC0414478 showed the highest biomass along with the chlorophyll and RWC in response to drought. Drought tolerance in EC0414478 is attributed to maintaining high moisture content and chlorophyll to sustain active metabolism and growth under limited water conditions. A detailed investigation is required to assess the drought tolerance potential of identified accessions under field conditions. For trait stability, this unique accession was evaluated under multi-location trial at four locations viz. ICAR-NBPGR, Issapur Farm, NBPGR, RS, Ranchi, ICAR-IARI,

New Delhi and ICAR-IIPR, Kanpur in *rabi* 2020-21 and this unique trait was expressed across the locations.

References

- Tripathi K, PG Gore, A Pandey, R Bhardwaj, N Singh, G Chawla and A Kumar (2019) Seed morphology, quality traits and imbibition behaviour study of atypical lentil (*Lens culinaris* Medik.) from Rajasthan, India. *Genet. Resour. Crop Evol.* 66(3): 697-706.
- Tripathi K, PG Gore and R Bansal (2021) Identification and revealing the potential traits of the unique germplasm with extended fuculus in pea (*Pisum sativum* L.). *Genet. Resour. Crop Evol.* <https://doi.org/10.1007/s10722-021-01275-5>.

51. IC251442 (INGR21226), a rice bean (*Vigna umbellata*) germplasm insensitive to photo-period and thermo-period

Aditya Pratap^{1*}, PS Basu, Sanjeev Gupta¹, Latha Madhavan² and NP Singh¹

¹Indian Institute of Pulses Research, Kanpur, Uttar Pradesh-208024, India

²ICAR-NBPGR Regional Station, Thrissur-680656, Kerala, India

*E-mail: adityapratapgarg@gmail.com

Mungbean and blackgram are the most popular pulse crops of the *Vigna* group and India is their largest producer, consumer and importer in the world (Pratap *et al.* 2012). Both these crops can be grown across a wide range of adverse soil and climatic conditions, and seasons (spring, summer, winter and rainy seasons) in different parts of the country as a sole, relay or intercrop (Pratap *et al.* 2013). Therefore, these crops also offer an opportunity for their horizontal as well as vertical expansion in large areas. However, the biggest hindrance in horizontal expansion of blackgram and mungbean in India is their photo- and thermo-sensitive behaviour which necessitates breeding of an array of genotypes for different agro-climatic zones of the country. Photo-thermo period sensitivity makes these crops vulnerable to photoperiod and temperature fluctuations, thereby affecting their yield potential drastically, especially when the same variety of these crops is grown across different seasons. Therefore, there is a need to develop cultivars which are largely insensitive to photo- and thermo-period and can be grown over large areas across seasons and agro-climatic zones. However, breeding for photo- and thermo-insensitivity requires robust donors for this trait without a possibility of linkage drag. Keeping this in view, this study aimed at identification of photo- and thermo-insensitive donors in the *Vigna* species so that these could be utilized in mungbean and blackgram improvement programmes through introgression breeding.

A set of 56 accessions of *Vigna* belonging to 13 species (eight accessions of *V. trilobata*, seven of *V. umbellata*, five each of *V. mungo* and *V. hainiana*, four each of *V. sylvestris* and *V. vexillata*, three each of *V. radiata*, *V. sublobata*, *V. dalzelliana* and *V. pilosa*, and one each of *V. glabrescens*, *V. trinernia* and *V. unguiculata*) and eight cultigens (four each of mungbean

and blackgram) was grown under natural field conditions in the tropical climatic conditions of Kanpur (26°28' N, 80°24' E) in two consecutive years (2011-13). All the individual plots of 56 accessions were observed every alternate day and the dates of important phenological events and characterization parameters as per NDUS guidelines (IIPR, 2010) were recorded. Viability of the fresh pollen samples in those accessions which survived through the rainy, summer and winter seasons was determined on the basis of observations on stainability of fresh pollen grains. On the basis of phenological events, physiological parameters as well as pollen viability studies, two accessions, viz., *V. umbellata* (IC251442) and *V. glabrescens* (IC251372) were identified to be largely photo- and thermo-period tolerant. Both these accessions behaved normally and were able to flower and set pods at extreme temperatures as high as 43.9°C and as low as 2.7°C. Pollen viability studies were also conducted which recorded viable pollen (>75% at 2.7°C and >85% at 41.9°C) and normal pollen tube growth at both the extremes of temperature. The identified *V. glabrescens* accession has long, constricted pods and dark green, mottled seeds while *V. umbellata* has smooth, curved pods and shining, oval, large seeds. Both these accessions have several other desirable characters besides photo- and thermo-period tolerance, such as long and bold pods, profuse branching and resistance to all major diseases of *Vigna* species, and therefore these could be potential donors for the above traits in *Vigna* through introgression breeding. Earlier *V. radiata* X *V. umbellata* and *V. mungo* X *V. umbellata* crosses have been successfully generated to transfer resistance to MYMV and other desirable traits into mungbean (Singh *et al.* 2003; Chaisen *et al.* 2013) and urdbean (Pal *et al.*, 2005). Both these accessions are currently being utilized in

developing photo-thermo tolerant genotypes in cultivated *Vigna* species.

References

- IIPR (2010) National Test Guidelines for the conduct of tests for distinctness, uniformity and stability of Mungbean (*Vigna radiata* L.) and Urdbean (*Vigna mungo* L.), 1—25. All India Coordinated Research Project on MULLaRP, Indian Institute of Pulses Research, Kanpur, India.
- Chaisan T, P Somta, P Srinives, S Chanprame, R Kaveeta and S Dumrongkittikule (2013) Development of tetraploid plants from an interspecific hybrid between mungbean (*Vigna radiata*) and rice bean (*Vigna umbellata*). *J. Crop Sci. Biotech.* 16: 45-51.
- Singh KP, PK Sareen, M Sareen and A Kumar (2003) Interspecific hybridization studies in *Vigna radiata* L. Wilczek and *Vigna umbellata* L. *Natl. J. Plant Improv.* 5: 16-18.
- Pal SS, JS Sandhu and I Singh (2005) Exploitation of genetic variability in interspecific cross between *Vigna mungo* X *V. umbellata*. *Indian J. Pulses Res.* 18: 9-11.

52. IPF 2014-13 (IC0640782; INGR21227), a pea (*Pisum sativum*) germplasm resistant to rust and powdery mildew

AK Parihar^{1*}, GP Dixit¹, Arpita Das², Deepa Saxena³, Deepak Singh⁴, KD Singha⁵, KPS Kushwaha⁶, Ramesh Chand⁷, RS Bal⁸, S Chandra⁹, Sanjeev Gupta¹, RK Mishra¹ and Anil K Singh¹

¹ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India

²Bidhan Chandra Krishi Viswavidyalaya, Nadia-741252, West Bengal, India

³Chandra Shekhar Azad University of Agriculture & Technology, Kanpur-208002, Uttar Pradesh, India

⁴ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

⁵Assam Agricultural University, Shillongani-782002, Assam, India

⁶G.B. Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India

⁷Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India

⁸Punjab Agricultural University, Gurdaspur-143521, Ludhiana, Punjab, India

⁹Narendra Deva University of Agriculture & Technology, Faizabad -224229, Uttar Pradesh, India

*Email: ashoka.parihar@gmail.com

Field pea is considered as an important winter season pulse crop of India and is being cultivated mainly in states of Uttar Pradesh, Madhya Pradesh, Bihar, Assam and Odisha (Anonymous 2021). Being a worthy source of quality protein, starch, minerals and vitamins, it is an important component in many food industries (Parihar *et al.* 2016). Considering the importance of this legume, significant contributions have been made in the recent past toward genetic improvement and cultivar development in our country. Unfortunately, biotic stresses particularly rust and powdery mildew have been the major constriction in field pea cultivation and both diseases can cause noteworthy yield loss under congenial condition (Parihar *et al.* 2020a). The *Uromyces viciae-fabae* (Pers de Bary) is the causal organism for pea rust in tropical and subtropical regions *viz.* India and China (Singh *et al.*, 2015; Das *et al.* 2019). This pathogen mainly appears on aerial parts during the reproductive stage of the crop which led towards reduction of photosynthetic area and subsequent yield losses ranges from 57– 100% (Upadhyay and Singh, 1994). The disease occurrence at early stages could result in total failure of the crop. Hence, management of rust is a crucial attempt for sustainable field pea production. However, chemical control is not holistic move towards controlling pea rust owing to intricacy in pathogen manners. This airborne pathogen has wider host range and lack of durability in resistance with quantitative nature of inheritance these factors complicating disease

management (Barilli *et al.*, 2009a). Therefore, exploitation of host pathogen resistance is the most modest approach of rust control (Rubiales *et al.*, 2013). However, so far in field pea, only incomplete resistance is reported against *U. viciae-fabae* (Xue and Warkentin, 2002; Chand *et al.*, 2006) and *U. Pisi* (Barilli *et al.*, 2009c). Thus, recognition of stable and durable resistance genotypes of field pea against rust, followed by utilization of these genotypes as donors in a resistance breeding program would be a best strategy for disease management in a trustworthy way. During recent past sincere efforts have been made and numbers of genotypes have been developed with good level of resistance to rust. As mentioned above resistance against this pathogen is partial and influenced by environmental factors. Therefore, the magnitude of environmental and genotype-by-environment interaction was assessed to understand the dynamism of resistance and identification of durable resistant genotypes through multi-location and multi- year evaluation for rust. A panel of 23 promising field pea genotypes was assessed under inoculated conditions for rust disease for two consecutive years at six locations in India. Genotype namely IPF-2014-16 and IPF- 2014-13 identified as “ideal” genotypes, which can be recommended for release and exploited in a resistance breeding program for the region confronting field pea rust.

The genotype IPF 2014-13 is tall type (177-211 cm) and leafy type. It has white colour flowers, white & round seed

and yellow cotyledon. It flowered and matured in 65-70 days and 120-122 days respectively with 20.0-22.0 gm 100- seed weight. The average yield of the genotype is more than 2.0t/ha. This genotype also has powdery mildew resistance and good yield potential (20-22 qt/ha). It can be grown on different type of soil; however, a well drained soil is essential to achieve good yield potential of this genotype. The field should be well prepared by two to three ploughings. The seed treatment should be done with fungicide like Thirum/ Captan/Carbendazim @ 3.0 g/kg seed + rhizobium culture @ 1 packet/10 kg + Trichoderma @ 4.0 g/kg at 4-5 days before sowing. The optimum sowing time is October 15-Novemebur 15 with 75-80 kg/ha seed rate. If available, about 20 tonnes of organic manures should be incorporated in the soil at the time of land preparation. This should be supplemented with 20-30kg/ha nitrogen as starter dose in basal dressing forms at the time of sowing. The phosphorus and potassium should be applied as a basal dose based on soil test. If soil is deficient in these nutrients, apply 40kg/ha P₂O₅ with 20-30 kg K₂O and 20kg Sulphur per hectare. For Zinc deficiency 0.5 per cent Zinc sulphate +0.25 per cent lime should be applied after the appearance of deficiency symptoms. First irrigation should be given at 45 days and second, if needed, at pod filling stage. This genotype has good worth as a donor in future fieldpea breeding programme towards development of fieldpea varieties with good level of resistance against rust and in other basic studies.

Reference

- Anonymous (2021) Project coordinators report, (2020-21) All India Coordinated Research Project (AICRP) on MULLaRP, ICAR-IIPR, Kanpur.
- Parihar AK, A Bohra and GP Dixit (2016) Nutritional Benefits of Winter Pulses with Special Emphasis on Peas and Rajmash. In: (ed. Singh et al 2016) Biofortifications of food crops, Springer publication, pp 61-71.
- Parihar AK, GP Dixit, A Bohra, DS Gupta, AK Singh, N Kumar, D Singh and NP Singh (2020a) Genetic Advancement in Dry Pea (*Pisum sativum* L.): Retrospect and Prospect. In: (Eds SS Gosal and SH Wani) Accelerated Plant Breeding, Volume 3, Springer, Springer Nature, Switzerland, pp 283-341.
- Singh D, AK Gupta, AK Singh, AK Singh and S Kumar (2015) Evaluation of field pea germplasm against rust disease caused by *Uromyces viciae fabae* de bary in glass house and field conditions. *Bangladesh J. Bot.* 44: 443–449. doi: 10.3329/bjb.v44i3.38552
- Upadhyay AL and VK Singh (1994) Performance of pea varieties/lines against powdery mildew and rust. *Indian J. Pulses Res.* 7, 92–93.
- Barilli E, JC Sillero, M Fernández-Aparicio and D Rubiales (2009a) Identification of resistance to *uromyces pisi* (pers) wint. in *Pisum* spp. germplasm. *Field Crop Res.* 114: 198- 203. doi: 10.1016/j.fcr.2009.07.017
- Rubiales D, JC Sillero and AA Emeran (2013) Response of vetches (*Vicia* spp) to specialized forms of *Uromyces vicia-fabae* and to *Uromyces pisi*. *Crop Prot.* 46: 38-43. doi: 10.1016/j.cropro.2012.12.011
- Xue AG and TD Warkentin (2001) Reaction of field pea varieties to three isolates of *Uromyces fabae*. *Can. J. Plant Sci.* 82: 253–255. doi: 10.4141/ P01-105
- Chand R, CP Srivastava, BD Singh and SB Sarode (2006) Identification and characterization of slow rusting components in pea (*Pisum sativum*). *Genet. Res. Crop Evol.* 53: 219–224. doi: 10.1007/s10722-004-6149-2
- Barilli E, JC Sillero, A Serrano and D Rubiales (2009c) Differential response of pea (*Pisum sativum*) to rusts incited by *Uromyces viciae-fabae* and *U. pisi*. *Crop Prot.* 28: 980– 986. doi: 10.1016/j.cropro.2009.06.010
- Das A, AK Parihar, D Saxena, D Singh, KD Singha, KPS Kushwaha, R Chand, RS Bal, S Chandra and S Gupta (2019) Deciphering Genotype-by- Environment Interaction for Targeting Test Environments and Rust Resistant Genotypes in Field Pea (*Pisum sativum* L.). *Front. Pl. Sci.* 10: 825. doi: 10.3389/fpls.2019.00825

53. DRMR 2018-37 (IC0640707; INGR21228), an Indian mustard (*Brassica juncea*) germplasm with white rust resistance

HS Meena*, PD Meena, VV Singh, KH Singh, Arun Kumar, BL Meena, HK Sharma, AK Thakur, MD Meena and PK Rai

ICAR-Directorate of Rapeseed Mustard Research, Bharatpur-321021, Rajasthan, India

*Email: singh_hari2006@yahoo.co.in

Indian mustard (*B. juncea* L.) is an important oilseed crop of the Indian subcontinent and contributes more than 80% of the total rapeseed-mustard production of the country. It has significant role in edible oil economy of India and perform amazing role in human and animal diet. It is cultivated under a wide range of cropping systems and principally grown as a winter (*Rabi* season) crop generally on conserved moisture or through pre-sowing irrigation. Rapeseed-mustard crops affected by several diseases at different growth stages cause high yield losses. Hence, a wide gap exists amongst the potential and realized yield at

the farmers' field. White rust is a major disease of *Brassica*, prevalent worldwide and causes high yield reductions of Indian mustard under severe conditions. The conventional management of using chemical pesticides is very difficult in mustard crop and a problem of reduced efficacy of pesticide arises due to development of resistance by pathogen. Thus, development of disease resistant varieties is the best approach to minimize the yield losses. Therefore, it is highly needed to have good sources of white rust resistance that can be exploited for development high-yielding resistant varieties.

The genotype DRMR 2018-37 was derived from a cross between DRMR 2019 x NRCDR 2 at ICAR-DRMR, Bharatpur. This genotype was isolated as a pure line through pedigree selection and found promising for white rust resistance. It was screened under AICRP-RM plant pathological trials during 2018-19 to 2020-21 at 6-12 locations under natural and artificial conditions. Further, it was also screened at Bharatpur during main *Rabi* season (2018-19 & 2019-20) and during off-season *Kharif* (2018 & 2019) at IARI Regional station, Wellington (Hot spot for white rust), Tamilnadu. White rust resistance of the proposed genotype was also confirmed through molecular markers (At541560 and At2g36360). Pooled summary over the years and locations indicates that proposed genotype DRMR 2018-37 has least WR disease severity (%), zero stag head (%) and revealed

immune reaction at hot spot as compared to resistant and susceptible checks (Table 1). The proposed genetic stock DRMR 2018-37 was found to possess AcB1-A5.1 WR resistant locus. Therefore, genotype DRMR 2018-37 revealed high resistance against white rust at both molecular and phenotypic level and it can be utilized in breeding programmes for development of high-yielding white rust resistant varieties. Genotype DRMR 2018-37 will be a very good addition to existing gene pool in germplasm repository for white rust resistance. Hence, this promising line needs protection through germplasm registration.

References

Annual Report (2018, 2019, 2020 & 2021) ICAR-Directorate of Rapeseed-Mustard Research, Sear, Bharatpur-321303 (Rajasthan).

Table 1: Pooled summary of reaction over the years on DRMR 2018-37 and checks to white rust under natural & artificial conditions in AICRP-RM pathological trials during 2018-19 to 2020-21 and at Wellington during *Kharif* 2018 & 2019

Entries	WR Severity (%)		Stag head (%)		WR (Scale: 0-9)
	Natural conditions (12)	Artificial conditions (6)	Natural conditions (7)	Artificial conditions (3)	Wellington (Hot spot for WR)
DRMR 2018-37	5.1	8.1	0.0	0.0	0
BIOYSR (RC)	19.2	11.8	7.1	19.9	3
Rohini (SC)	29.8	35.1	18.3	20.8	9

*Values in parenthesis representing the number of locations

54. PBS 29079B (IC0642010; INGR21229), groundnut (*Arachis hypogaea* subsp. *hypogaea*) germplasm with high hundred kernel weight (85.36 g)

Kona Praveen^{1*}, Gangadhara K², Ajay BC¹, Narendra Kumar¹, SK Bera¹, AL Rathnakumar³, Radhakrishnan T¹, Kirti Rani¹, Dagla MC⁴, Hariprasanna K⁵, Manivel P⁵, Mathur RK⁷, Chuni Lal⁸ and HK Gor¹

¹ICAR-Directorate of Groundnut Research, Junagadh-362001, Gujarat, India

²ICAR- CTCRI Research Station, Kandukur-534456, Andhra Pradesh, India

³ICAR-Indian Institute of Oilseeds Research, Hyderabad-500030, Telangana, India

⁴ICAR-Indian Institute of Maize Research, Ludhiana -141004, Punjab, India

⁵Centre for Rabi Sorghum, ICAR-IIMR, Solapur-413006, Maharashtra, India

⁶CTRI, Research Station, Vedasandur-624710, Tamil Nadu, India

⁷ ICAR-Indian Institute of Oil Palm Research, Pedavegi-53450, Andhra Pradesh, India

⁸ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

*Email: kona.praveen@icar.gov.in

Kernel with good quality attributes determines the export potential of groundnut. Large/bold seed with high hundred kernel weight (>55 g) coupled with some quality attributes is one of the major prerequisite for exploiting any groundnut variety for confection purpose (Nigam *et al.*, 1989; Dwivedi and Nigam, 1995). At ICAR-Directorate of Groundnut Research, Junagadh a novel advanced breeding line of groundnut, PBS 29079B was developed from the cross Somnath x J 11 using pedigree method.

It is a Virginia runner with decumbent growth habit and semi spreading type. It bears alternate flowering with compound inflorescence. Leaves are dark green with ovate shape and less hairy. Pods are medium reticulated with shallow constriction and slightly beaked and tan seed colour. It recorded significant difference for seed characters like hundred kernel weight (HKW), kernel length (KL), kernel width (KW) when compared with checks, RG 599-3, Mallika and Girnar 2 over 2018 to 2020 year seasons (Table 1). At

Bikaner it recorded large mean seed size (HKW -121.9 gm; KL- 2.21 cm and KW- 1.03 cm) with moderate oil (48%) and high protein 30.39%) in two seasons. The overall mean for seed size in four seasons is 85.36 g of HKW, 1.84 cm of KL and 0.88 cm of KW.

In addition to seed size this line contains good amount of protein (30%) and moderate oil (45-48%). It is highly suitable for confection purpose and gives good yield under sandy soils especially in Rajasthan. General package of practices for large seed groundnut crop production are applicable to this advanced breeding line production.

References

- Dwivedi SL and SN Nigam (1995) Breeding for improved seed quality in groundnut (*Arachis hypogaea* L.) with special reference to export promotion: issues and opportunities. Paper presented at workshop on Status of Confectionery Groundnut Research in India and Strategies for Export Promotion 28-29 April 1995. BARC, Trombay, India.
- Nigam SN, SL Dwivedi, LJ Reddy and MJ Vasudeva Rao (1989) An update on groundnut breeding activities at ICRIAT centre with particular reference to breeding and selection for improved quality. Proceedings of the Third Regional Groundnut Workshop, held during 13-18 March 1988, Lilongwe, Malawi, pp 115-25.

Table 1: Comparison of PBS 29079B genotype with best check over seasons for different traits

	HKW	KL	KW			HKW	KL	KW	% of superiority over check
<i>Kharif, 2018</i>									
PBS29079B	79.64	1.98	0.99	Best Check	Mallika	54.36	1.35	0.8	31.74
<i>Summer, 2019</i>									
PBS29079B	71.27	1.81	0.93	Best Check	GJGHPS1	51.33	1.61	0.8	27.97
<i>Kharif, 2019</i>									
PBS29079B									
Junagadh	73.2	1.71	0.74	Best Check	Mallika	49.04	1.69	0.69	33.00
Bikaner	121.97	2.26	1.03		RG559-3	87.44	1.92	0.94	28.31
<i>Summer, 2020</i>									
PBS29079B	72.69	1.92	1.12	Best Check	GJGHPS1	54.35	1.6	0.94	25.23
<i>Kharif, 2020</i>									
PBS29079B									
Junagadh	75.33	1.7	0.8	Best Check	Mallika	52.33	1.6	0.73	30.53
Bikaner	121.97	2.17	1.06		RG559-3	88.33	1.98	0.89	27.58

55. M-571 (IC0642011; INGR21230), a dwarf pistillate line of castor (*Ricinus communis*) condensed internodes, convergent branching, cup shaped leaves and loose spike showing resistant to *fusarium* wilt and leafhopper

C Lavanya*, Santhalakshmi PM and Duraimurugan P

ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500030, Telangana, India

*Email: c.lavanya@icar.gov.in

M-571 is an S type pistillate line developed through mutation breeding using gamma ray irradiation of VP-1 seed followed by pedigree method of selection for wilt resistant pistillate line in wilt sick plot. Morphological characters were recorded as red stem color, triple bloom, condensed internodes, 10-15 nodes to primary, cup shaped leaves, convergent branching, conical, long (45-50 cm) spike with loose capsules, pistillate with ISF, spiny capsules (Lavanya and Gopinath, 2008). It is distinct to other registered pistillate lines like IPC-15 (INGR 19017) with papaya leaf type and DPC-16 (INGR 140003) with purple stem and zero bloom.

M-571 is also a good combiner for number of effective spikes per plant (Lavanya and Chandramohan, 2003, Lavanya *et al*, 2006) and used for development of several high yielding experimental castor hybrids. Castor wilt (*Fusarium oxysporum* f. sp. *ricini* Nanda and Prasad) is the most important disease of castor resulting in 30-100% loss of plant population in wilt endemic areas where mono-cropping is followed without crop rotation. Screening of M-571 consecutively for three years (2013-14, 2014-15 and 2018-19) at IIOR-Hyderabad in wilt sick plot using standard screening procedures used in AICRP on castor indicated <10% to <20% wilt incidence (Santhalakshmi *et al*, 2016).

M-571 also showed resistant reaction to leafhopper (hopper burn grade of 0 to 1 on 0–4 scale, while susceptible check DPC-9 recorded maximum hopper burn grade of 4 consecutively for two years (2013-14 and 2014-15) at ICAR-IIOR, Hyderabad. Screening at three hot spot locations-IIOR, Hyderabad, Palem (Telangana) and Yethapur (Tamil Nadu) during 2015-16 revealed resistant reaction of M-571 with hopper burn grade of 1 on 0–4 scale and low infestation of leafhopper (7.4 to 35.3 leafhoppers/ 3 leaves/plant) in all three locations. Susceptible checks (DCS-107, DCH-177 and DPC-9) recorded susceptible reaction of 3-4 hopper burn grade and high infestation of leafhopper (40.2 to 84.9 leafhoppers/3 leaves/plant) (Source: DOR/IIOR Annual Report, 2013-14 to 2015- 16).

56. IC0610001-60/Pune 2 (INGR21231), an oil palm (*Elaeis guineensis*) germplasm with Short stature (28.9 cm), high FFB (243.91 kg) and more number of bunches

Bhagya HP^{1*}, RK Mathur¹, G Ravichandran¹, P Murugesan², K Sunil Kumar², D Ramajayam³, Anitha P¹, B Kalyana Babu¹, G Somasundaram⁴ and SN Rahana⁴

¹ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India

²ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India

³ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India

⁴ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India

*Email: Bhagya.HP@icar.gov.in

Oil palm is very important crop for fulfils the edible oil requirement of our country. As compared to other annual oil yielding crop this is giving more oil yield (5-6 t/ha). Oil palm breeding programme mainly depending male (sterile *Pisifera*) and female parent (fertile *Dura*) for hybrid seed production. Commercial material for farmer cultivation is *Tenera*, this can be obtained by crossing of fertile *Dura* and sterile *Pisifera*.

Harvesting is a major problem in oil palm plantation due to more height of the palm, upto 15 years we can easily harvest by using chisel and aluminium pole. After 20-year plantation by using poles we can harvest but risk factors are more due to unbalancing of pole and chances of falling bunches on person and identification of right stage of ripening etc. If we develop low height increment hybrids, life of plantation can be extended for few years instead of uprooting plantation. For developing low increment *Tenera* hybrid, we need low height increment *Dura* genotype and dwarf *pisifera*. But dwarf *pisifera* is very rare, so we have to select elite *dura* with low height increment will lead to development of dwarf

References

- Santalakshmi MP, E Bharathi, C Lavanya and AJ Prabakharan (2016) Parental lines and advanced breeding material of castor resistant to wilt disease. *Ind. Phytopath.* 69(4): 721-723.
- Lavanya C and V Gopinath (2008) Inheritance studies for morphological characters and sex expression in pistillate lines of castor (*Ricinus communis* L.). *Indian J. Genet.* 68(3): 275-282.
- Lavanya C and Y Chandramohan (2003) Combining ability and heterosis for seed yield and yield components in castor (*Ricinus communis* L.). *J. Oilseeds Res.* 20(2): 220-224.
- Lavanya C, PV Ramanarao and V Venkata Gopinath (2006) Studies on combining ability and heterosis for seed yield and yield components in castor, *Ricinus communis* L. hybrids. *J. Oilseeds Res.* 23(2): 174-177.

hybrids. By this we can improve the yield and hasten the life of plantation and harvesting can be made easy. More number of bunches and high yield genotypes are ideal for developing dwarf hybrids for commercial production. This identified genotype is belonging to base collected germplasm from ICAR-IIOPR and it is 28.9 cm annual height increment with high FFB yield of 243.91 kg and total dry matter of 364.56 kg and more number of bunches (14) (Table 1). So this *dura* will serve as base genetic material for development of mother *dura* blocks for commercial production of *Tenera* hybrid in oil palm breeding programme.

References

- Bhagya HP, B Kalyana Babu, PM Gangadharappa, BN Mahantesha, Naika, D Satish and RK Mathur (2020) Identification of QTLs in oil palm (*Elaeis guineensis* Jacq.) using SSR markers through association mapping. *J. Genetics.* 99:19. <https://doi.org/10.1007/s12041-020-1180-4>.
- Bhagya HP and P Anitha (2021). Identification of elite genotype in germplasm block. *ICAR-IIOPR News.* 25(2): 3

Table 1: Trait description accession: IC061001-60 (Pune-2)

Traits	2015-16	2016-17	2018-19	Average
Annual height increment (cm)	28.28	28.06	30.37	28.90
Number of bunches	14	14	11	13
FFB yield (Kg/palm/year)	267	267.48	197.26	243.91
Average bunch weight (kg)	19.07	19.11	17.93	18.76
Total Dry matter (kg)	372.88	357.37	363.43	364.56

57. IC0610001-59/Pune 1 (INGR21232), an oil palm (*Elaeis guineensis*) germplasm with low annual height increment (25.25cm) and high FFB (211.33 kg)

Bhagya HP^{1*}, RK Mathur¹, G Ravichandran¹, P Murugesan², K Sunil Kumar², D Ramajayam³, Anitha P¹, B Kalyana Babu¹, G Somasundaram⁴ and SN Rahana⁴

¹ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India

²ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India

³ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India

⁴ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India

*Email: Bhagya.HP@icar.gov.in

Oil palm is very important crop for fulfils the edible oil requirement of our country. As compared to other annual oil yielding crop this is giving more oil yield (5-6 t/ha). Commercial material for farmer cultivation is *Tenera* due to high mesocarp and high oil content. Now a day's demand for the edible oil is increasing and it's very difficult to fulfil by any other oil yielding crops, but there is a chance to reduce the import of oil from other country by increasing the oil palm yield by using elite germplasm material. If yield of the oil palm is increasing, definitely oil yield also will increase. For this we need high yielding *Tenera* genotypes and also low height increment genotypes due to harvesting problem after 15 to 20 year of plantation.

Fertile *Dura* (Female parent) and Sterile *Pisifera* (Male parent) are very important for commercial production of *Tenera* seedlings for commercial plantation. Sterile *Pisifera* population is scarce and we need to develop and maintain in field genebank for pollen collection. For getting *Pisifera* population also need to go for *Tenera* selfing, by selfed bunches, 1:2:1 ratio *Dura*, *Tenera* and *Pisifera* population will obtain. In this, sterile *Pisifera* can be identified and these can be utilized in breeding programme for commercial

Tenera production. *Tenera* X *Pisifera* crossing can be made to obtain 1:1 ratio of *Tenera* and *Pisifera* population and by this also we can select sterile *Pisifera* for utilization in breeding programme as male parent. These types of elite *Tenera* genotypes can be directly used in multiplication by tissue culture for getting true to type plants once the tissue culture protocol standardized. This identified genetic stock is having annual height increment of 25.25 cm with high FFB yield of 211.33 kg per palm per year (30.22 t/ha) and high average bunch weight of 23.48 kg/palm/year (Table 1). So elite *Tenera* genotypes can be used in T X T, T X P for production of *Pisifera* and direct multiplication by vegetative method (Tissue culture) for production of uniform saplings.

References

- Bhagya HP, BK Babu, PM Gangadharappa, Mahantesha, BN Naika, D Satish and RK Mathur (2020) Identification of QTLs in oil palm (*Elaeis guineensis* Jacq.) using SSR markers through association mapping. *J. Genetics*. 99: 19. <https://doi.org/10.1007/s12041-020-1180-4>.
- Bhagya HP and AnithaP (2021) Identification of elite genotype in germplasm block. ICAR-IIOPR News. 25(2): 3

Table 1: Trait description Accession: IC061001-59 (Pune-2)

Traits	2015-16	2016-17	2018-19	Average
Annual height increment (cm)	25.17	25.16	25.20	25.29
Number of bunches	11	11	10.33	9
FFB yield (Kg/palm/year)	274	274.89	253.40	211.33
Average bunch weight (Kg)	24.90	24.99	24.45	23.48
Total Dry matter (kg)	346.46	306.83	319.61	305.55

58. IC0610051-71/TG 9 (IC0610051; INGR21233), an oil palm (*Elaeis guineensis*) germplasm with high yield (261.71kg), more number of bunches (16.66)

Bhagya HP^{1*}, RK Mathur¹, G Ravichandran¹, P Murugesan², K Sunil Kumar², D Ramajayam³, Anitha P¹, B Kalyana Babu¹, G Somasundaram⁴ and SN Rahana⁴

¹ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India

²ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India

³ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India

⁴ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India

*Email: Bhagya.HP@icar.gov.in

Oil palm (*Elaeis guineensis* Jacq.) is monocious and highly cross pollinated crop and in this crop fruit forms are very important and it is having mainly 3 fruit forms viz. *Dura*, *Tenera* and *Pisifera*. *Dura* is mainly used as female parent and *pisifera* is used as male parent for development of thin shell *Tenera* hybrid for more oil yield and *Tenera* is commercially cultivated variety throughout the world. *Dura* is mainly used as mother palm in production of hybrid in oil palm breeding programme. In germplasm block we have evaluated and found high yielding *dura* with 37.42 tonnes/ha Fresh Fruit Bunches (FFB) yielding genotype with more number of bunches (16.66) and oil to bunch ratio 20.78 %. As per minimum standards of oil palm mother palm selection these all traits were high and it is elite genotype for development of mother seed garden for improving yield and development of high yielding hybrids. For selection of *dura* unknown sources should be 18 % oil to bunch ratio and FFB yield should be 220 kg/palm/year (Table 1).

This *dura* genotype is also having other morphological traits like high TDM (305.55 kg) and average bunch weight (15.73 kg) with bunch index was 0.43. This base material for production of mother *dura* blocks for production of dwarf *Tenera* hybrids with high FFB yield for commercial production to fulfil the requirement of planting material supply to the farmers field and it will help in fulfil the

requirement of edible oil in our country and can reduce the import of oil from other countries. This dwarf trait can be utilized in further breeding programme. This genotype already utilizing in breeding programme for development of *dura* mother palms.

Reference

- Annual Report (2019) (Eds: Dr. R K Mathur, Dr. K Suresh, Mrs. A. Bhanusri, Dr. B Kalyana Babu, Dr. K Manorama and Dr. P. Anitha) Research achievements- Collection, Conservation, Cataloguing and evaluation of oil palm germplasm. ICAR-Indian Institute of oil palm Research Pedavegi. pp 19-22.
- Bhagya HP, BK Babu, PM Gangadharappa, Mahantesha, BN Naika, D Satish and RK Mathur (2020) Identification of QTLs in oil palm (*Elaeis guineensis* Jacq.) using SSR markers through association mapping. *Journal of Genetics*. 99: 19. <https://doi.org/10.1007/s12041-020-1180-4>.

Table 1: Trait Description Accession: IC0610051-71 (*Dura*)

Trait	2015-16	2016-17	2018-2019	Average
Number of bunches	16	18	16	16.66
FFB yield (kg/palm/year)	238.47	269.48	277.18	261.71
Average Bunch Weight (Kg/palm)	14.90	14.97	17.32	15.73
Bunch Index	0.48	0.45	0.37	0.43
Oil to Bunch ratio	21.73	19.84	20.79	20.78

59. Jor Lab SM-2 (IC0642007; INGR21234), a taro (*Homalomena aromatica*) germplasm with high rhizome essential oil yield (1.20%dwb) basis

Mohan Lal

CSIR-North East Institute of Science and Technology, Jorhat-785006, Assam, India

*Email: drmohanlal80@gmail.com

Homalomena aromatica Schott., commonly known as 'Sugandhmantri' due to its aromatic nature belongs to the family Araceae (Roy *et al.*, 2019). Essential oil of *H. aromatica* has several applications in perfumery, flavour, and pharmaceutical industries. The essential oil of aromatic rhizomatous plants possesses numerous biological activities like larvicidal, nematicidal, anti-inflammatory, antimicrobial, antidepressant, antioxidant, anti-helmintic, etc (Lal *et al.*, 2021). Similarly, the rhizome of *H. aromatica* was reported to possess various medicinal properties like anti-inflammatory, analgesic, antiseptic, antidepressant, skin infections, joint pain, sedative, etc (Policegoudra *et al.*, 2012; Kehie *et al.*, 2017).

The aim and objective of the present study was to identify high and stable essential oil-rich genotype from collected germplasm of *H. aromatica*. During the year 2014, a total of 49 germplasm were collected from different parts of NE India. All the collected germplasm was planted in the year 2015 with three replications in CRBD at the experimental farm of

CSIR- NEIST, Jorhat. The same genotypes were again planted during 2017 with the same design. All the agronomical and essential oil data were recorded and analyzed. Based on two crops season (2015-16 and 2017-18) of the selection trial, a new essential oil 1.20% rich strain (RRLJ HA-18) with a high dry rhizome yield of 1454.53 kg/ha/crop season was selected. The identified accession was later renamed as Jor Lab SM-2. The stability of the identified germplasm (RRLJ HA-18) was confirmed by testing in multilocation trial in four different locations for two years i.e., one crop season (2019-2020) along with two check varieties. The stability analysis for the economic character like dry rhizome yield, essential oil% and total essential oil yield/ha showed the high mean value and were stable in all the four locations with $\beta_1=1.05$, $\beta_2=1.09$, and $\beta_3=1.14$ respectively (Table 1a, 1b). The GC/MS profiling of the essential oil extracted from the rhizome of *H. aromatica* revealed linalool (66.27%) major compounds followed by α -cadinol, τ -muurolol, linalool oxide, neointermedeol, and 3-carene as other compounds. The stable germplasm Jor Lab

Table 1(a): Estimation of mean and stability parameters of plant height, number of leaf per plant, leaf width, leaf length, length of rhizome and fresh rhizome genotype (Jor Lab SM-2) of *H. aromatica* in MLT trials

Genotypes	Plant height (cm)			Number of leaf/plant			Leaf width (cm)			Leaf length (cm)			Length of rhizome (cm)			Fresh rhizome weight/plant (gm)		
	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$
Jor Lab SM-2	75.41	0.95	-	16.84	1.26***	0.40	20.78	1.05	0.19	28.11	0.79**	0.16	32.38	1.93**	0.18	183.95	0.94	2.26***
Mizoram local	72.92	1.01***	0.35***	13.50	1.06***	0.41	20.99	0.65*	-	25.52	1.07***	0.55***	22.95	0.47*	0.61**	149.98	1.08***	2.16***
Tura local	70.81	1.04***	0.36***	12.29	0.68***	0.42	19.99	1.30***	-	24.76	1.14***	0.14	22.41	0.60***	1.06***	125.59	1.08***	1.99***
Population mean	73.05			14.03			20.59		0.23	26.13			25.91			153.17		

*Significant at P<0.10, **Significant at P<0.05, *** Significant at P<0.01

Table 1(b): Estimation of mean and stability parameters of dry rhizome recovery, rhizome diameter, fresh rhizome yield, dry rhizome yield, essential oil yield% and total essential oil yield/ha of genotype (Jor Lab SM-2) of *H. aromatica* in MLT trials

Genotypes	Dry rhizome recovery (%)			Rhizome diameter (cm)			Fresh rhizome yield (kg/ha)			Dry rhizome yield (kg/ha)			Essential oil yield (%)			Total essential oil yield/ha on dry weight basis (kg/ha)		
	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$	μ	β_i	$\sigma^2 di$
Jor Lab SM-2	18.89	0.90	0.64***	5.12	0.58**	0.01	7725.69	0.97	12157.06	1458.86	1.05	85.86	1.20	1.09	0.00	1753.98	1.14	47.07
Mizoram local	17.24	0.93***	0.55***	4.26	1.22***	0.00	6299.06	0.93**	10634.34	1086.83	1.65**	60.95***	0.55	1.35*	0.00	598.95	0.42	525.51*
Turalocal	16.90	1.17***	0.42***	4.12	1.20***	0.02***	5274.57	1.17**	13322.19***	890.64	0.91*	257.60	0.51	1.06***	0.00	452.69	0.88	646.35***
Population mean	17.68			4.50			6433.11			1145.44			0.75			935.20		

*Significant at P<0.10, **Significant at P<0.05, *** Significant at P<0.01

SM-2 was found to be more than twice superior compared to the check varieties in terms of essential oil yield. All the studied traits of Jor Lab SM-2 were significantly and distinctly higher than the check varieties. As per our knowledge, no essential oil-rich variant of *H. aromatica* is reported so far; therefore, this is the first report on the identification of a superior and stable line of *H. aromatica*.

References

Roy SJ, PS Baruah, L Lahkar, L Gurung, D Saikia and B Tanti (2019) Phytochemical analysis and antioxidant activities of *Homalomena aromatica* Schott. *J. Pharmacogn. Phytochem.* 8(1): 1379-1385.

Lal M, S Munda, T Begum and SK Pandey (2021) Identification of a Stable Rhizome Essential Oil-Rich Variety (JorLab SM-2) of *Homalomena aromatica* Schott., Through Biometrical Method, *J. Essent. Oil. Bear. Plants.* (24) doi: 10.1080/0972060X.2021.1995510

Policegoudra RS, S Goswami, SM Aradhya, S Chatterjee, S Datta, R Sivaswamy, P Chattopadhyay and L Singh (2012) Bioactive constituents of *Homalomena aromatica* essential oil and its antifungal activity against dermatophytes and yeasts. *J. Mycol. Med.* 22: 83- 87.

Kehie M, P Kehie and NL Pfoze (2017) Phytochemical and ethnopharmacological overview of endangered *Homalomena aromatica* Schott: An aromatic medicinal herb of Northeast India. *Indian J. Nat. Prod. Resour.* 8(1): 18-31.

60. DBM-4 (IC0642012; INGR21235), a brahmi (*Bacopa monnieri*) germplasm with high Bacoside-A content and API quality parameters

Parmeshwar Lal Saran*, Hiteksha I Damor, Manish Kumar Suthar and Kuldeep singh A. Kalariya

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

*Email: plsdehradun@gmail.com

Jal brahmi (*Bacopa monnieri* L. Pannell) is a creeping, branched succulent perennial herb belonging to family *Plantaginaceae* used in indigenous system of medicine as a nerve tonic and for epilepsy and insanity. Owing to its inherent potential of enhancing memory and vitality, this miracle plant is gaining attention globally for its commercial cultivation. 'DBM-4' is diverse in morphological, qualitative and molecular characters (DMAPR Annual report, 2020). Distinct character like maximum pedicel length (2.80-2.97 cm) was observed as morphological marker as compared to check (Cim Jagriti); Saran *et al.*, 2022; Saran and Damor, 2021; DMAPR Annual report 2020). It also contains maximum Bacoside-A (2.64-3.65 % W/W) and Total Bacosides (5.27% w/w) content in dry herbage. Maximum bacoside-A content in DBM-4 (3.65% W/W) and minimum was recorded in CIM Jagriti (1.82% W/W) on dry weight basis (Saran *et al.*, 2022; Saran and Damor, 2021; DMAPR Annual report 2020). DBM-4 with the distinct morphological and chemical traits was developed through selection method and conservation carried out at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The herb is the small creeping type prostate with the numerous succulents, glabrous branches. The leaves of herb are oblanceolate, relatively thick, succulent and arranged oppositely on the stem/stolon. Small, actinomorphic flowers are borne in leaf axils, which are whitish purple to medium purple in colour with maximum of flower-stalk length. Further, morphological variation also observed for stolon colour, stolon length and stolon thickness in different accessions of Jal brahmi. Other important quality parameters as per Ayurvedic Pharmacopoeia of India (API) like minimum loss of drying (11.13%W/W), total ash (8.38%W/W), acid soluble ash (0.20%W/W) were higher in DBM-4. At the same

time maximum alcohol soluble extractive (14.75% W/W) and water-soluble extractive (28.57% W/W) was observed (Saran *et al.*, 2022).

Jal brahmi grow well in low lying area having poorly drained soils under subtropical area, especially in rice growing regions. It is cultivated through vegetative propagation using soft herbaceous cuttings (Saran and Patel, 2019). In north India, Jal brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. For planting one-hectare area on an average 3-3.5 quintals herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes are transplanted directly in the field at spacing of 10x10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On an average 130-145 q ha⁻¹ dry herbage can be obtained from a multiple harvest (Saran, 2020). The accession DBM-4 was found suitable for commercial cultivation in low-lying rice-wheat cultivation systems and farmers can get approximately Rs. 4.62 lakhs ha⁻¹ year⁻¹ net return.

References

ICAR-DMAPR Annual Report, (2020) <https://dmapr.icar.gov.in/Publications/AnnualReport/E%20Annual%20Repor%202020.pdf>

Saran PL and RB Patel (2019) Plastering technique: An easy and cost-effective way of *Bacopa monnieri* L. Pannell multiplication, *Academic J. Med. Plants.* 7(8): 181-186.

Saran PL (2020) "Jal brahmi ki kheti" Extension Bulletin 17, pages 28, Published by Director, ICARDMAPR, Anand, Gujarat ([http://dmapr.icar.gov.in/Publications/Bulletine/ialb hramibulletin.pdf](http://dmapr.icar.gov.in/Publications/Bulletine/ialb%20hramibulletin.pdf)).

Saran PL and HI Damor (2021) Morphogenetic diversity in DBM-4 accession of jal brahmi. *Indian Horti*, May-June 2021.

Saran PL, HI Damor, DH Lodaya, MK Suthar, KA Kalariya and S

Roy (2022) Identification of potential accessions of *Bacopa monnieri* L. for herbage yield and bacosides A content. *Ind. Crops Prod.* 176: 114348.

61. DBM-2 (IC0642013; INGR21236), a brahmi (*Bacopa monnieri*) germplasm with Curved/Twisty top leaf of stolon and rich in bacopaside I

Parmeshwar Lal Saran^{1*}, Hiteksha I Damor¹, Susheel Singh², Kuldeepsingh A Kalariya¹ and Manish Kumar Suthar¹

¹ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

²Food Quality Testing Laboratory, N.M. College of Agricultural, NAU, Navsari, Gujarat, India

*Email: plsdehradun@gmail.com

In India, brahmi has been largely used as a rejuvenating herb for the last 3000 years. In Ayurvedic systems, brahmi is applicable for promoting mental strength (Balya), longevity (Ayushya), life energy (Jivaniya) and Sleep (neendranjan). A distinct morphological character “curved leaf at top of the stolon” and “maximum size or area of basal leaf” identified in DBM-2 (1.653 cm²) which is minimum in CIM Jagriti (0.736 cm²) as a morphological marker (Saran et al., 2021; Saran and Damor, 2021). At the same time, the germplasm “DBM-2” reported maximum bacopaside I (1.50% w/w) from total herbage as compared CIM Jagriti (0.65% w/w) using HPLC analysis. DBM-2 with the distinct morphological and chemical traits was developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The Jal brahmi herb is the small creeping type prostate with the numerous succulents, glabrous branches. Different morphological parameters including solitary axillary flowers (five petals) with sessile, succulent and thick leaves grown appositively on stem having different leaf size (Maximum basal leaf area), leaf shape (Oblanceolate), leaf apex (Obtuse) and leaf base (Acuminate type), leaf colour (medium dark green) and flower colour (Purple colour). Further, morphological variation also observed for stolon colour, stolon length, stolon thickness and flower pedicel length in different accessions of Jal brahmi.

Jal brahmi grow well in low lying area having poorly drained soils under subtropical area, especially in rice growing regions. It is cultivated through vegetative propagation using soft herbaceous cuttings (Saran and

Patel, 2019). It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran et al., 2022). In north India, Jal brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. For planting one-hectare area on an average 3-3.5 quintals herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes are transplanted directly in the field at spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On an average 130-145 q ha⁻¹ dry herbage can be obtained from a multiple harvest (Saran, 2020).

References

- Saran PL and RB Patel (2019) Plastering technique: An easy and cost-effective way of *Bacopa monnieri* L. Pannell multiplication, *Acad. J. Med. Pl.* 7(8): 181-186.
- Saran PL (2020) “Jal brahmi ki kheti” Extension Bulletin 17, pages 28, Published by Director, ICARDMAPR, Anand, Gujarat (http://dmapr.icar.gov.in/Publications/Bulletine/ialb_hramibulletin.pdf).
- Saran PL, HI Damor and KA Kalariya (2021) Physiologically diverse morphotypes of *Bacopa monnieri* L. PANNELL. *J. Pl. Dev.* (131): 779-783.
- Saran PL and HI Damor (2021) Morphogenetic diversity in DBM-4 accession of jal brahmi. *Indian Horti*. May-June 2021.
- Saran PL, HI Damor, DH Lodaya, MK Suthar, KA Kalariya and S Roy (2022) Identification of potential accessions of *Bacopa monnieri* L. for herbage yield and bacosides A content. *Ind. Crops Prod.* 176: 114348.

62. DBM-5 (IC0642014; INGR21237), a brahmi (*Bacopa monnieri*) germplasm with Light purple flowers and high Jujubogenin (1.43% w/w) and Bacopaside C (1.29% w/w) content

Parmeshwar Lal Saran^{*}, Hiteksha I Damor, Kuldeepsingh A Kalariya and Manish Kumar Suthar

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

*Email: plsdehradun@gmail.com

Bacopa monnieri (L.) Penn. commonly known as 'Neera Brahmi' belongs to the family *Scrophulariaceae* is a perennial, prostrate, and creeping herb that is identified in habitats including wetlands and muddy shores. Jal Brahmi, a nootropic herb being used as a promising agent in the modern Ayurveda system owing to its antioxidant, cholinergic, anti-beta amyloid property. The evaluated germplasm 'DBM-5' varied in morphology, herbage yield, qualitative as well as quantitative parameters. The germplasm has an exceptionally whitish (light purple) flower colour (Purple 76 D; as compared to Violet 85A in Check as per the RHS colour chart (Saran et al., 2022). The maximum dry herbage yield was recorded in DBM-5 (19.71 t h⁻¹y⁻¹) as compared to check (17.55 t h⁻¹y⁻¹) variety CIM-jagriti (DMAPR Annual Report, 2020; Saran and Damor, 2021; Saran et al., 2022). The growth habit of germplasm is spreading type while check having a semi spreading type branches. The germplasm DBM-5 also contains significantly maximum Jujubogenin (1.43% w/w) and Bacopaside C (1.29% w/w) content as compared to CIM Jagriti (0.35% and 0.56% w/w, respectively). Germplasm DBM-5 having distinct morphological and chemical traits was developed through selection method and conservation of distinct germplasm carried out at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

Jal Brahmi has different morphological parameters including solitary whitish flowers with sessile, oblanceolate, succulent, and relatively thick leaves with larger leaf area, and are arranged oppositely on the stolon. Further, morphological variation was also observed for a number of stolons, stolon length, and stolon thickness in different accessions of Jal Brahmi.

Jal Brahmi performs exceptionally well in poorly drained soils and waterlogged areas under subtropical conditions.

Vegetative cuttings are a suitable propagation technique for commercial cultivation of the Jal Brahmi. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran et al., 2022). In North India, it can grow in a wide range of temperatures (15–40 °C) and soil pH (5–7.5). It becomes dormant during the winter months except when grown in the vicinity of running water. In the south and central India, it can be grown throughout the year. For planting a one-hectare area on an average 3–3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4–5 cm long, each with two-three nodes is transplanted directly in the field at a spacing of 10×10 cm using the plastering method during the month of July–August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On average 130–145 q ha⁻¹ dry herbage can be obtained from multiple harvests (Saran, 2020). Overall, germplasm was found diverse, unique, and rich in quality herbage for commercial cultivation

References

- ICAR-DMAPR Annual Report (2020) <https://dmapr.icar.gov.in/Publications/AnnualReport/E%20Annual%20Repor%202020.pdf>
- Saran PL and RB Patel (2019) Plastering technique: An easy and cost-effective way of *Bacopa monnieri* L. Pannell multiplication, *Academic J. Med. Plants*. 7(8): 181-186.
- Saran PL (2020) "Jal brahmi ki kheti" Extension Bulletin 17, pages 28, Published by Director, ICARDMAPR, Anand, Gujarat (<http://dmapr.icar.gov.in/Publications/Bulletine/ialb%20hramibulletin.pdf>).
- Saran PL and HI Damor (2021) Morphogenetic diversity in DBM-4 accession of jal brahmi. *Indian Horti*. 66(3).
- Saran PL, HI Damor, DH Lodaya, MK Suthar, KA Kalariya and S Roy (2022) Identification of potential accessions of *Bacopa monnieri* L. for herbage yield and bacosides A content. *Ind. Crops Prod*. 176: 1143-48.

63. DBM-10 (IC0642015; INGR21238), a brahmi (*Bacopa monnieri*) germplasm with maximum number of leaves (760.83) and minimum leaf size (0.47-0.48 cm²)

Parmeshwar Lal Saran*, Hiteksha I Damor, Manish Kumar Suthar and Kuldeepsingh A Kalariya

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

*Email: plsdehradun@gmail.com

Brahmi (*Bacopa monnieri* L. Pannell) has been identified as a member of the seven important medicinal plants recommended for immediate attention and included in the list of highly endangered medicinal plants of India. It is also known as 'Herpestis monnieri', 'Jal brahmi', 'water hyssop', 'Neera-brahmi', and 'Jalanimba'. Morphological distinct characters especially a maximum number of leaves (760.83) with minimum leaf size or least leaf area was observed in DBM-10 (0.47-0.48 cm²) as compared to CIM Jagriti (465.83 and 0.55-0.60 cm²), respectively (DMAPR Report 2020; Saran et al., 2021; Saran and Damor, 2021). At the same time the

germplasm "DBM-10" reported diversity for a maximum number of leaves with minimum leaf size after 55 days of transplanting and at full flowering (Saran et al., 2021). DBM-10 with the unique morphological traits and yield associated traits was developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The herb can be grown up to a height of 40 cm with 10-35 cm long branches. It is a tender herb having various branches with rooting at all nodes. The leaves are sessile,

entire, opposite, simple, fleshy, and obscurely veined. Leaves are oblanceolate in shape with 2 cm long and 3 mm broad. In summer fruits and flowers are seems. It has normally light purple-colored flowers.

Jal Brahmi grows well in low-lying areas having poorly drained-water logged soils under subtropical climatic conditions. Normally it is propagated through stem cuttings. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran *et al.*, 2022). In north India, Jal Brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. The leaves under shade conditions made efficient use of the less intense irradiation reaching up to them like *rauwolfia*, patchouli, turmeric, Shatavari, and Brahmi (Saran *et al.*, 2019). For planting a one-hectare area on an average 3-3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes is transplanted directly in the well prepared FYM-rich field at a spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. The herbage portion including stem and leaves are harvested and shade dried. On average 130-145

q ha⁻¹ dry herbage can be obtained from a multiple harvest (Saran, 2020).

References

- Saran PL and RB Patel (2019) Plastering technique: An easy and cost-effective way of *Bacopa monnieri* L. Pannell multiplication. *Acad. J. Med. Pl.* 7(8): 181-186.
- Saran PL, S Singh, VH Solanki, KA Kalariya, RP Meena and RB Patel (2019) Impact of shade-net intensities on root yield and quality of *Asparagus racemosus*: A viable option as an intercrop. *Ind. Crops Prod.* 141: 111740. <https://doi.org/10.1016/j.indcrop.2019.111740>.
- ICAR-DMAPR Annual Report (2020) <https://dmapr.icar.gov.in//Publications/AnnualReport/E%20Annual%20Repor%202020.pdf>
- Saran PL (2020) "Jal brahmi ki kheti" Extension Bulletin 17, pages 28, Published by Director, ICARDMAPR, Anand, Gujarat (http://dmapr.icar.gov.in/Publications/Bulletine/ialb_hramibulletin.pdf).
- Saran PL, HI Damor and KA Kalariya (2021) Physiologically diverse morphotypes of *Bacopa monnieri* L. PANELL. *J. Pl. Dev.* (131): 779-783.
- Saran PL and HI Damor (2021) Morphogenetic diversity in DBM-4 accession of Jal Brahmi. *Indian Horti.* 66(3).
- Saran PL, HI Damor, DH Lodaya, MK Suthar, KA Kalariya and S Roy (2022) Identification of potential accessions of *Bacopa monnieri* L. for herbage yield and bacosides A content. *Ind. Crops Prod.* 176: 1143-48.

64. DBM-13 (IC0642016; INGR21239), a morphotype brahmi (*Bacopa monnieri*) having light green leaf colour, purplish white flower color and low chlorophyll content (0.74-1.07 mg g⁻¹)

Parmeshwar Lal Saran*, Hiteksha I Damor, Kuldeepsingh A Kalariya and Manish Kumar Suthar

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

*Email: plsdehradun@gmail.com

Jal Brahmi (*Bacopa monnieri* (L.) Wettst. is an important prostrate herb belonging to the family *Platanaceae*. It is a diverse family comprising approximately 90 genera and 1900 species. It is precious as a revitalizing herb and used by Ayurvedic practitioners for nearly 3000 years ago. This miracle herb has the inherent potential of enhancing memory and vitality, therefore, gaining attention for its commercial cultivation globally (Saran and Patel, 2019) and required to understand the existing genetic variability for successful retrieval. DBM-13 accession of *B. monnieri* has been identified for variation in morphological characters viz., light green leaf colour (Yellow Green 146B) and purplish-white flower colour (Purple 76B petal with Violet 84C petal veins colour), while check has Green N137C (leaf) and Violet 85A (flower colors) using RHS colour chart in DBM-13 (Saran *et al.*, 2021). For total chlorophyll content, accessions DBM-13 showed the lowest total chlorophyll content (0.74- 1.07 mg g⁻¹) compared to check (0.92-1.50 mg g⁻¹) and among all the studied accessions (Saran *et al.*, 2021). DBM-13 with the

distinct light green colour leaves with the lowest chlorophyll content was identified and developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The Jal brahmi herb is the small creeping type prostate with numerous succulents, glabrous branches. Different morphological parameters including solitary axillary flowers with 0.5 cm to 4.0 cm pedicels length, small-tubular, five-petaled flowers are white-purple in colour. Leaves are sessile, succulent, and thick grown appositively on 40-45 cm long stem with different leaf shape (Obovate), leaf apex (Rounded) and leaf base (Acuminate type). The fruit is oval and sharp at the apex, while seeds are oblong and pale-colored.

The perennial herb performs exceptionally well in poorly drained soils and water-logged areas. Near-neutral, clayey loam to clayey soils is best suited for its growth. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level. It is cultivated

through vegetative mass propagation using soft herbaceous cuttings. In north India, Jal Brahmi can grow in a wide range of temperatures (15–40 °C) and soil pH (5–7.5) at temperatures (30–40 °C) and humidity (65–80%). In south India, it can be grown throughout the year. For planting a one-hectare area on an average 3–3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4–5 cm long, each with two–three nodes is transplanted directly in the well-prepared FYM-rich field at a spacing of 10×10 cm using plastering method during the month of July–August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On average

130–145 q ha⁻¹ dry herbage can be obtained from multiple harvests (Saran, 2020).

References

- Saran PL and RB Patel (2019) Plastering technique: An easy and cost-effective way of *Bacopa monnieri* L. Pannell multiplication, *Acad. J. Med. Pl.* 7(8): 181–186.
- Saran PL (2020) “Jal brahmi ki kheti” Extension Bulletin 17, pages 28, Published by Director, ICARDMAPR, Anand, Gujarat ([http://dmapr.icar.gov.in/Publications/Bulletine/ialb hramibulletin.pdf](http://dmapr.icar.gov.in/Publications/Bulletine/ialb%20hramibulletin.pdf)).
- Saran PL, HI Damor and KA Kalariya (2021) Physiologically diverse morphotypes of *Bacopa monnieri* L. PANNELL. *J. Pl. Dev.* (131): 779–783.

65. Jor Lab CL-1 (IC0642017; INGR21240), a turmeric (*Curcuma longa*) germplasm with high leaf essential oil (1.2%)

Mohan Lal

CSIR-North East Institute of Science and Technology, Jorhat-785006, Assam, India

*Email: drmohanlal80@gmail.com

Curcuma longa, which belongs to the family Zingiberaceae, is an important crop plant having important medicinal properties. India is a leading producer of turmeric. The commercially available material (i.e. turmeric powder) in Europe is obtained mainly from India and somewhat from other south eastern Asian countries (Murugananthi *et al.*, 2008). The essential oil is the one that provides the *C. longa* rhizome a particular spicy and aromatic flavour with its distinctive chemical composition (Saiz, 2014; Luthra *et al.*, 2001). It is reported to possess potential applications in the agri-food industry, such as antimicrobial, weedicide and as food preservative agent (Ibáñez and Blázquez, 2021). The essential oil of this species is rich in various valuable chemical compounds, which are useful for pharmaceutical, industrial as well as food purposes. In this present investigation, a total of 352 germplasm of *C. longa* germplasm were collected from different regions of India, from 2014 to 2016 and planted in RBD design at CSIR-NEIST Jorhat Assam during March, 2016. After two year of the evaluation trial a high leaf essential oil rich germplasm was identified and named as Jor Lab CL-1. To identify the constituents, extraction of leaf essential oil was done using hydro- distillation and GC/MS analysis. The identified germplasm was planted in

multi-location trial, along with the standard check variety during the year 2019. The average leaf essential oil yield of the newly identified germplasm in the five different locations was 1.20%, which is much higher as compared to the check variety that showed essential oil yield of 0.60%. This selected germplasm also showed better agronomical traits in comparison to the check variety as it has an average of 96cm of plant height, 5 number of tillers per plant, 44cm of leaf length, 29% dry rhizome recovery, and fresh rhizome yield of 17.9t/ha. This new identified line was named as “Jor Lab CL –1” and is suitable for commercial cultivation and essential oil production.

References

- Murugananthi D, S Selvam, N Raveendaran and ST Meena (2008) A study on the direction of trade in the Indian turmeric exports: Markov chain approach. *IUP J Agr Econ.* 4: 20–25.
- Saiz de Cos P (2014) Cúrcuma I (*Curcuma longa* L.). *Reduca Ser. Botánica.* 7: 84–99.
- Luthra PM, R Singh and R Chandra (2001) Therapeutic uses of *Curcuma longa* (turmeric). *Indian J. Clin. Biochem.* 16: 153–160.
- Ibáñez MD, MA Blázquez (2021) *Curcuma longa* L. rhizome essential oil from extraction to its agri-food applications. a review. *Pl.* 10(1): 44.

66. IC-625596 (IC0625596; INGR21241), a ber (*Zizyphus mauritiana*) germplasm with small proportion of stone (7%) and excellent blend of high T.S.S. (17-18 °B), acidity (0.35 %) and Vitamin C (51.2 mg/100 gm). Superior in taste and fruit weight (23 gm) compared to stone less landrace (INGR No. 19100)

Vijay Singh Meena^{1*}, Rakesh Bhardwaj¹, RR Sharma², Manoj Mahawar³, VK Sharma⁴ and Kuldeep Singh⁴

¹ICAR-NBPGR Regional Station, Jodhpur-342001, Rajasthan, India

²ICAR-CIPHET, Abohar-152117, Punjab, India

³ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India

⁴ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

*Email: vijay.meena1@icar.gov.in

Ber (*Zizyphus mauritiana* L.) is an indigenous fruit crop grown extensively in arid and semi-arid part of India. Presently, its cultivation is gaining popularity across the country because of its low maintenance cost, ability to grow in saline and drought condition, high nutrition value and high yield and money returns. But, bigger size of stone is major hindrance for its processing. Less proportion of stone is trait of interest and prime need of breeder for improvement of this fruit crop. Hence 12 germplasm (Banarashi Karka, Umran, Chhuhara, Gola, Kaithili, Seb, Jogia, Saharanpur narnaul, Katha Phal, aliganj, Delhi local and IC0625596) of ber maintained at Exp. Station Issapur farm, ICAR-NBPGR, New Delhi were evaluated during 2017-18, 2018-19, 2019-20 and 2020-21 for superior fruit characteristics and chemical analysis under randomized block design (RBD).

A germplasm IC0625596 found promising in term of least stone/ kernel length (2.66 cm) and width (0.6 cm). This accession attained maturity during February with average stone weight (0.63 gm) that is only 7 % compared to more than 20 percent in other genotype. Fruit were oblong in shape

with smooth surface and turn greenish yellow at the time of maturity. Fruit was soft with apex as broadly pointed and pulp colour was white. The pulp to stone ratio found (21.15) which is highly desirable for breeding purpose. It has excellent blend of T.S.S. of 17 °B and acidity (0.35 %) which makes it tasty and juicy over stone less landrace of ber (INGR No. 19100) that consist very small fruits (1-2 gm) which gives gumminess feeling after eating. This accession rich in Vitamin C in (51.2 mg/100 gm), total phenolic content found (201.5 mg GAE/100gm) and antioxidant activity expressed as AOX (11.5 µmol trolor/gm).

References

- Bisla SS and BS Daulta (1986) Studies on variability, heritability and genetic advance for quality traits in ber (*Zizyphus mauritiana* Lamk.). *Haryana J. Horti. Sci.* 15(34): 175-178.
- Godi NS, VR Joshi and VS Supe (2016) Physical fruit characteristics assessment of selected ber (*Zizyphus mauritiana* L.) genotypes. *Int. J. Appl. Res.* 2: 757-61.
- Pareek OP (2001) *Fruits for the Future Ber*. International centre for Underutilized crops, University of Southampton, Southampton UK.

67. CZCM-2001 (IC642018; INGR21242), a carissa (*Carissa carandas*) germplasm with multiple flowering/fruitletting in a year

PR Meghwal and Akath Singh

ICAR-Central Arid Zone Research Institute, Jodhpur-342003, Rajasthan, India

*Email: PR.Meghwal@icar.gov.in

Karonda (*Carissa carandas* L.) is an Indigenous underutilized fruit plant with high phyto-therapeutic and nutritive value. It is a multipurpose plant with ability to grow and sustain in diverse agro-ecological conditions including arid and semi-arid regions. A unique genotype i.e. CZCM-2001 has been identified at Central Arid Zone Research Institute, Jodhpur. It bears flowers and fruits thrice in a year as against single flowering/fruitletting season in other accessions and popular varieties. It may be of more valued due to higher fruit yield and ornamental purposes round the year. The genotype was identified during long term evaluation of karonda germplasm. It is a selection from seedling population of the parent materials originally

collected from one of the home gardens in Jodhpur city of Rajasthan state. In subsequent years, true to type plants were multiplied from single selected plant by air layering where the same trait was confirmed subsequent years.

The data on vegetative growth and fruit yield were recorded in CZCM-2001 along with other accessions and a released variety Pant Manohar (Table1). Since, karonda is basically a spreading bush, there was not much variation in plant height but significant differences in canopy area and fruit yield were recorded with highest value in CZCM-2001. Because of multiple fruitletting, the cumulative fruit yield in CZCM-2001 was higher by 25 to 68 % over the fruit yield of

Table 1: Vegetative growth and fruit yield of CZCM-2001 and other genotypes/variety (7th year onwards)

Genotype	Plant height (m)	Canopy area (m ²)	Fruit yield (kg plant ⁻¹)				
			2012	2013	2014	2015	Mean
CZCM-2001	3.06	7.45	25.60	29.8	26.5	30.1	28.25
CZCM-2021	2.56	6.73	15.52	17.3	16.8	17.5	16.78
CZCM-2022	2.38	5.14	22.2	21.4	22.8	23.7	22.52
CZCM-2031	3.15	6.76	18.20	20.1	22.6	21.2	20.50
Pant Manohar	2.82	6.92	16.80	18.3	23.5	20.2	19.70
CD(p=0.05)	NS	2.1	3.2	3.7	4.6	4.45	

Table 2: Flowering and fruiting pattern and fruit characteristics in CZCM-1 and other varieties/genotypes of karonda

Genotypes	Flowering time	Fruit maturity time	Mean fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	No. of seeds/fruit
CZCM-2001	March-April	June-July	3.50	2.12	1.52	5.10
	July-August	September-October	3.10	2.07	1.65	4.40
	October-November	December-January	3.20	2.18	1.69	4.50
CZCM-2012	March-April	July-August	2.96	2.30	1.83	3.60
CZCM-2021	March-April	July-August	2.76	1.93	1.60	6.60
CZCM-2022	March-April	July-August	4.18	2.25	1.91	4.90
CZCM-2031	March-April	July-August	4.21	2.26	1.96	5.40
Pant Manohar	March-April	July-August	3.34	2.15	1.71	3.50

other genotypes/Pant Manohar which can be attributed to higher canopy area and multiple fruiting. The variation in vegetative growth and fruit yield among different genotypes confirms the earlier publication on karonda (Meghwal *et al.*, 2014 and Meghwal, 2018).

The data on flowering/fruiting frequencies and fruit morpho-physico characteristics (Table 2) of CZMCM-2001 along with other genotypes indicated that except CZCM-2001, all other genotypes had single flowering/ fruiting habit while CZCM-2001 gave flowering/ fruiting three times in a years as depicted Table 2.

The species responds well to air layering for multiplication of cent per cent true to type plant. However, for large scale propagation seeds from ripened fruits can be used for propagation which should be sown immediately after extraction. The planting can be done in July-August or during February-March in blocks or in hedge row for live fencing. Spacing may differ from 3 to 5 meters either way while about 2 m between the plants is kept in hedge. Bearing bushes usually do not require pruning, however, to

give desired shape, additional twigs are pruned. Diseased or broken twigs are also need to be removed. Old hedges may be headed back to induce new growth. Karonda once established do not require much water as it behaves as xerophytic plant. New plantations need to be irrigated at every weekly and fortnightly interval in summer in winter season respectively. Irrigation in April and June is helpful for survival of the plants for longer duration. There are no major diseases and pests on karonda except die back and anthracnose which sometimes attack the foliage of the plants. The anthracnose can be controlled by spraying with Blitxo-50 or Fytolon @ 2 g/litre water while dieback can be kept under check by spraying Benomyl @ 0.2%.

References

- Meghwal PR, SK Singh, A Singh and R Pathak (2014) Characterization of karonda accession under arid regions. *J. App. Hort.* 16(2): 157-160.
- Meghwal PR (2018) Collection, evaluation and improvement of some underutilized fruits in hot Indian desert. *Indian J. Arid Horti.* 13(1&2): 59-64.

Referees for Volume 36 (1, 2 & 3) 2023

The Editors gratefully acknowledge the help rendered by following referees in reviewing the manuscripts published during 2023.

A. Mohan Rao

Professor

Genetics and Plant Breeding & Scheme Head AICRN on
Potential Crops Organic Farming Building, GKVK
University of Agricultural Sciences (UAS)
Bangalore-560 065, Karnataka
Email: amrao8@rediffmail.com

Ambika Baldev Gaikwad

Principal Scientist

Division of Genomic Resources ICAR-National Bureau of
Plant Genetic Resources Pusa Campus,
New Delhi-110 012
Email: ambika.Gaikwad@icar.gov.in

Amish Kumar Sureja

Principal Scientist

Division of Vegetable Science ICAR-Indian Agricultural
Research Institute Pusa Campus, New Delhi-110012
Email: aksureja@gmail.com

Amit Kesarwani

Assistant Professor

Department of Agronomy
G.B. Pant University of Agriculture and Technology
Udharn Singh Nagar, Pantnagar-263145, Uttarakhand
Email: getkesar@gmail.com

Arpita Das

Assistant Professor

Genetics & Plant Breeding Bidhan Chandra Krishi
Viswavidyalaya Mohanpur, Nadia-741252, West Bengal
Email: arpitacoh@gmail.com

B. Varalakshmi

Principal Scientist

Division of Vegetable Crops
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bengaluru-560 089, Karnataka
Email: Varalakshmi.B@icar.gov.in

D.R. Pani

Principal Scientist

ICAR-NBPGR, Regional Station, Cuttack NRRI Campus,
Cuttack-53006, Orissa
E-mail: diptiranjana.pani@icar.gov.in

Deepika Cheruku

Scientist (Genetics and Plant Breeding)

ICAR-Indian Institute of Millets Research Rajendranagar,
Hyderabad-500 030, Telangana
Email: deepika@millets.res.in

Gayacharan

ARS (Agri. Biotechnology)

ICAR-National Bureau of Plant Genetic Resources New
Delhi -110012
Email: Gayacharan@icar.gov.in

Giriraj Kumawat

Senior Scientist

ICAR-Indian Institute of Soybean Research
Khandwa Road, Indore-452001, Madhya Pradesh
E-mail: Giriraj.Kumawat@icar.gov.in

Gograj Singh Jat

Division of Vegetable Sciences

ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012
Email: singhgograj@gmail.com

Gowthami R.

Scientist

Tissue Culture and Cryopreservation Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Gowthami.R@icar.gov.in

Hima Bindu Aatla

Assistant Professor (Hort.)

College of Horticulture Dr. Y.S.R. Horticultural University,
Parvathipuram, Vizianagaram (Dist.)
Andhra Pradesh-534101
Email: himabindu291188@gmail.com

Jai Prakash

Principal Scientist (Horticulture)

Division of Fruits & Horticultural Technology ICAR-Indian
Agricultural Research Institute Pusa Campus, New
Delhi-110 012
Email: singhjai2001@rediffmail.com

Jayasudha Srinivasa

Assistant Professor

Banaras Hindu University (BHU)
Varanasi-221002, Uttar Pradesh
Email: jkomalaster@gmail.com

Jyoti Kumari

Principal Scientist (Plant Breeding)

Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources Pusa
Campus, New Delhi-110012
Email: jj_gene@gmail.com

K. Pradheep

Principal Scientist

ICAR-NBPGR Regional Station – Thrissur
Vellanikkara, KAU P.O. Thrissur-680 656, Kerala
Email: K.Pradheep@icar.gov.in

K.C. Bhatt

Principal Scientist

Division Plant Exploration and Germplasm Collection
ICAR- National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012
E-mail: kailash.bhatt@icar.gov.in

Kannan CS Warriar

Scientist F

ICFRE-Institute of Forest Genetics and Tree Breeding
Forest Campus, Cowley Brown Road, R.S. Puram
Coimbatore-641 002, Tamil Nadu
Email: kannan@icfre.org

Kuldeep Tripathi

Scientist

Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Kuldeep.Tripathi@icar.gov.in

Lalit Arya

Principal Scientist

Division of Genomic Resources ICAR-National Bureau of
Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Lalit.arya@icar.gov.in

M. Bala Barathi

Department of Genetics and Plant Breeding
Acharya N.G. Ranga Agricultural University
Agricultural College Bapatla-522101, Andhra Pradesh
E-Mail: balu3modugula@gmail.com

M. Latha

Principal Scientist

ICAR-NBPGR Regional Station, Thrissur
Vellanikkara, KAU P.O. Thrissur-680 656, Kerala
E mail: M. Latha@icar.gov.in

M. Saravanan

Senior Scientist (Plant Breeding)

Division of Crop Improvement
ICAR-Central Institute for Cotton Research
Shankar Nagar, Nagpur-440 010, Maharashtra
Email: M.Saravanan@icar.gov.in

M. Sujatha

Former Director

ICAR-Indian Institute of Oilseeds Research
Rajendranagar, Hyderabad-500030, Telangana
E-mail: sujatador@gmail.com

M. Vignesh

Senior Scientist

Division of Genetics ICAR-Indian Agricultural Research
Institute Pusa Campus, New Delhi-110012

Manjunatha Gowda D.C.

Scientist

Division of Vegetable Crops
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bengaluru-560 089, Karnataka
Email: dc.manjunath@icar.gov.in

Manjusha Verma

Principal Scientist

Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012 Email: Manjusha.
Verma@icar.gov.in

Mankesh Kumar

Assistant Professor (Genetics & Plant Breeding)
Bihar Agricultural University (BAU)
Sabour Bhagalpur-813210, Bihar
Email: mankesh2008@gmail.com

N. Sivaraj

Principal Scientist (Economic Botany)

ICAR-NBPGR Regional Station
Rajendra Nagar, Hyderabad-500030, Telangana
E mail: sivarajn@gmail.com

Parvaze A Sofi

USDA Norman Borlaug Fellow

Visiting Scientist Kansas State University
Visiting Scholar Sustainable Intensification Innovation Lab
KState
Professor (Genetics & Plant Breeding)
FOA, SKUAST-K, Wadura-193201, Jammu & Kashmir
Email: parvazesofi@gmail.com

Pradeep Kumar Chand

Professor (Retired)

Plant Biotechnology Laboratory, Post Graduate
Department of Botany, Utkal University
Vani Vihar, Bhubaneswar-751004, Odisha
Email: pkchand13@gmail.com

Pragya

Principal Scientist

Germplasm Exchange & Policy Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Pragya@icar.gov.in

Prananath Barman

Scientist (Senior Scale)

ICAR-CISH Regional Research Station, Malda
Malda-732101, West Bengal
Email: prananath.barman@icar.gov.in

Priyamedha

Senior Scientist (Plant Breeding)
ICAR-NRRI-Central Rainfed Upland Rice Research Station,
Hazaribagh-825301, Jharkhand
Email: priyamedha.pb@gmail.com

R. Anandalakshmi

Scientist F
ICFRE-Institute of Forest Genetics and Tree Breeding
Forest Campus, Cowley Brown Road, R.S. Puram
Coimbatore-641 002, Tamil Nadu
Email: lakshmir@icfre.org

R. Parimalan

Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email- r.parimalan@icar.gov.in

R.S. Pal

Senior Scientist (Plant Biochemistry)
ICAR-Vivekananda Institute of Hill Agriculture
Almora-263601, Uttarakhand
Email: Ramesh.Pal@icar.gov.in

Raj Kumar Gautam

Principal Scientist
Division of Germplasm Evaluation
ICAR-NBPGR, New Delhi-110012
Email: Raj.Gautam@icar.gov.in

Rajasekharan P.E.

Principal Scientist
Division of Ornamental and medicinal crops
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake, Po Bangalore-560 089, Karnataka
Email: rajasekharan.pe@icar.gov.in

Rajesh Kumar

Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012 Email: Rajesh.
Kumar13@icar.gov.in

Rajiv Kumar

Principal Scientist
Division of Floriculture,
ICAR-IIHR, Hessaraghatta lake post Bengaluru-560089,
Karnataka
Cell No. 9986794620
Email: rajiv.kumar11@icar.gov.in

Rajkumar Zunjare

Scientist (Plant Breeding)
Division of Genetics, ICAR-Indian Agricultural Research
Institute Pusa Campus, New Delhi-110 012
Email- raj_gpb@yahoo.com

Rakesh K Dubey

Principal Scientist
Vegetable Breeding & PGR Management
ICAR-Indian Institute of Vegetable Research
Jakkhini, Varanasi-221 305, Uttar Pradesh
Email: Rakesh.Dubey1@icar.gov.in

Sangita Bansal

Principal Scientist
Tissue Culture and Cryopreservation Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
E-mail: sangita.bansal@icar.gov.in

Sherry R. Jacob

Senior Scientist
Division of Germplasm Conservation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Sherry.Jacob@icar.gov.in:

Shubha Kumari

Scientist (Vegetable Science)
ICAR Parisar, ICAR Research Complex for Eastern Region
B V College, Patna-800 014, Bihar
Email: Kumari.shubha@icar.gov.in

Sudip Kumar Dutta

Senior Scientist (Horticulture)
ICAR Research Complex for NEH Region, Sikkim Centre
Tadong, Gangtok-773102, Sikkim
Email: Sudip.Dutta@icar.gov.in

Surendra Barpete

National Associate Scientist
ICARDA-Food Legume Research Platform
Amlaha, Sehore-466 113, Madhya Pradesh
Email: surendrabarpete@gmail.com

T. Boopathi

Senior Scientist
ICAR-Indian Institute of Oilseeds Research
Rajendranagar, Hyderabad,500030, Telangana
Email: boopathi.thangavel@icar.gov.in

V. Thondaiman

Associate Professor (Horticulture)
Department of Horticulture
Central University of Tamil Nadu
Neelakudi Campus, Thiruvavur-610005, Tamil Nadu
E mail: thondaiman@cutn.ac.in

Vandana Tyagi

Principal Scientist
Germplasm Exchange & Policy Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012
Email: Vandana.tyagi@icar.gov.in

Vartika Srivastava

Scientist (Senior Scale)
Division of Germplasm Conservation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delh-110 012
Vartika.Srivastava@icar.gov.in

Vijayata Singh

ARS Scientist (Genetics and Plant Breeding)
ICAR-Central Soil Salinity Research Institute
Karnal-132001, Haryana
Email: vijayata.singh@icar.gov.in

Zakaullah Khan

Principal Scientist
Division of Plant Quarantine
ICAR-National Bureau of Plant Genetic Resources Pusa Campus, New Delhi-110 012
Email: zakaullah.khan@icar.gov.in

AUTHOR GUIDELINES

The Indian Journal of Plant Genetic Resources (IJPGR) is the official publication of the Indian Society of Plant Genetic Resources (ISPGR). For publication in the journal, the authors must be a member of the Society. IJPGR publishes full-length papers or short communications of original scientific research in the field of plant genetic resources (PGR). Review articles (with prior consent or invitation only) summarizing the existing state of knowledge in topics related to PGR will also be published.

Contributions should be as concise as possible. The maximum length of the review article, full-length papers and short communications is usually restricted to 12, 6, 3 printed pages including illustrations and tables, respectively.

SCOPE

- Basic research on biosystematics, genetics and genomics related to PGR
- Applied research on field and laboratory evaluation of PGR
- Supportive research in conservation and quarantine of PGR
- Policy research on access and benefit sharing; IPRs
- Status reports on ecology, conservation, traditional knowledge and use of PGR

Title Page: The title page of the manuscript should be the first page and should include the title, names and addresses of the authors, abstract and keywords.

Title: Keep the title brief, specific and informative and amendable to indexing. It should be typed in running text with first letter of word as capital and Latin names in italics.

Name and Address: The name of authors and the address of the institution where the work was carried out should be mentioned below the title. Present address of correspondence, if different, should be given as footnote indicating by asterisk (*) the author to whom the correspondence and reprint requests are to be made. E-mail addresses should also be indicated.

Abstract: The abstract should clearly state the rationale, objectives, methods, and important conclusions of the study. It should not exceed 150 words.

Key Words: The abstract should be followed by not more than five key words (following alphabetic order) indicating the contents of the paper and useful for abstracting purposes.

Main Text: The main text of the paper should start from the second page which should contain the title of the paper followed by the text divided into following main headings which are to be typed in running text and flushed with the margin: Introduction, Materials and Methods, Results, Discussion, Acknowledgements, References. Only relevant references should be included in reference section. Wherever appropriate, results and discussion can be combined and acknowledgements be omitted.

Introduction should be brief and limited to the statement of the problem and aim of the experiment.

Materials and Methods should include relevant details on the nature of material, experimental design, the techniques/ methodology employed and the statistical method used. For well-known methods, citation of reference will suffice.

Results and Discussion should be clear to readers in different disciplines. Units of measurement should be SI.

Tables should be typed on separate sheets, each with a heading stating its contents clearly and concisely. Numerical data and calculations should be thoroughly checked.

Figures of only good quality that are essential to a clear understanding of the paper shall be accepted. Legends to the illustrations should be typed on separate paper. Information in the legend should not be repeated in the text and similarly, the same data should not be represented in both graph and table form. All figures, whether photographs, maps, graphs or line drawings should be numbered consecutively. Illustration number and title of the article with authors' name may be given at the back of the plates in soft pencil.

Line diagrams of high quality, preferable in the desired final size would be accepted. The inscriptions should be clearly legible.

Photographs for publication should be of high contrast, black and white/coloured, glossy print, trimmed at right angles. Magnification should be indicated with a bar scale on the photo. Authors need to indicate colour reproduction of photographs. Color photographs will be published free of cost however, cost of colour printing will be borne by the authors, if hard copy is required by author(s).

Acknowledgements should mention only guidance or assistance received in real terms, and financial grant provided by a funding agency. Acknowledgements for inspiration, typing etc., need not be mentioned.

References in text should be cited by author, year of publication (e.g. Joshi, 1995; Joshi and Rao, 1995) and multiple citations should be in chronological order (Withers and Englemann, 1998; Rao *et al.*, 2001). References should be listed in alphabetical order under the first authors' name. The names of journals should be abbreviated according to the latest edition of the World List of Scientific Periodicals (eds P Brown and GB Stratton), Butterworths, London.

The following examples may be used for citations:

- Chao CCT and RR Krueger (2007) The date palm (*Phoenix dactylifera*); an overview of biology, uses and cultivation. *Hort. Sci.* 42(5): 1077-82.
- Muralidharan CM, SBS Tikka and P Verma (2008) Date palm cultivation in Kachchh, Technical Bulletin-2, Date palm Research Station, Sardarkrushinagar Dantiwada Agricultural University (SDAU), Mundra, Gujrat, India, p36.
- Wither LA and F Englemann (1998) In vitro conservation of plant genetic resources. In: A Altman (ed) *Agricultural Biotechnology*. Marcell Dekker Inc., New York, pp 57-58.
- WOI (1985) Wealth of India – Raw Materials. A Dictionary of Indian Material and Industry Products – Raw Material Vol 1: A (Revised). Publication and Information Directorate, Council of Scientific and Industrial Research, New Delhi, 513 p.
- Engels JMM and V Ramanatha Rao (eds) (1998) Regeneration of seed crops and their wild relatives. *Proceedings of a Consultation Meeting*, 4-7 December 1995, ICRISAT, Hyderabad and IPGRI, Rome, Italy, 167 p.

Short Communications

The style and format as mentioned for full-length papers should be followed for Short Communications. However, the abstract should be restricted to not more than 50 words and the remainder text should be continuous (without headings). Illustrative material should be kept at minimum, usually not more than one table or figure and only few references should be included (not more than 10). Authors can also submit meeting reports after consulting Editor-in-Chief, IJPGR.

Submission of the Manuscript Submission of an article will be held to imply that it has not been previously published or submitted for publication elsewhere. A cover letter including a statement to this effect should be submitted with the manuscript. Article are submitted through online submission system:

https://ispgr.in/index.php/ijpgr/about/submissions=manuscript_submission or by email to:

Editor-in-Chief, Indian Journal of Plant Genetic Resources

E-mail: ispgr2015@gmail.com

- Experts in the subject will review all the submitted manuscripts and the final decision about the acceptance of the manuscript rests with the Editorial Board. If manuscript is accepted for publication, the revised manuscript should be accompanied by electronic copy on CD or through electronic mail.
- Publication of a paper in the Journal does not imply the responsibility for an agreement with the statements or view written therein, and rests entirely on the authors thereof.
- The authors will receive page proofs, which should be corrected and returned maximum within 3 days. Corrections must be kept to the minimum, and the proof stage should not be regarded as an opportunity for further editing and additions. Although, every effort is made by the editors to correct proofs of all the papers they assume no responsibility for errors that may remain in the final print.

ETHICS STATEMENT

IJPGR approves the spirit of the guidelines for journal editors developed by the Committee on Publication Ethics (COPE).

- Manuscripts submitted to IJPGR are evaluated entirely on the basis of their scientific content and relevance to PGR research community.
- IJPGR does not levy any publication charges to members of ISPGR.
- ISPGR, the publishers of the Journal, take all possible measures to uphold the highest standards of publication ethics and to prevent any malpractices.
- Authors who submit manuscripts to IJPGR declare that the submissions are original and unpublished and are not under consideration for publication elsewhere.

- Authors also declare that the manuscript is based on their own original work devoid of any nature and amount of plagiarism.
- IJPGR makes full efforts to eliminate any kind of conflict of interest of authors, editors or reviewers, resulting from competitive, collaborative or other relationship with any person, institution or agency connected to the submissions.

Ethics expected to be followed by IJPGR Editors:

- IJPGR Editorial Team is fully responsible for the decision on acceptance or rejection of a manuscript submitted to the Journal. An established procedure is followed to ensure unbiased decision making. Submissions are handled by different Editors based on their specialization. Editors obtain the reports of three referees with expertise in the topic dealt in the submission. Each Editor recommends rejection or acceptance (direct or after revisions) to the Editor-in-Chief who takes the final decision.
- The evaluation of manuscripts is made on the basis of their scholarly content in terms of relevance, novelty and scope as well as their presentation in terms of language and syntax. IJPGR does not consider any other factors like gender, race, religious belief, ethnic origin, citizenship, or political philosophy of the authors.
- IJPGR strictly follows transparency in the evaluation process and confidentiality of the submission. Reviewers, as on today, remain anonymous to authors.

Ethics expected to be followed by IJPGR Reviewers

- Peer review is the backbone of IJPGR manuscript flow. IJPGR depends upon the services of reviewers for maintaining ethical integrity and scholarly quality.
- IJPGR does not follow double blind review and, therefore, the reviewers are expected to maintain absolute confidentiality with regard to the contents of manuscripts.
- The reviews are conducted objectively with every comment/decision supported by clear reasons. Reviewers follow a non-ranking format provided by the IJPGR to facilitate decision making by Editor.

Ethics expected to be followed by Authors

- Authorship should be restricted to only those persons who have made a significant contribution to the conception, design, execution, or interpretation of the reported study. In recent times, symbiotic authorship has become a serious ethical issue which should be avoided.
- The authors must ensure that the experiment and manuscript are both entirely original works written in good English without any ambiguity. Every instance of use of work and/or words of other authors must be appropriately cited or quoted. Any kind of plagiarism detected at review stage results in rejection of the manuscript. If the plagiarism is detected post-publication, the article will be summarily retracted. If any fundamental errors are found in published papers, authors will inform IJPGR which will take corrective measures including retraction.
- IJPGR persuades authors to provide the basic data related to manuscripts such as description of germplasm and its availability to ensure greater utilization of diverse germplasm. Authors are also encouraged to provide relevant raw data for editorial review. Authors must prepare such data in a format to provide public access. Specific requests of data confidentiality shall be entertained by IJPGR on case-to-case basis.
- Authors must avoid any kind of duplication in their submissions *i.e.* attempting to publish same/significantly similar manuscripts in more than one journal. IJPGR does not consider the following as a prior publication: (i) Abstract in a conference/symposium; (ii) Academic thesis/dissertation; (iii) Invited talks and interviews on specific topics.
- Submission to IJPGR implies that authors have complied with ethical and technical standards of use of hazardous material, use of animal or human subjects, access and use of genetic resources, access and use of IP protected data. It is authors' duty to ensure no national or international legal requirement is compromised.
- Submission of a manuscript to IJPGR implies that the corresponding author has ensured that all co-authors have seen and approved the final version of the paper and have agreed to its submission for publication to IJPGR. All sources of financial support should also be disclosed.

PUBLISHER/EDITORIAL OFFICE ADDRESS

#H-204, ICAR-National Bureau of Plant Genetic Resources Pusa Campus (NBPGR), New Delhi-110012, India

E-mail: ispgr2015@gmail.com

Publisher website: www.nbpgr.ernet.in/ispgr

Journal hosting and online submission of manuscript: <https://ispgr.in/index.php/ijpgr/about/submissions>

Online Access to IJPGR

All the issues of Indian Journal of Plant Genetic Resources from 1988 [Vol 1(1)] till date [Vol 36(1)] are accessible as pdf files of individual papers.

- The access is provided to life members only
- Access is through user ID and password
- Login credentials have been emailed to all life members by ispgr.in (if any life member has not received the user ID and password, please contact IJPGR office *via* E-mail: ispgr2015@gmail.com)
- Open the home page of IJPGR at <https://ispgr.in/index.php/ijpgr/index>
- You may also reach IJPGR home page *via* Google search of "Indian Journal of Plant Genetic Resources"
- Click on the LOGIN button and enter the user ID and password
- If you are a new member, then click on the REGISTER option, and register as AUTHOR.
- For a new submission, click on MAKE A SUBMISSION, or check our AUTHOR GUIDELINES.
- The login credentials are for the personal use of IJPGR life members. Please do not share with others.

Online Access to IJPGR

All the issues of Indian Journal of Plant Genetic Resources from 1988 [Vol 1(1)] till date [Vol 36(1)] are accessible as pdf files of individual papers.



- The access is provided to *life members only*
- Access is through user ID and password
- Login credentials have been emailed to all life members by ispgr.in (if any life member has not received the user ID and password, please contact IJPGR office at ispgr2015@gmail.com)



- Open the home page of IJPGR at <https://ispgr.in/index.php/ijpgr/index> You may also reach IJPGR home page via Google search of “Indian Journal of Plant Genetic Resources”
- Click on the LOGIN button and enter the user ID and password
- If you are a new member, then click on the REGISTER option, and register as AUTHOR.
- For a new submission, click on MAKE A SUBMISSION, or check our AUTHOR GUIDELINES.
- The login credentials are for the personal use of IJPGR life members. Please do not share with others

CONTENTS

Potato Genetic Resources and their Utilization in India <i>Satish K. Luthra and Vinod Kumar</i>	1
Molecular Profiling of Erucic Acid Biosynthesizing FAE1 Gene of Indian Mustard Varieties <i>Rajesh Kumar, S. Rajkumar and J. Radhamani</i>	20
High Popping Quality Finger Millet (<i>Eleusine coracana</i>) Genotypes <i>Y. A. Nanja Reddy, P. Jayalakshmi, T. Lavanyabai, K. Geetha, M. Deepika and M. V. C. Gowda</i>	24
Molecular Characterization of Garden Rose Germplasm using SSR Markers <i>Shephalika Amrapali, Sunil Archak, Namita and Ambika B. Gaikwad</i>	31
SSR Markers based Diversity Analysis in Elite Genotypes of Pearl Millet <i>J. Jorben, Mukesh Sankar S., Anju M. Singh, C. Tara Satyavathi1, Tripti Singhal, Thribhuvan R. and S. P. Singh</i>	39
Multi-crop Exploration in Unexplored Areas of Garo Hills, Meghalaya <i>Sanjeev K. Singh, Ranbir S. Rath, Kailash C. Bhatt, Subarna Hajong and Naorem A. Singh</i>	47
Evaluation of Recombinant Inbred Lines of <i>Oryza glaberrima</i> and Improved Samba Mahsuri for Antixenosis and Tolerance against <i>Nilaparvata lugens</i> (Stal) <i>Neha Chhabra, Preetinder S. Sarao, R. M. Sundaram and Gurjot Kaur</i>	56
Collection, Characterization and Identification of Elite Genotypes of Wild/Semi-Domesticated Bitter Gourd (<i>Momordica charantia</i> var. <i>muricata</i>) for Utilization and Conservation <i>Asna A. C., Jiji Joseph, Joseph K. John, Sainamole Kurien P and C. Beena</i>	62
Evaluation of <i>Saccharum spontaneum</i> Clones for Water Deficit Stress Tolerance <i>Vinu V., T. L. Pathy, Mahadevaswamy H. K., R. Valarmathi, Manju M. Paul and R. A. Kumar</i>	73
Variability, Heritability, and Correlation Studies for Economic Traits in Grain Amaranth (<i>Amaranthus</i> spp.) <i>Ved Prakash, Gajala Ameen, Vivek K. Sandilya and Jitendra K. Tiwari</i>	80
Microsatellite Markers Reveal the Genetic Integrity of Stored Accessions of Cotton (<i>Gossypium arboreum</i> L.) in the Indian National Genebank <i>Anto James, Shipra Deo, Anjali Kak and Mukesh K. Rana</i>	90
Studies on Traditional Melon 'Vellari' (<i>Cucumis melo</i> Var. <i>momordica</i> L.) in Tamil Nadu, India <i>Prabhu P, Anjula Pandey, S Rajkumar, Harish GD, Chithra Pandey and Rakesh Bharadwaj</i>	97
Acclimatization Pattern of Cultivated <i>Capsicum</i> spp. in an Agro-Ecologically Diverse Habitat, Kerala, India <i>Asish I. Edakkalathur, Presannakumari K.T., Latha M, Minimol J.S., Manju P., Pradeepkumar T., Krishnan S. and Sivaraj N.</i>	105
Genetic Diversity, Variability, and Correlation Studies in South Indian Culinary Melon (<i>Cucumis melo</i> ssp. <i>agrestis</i> var. <i>acidulus</i>) Accessions <i>Ratnakar M. Shet, Virupakshi Hiremata, Raghavendra Gunnaiah and Santosha Rathod</i>	118
Performance of Exotic and Indigenous Coconut Genotypes for Growth, Fruit Yield, Fruit and Nut Characters under Assam Conditions of North East Region of India <i>Leichombam S Singh, Niraj Vittal, Gobinda C Acharya and Manju Chaithra</i>	125
Plant Germplasm Registration Notice	131
Author Guidelines	

