Vol. 33 No. 1 2020

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

Indian Journal of Plant Genetic Resources

An International Journal for Conservation and Use of Plant Diversity

ISPGR 1987

Indian Society of Plant Genetic Resources
New Delhi, India

INDIAN SOCIETY OF PLANT GENETIC RESOURCES

(Registration No. S/18336)

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ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

Vol. 33 No. 1 2020

INDIAN SOCIETY OF PLANT GENETIC RESOURCES
NBPGR CAMPUS, NEW DELHI-110012, INDIA
Web: ispgr.nbpgr.ernet.in

CONTENTS

Commentary

COVID19: The Pandemic of Neglected Biodiversity 1
Prof SK Sharma

Special Article

Managing Agrobiodiversity of Indian Drylands for Climate-Change Adaptation 3
OP Yadav, JP Singh, RK Kakani, HR Mahla, MP Rajora, Akath Singh, PR Meghwal and Archana Verma

Review Article

Arid Horticultural Crops: Status and Opportunities under Changing Climatic Conditions 17
PL Saroj, Chet Ram and Kamlesh Kumar

Meeting Report

Expert Consultation Meeting on Global Crop Conservation Strategies 32
Sherry Rachel Jacob

Expert Consultation Workshop on "Global Conservation Strategy for Crops in the *Cucurbitaceae* Family" 34
Chithra Devi Pandey

Research Article

Development and Documentation of DUS Traits for *Melia dubia* Cav. Genetic Resources 36
TM Akhilraj and KT Parthiban

Survey of Major Ethnomedicinal Plants of District Kinnaur, Himachal Pradesh 43
Meenakshi Bhardwaj, LS Kandari and Tripti Negi

Genetic Diversity for Yield and Water Use Efficiency related Traits in Groundnut (*Arachis hypogaea* L.) 52
K Gangadhara, AL Rathnakumar, PP Thirumalaisamy, BC Ajay and HK Gor

Evaluation of Teosinte derived Maize Lines for Drought Tolerance 60
Amarjeet Kumar, NK Singh, AS Jeena, JP Jaiswal and SS Verma

Assessing Genetic Diversity of Newly Developed Winter Maize (*Zea mays* L.) Inbred Lines 68
SB Singh, RK Kasana, Santosh Kumar and Ramesh Kumar

Notes on Diversity Distribution and Systematics Study of *Abelmoschus tuberculatus* Pal & Singh: A Close Wild Relative of\ Okra from India 77
Anjula Pandey, S Nivedhitha, Vidya Sagar, Pavan K Malav, Shashikant Sharma and SP Ahlawat

Short Communication

Exploiting Genetic Diversity for Identification of Protein Dense Seed Parent in Pearl Millet 85
Mukesh K Berwal, Preeti Goyal, LK Chugh, Ramesh Kumar and Dev Vart

Studies on Reproductive Behavior of Fifteen Elite Wheat Genotypes in Relation to Hybrid Development 90
Krishnendu Guin, Sudhir Kumar Sethi and Rajesh Kumar Arya

Collection and Evaluation of Henna (*Lawsonia inermis* L.) Germplasm from South India 94
PC Shiji and EA Siril

Variability in Fruit and Seed Parameter of *Manilkara hexandra* (Roxb.) Dubard in Rajasthan 98
Keerthika A, AK Shukla, DK Gupta, MB Noor Mohamed, BL Jangid and Mahendra Singh

Diversity in Seed Characters for Morphological Characterization of Date Palm (*Phoenix dactylifera* L.) Varieties 102
RS Singh, R Bhargava and BD Sharma

PGR Note

Larnoo Purple: A High Yielding, Early Maturing, Cold Tolerant Maize Line with High Carotenoid and Protein Content 106
M Ashraf Ahangar, ZA Dar, Showkat A Waza, Asif B Shikari, FA Sheikh, S Sapna, NA Teeli and Ajaz A Lone

Empowering Ethnic Groups through Farmers' Variety Protection by NBPGR: Success Story from Telangana State 109
SR Pandravada, N Sivaraj, V Kamala, M Swapna and B Sarath Babu

Tubocapsicum anomalum (Franch. & Sav.) Makino: A New Record to the Flora of Arunachal Pradesh, India 115
RS Rathi, KC Bhatt, Anjula Pandey, UK Tiwari, K Pradheep, NS Panwar and SP Ahlawat

Referees for Volume 32 (1, 2 & 3) 2019 119

Guidelines to Authors 122

Indian J. Plant Genet. Resour. 33(1): 1–2 (2020)
DOI 10.5958/0976-1926.2020.00001.7

COMMENTARY

COVID19: The Pandemic of Neglected Biodiversity

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(Received: 24 May, 2020; Revised: 05 June, 2020; Accepted: 06 June 2020)

The year 2020 was supposed to be a Super Year for biodiversity, as two important programmes of the United Nations, The Decade on Biodiversity and the Strategic Plan for Biodiversity 2011-2020, were to be concluded by the year end. Besides, two key global inter-governmental meetings were planned during the year towards addressing the twin environmental crises of recent times: biodiversity loss and climate change. The Convention on Biological Diversity (CBD) COP 15 was to establish a post-2020 global biodiversity framework, while the UN climate change conference COP 26 was to address the challenges of climate change. These meetings have been postponed owing to COVID-19 pandemic. Nature, it seems, had other plans. The corona virus pandemic has put pretty much all of that at the back-burner. The International Day for Biological Diversity was observed on May 22 to raise the awareness and understanding of biological diversity and issues related to it. The theme of the current year is "Our Solutions are in Nature", which shows that nature, including biodiversity, is pivotal to answer a number of sustainable development challenges and the current pandemic that we all are fighting.

Some of the diseases that emerge in humans come from both domestic and wild animals, who are the carriers of such pathogens which are contagious in nature. Pandemics, however, are caused by activities that bring increasing numbers of people into direct contact with the deceased; hence, a single infected person can result in the disease spread. COVID-19 is believed to have originated in a wet market in Wuhan, China, where live animals are traded and carcasses of wild animals such as bats, rats, snakes, pangolins, baby crocodiles, etc. are marketed and displayed.

Biodiversity provides various ecosystem goods and services in different ways that are not always apparent or appreciated. Thriving ecosystems also provide a variety of benefits to surrounding humanity - from fresh water to food to fertile soil. Over the past 50 years, through increased population and climate change, humans consumed and degraded biodiversity and ecosystems more rapidly than during any other time in human history. The impact of biodiversity loss and ecosystem degradation has broad and systemic implications that are connected to many pressing challenges that humanity face today.

Researchers today believe that it is actually humanity's destruction of biodiversity and ecosystem services which led to the appearance of new viruses and diseases such as COVID-19 with profound health and economic impact in rich and poor countries alike. Some of the activities contributing to biodiversity and ecosystem services loss are logging, mining, road construction in remote places, building of dams and irrigation projects, development in coastal areas, rapid urbanization, population growth, etc. Forest fires alter habitats, yield less food and send foraging wildlife in contact with nearby humans and thereby creating greater opportunities for the vectors of zoonotic bacteria, viruses and parasites.

Another important factor is the climate change, which is, both a cause and an effect of biodiversity loss. Climate change has severe direct and indirect impact on biodiversity and is predicted to be a dominant driver of future biodiversity loss. Several other drivers of biodiversity loss include habitat degradation/destruction and the introduction of invasive alien species to ecosystems, which get magnified by the effects of climate change. The loss of species and habitats contributes to climate disruption, which in turn can accelerate biodiversity loss — both of which can contribute to the rise of pandemics. The consumption and import/export

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thereof of exotic animals have two major consequences: i) increasing the risk of an epidemic by putting human beings in contact with rare infectious agents and ii) putting enormous pressure on wild populations resulting in the loss of biodiversity.

The Regional Assessment Report on Biodiversity and Ecosystem Services released by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) at Medellin, Colombia during 2018 indicated that biodiversity is declining in all regions of Asia-Pacific including India. The IPBES Global Assessment Report (2019) has evaluated the progress in achieving key international goals ranging from the Sustainable Development Goals (SDGs) and Aichi Biodiversity Targets, to the Paris Climate Agreement. The report concludes that if biodiversity loss needs to be halted, deterioration of nature must be slowed down and the biodiversity, climate and sustainable development goals must be achieved by 2030. "Business as usual" will not work; instead societies and economies will be driven to greater risks.

Until some effective vaccine is made available to control the COVID-19, increasing immunity is being advocated to avoid the infection. Ayurveda, the Indian Traditional System of Medicines, lays emphasis on promotion of health concept by strengthening host-defence system thereby attaining resistance against different diseases. Herbal drugs are known to possess excellent immuno-modulatory properties. Besides, these plants have other properties like delaying the onset of senescence and improving the mental functions. This concept has been described as *Rasyana* in Ayurveda and known to employ around 700 plant species. Besides, there are large number spices, fruits, nuts, and vegetables, which are consumed to improve immunity since time immemorial. These are very valuable components of the biodiversity and need to be protected and used.

The biodiversity protection and climate change mitigation go hand-in-hand and are mutually dependent. Managing and protecting biodiversity will mitigate the negative impact of climate change and help humans adapt to it. Policies and actions aiming at limiting the effects of climate change will contribute to the protection of biodiversity. The focus on biodiversity conservation should be on a growing movement towards nature-based solutions, which harness the power of ecosystem services to mitigate the effects of climate crisis, non-sustainable food systems, water pollution and other environmental challenges. To protect nature and avoid lethal pandemics, environmental regulations must be strengthened and enforced, and stimulus packages that offer incentives for more sustainable activities must only be deployed.

There are high hopes that the post-2020 global biodiversity framework will take an ambitious but practical approach in addressing these concerns, improving on the Aichi Biodiversity Targets to increase the area of protected land and water worldwide. Besides, it will have to address the drivers of biodiversity loss, emphasize that biodiversity loss and climate change are related problems, and give the policy measures some teeth. Protecting nature is our foremost duty to safeguard human health and strengthen the nations. Successful drug development is not always about advanced synthetic biology; there is also a link to nature-based solutions and biodiversity as researchers are increasingly reverting to nature to look for new therapeutic options.

The COVID-19 pandemic is a wakeup call for a healthier planet. Protecting nature and ensuring the sustainable use of natural resources could help prevent the next pandemic. Future pandemics are likely to happen more frequently, spread more rapidly, have greater economic impact and kill more people if we are not extremely careful about the possible impact of the choices we make today. The right mix of policies for protecting nature, sustainable use of natural resources and educating local communities about the dangers of zoonotic diseases, could play a significant role in sustainable development with important co-benefits for people, biodiversity and the climate. Community of plant genetic resources researchers have responsible role to play.

Indian J. Plant Genet. Resour. 33(1): 3-16 (2020)
DOI 10.5958/0976-1926.2020.00002.9

SPECIAL ARTICLE

Managing Agrobiodiversity of Indian Drylands for Climate-Change Adaptation

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Agrobiodiversity in drylands consisting of large number of field crops, horticultural crops, grasses, shrubs and multi-purpose trees plays a very critical role in providing food, fodder, nutritional and environmental security to the inhabitants of drylands. Despite several bio-physical constraints, the drylands support high human and livestock population with limited resources resulting in over-exploitation of the natural resources. Moreover, drylands are more vulnerable to global warming-mediated climate changes such as intense drought, sudden rainfall burst, high ambient temperature and appearance of new unforeseen diseases and pests. In addition to other technological interventions, the management of agro-biodiversity in drylands is expected to be a key factor for sustainability, food and fodder security and for improving livelihood in drylands.

Genetic resources of dryland species include local landraces, improved elite material, traditional cultivars, genetic stocks and wild relatives of coarse cereals (pearl millet, barley, sorghum, maize and small millets), legumes (chickpea, mungbean, mothbean, clusterbean), horticultural crops, grasses, shrubs, medicinal plants and multi-purpose trees. A large numberof exotic and indigenous germplasm accessions are conserved in National Gene Bank or Field Gene Banks at the ICAR-National Bureau of Plant Genetic Resources (NPBGR) and elsewhere across globe. Characterization of genetic resources using prescribed descriptors has largely indicated existence of large variation for phenotypic, phenological, nutritional and stress-adaptation traits among available germplasm.

Research conducted so far has indicated that the genetic resources from drylands hold a unique advantage as they have evolved over centuries by natural and human selection under drought, high temperature or saline conditions. They are better adapted to the local conditions and would contribute in enhancing the resilience at the farm level. These resources could be of immense importance especially as sources of native genes conditioning resistance to various biotic and abiotic stresses and also make unique study material to understand the mechanism of adaptation to abiotic stresses. They could also serve as an excellent genomic resource for isolation of candidate genes for tolerance to climatic and edaphic stresses for accelerating further genetic improvement. However, only a very small fraction of these accessions has been utilized so far because of operational difficulties in dealing with large number of germplasm accessions. The development of core and mini-core in recent past is expected to improve this situation. Formation of trait-specific gene pools is also likely to enhance the utilization of genetic resources to a greater extent.

There are multiple and complex challenges for agrobiodiversity in drylands due to habitat destruction, high grazing/browsing pressure, invasion of other species, unsustainable exploitation of natural resources and dilution of customary conservation practices. Critical assessment is needed for identifying geographical and trait-diversity gaps using GIS and other modern tools.

Additional explorations are needed in the regions where collection gaps have been indicated. *Ex situ* conservation of genetic resources from such regions and distribution of germplasm to the stakeholders on regular basis would remain very crucial especially in the present scenario of climate change. Developing e-resources with detailed information like passport data, characterization and evaluation data with respect to individual accessions would certainly help in enhancing the utilization of genetic resources to broaden crop genetic base which is very essential to reduce the chances of disease epidemics and to adapt to the effects of climate change.

Key Words: Agrobiodiversity, Arid and semi-arid regions, Climate change, Genetic resources and Indian drylands

Introduction

The drylands in India occupy about 80 million ha and are spread over arid, semi-arid and sub-humid climatic zones presenting nearly 56% of the net cultivated area. The drylands are characterized by low precipitation, highly variable rainfall patterns, high evapotranspiration

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rates, inadequatly available nutrients in majority of native soils, poor quality of ground water, severe land degradation, short growing period and low crop yields. Despite these bio-physical constraints, the drylands support high human and livestock population, which mostly depend on agriculture and allied activities with limited natural resources resulting in over-exploitation of the resources. Presently, degradation of natural resources (land, water and biodiversity), decreasing farm profitability and environmental pollution (soil and water) are threatening the sustainability of agricultural production in the drylands. Moreover, drylands are more vulnerable to global warming-mediated climate change reflected in the form of more intense drought, sudden rainfall burst, high ambient temperature and appearance of unforeseen diseases and pests. Along with other technological interventions, the management of agro-biodiversity in drylands is expected to be a key factor for sustainability, food and fodder security and for improving livelihood in drylands.

Drylands are critically important in terms of cultivation of landraces, traditional varieties and wild relatives of field crops in addition to huge variation in number of horticultural crops, grasses, shrubs, multi-purpose tress etc. With this background, an attempt has been made to assess the status of conservation, evaluation and utilization of genetic resources of drylands, and the role of agro-biodiversity in combating climate change in the Indian drylands.

Conservation

Plant genetic resources (PGR) of drylands consist of landraces, cultivars, genetic stocks, elite germplasm and, wild and weedy relatives of large number of cereals, legumes, horticultural crops, grasses, medicinal plants, shrubs and multi-purpose trees.

Cereals

The most important cereals in drylands include pearl millet [*Pennisetum glaucum* (L.) R.Br.], sorghum [*Sorghum bicolor* (L.) Moench.], maize (*Zea mays* L.), barley (*Hordeum vulgare* L.) and small millets consisting of six species viz., finger millet [*Eleusine coracana* (L.) Geaertn.], foxtail millet [*Setaria italica* (L.) P. Beauv.], little millet (*Panicum sumatrense* Roth ex Roem. & Schult.), kodo millet (*Paspalum scrobiculatum* L.), proso millet (*Panicum miliaceum* L.) and barnyard millet [*Echinochloa crusgalli* (L.) P. Beauv]. Efforts made at national and international levels have resulted in the collection and conservation of a large number of germplasm from different parts of the world providing the scientific community an access to a large pool of genetic resources to meet challenges in drylands. Details of germplasm accessions of cereals at ICAR-NBPGR, New Delhi is given in Table 1.

Table 1. Germplasm accessions of dryland cereals at ICAR-NBPGR, New Delhi

Crop	Indigenous	Exotic	Total
Pearl millet	8006	830	8836
Sorghum	11938	9067	21005
Maize	8616	141	8757
Barley	5937	1149	7086
Foxtail millet	4500	81	4581
Finger millet	11075	109	11184
Little millet	2095	01	2096
Kodo millet	2372	01	2373
Barnyard millet	1923	08	1931
Proso Millet	998	0	998
Total	57460	11387	68847

Source: NBPGR, PGR Portal, 2019

Pearl millet: At global level, pearl millet germplasm collection consists of 65,447 accessions (FAO, 2010a) in more than 1750 gene banks of 46 countries (FAO, 2010b). Six large *ex-situ* holders are ICRISAT, India (33%); CNPMS, Brazil (11%); NBPGR, India (9%); ORSTOM, France (6%) and ICRISAT, Nairobi (4%). ICRISAT is holding 23,841 germplasm accessions which include 20,628 traditional cultivar/landraces, 2268 breeding material, 816 wild relatives and 129 advanced or improved cultivars from 50 countries (ICRISAT, 2019). Indigenous collections of ICAR-NBPGR are from 17 states and union territories (Yadav *et al*., 2017)

*Sorghum***:** Global germplasm collections of sorghum consist of 2,35,688 accessions (FAO, 2010a). Largest global collection of sorghum from 93 countries is conserved at ICRISAT, Patancheru (Upadhyaya *et al*., 2017). ICRISAT has a total of 41,023 accessions in the gene bank which include 35,632 landraces or traditional cultivars, 4841 breeding material, 461 wild relatives and 89 improved cultivars (GENESYS-PGR, 2019). China had also collected 12,836 accessions throughout the country and 10,414 of these have been registered and preserved in National Genetic Germplasm Resources Bank.

Indigenous collections in NBPGR are from 30 states and union territories with majority from Maharashtra (2,525), Andhra Pradesh (1,654), Madhya Pradesh

(1,224), and Karnataka (1,144). A total of 42,048 sorghum accessions have been stored in ICAR-IIMR Gene Bank, which are readily supplied to the AICRP centers for utilization. This collection includes landraces, mapping populations, breeding material, varieties, hybrids and parental lines of hybrids.

Maize: Global germplasm collection of maize consists of 3,27,932 accessions (FAO, 2010a). CIMMYT is working as a global repository of maize germplasm collection and is conserving 28,193 accessions from 64 countries. Apart from the germplasm collection, there is one primary maize bank especially for genes, the Maize Genetic Stock Centre. This centre has conserved and annotated the maize mutant stocks (nearly 80,000) and are available to maize geneticists.

Indigenous collection of 8,616 accessions in NBPGR are from 30 states and union territories with majority from Himachal Pradesh (976), Delhi (635), Mizoram (503), Andhra Pradesh (500), Uttarakhand (472) and, Jammu and Kashmir (400), whereas the exotic collections are from three countries mainly from Indonesia (97), Argentina (22) and Thailand (9). A detailed report on germplasm collection status, diversity mapping and gap analysis in India was recently published (Pandey *et al*., 2015)

*Barley***:** Global barley collection in different gene banks throughout the world are 4,66,531 (FAO, 2010a) stored in 49 gene banks across five continents. Among the national collections, highest collections are maintained in Canada (39,852) followed by USA (29,838), Brazil (29,227), UK (23,603) and Germany (22,106) (Anonymous, 2008). As a global collection centre, ICARDA has 32,790 accessions which include 18,935 traditional cultivar/ landraces, 8,458 breeding material, 2,392 wild and 46 wild relatives.

Indigenous collections in NBPGR are from 20 states and union territories with majority from Himachal Pradesh (1,177), Haryana (637), Uttarakhand (442) and Delhi (441). A total of 8,159 germplasm (both indigenous and exotic) are being maintained in medium-term storage facility at Karnal (IIWBR, 2019).

Small millets: Dwivedi *et al*. (2012) summarized the collection of cultivated and wild relatives of different small millets across the continents, in national and international gene banks. The major collection of germplasm accessions are stored in gene banks viz., foxtail millet at China, India, France and Japan; finger millets in India and African countries; proso millet in Russian Federation, China, Ukraine and India; barnyard millet in Japan and India; kodo millet in India and USA; and little millet in India (Upadhyaya *et al.,* 2016c; Vetriventhan *et al.,* 2016). ICRISAT is holding the global germplasm of small millets (Table 2).

Table 2. Small millet germplasm holdings at ICRISAT

Crop	Cultivated	Wild	Total
Finger millet	5880	204	6084
Foxtail millet	1488	54	1542
Little millet	473	-	473
Kodo millet	665	-	665
Proso millet	849	-	849
Barnyard millet	749	-	749
Total	10,104	258	10,362

Indigenous collection in ICAR-NBPGR for foxtail millet is from 26 states with maximum from Tamil Nadu (597) followed by Andhra Pradesh (506). The collection of finger millet is from 26 states with maximum from Uttarakhand (890) followed by Andhra Pradesh (852); little millet from 20 states with maximum from Andhra Pradesh (447) followed by Madhya Pradesh (250); kodo millet from 13 states with maximum from Madhya Pradesh (402); and barnyard from 18 states with maximum from Uttarakhand (186) (NBPGR, 2019). AICRP on small millets is maintaining germplasm at National Active Germplasm Site (NAGS) (AICRPSM, 2018).

Legumes

The major legumes of drylands are chickpea (*Cicer arietinum* L.), mungbean [*Vigna radiata* (L.) Wilczek], clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] and mothbean [*Vigna aconitifolia* (Jacq.) Marechal]. Globally over 86,533 cultivated and 1032 wild germplasm accessions of chickpea are conserved in world gene banks. ICRISAT (20,267), International Centre for Agricultural Research in Dry Area (13,362) and NBPGR (15,084) have the major holdings of chickpea collections. Worldwide, a total of 43,027 mungbean accessions are held *ex situ* (Nair *et al*., 2012). ICRISAT holds 13,783 accessions of pigeonpea while more than 10,000 accessions are being maintained by the All India Coordinated Pigeonpea Improvement centers. Majority of clusterbean and mothbean germplasm collections are confined to Indian arid regions with some contribution from Pakistan in clusterbean. In India, NBPGR has been mandated for collection and conservation of germplasm (Table 3).

Table 3. Germplasm holdings of major legumes at ICAR-NBPGR, New Delhi

Crop	Landrace	Elite/breeding lines	Wild	Others	Total indigenous	Exotic	Total
Chickpea	4567	622	47	6765	12001	3083	15084
Pigeonpea	3715	1157	17	6132	11021	308	11329
Mungbean	887	146	13	2301	3347	405	3752
Mothbean	176	35	53	1195	1459	31	1490
Clusterbean	203	103	2	3659	3967	31	3998

Chickpea and pigeonpea germplasm have been collected from almost all parts of the country. Major areas of collections in clusterbean include Rajasthan (1,376), Haryana (243), Punjab (155) and Gujarat (105) while in mothbean the majority of collectioins have come from Rajasthan (541), Gujarat (167) and Haryana (78).

Grasses

Economy of the arid regions of drylands is closely linked to the raising of livestocks which mainly depend upon the native rangelands for their sustenance. About 106 species of grasses are found in western Rajasthan, though buffelgrass (*Cenchrus ciliaris* L.), birdwood grass (*Cenchrus setigerus* Vahl), sewan (*Lasiurus sindicus* Henr.), marvel grass [*Dichanthium annulatum* (Forsk) Stapf], blue panic (*Panicum antidotale* Retz.), murat (*Panicum turgidum* Forsk.) etc. are the main range grasses dominating the arid regions of drylands. Details of germplasm collections of grasses acquired mostly from arid regions of Rajasthan are given in Table 4.

Medicinal Plants and Shrubs

Drylands harbour a number of plants and shrubs that have a great relevance for medicinal purposes. Aloe [*Aloe vera* (L.) Webb. & Berth] is an important medicinal crop of arid and semi-arid regions of drylands and can withstand water scarcity. A total of 123 accessions of *A. vera*, have been collected and conserved from arid regions of Rajasthan and Gujarat. Guggual [*Commiphora wightii* (Arn.) Bhandari] is a commercially high-valued medicinal species as it yields oleo gum-resin of immense pharmacological importance. Only 19 collections of *C. wightii* are reported and deposited in NBPGR from ICAR-CAZRI, Jodhpur. Henna (*Lawsonia inermis* L.) is a hardy aromatic shrub capable of growing on diverse soil and climatic conditions. A total of 111 accessions from various states are with ICAR-NBPGR.

Shrubs like bawli (*Acacia jacquemontii* Benth.), phog (*Calligonum polygonoides* L.), kair [*Capparis decidua* (Forsk.) Edgew.], khara lana [*Haloxylon recurvum* (Moq.) Bunge ex Boiss.], lana [*H. salicornicum* (Moq.) Bunge ex Boiss.], kheep [*Leptadenia pyrotechnica* (Forsk.) Decne], bordi [*Ziziphus nummularia* (Burm.f.) Wight &Arn.] etc. have unique adaptability to harsh arid climatic conditions. During the last two decades, a wide range of unique germplasm have been collected from western Rajasthan and conserved in field gene banks of ICAR-CAZRI (Table 5).

Horticultural Crops

The drylands are suitable for growing many fruit species despite climatic constraints and limited irrigation facilities. These include ber (*Ziziphus mauritiana* Lam.), khejri [*Prosopis cineraria* (L.) Druce], peelu (*Salvadora oleoides* Decne.), pomegranate (*Punica granatum* L.), aonla (*Emblica officinalis* Gaertn.), date palm (*Phoenix dactylifera* L.), bael [*Aegle marmelos* (L.) Corr.], lasora (*Cordia myxa* L.), karonda (*Carissa carandas* L.), kair (*Capparis decidua*) etc. These fruit crops are very rich in nutraceuticals and can provide income security besides contributing to environmental amelioration. Great deal of variability exists in these species both at genotypic and phenotypic level as they are primarily propagated by seeds. The role of germplasm in the improvement of arid fruit crops has been well recognised and a large number of collections are maintained at different stations (Table 6).

Table 4. The number of germplasm collections of grasses in the field gene banks at ICAR-CAZRI, Jodhpur

Species	Number
Cenchrus ciliaris	85
Cenchrus setigerus	42
Cymbopogon jwarancusa	09
Lasiurus sindcus	111
Panicum antidotale	44
Panicum turgidum	01

Table 5. The number of germplasm collections of shrubs in the field gene banks

Species	No. of germplasm	Location of field gene bank
Acacia jacquemontii	26	ICAR-CAZRI, RRS, Bikaner
Calligonum polygonoides	32	ICAR-CAZRI, RRS, Bikaner
Capparis decidua	35	ICAR-CAZRI, RRS, Jaisalmer
Haloxylon salicornicum	55	ICAR-CAZRI, RRS, Bikaner
Haloxylon recurvum	2	ICAR-CAZRI, RRS, Bikaner

Multi-purpose Trees

The most important tree species in the drylands include khejri (*Prosopis cineraria*), kumat [*Acacia senegal* (L.) Willd.], rohida [*Tecomella undulata* (Sm) Seem.], meethajal (*Salvadora oleoides* Decne.) and kharajal (*S. persica* L.). Global collection of agroforestry tree species is mainly from India and African-Arab countries. The species like *P. cineraria* and *A. senegal* involve accessions from India, Oman, Yemen, Algeria, Mali, Pakistan, Ethiopia, Israel, Senegal, Sudan, Mali, Kenya, Tanzania and Niger. Though, no record for global collection of *T. undulata* and *Salvadora* species are available. India and Pakistan are the major contributors of *P. cineraria* germplasm with 9 and 11 accessions, respectively. Few accessions from Middle-East countries like Oman (4) and Yemen (2) were also recorded in global collection of *P. cineraria* whereas, collection of *A. senegal* was mainly from African and Asian countries *viz.* Sudan (13), Senegal (11), India (6), Niger (6), Pakistan (5) and Kenya (4).

Indigenous collections at ICAR-NBPGR include 48 accessions of *P. cineraria* mainly from Rajasthan and Gujarat and 340 accessions of *T. undulata*. Several accessions of *A. senegal* were collected from

Table 6. Conservation status and major diversity states of germplasm of different arid fruit crops

Crop	Conservation centres	Number of accessions	Conservation status	Major states of diversity
Punica granatum (Pomegranate)	NBPGR	360	Field gene bank	Maharashtra, Gujarat, Karnataka, Rajasthan, Tamil Nadu, H.P., U.P., J&K
	NRCP, Sholapur	375	Field gene bank	
	IIHR, Bangalore	203	Field gene bank	
	CIAH, Bikaner	154	Field gene bank	
	CAZRI, Jodhpur	28	Field gene bank	
	MPKV, Rahuri	170	Field gene bank	
Ziziphus mauritiana (Indian jujube, ber)	NBPGR	285	Field gene bank	Rajasthan, U.P., Haryana, Gujarat, M.P., A.P., Karnataka, Tamil Nadu, Maharastra
	CIAH, Bikaner	318	Field gene bank	
	CAZRI, Jodhpur	40	Field gene bank	
	HAU, Hisar	39	Field gene bank	
	PAU, Ludhiana	35	Field gene bank	
Aegle marmelos (Bael)	NBPGR	427	Cryo-bank (265) and field gene bank (162)	Jharkhand, U.P., Orissa, West Bengal, Rajasthan, Gujarat, Bihar, Chhattisgarh, H.P., A.P., M.P., Maharashtra, Kerla
	NDUAT, Faizabad	12	Field gene bank	
	CISH, Lucknow	54	Field gene bank	
	CIAH, Bikaner	17	Field gene bank	
	GBPUAT, PantNagar	10	Field gene bank	
	CAZRI, Jodhpur	8	Field gene bank	
Capparis decidua (Ker)	NBPGR	35	Cryobank (265)	Rajasthan, Gujarat
	CIAH, Bikaner	3	Field gene bank	
	CAZRI, Jodhpur	4	Field gene bank	
Cordia myxa (Lasora)	NBPGR	231	Cryobank (12), Field gene bank	Rajasthan, Haryana, H.P., Gujarat, Maharashtra, U.P., M.P., Jharkhand,Chhattisgarh
	CIAH, Bikaner	65	Field gene bank	
	CAZRI, Jodhpur	17	Field gene bank	
Emblica officinalis (Aonla)	NBPGR	51	Field gene bank	U.P., Gujarat, Rajasthan, M.P., Bihar, Tamil Nadu, Jharkhand Chhattisgarh
	NDUAT, Faizabad	22	Field gene bank	
	CIAH, Bikaner	50	Field gene bank	
	CAZRI, Jodhpur	8	Field gene bank	
Phoenix dactylifera (Date palm)	CIAH, Bikaner	61	Field gene bank	Gujarat, Rajasthan, Punjab
	RAU, Bikaner	35	Field gene bank	
	PAU, Research Station Abohar	31	Field gene bank	
	GAU, Research Station Mundra	24	Field gene bank	
	CAZRI, Jodhpur	23	Field gene bank	
Carissa Carandas (Karonda)	NBPGR	29	Field gene bank	Bihar, West Bengal, Chhattisgarh, Orissa, U.P., M.P., Jharkhand, Rajasthan, Gujarat, Maharashtra, Kerala, Karnataka, Haryana
	CIAH, Bikaner	8	Field gene bank	
	CAZRI, Jodhpur	5	Field gene bank	
	GBPUAT, Pantnagar	8	Field gene bank	

Updated from Malik SK, Rekha Choudhary, OP Dhariwal and DC Bhandari. 2018. Genetic resources of tropical and underutilized fruits in India. NBPGR, New Delhi. 168p.

different parts of country. However, no study on gap analysis of arid zone tree species has been done but on the basis of economic importance and conservation status, Ministry of Environment and Forests & Climate Change (MOEF & CC) has prioritized large number of forest tree species for conservation. Asia Pacific Forest Genetics Resource Programme and Food and Agriculture Organisation (FAO) had identified priority species for tree improvement and conservation programme. Lack of information on reproductive and population biology of many agroforestry trees along with the poor knowledge of gene pool diversity has led to lack of efforts for the conservation process. There is also limited knowledge on seed viability testing methods, maintenance of field gene banks, and susceptibility of genetic material to pest and pathogens.World Agroforestry Centre has over 500 accessions representing 120 agroforestry tree species, duplicated in a black box at the Svalbard Global Seed Vault, Norway.

Evaluation

Cereals

Almost full set of germplasm accessions of pearl millet for 23 morpho-agronomic traits have been evaluated for various phenotypic and phenological traits, and a huge variation has been observed for all traits (Yadav *et al*., 2017). Specific germplasm accessions have also been identified for use in resistance/tolerance to different biotic and abiotic stresses. Specific accessions have also been identified as a source of superior quality traits. Similarly, a total of 36,325 sorghum accessions have been characterized for important morpho-agronomic characters (Reddy *et al*., 2007). The range of variability available in cultivated races and their wild relatives is extensive, both for qualitative and quantitative traits. There was a wide range for qualitative traits like plant pigmentation from tan to pigmented, midrib colour from white to brown, panicle compactness and shape from very loose stiff branches to compact oval, glume colour from straw to black, glume fully covered to noncovered, grain colour from white to black, endosperm texture from completely starchy to completely corneous, threshability from freely threshable to difficult-to-thresh; grain lustre from lustrous to non-lustrous; and subcoat from presence or absence (Reddy *et al*., 2007). A total of 5,000 accessions maintained at IIMR, Hyderabad had also been characterized (Kudadjie, 2006; Elangovan *et al.,* 2007; Upadhyaya *et al*., 2008a; Durrishahwar *et al.,* 2012). The extent and pattern of genetic diversity within the world sorghum collections have also been investigated (Dje *et al*., 2000; Grenier *et al*., 2000; Casa *et al.,* 2005; Figueiredo *et al*., 2006, Upadhyaya *et al*., 2016b).

The entire set of accessions of barley maintained at IIWBR, Karnal has been evaluated for different biotic and biotic stresses as well as malting quality. A total of 21 genetic stocks have been registered in barley for disease resistance, quality traits, male sterility and altered botanical characters (IIWBR, 2019). Based on evaluation of 5,337 accessions including 2,801 indigenous and 2,536 exotic, germplasm was classified in different groups for various growth and qualitative traits (Sarkar *et al*., 2010).

The small millet germplasm accessions have been evaluated for morpho-agronomic traits (>10 traits) and there was large genetic variation in foxtail millet (Upadhyaya *et al.*, 2008b), finger millet (Upadhyaya *et al*., 2006a), proso millet (Upadhyaya *et al*., 2011), barnyard, kodo and little millet (Upadhyaya *et al*., 2014a). The diversity in entire and core collections of small millets has been reviewed (Vetriventhan *et al*., 2016 and Upadhyaya *et al*., 2016b).

Legumes

Upadhyaya (2003) assessed the pattern of diversity in chickpea based on 21 traits from 16,820 accessions representing 43 countries. Based on geographical pattern of diversity, means for different agronomic traits differed significantly between regions and variances for all the traits among regions were heterogeneous. Majumder and Singh (2005) underlined that Indian sub-continent is the major area of genetic diversity in pigeonpea for a number of traits related to growth habit, duration, yield-contributing traits and resistance/tolerance to biotic stresses and abiotic stresses. Available germplasm accessions of legume crops have been evaluated (Kumar and Singh, 2009) and a large variation has been documented for most of the agronomic traits in chickpea (Archak *et al.,* 2016), pigeon pea (Dua *et al.,* 2007, 2009; Saxena, 2008), green gram (Bisht *et al.,* 1998), clusterbean (Dabas *et al.,* 1989; Dwivedi and Bhatnagar, 2002a) and mothbean (Dwivedi and Bhatnagar, 2002b).

Grasses

Variability in morphological and physiological characters in 10 strains of *Cenchrus setigerus* led to identification of strain 175 that was the most suitable for adaptation to arid zone owing to its higher forage yield, highest

basal and crown diameters capacity for maximum tiller production, dark green leaf with longer and broader leaf blade and ability to sustain grazing pressure and to rejunivate (Chakravarty and Bhati, 1968). Wide genetic variation was observed in the characters contributing to forage yield, forage quality and underground biomass for *Cenchrus ciliaris*, *C. setigerus*, *Lasiurus sindicus* and *Dichanthium annulatum* (Yadav *et al*., 1980; Yadav, 1981; Yadav and Krishna, 1986; Rajora, 1998; Rajora *et al*., 2009). Genotypes of *C. ciliaris* exhibited significant variation with respect to earliness, plant height, tillering, leafiness and dry matter accumulation (Rajora, 1998; Rajora *et al.,* 2009). According to Dabadghao *et al.* (1963), *L. sindicus* exhibited maximum depth (4.03 m) of root penetration into the soil and also their horizontal spread, hence this is the most drought-resistant grass, because it can draw moisture from a broader horizon as compared to other arid zone grasses and remain alive under extreme arid condition.Wide range of variations was observed in the strains for fodder quality (Gupta *et al*., 1985).

Horticultural crops

Most of the present day commercial cultivars are selections from the variability generated by the germplasm collected/introduced in the past. Ber (*Ziziphus mauritiana*) which is commercially important has more than 300 varieties and this enormous diversity may be attributed to sexual propagation, heterozygosity, cross pollination and natural polyploidy. Khoshoo and Singh (1963) reported that segmental alloploidy also plays an important role in creation of variability in *Ziziphus* species. Pomegranate (*Punica granatum*) has a very narrow genetic variability with maximum variability occurring in Maharashtra, Karnataka, Tamil Nadu, Gujarat and Rajasthan. The genetic variability in aonla (*Emblica officinalis*) is widespread particularly in Uttar Pradesh (Pratapgarh), Gujarat, Rajasthan and Maharashtra with Banarasi, Francis, Banshi Red, Chakaiya, and Deshi being well-known old cultivars. Recent cultivars include NA6, NA7, NA10, Krishna, Kanchan, Anand-2 etc.. Evaluation of aonla cultivars in arid areas of Rajasthan revealed variation in growth attributes and physico-chemical parameters of fruits in different varieties (Meghwal and Azam, 2004). There are three major species of date palm grown in India viz., *Phoenix dactylifera*, *P. sylvestris* (L.) Roxb. and *P. canariensis* Chabaud. *P. Dactylifera* is grown commercially. Owing to superior quality edible fruits. At present, 35 date palm varieties are conserved at Date Palm Research Station, Bikaner, 19 cultivars at ICAR-CAZRI, Jodhpur, while only 5-6 varieties are recommended for commercial cultivation. In lasora (*Cordia myxa*), there are no well-defined cultivars, though great variation exists in size of fruits and their pulp content.

In karonda (*Carissa carandas*), some promising types No. 13, 16, 12 and 3 have been identified at Rahuri, Maharashtra (Karale *et al.,* 1989). Phenotypic variability in Karonda was also observed in plant growth, fruit size, shape and colour of fruit at CAZRI, Jodhpur (Bankar and Prasad, 1992; Bankar *et al*., 1992; Meghwal *et al*., 2014a). Singh *et al*. (2007) studied the *in-situ* variability in morphological and fruit traits of *C. decidua* from arid and semi arid-regions. Mahla and Singh (2013) evaluated 45 accessions of *C. decidua* and observed a wide range of fruit diameter, fruit weight, number of seeds per fruit, root length, shoot length and root:shoot ratio. Characterization for fruit and seed characters as per IPGRI descriptors of 30 accessions of *C. decidua* was also done at NBPGR (Anonymous 2017). Pilu (*Salvadora oleoides*), grown naturally in arid areas, showed great variability in growth and quality attributes (Jindal *et al.,* 2006).

Medicinal plants

Of the 123 accessions of *Aloe vera*, collected from arid region, two broad groups were identified: bitter and non-bitter types having significantly different aloin content which ranged from 0.033 to 0.061% in non-bitter types and 6.76 to 12.43% in bitter types (Azam *et al*., 2009). Morphologically, of the 11 floral characters studied, eight characters of non-bitter *A. vera* were significantly different from those of bitter *A. vera* (Azam *et al*., 2012). Jindal *et al.* (2005) recorded considerable variation in morphology and seed traits in natural population of *Commiphora wightii*. Phenophytic observations of *Lawsonia inermis* indicated prevalence of two types of the yellow-flowered henna i.e '*desi'* and '*muralia'* type and both types exhibited diverse morphological and reproductive behavior (Singh *et al*., 2005a). Considerable variability in 'desi' henna has been observed in terms of plant height, canopy spread, leaf length and width, dry leaf yield and dye content of the plant. It is observed that *Lawsonia* from Sojat has more lawsone content than henna produced in other parts of country. Two superior henna germplasm *viz*., Sojat-8 and Sojat-22 were identified and multiplied at ICAR-CAZRI, RRS, Pali, Rajasthan. Evaluation of various

accessions of *Cassia angustifolia* for morphological traits under rainfed conditions at Jodhpur and irrigated conditions at Bikaner, did not reveal any significant variation (Singh *et al*., 2005a).

Shrubs

There was a remarkable variability in shape and size of 70 accessions of *Calligonum polygonoides* collected from 50 diverse sites of western Rajasthan (Beniwal *et al*., 2005). Vyas *et al.* (2012) reported high level of genetic diversity among different collections of *C. polygonoides*, wherein 90.18% RAPD markers were polymorphic. However, the RAPD patterns were not systematic with respect to classification of sampling accords to regions which leads to an uncharacterized diversity in the dendogram. Wide variation was reported among 65 accessions of *Haloxylon salicornicum* for agro-morphological characters (Singh *et al.,* 2015a). Meghwal *et al.* (2014) examined 21 genotypes of *Haloxylon* species with 10 RAPD primers and four primers produced 28 scorable bands all of which were polymorphic.

Multi-purpose Trees

Characterization and evaluation of 16 accessions of *Prosopis cineraria* for various horticultural traits indicated huge morphological variation (Arshad *et al.,* 2006; Sivalingam *et al*., 2011).The variability in vegetative vigour of *P. cineraria* has also been reported by Mann and Saxena (1980), Muthana (1980) and Kaul *et al.,* (1991). Recent survey of khejri germplasm for desirable pod types for culinary purpose led to identification of two superior types which had longer pods and were thornless (Anonymous, 2008b). Thar Shobha is a selection from naturally occurring trees from Bikaner. Jindal *et al.* (1987) and Meena *et al*. (2015) assessed more than 100 accessions of *Tecomella undulata* from different regions and reported a wide variation in several morphological traits. Fast growing accessions of *Acacia senegal* were identified at ICAR-CAZRI, Jodhpur (Jindal *et al*., 2000). Fakuta *et al*. (2015) reported variation in the yield of gum in different accessions of *A. senegal* from Sudan and Sahel. *Salvadora oleoides* accessions collected from Gujarat and Rajasthan were evaluated for diversity in seed size, oil content, seed germination and juvenile traits (Jindal *et al*., 2006). Malik *et al*. (2010) also characterized the fruit and seed characters in 17 accessions of *Salvadora* spp. originating from Rajasthan and Haryana and identified useful accessions for specific traits.

Utilization

Selected genetic resources play a major role in crop improvement programmes. Over the years, systematic evaluation of germplasm accessions available in gene banks has led to the identification of several sources of phenotypic, quality and adaptation traits, and biotic and abiotic stress resistance in a number of species of drylands. Several genetic stocks have also been identified and used as sources of biotic and abiotic stress resistance/ tolerance (Dwivedi and Bhatnagar, 2002a; Kumar and Singh, 2009; Verma *et al*., 2015).

Systematic evaluation of pearl millet germplasm led to the identification of accessions for specific traits including abiotic stress tolerance, biotic stress tolerance and nutritional traits (Yadav *et al*., 2017). In general, Indian pearl millet landraces have mainly contributed for earliness, high tillering, high harvest index and local adaptation (Yadav and Bidinger, 2007), whereas African material has been a good source of high head volume, large seed size and disease resistance (Kumar and Appa Rao, 1987). Several germplasm accessions have been used directly as cultivars after a few cycles of mass selection (Rai *et al*., 1990; Yadav, 2004; Upadhyaya *et al*., 2007; Yadav and Rai, 2013).

Sorghum germplasm accessions have also been identified for different traits like earliness, resistance to diseases and insect-pests (Prom *et al.,* 2007; Prom *et al*., 2011; Erpelding, 2011). Several sorghum germplasm accessions have been directly released as cultivars in 17 countries (Reddy *et al.,* 2006; Upadhyay*et al*., 2014b).

Kaul *et al*. (2018) evaluated maize accessions (registered at NBPGR for specific traits) for tolerance to various diseases, insects, early maturity, medium maturity, high tryptophan content, QPM (quality maize protein) etc. In small millets, germplasm accessions have been identified as source for specific traits by various researchers (Vetriventhan *et al*., 2016; Upadhyaya *et al*., 2016b).

In pomegranate, varieties like Muskat, Bassein Seedless, Dholka, Jalore Seedless and Jodhpuri Red are the traditional cultivars derived from local material. Selections P-23 and P-26 from Muskat, Ganesh from Alandi, G-137 from Ganesh, IIHR selection from Basein seedless and Yercaud-1 (Sayed *et al*., 1985) have been made. The cultivar Mridula has been developed at Rahuri, from the open-pollinated progeny raised from the F_1 population, derived from Ganesh × Gul-e-Shah

Red (Anonymous, 1994). It has red arils with very soft seeds. At Hisar, Shirin Anar and Russian seedlings possessed resistance to bacterial leaf (Singh and Rana, 1993). Evaluation of nine pomegranate cultivars under arid conditions of Jodhpur revealed significant variation in plant growth, fruit yield and physico-chemical properties of fruits (Prasad and Banker, 2000). The pomegranate orchard in Jalore and Jodhpur district in western Rajasthan have spread through seed propagation with lot of variability (Vashistha *et al*., 2003). Presently, Bhagwa is the most popular variety occupying maximum area under cultivation in India. It has been released by MPKV, Rahuri, Maharashtra by selection from F_2 progeny of the cross between Ganesh × Gul-e-Shah Red. It is a high yielder with an average fruit yield of 20-25 kg/plant. Due to bigger fruit size, sweet and glossy red rind with bold deep red arils, it fetches a very good price in the market and has a heavy demand for export. The fruit matures in about 170-180 days.

Long term evaluation of lasora (*Cordia myxa*) germplasm at ICAR-CAZRI, Jodhpur led to identification of five high yielding genotypes i.e. CZCM-2011, CZCM-2012, CZCM-2021, CZCM-2025 and CZCM-2062. The accession CZCM-2025 has been released as Maru Samridhi from CAZRI with fruit yield more than 100 kg per plant. Evaluation of karonda (*Carissa carandas*) germplasm over a period of eight years for fruit yield and other desirable attributes, led to identification of the accessions *viz*., CZCC-2011, CZCC-2022 and CZCC-2031 for hot arid zone. Subsequently, one of the accessions, (CZCC-2011) was released as Maru Gaurav, an improved high yielding variety from ICAR-CAZRI Jodhpur. The variety Thar Kamal has been released recently from ICAR-CIAH, Bikaner (Singh *et al*., 2015b) while Pant Manohar, Pant Suverna and Pant Sudarshan were released earlier from GBPUAT, Pantnagar.

Despite collection and conservation of large number of germplasm accessions, only fraction of these resources have been utilized in genetic improvement programmes across the world. Formation of trait-specific gene pools, core and mini core collections are likely to enhance the utilization of genetic resources to a greater degree. The core collection (10% of entire collection) and mini-core collection (10% of core collection or 1% of entire collection) of many drylands field crops have been established which may enhannce the utilization of germplasm (Grenier *et al*., 2001; Upadhyaya *et al.,* 2006a, 2006b; Bhattacharjee *et al.*, 2007 Upadhyaya *et al.,* 2008b; Upadhyaya *et al*., 2009; Yong-Bi Fu and Horbach 2012; Vančetović *et al*., 2015).

Access to Germplasm Collections

The ICAR-NBPGR, New Delhi is the nodal agency for supply of plant germplasm, within India to researchers under the material transfer agreement. The bureau also facilitates import of germplasm from the countries having treaty as per convention of biological diversity act. As per agreement with the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), CGIAR centres like ICRISAT, ICARDA, CIMMYT supply germplasm free of cost to global research community using the Standard Material Transfer Agreement (SMTA) to strengthen breeding programmes. Various systems are in place to retrieve information on many aspects of germplasm collections, such as PGR portal of ICAR-NBPGR, Genebank Information Management System (GIMS) at ICRISAT, GRIN-Global used at USDA ARS and SINGER at CGIAR centers.

Effect of Climate Change on Dryland Agro-biodiversity

Climate has been the main motivating force in the nature for evolution of biological systems. Climate change, happening at a much faster rate in terms of frequency and extent of extreme of weathers, floods and droughts, might have negative impact on agrobiodiversity. This may threaten the livelihood of dryland inhabitants, which is closely intertwined with the diversity cherished by them since long. Climate change will affect the plant species with respect to their distribution, reproduction timings, length of growing seasons etc. Thus, it will modify the topography of plant or crop suitability. Moreover it will affect the crop wild relatives, which are an important component of agrobiodiversity. Climate change will significantly reduce the suitable areas of some of the crops like wheat and oats. However, suitable areas for some of the dryland crops like pearl millet and small millets are likely to increase.

Role of Agrobiodiversity in Imparting Adaptation to Climate Change

Agrobiodiversity holds potential solution for adaptation to climate change. Adaptive traits of dryland organisms will be of immense value in coping with climate change. Larger genepool of various arid crops will facilitate breeding of genotypes better adapted to shifts in climatic conditions. Crop species such as pearl millet, mothbean, clusterbean, forage grasses (*Lasiurus, Cenchrus,*

Cymbopogon) can provide invaluable genes imparting tolerance to abiotic stresses. Woody perennial species having wide range of adaptability need greater attention in climate change scenario. Genera like *Acacia, Ziziphus, Cordia, Grewia, Indigofera, Crotalaria, Maytenus, Balanites* etc. need greater attention. Moreover, genetic resources from arid rangelands would play a significant role as valuable source of diverse genetic material needed for rehabilitation and improvement of degraded arid rangelands to the level of a multitiered silvi-pastoral systems.

Threats to Drylands Agrobiodiversity

The agrobiodiversity of drylands is facing serious threat due to climatic and anthropogenic factors. Habitat destruction/change in land use pattern is one of the major threats to dryland agrobiodiversity. Conversion of key grasslands in hot arid areas into cropping is threatening the existence of native grasslands particularly *Lasiurus sindicus* and *Panicum turgidum* grasslands. Conversion of *P. turgidum* dominated grasslands into croplands in Jaisalmer district is a great loss to natural habitat of *Caralluma edulis* which is one of the threatened species of great Indian Thar Desert.

Grazing intensity of small and large ruminants in arid and semi-arid regions is 3-5 times higher than what can be called as sustainable in these regions. Increased livestock population is leading to deterioration in composition of forage species. There is a significant loss of diversity in key palatable species.

Unsustainable practices are leading to exhaustion of genetic stocks and erosion of biodiversity. Non-scientific methods of gum and resins collection in certain shrubs of drylands are causing a decline in population of certain species. For example, loss of diversity and plant population in guggal (*Commiphora wightii*), in Jaisalmer district, is a major concern due to its overexploitation for oleo-gum resin. Further, unsustainable harvesting practices particularly in those medicinal plants which have underground and reproductive parts is also a serious concern in important species like *Ceropegia, Urginea* and *Dipcadi* in western Rajasthan. Large scale root digging for fuel wood in key species like Phog (*Calligonum polygonoides*) in western Rajasthan has threatened this important rangeland shrub of Thar Desert.

Species like *Prosopis juliflora* in drylands of Rajasthan and Gujarat, *Lantana camara, Parthenium hysterophorus* in semi-arid regions are the problematic invasive species. Proliferation of *Prosopis juliflora* in Kutch region of Gujarat and Gajner century of Bikaner, Rajasthan is threatening the habitat of indigenous Banni grasslands and *Heliotropium rariflorum,* respectively.

Dilution of traditional management practices is also an important factor for loss of biodiversity**.** Traditional management of *Orans* (sacred groves), *Gauchars* (common grazing lands), *Agors* (catchment areas for water harvesting) in western Rajasthan that were harbouring agro-biodiversity are the best examples which are losing their relevance in current scenario.

Afforestation with inappropriate woody perennial (replacing native species with exotic ones) is also one of the threats to biodiversity as it affects the ecosystem services at local scale.

Measures for Conservation of Dryland Agro-biodiversity

Tremendous efforts have been made towards *ex situ* conservation of agrobiodiversity from drylands. However, desired attention has not been paid for *in situ* conservation of genetic resources of drylands. Farmers need to be incentivised for preservation of agrobiodiversity in their agricultural fields. Planting of locally adapted multipurpose shrubs and woody perennials on farm boundaries is one example of conserving biodiversity and also from climate change mitigation point of view. Dryland farmers cultivating traditional landraces of crops and rearing native breeds need to be suitably recognized and rewarded.

Certain traditional farming systems and specific habitats do play a very critical role in conservation of genetic resources. For instance, saline depressions (Playas) or lakes are scattered throughout drylands in Rajasthan. Significant *ranns* may be seen in the district of Barmer, Bikaner, Jaisalmer, Jodhpur and Nagaur where several important halophytes are abundantly found. Another good example comes from runoff farming system (*Khadins*) in western Rajasthan that plays an important role in on-farm conservation of agro-biodiversity of traditional varieties of crops like pearl millet, clusterbean, wheat, chickpea, mustard and indigenous trees on bunds.

Communities play a great role in management of genetic resources in drylands agro-ecosystems. There is a greater need to capacity building and raising

awareness among the drylands farmers for promotion and conservation of agrobiodiversity.

Conclusion

Agrobiodiversity in drylands has undoubtedly played an extremely critical role in achieving food and fodder security, in addition to raising the resilience to climatic stresses of drylands. However, the agro-biodiversity is facing several complex challenges due to global warming-mediated climate changes and due to several anthropogenic factors like habitat destruction, high grazing/browsing pressure, unsustainable exploitation of natural resources and dilution of customary conservation practices. This situation calls for several interventions at scientific and policy fronts to conserve the genetic diversity. Genetic resources of drylands are potential sources of native genes conditioning resistance to various biotic and abiotic stresses, present unique study material to understand the mechanism of adaptation to abiotic stresses and are likely to serve as an excellent genomic resource for isolation of candidate genes for tolerance to climatic and edaphic stresses for accelerating further genetic improvement. Because of these reasons, enormous efforts have been made, in the past, to collect and conserve them. Given that agrobiodiversity is dyanamic in nature, continuous explorations are needed in the regions where collection gaps have been indicated, taking help of GIS and other modern tools. *Ex situ* conservation efforts are to be strengthend and e-resources to be developed to enhance the utilization of genetic resources in order to broaden crop genetic base which is very essential to mitigate the effects of climate change.

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Indian J. Plant Genet. Resour. 33(1): 17–31 (2020)
DOI 10.5958/0976-1926.2020.00003.0

REVIEW ARTICLE

Arid Horticultural Crops: Status and Opportunities under Changing Climatic Conditions

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Arid ecosystem, especially 'Thar Desert' of India possess highest flora and fauna among the desert ecosystems of the world. It has a very rich floral diversity consisting about 628 species, 352 genera and 87 families, mainly occupied by dry grassland, trees, thorny bushes, and arid fruits and vegetables of economic importance. The adapted species of hot arid zone have specific traits of high significance in future for climatic changes and/or the emergence of new diseases. On the other hand, herbal nutraceuticals and antioxidants are gaining momentum world over for human being as well as animal's health care and arid flora are treasure house of such traits. Mining of unique genes from arid flora provides ample scope for imparting abiotic stress tolerance in the high yielding commercial crop cultivars. Most of the native flora of this region viz. *Khejri, ker, kumat*, karonda, *kachri, pilu*, lasora, bitter apple, cactus pear, *phog, kheep*, etc are unexploited and underutilized which require sincere research efforts for their conservation and sustainable utilization at commercial level. Nutraceutical and nutritional profiling of selected indigenous and traditional crops and varieties, and their bioavailability can help to determine which crops should be promoted and marketed for the health benefits. Besides, arid regions have an ample scope for introducing a number of crops from isoclimatic regions for crop diversification and promotion of nutritional security. Furthermore, the Indira Gandhi Canal Project has increased the over-exploitation of 'Thar Desert' for agricultural activities which enhanced the domestication of animals, particularly dairy animals like cows, buffalos, goats and other ruminants in the region. Also, the area under fruits, vegetables and spices has increased substantially since past few decades. Thus, sustainable management of these arid horticultural native crop plants certainly reduces the poverty, malnutrition and improves the nutritional quality of the foods and ultimately ensure nutritional security of resource poor people living in hot arid climate. This review will be helpful in conserving native flora of arid region and their sustainable use during the scenario of climate change.

Key Words: Abiotic stresses, Arid horticulture, Biodiversity, Climate change

Introduction

Climate change is one of the major challenges in plant biodiversity which adversely affect the growth, yield and quality attributes of the plants. In the present scenario, global climate change is a major threat for socioeconomic activities including agriculture and forestry and is a major hazard for biodiversity and ecosystem (Lepetz *et al.*, 2009). India with diverse soil and climatic conditions comprised with several agroecosystems, provides a huge opportunity to cultivate a variety of horticultural crops but an arid ecosystem is most vulnerable to climate change. In the arid ecosystem, 'Thar Desert' is the ninth largest desert of the world, but it has abundant biodiversity status. The vegetation of this region is adapted to xerophytic conditions. It is a biodiversity hotspot of a huge flora and fauna which are flourishing under such a harsh conditions.

Arid region is characterized by low and erratic rainfall, frequent droughts, extremes of diurnal and annual temperatures, low humidity, poor availability of nutrients, high evapotranspiration rate and high wind velocity. During summer (March to June), the maximum temperature generally varies between 45°C and 50°C, while temperatures in winters (November to February) range between 15-25°C (Fig. 1 and 2). More than 88% of total annual rainfall received less than 25 cm during Monsoon season (July to October) [Fig. 3]. The soil of the 'Thar Desert' is characterized by poor soil fertility. It is dominantly sandy with 60-90% fine sand and 2-10% of silt-clay in the topsoil and it has very less organic matter. The sifting sand dunes is a natural phenomenon of this region. The soil has low to medium available phosphorus and medium to high available potassium. The average pH of the soil of the desert ranges from 7.6 to 8.5. Salinity and sodicity of the soil in some

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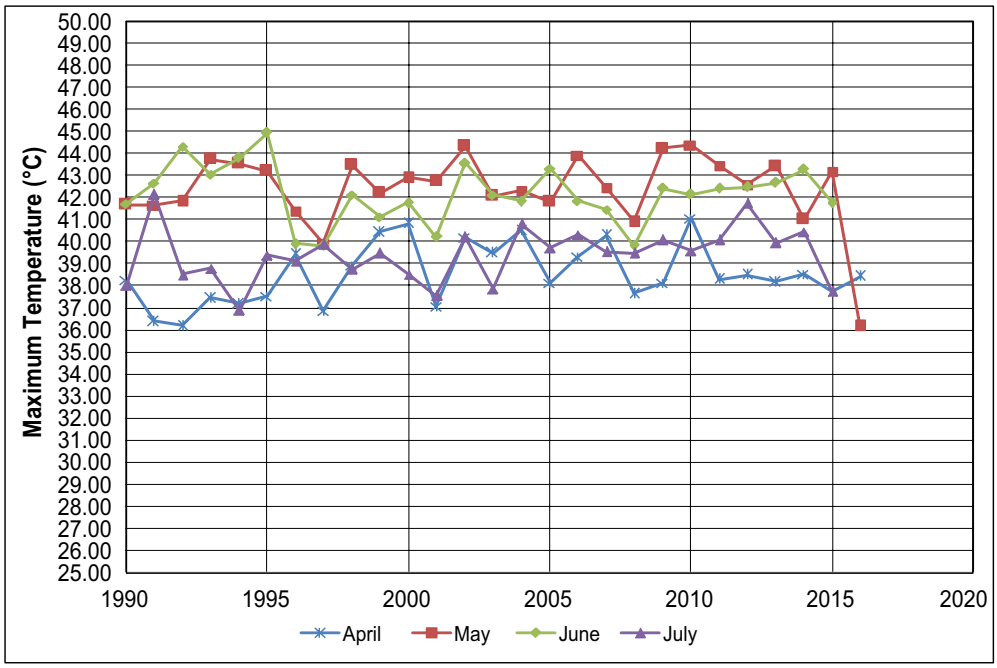

Fig. 1. Variations in the maximum temperature over the past 25 years during summer season

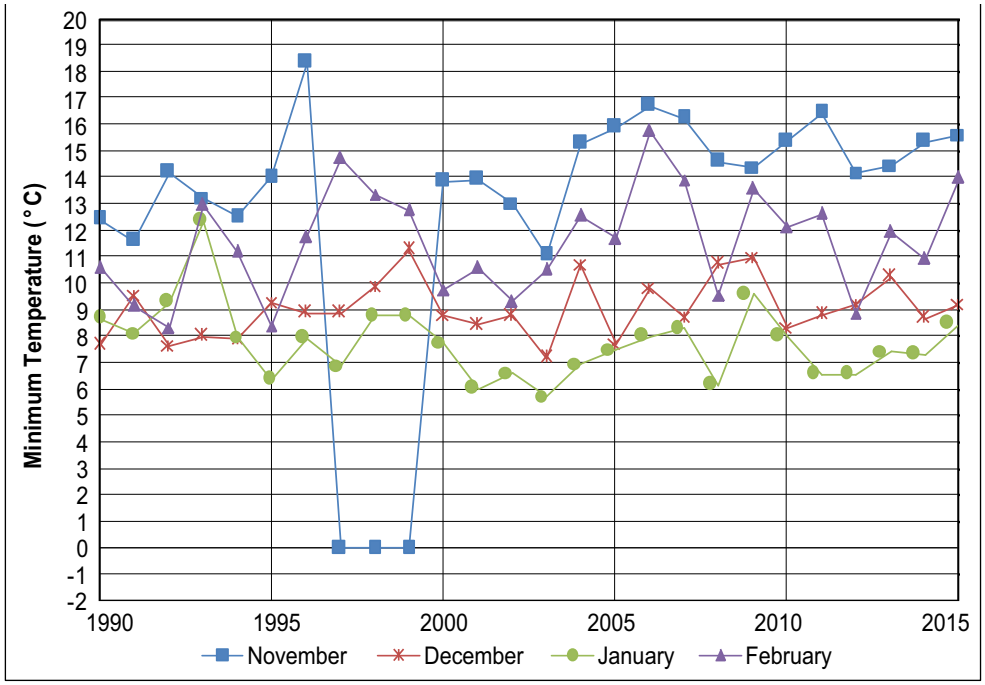

Fig. 2. Variations in the minimum temperature over the past 25 years during winter season

areas of the desert is higher, which is mostly confined to areas with depressions (Charan and Sharma, 2016). The isohyets map of Rajasthan shows that the eastern part of the desert receives high rainfall (up to 400 mm) as compared to the western part (about 100 mm) and hence, vegetation cover is comparatively dense in the eastern part. The vegetation of the region has adapted to these edapho-climatic extremities, which helps the plants to grow and sustain the adverse xerophytic conditions. It is reported that the 'Thar Desert' represents only 5%

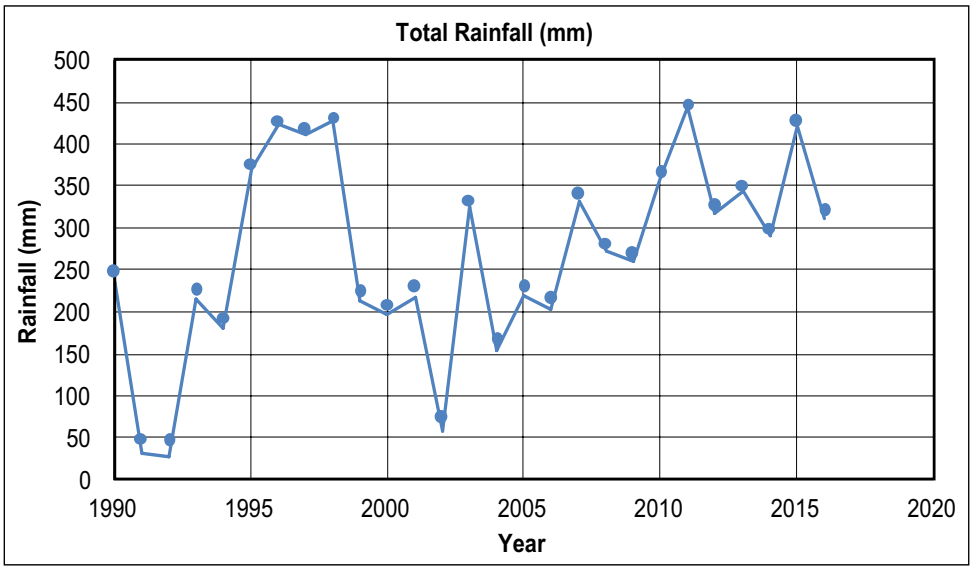

Fig. 3. Variation in total annual rainfall over the past 25 years

of the flora of India, which has about 17,500 flowering plants. The average population density in the 'Thar Desert' is 83 persons/ km^2 while in other deserts of the world; the population density is just 7 persons/square km. In India, more than 60% of the geographical area of the 'Thar Desert' lies in the Rajasthan state (Charan and Sharma, 2016).

For the last fifty years, the climatic regime has adversely affected, especially due to anthropogenic causes, at local as well as global level. A report of the Inter-Governmental Panel on Climate Change has projected hotter days and warm nights and a reduction in rainfall in arid regions by the 21st century. It is reported that the consequences of climate change may be very adverse for the biological diversity of the arid region (Charan and Sharma, 2016) and adversely affects the production and yield of crop plants. Perennial desert flora like *khejri, ker, phog, pillu, ber,* etc. provides a natural habitat for numerous herbaceous plants and soil microbes in arid zone. It is reported that most of the plants of the 'Thar Desert' are having different medicinal properties and therefore, they are being used by tribes for curing their ailments. In order to increase the function of terrestrial species of arid ecosystem, there is an urgent need to conserve and manage the flora of arid ecosystems. Moreover, horticultural crops are also sensitive to climate change through changes in atmospheric temperature, rainfall, soil moisture, humidity and wind velocity (Malhotra, 2017; Saroj, 2018). The major consequences of climate change on horticultural crops in this region are erratic rainfall patterns and unpredictable high temperature during dry spells which consequently reduce crop productivity and quality. However, it is not always to put adverse effects on crop plant, especially on arid horticultural crops. The sharp fluctuations in day and night temperature during autumn, spring and summer help in development of sweetness in sweet orange, kinnow, ber and date palm and arils colour and sweetness in pomegranate and *mateera* pulp (Sharma *et al*., 2018). Therefore, the conservation, characterization and utilization of arid biodiversity in terms of arid fruits and vegetables are the most important aspects in the present climate change scenario *per se*.

Effect of Weather Aberrations on Arid Crops

Weather aberrations from the normal climatic pattern, sometimes have adverse influence on various crops in the arid region. For example, in general, frost occurrence is a common phenomenon in arid regions during December–January, but sometimes it was happened in first fortnight of February. Similarly, severe hailstorm of marble size was occurred in Bikaner district of Rajasthan in the month of March, 2016, which badly affected cultivated crops especially, date palm, rapeseed and mustard. In 2019, prolonged winter and rains in the month of February-March significantly affected few crops like date palm and lasoda (*Cordia myxa*) and thereby delayed flowering. Generally, in date palm spathe emergence starts from the last week of January and completes up

to February and flowering commences in the month of March. But this year, due to a prolonged winter coupled with rains during February-March delayed the spathe emergence and subsequent flowering in date palm. Also, flowering in date palm, completed in April, 2019 which ultimately will delay the fruit ripening. The fruits will ripe during rainy season in the month of July instead of June which will badly affect the fruit quality. Since, date palm harvested in arid regions at *doka* stage for commercial consumption and *pind* stage (attained during June-July) is not suitable for Indian conditions because of monsoon rains with dust storms occurred during June-July. Likewise, in phalsa also, under arid region, flowering mainly commences from the second fortnight of February and completes up to 20th March, and fruit harvesting/picking starts from third week of April and completed up to first week of May. This year due to prolonged winter, flowering commenced in the month of April, 2019, therefore fruit ripening started from the second week of May ultimately fruit picking/harvesting delayed by about 20-25 days. Sometimes, sudden rise in temperature during March (>40 ºC) may also affect arid vegetables mostly cucurbits. Early break of monsoon followed by prolonged cessation of rains will lead to total failure of arid vegetables. Such weather aberrations not only affect horticultural crops in arid region but also effect field crops, pulses, oilseed crops, etc.

Biodiversity of Hot Arid Region

India represents one of the greatest emporia of ethnobotanical wealth. Like other parts of India, in hot arid regions too, rural and tribal communities have precious information about utilization of indigenous plants. Besides, identification of plants as food, fodder, medicine, etc., their also exists similar experience on life sport species for exigencies like drought and famines, which is less utilized so far. Several researches made contribution on ethnobotanical aspects of 'Thar Desert' of western Rajasthan (Singh and Rathore, 2018). Traditional species of economic importance of the hot arid region have immense value as evolved in nature to survive under abiotic stress conditions. They have become adapted to cope with many natural hazards created due to global climate change and also developed resistance to the pest and diseases. Oozing of essential oil/gums by certain arid plants appears to play a vital role in protecting them against drought and higher temperature. Now a day, herbal nutraceuticals, antioxidants, adaptogen herbs, etc., are gaining momentum world over for human being as well as animal health care. The adapted species of hot arid zone have specific traits; such of these traits could prove very important in future for climatic changes or the emergence of new diseases (Singh and Rathore, 2018). The 'Thar Desert' has a very rich floral diversity, including dry grassland, trees, thorny bushes, and arid fruits and vegetables of economic importance. Among them, *khejri* (*Prosopis cineraria*) is known as *Kalpavriksh* and considered as the lifeline of hot arid zone of India which is integral part of an arid ecosystem.

One of the important geological features of the 'Thar Desert' is the presence of some ephemeral rivers, including Luni, Sookdi, Ghagghar, Bandi and Jojri river, which play an important role on micro-climatic conditions of the regions through which they traverse and hence, they affect the vegetation of the 'Thar Desert' (Charan and Sharma, 2016). A total of 62 families, 157 genera and 206 species were documented from the desert area. Among the existing families, Fabaceae is the largest family with 29 species, followed by Poaceae (26 species) and Asteraceae (15 species), Amaranthaceae (10 species), Cucurbitaceae (9 species), Convolvulaceae (6 species), Boraginaceae, Euhorbiaceae and Lamiaceae (5 species each), Acanthaceae, Brassicaceae, Capparaceae, and Zygophyllaceae (4 species each), Solanaceae, Apocynaceae, Asclepiadaceae, Menispermaceae, Tiliaceae, Malvaceae and Chenopodiaceae (3 species each), Aizoaceae, Caesalpinioideae, Cleomaceae, Cyperaceae, Hydrocharitaceae, Moraceae, Nymphaceae, Molluginaceae, Pedaliaceae, Plantaginaceae, Rhamnaceae, Salvedoraceae and Tamaricaceae (2 species each), while rest of 29 families are represented with one species. The habit wise analysis of the study shows that herbaceous vegetation (60.10%) were highest prevailing vegetation in 'Thar Desert' followed by shrubs (16.26%), trees (14.29%) and climber (9.36%) according to Charan and Sharma (2016).

Biodiversity of Horticultural Crops

Globally, drylands are a typical terrestrial system of the earth constrained with low water availability. Drylands occupy about 41.3% of the land surface in the world, where major proportion is arid and semi-arid regions (25.80%). Traditionally drylands have been largely used for livestock, but they are increasingly being converted into horticultural land. The livelihood of more than 1 billion people in some 100 countries is threatened by desertification. Nearly 1 billion of the

poorest and most marginalized people, who live in the most vulnerable areas, may be the most severely affected by desertification. The total dryland population is 2.1 billion, indicating the home to one in three people in the world today. As far as India is concerned, arid region alone occupies about 12.02% of the geographical area. The hot arid region is spread over about 31.7 million ha area mainly in the states of Rajasthan, Gujarat, Andhra Pradesh, Punjab and Haryana, which inhabit on an average 61 persons per square km, making up a population of nearly 20 million people. The direct land degradation factor of dry lands are extremely low precipitation, low soil moisture, high evapotranspiration and indirect drivers are mostly human derived and include poverty, low adoption rate of advance technologies, traditional marketing system and sociopolitical dynamics (Saroj, 2018).

Arid fruit crops: Large number of fruit crops are being cultivated in arid regions. Some fruit crops are grown at the commercial level like pomegranate, date palm, ber, aonla, tamarind, custard apple, citrus, *etc*. In past few decades, considerable area has come up under fruits like aonla, ber, pomegranate, annona, fig and phalsa in different parts of the country. Ber has spread from northern states to the western and southern India from a mere 12,000 ha in 1978 to nearly 86,000 ha in 2015-2016 with a production of about 0.90 million tonnes. Similarly, the area under pomegranate has also leaped to over 2.16 lakh ha. Likewise aonla, presently cultivated on 80,000 ha with the production of 2, 80, 000 tonnes. This has become possible as a result of the research and developmental efforts of the different organizations of NARS. Under-utilized horticultural crops like., bael, jamun, karonda, mulberry, phalsa, lasoda, chirounji, *pilu*, mahua, wood apple, manila tamarind, *ker*, khirni, cactus pear etc. are not exploited well. Such fruit trees are not only hardy but have high nutritional and nutraceutical values which need proper attention. A list of arid fruits with other details are given in Table 1 (Vashishtha, 2005).

After massive research work on arid fruits, a large number of varieties have been released by different R&D organizations which are recommended for commercial cultivation in arid and semi-arid regions of the country (Table 2).

Underutilized arid flora: In the hot arid region of India, a large number of naturally grown plant biodiversity can be seen across the roadsides and on the sand dunes of barren lands (Table 3). These flora are totally grown under rainfed conditions and show typical characteristic of adaptation under harsh situation of an arid ecosystem. Other than cultivated fruit and vegetable crops in arid regions, these flora have economic importance for livelihood of this region and play a greater role to maintain

Table 1. List of major arid fruits in India

Botanical Name	Common name(s)	Family	Chromosome no. (2n)	Origin/distribution
Aegle marmelos (L.) Correa	Bael fruit, Bael	Rutaceae	36	Northern India
Opuntia ficus-india L. Mill.	Cactus pear, Prickly pear	Cactaceae	22-88	Mexico
Capparis decidua (Forsk.) Edgew	Capparis, Ker, Teet	Capparidaceae	14, 16 (2x)	Arid region of India
Buchanania lanzan L.	Almondette tree, Chironji	Anacardiaceae	-	Western Peninsula
Cordia myxa Roxb.	Cordia, Lasoda, Gonda	Boraginaceae	-	India
Annona squamosa L.	Custard apple, Sarifa	Annonaceae	14, 16	Tropical America
Phoenix dactylifera L.	Date plam, Khajur	Palmaeae	36	Around Persian Gulf, Iraq
Ficus carica L.	Fig, Anjir	Moraceae	26	South-East Asia
Emblica officinalis Gaertn	Indian gooseberry, Aonla	Euphorbiaceae	18, 28	Peninsular India
Zizyphus mauritiana Lamk.	Indian jujube, Ber	Rhamnaceae	24	Indian sub-continent
Syzygium cumini (L.) Skeels	Java plum, Jamun	Myrtaceae	40	Indian sub-continent
Carissa carandas L.	Karanda, Karonda	Apocynaceae	12	India
Prosopis cineraria (L.) Druce	Khejri, Jand, Sami	Leguminosae, Mimosaceae	-	Thar Desert of India
Morus alba L.	Mulberry, Tut	Moraceae	308	Northern China/Japan
Grewia subinaequalis DC.	Grewia, Phala	Tiliaceae	36	India
Salvadora oleoides Decne	Pilu	Salvadoraceae	24	India/Tropical Africa
Punica granatum L.	Pomegranate, Anar	Punicaceae	18	Iran, Afghanistan to Himalayas
Tamarindus indica (L.) Gaertn.	Tamarind, Imali	Caesalpiniaceae	24	Tropical Africa
Feronia limonia (L.) Swingle	Wood apple, Kainth	Rutaceae	18	India, Sri Lanka

Table 2. Recommended varieties of fruits for arid and semi-arid regions

Crops	Varieties suitable for arid and semi-arid ecosystem
Pomegranate	Ganesh, Dholka, Jalore Seedless, Mridula, Phule Arakta, Ruby, Amalidana, G-137, Jyoti, Basin Seedless, Goma Khatta, Bhagwa, Super Bhagwa, Solapur Lal
Ber	Gola, Seb, Umran, Banarasi Karaka, Kaithali, Mundia, Goma Kirti, Thar Bhubharaj, Thar Sevika, Thar Malti, Narendra Ber Sel-1 & 2
Bael	NB-5,NB-9, PantAparna, PantUrvashi, Pant Shivani, Pant Sujata, CISH Bael-1 & CISH Bael-2, Goma Yashi, Thar Divya, Thar Nilkanth
Aonla	Banarasi, Chakaiya, NA-6, NA-7, NA-10, Kanchan, Krishna, Anand-1, Anand-2, Lakshmi-52, BSR-1
Custard apple	Balanagar, Mammoth, Island Gem, APK (Ca) 1, ArkaSahan, Phule Janki
Fig	Poona Fig, Dinkar, Dianna, Conadria, Excel
Date palm	Halawy, Barhee, Medjool, Khalas, Khuneizi, Khadrawy, Zahidi
Lasoda	Thar Bold, Karan Lasoda, Maru Samridhi
Tamarind	PKM 1, Pratisthan, Yogeshwari, Ananta Rudhira
Guava	Allahabad Safeda, L-49, Chittidar, Lalit, Hisar Surkha, Pant Prabhat,
Phalsa	Thar Pragati
Wood apple	Thar Gaurav
Jamun	Goma Priyanka, Thar Priya
Chirounji	Thar Priya
Khirni	Thar Rituraj
Mulberry	Thar Lohit, Thar Harit

Table 3. Unexploited and economically important plant biodiversity of the arid region

S.No.	Common Name	Botanical Name	Uses
1	*Ker*	*Capparis decidua*	Pickle and vegetable
2	*Kumat*	*Acacia senegal*	Ingredient of panchkuta
3	*Pilu*	*Salvodora oleoides*	Tooth-paste making, fuel and furniture
4	*Fog*	*Caligonum polyconides*	Culinary utilization
5	*Kheep*	*Leptadenia pyrotechnica*	Vegetable and shelter
6.	*Tumba*	*Citrullus colocynthis*	Medicinal value and bio-pesticide

agro-ecological balance of an arid ecosystem. Besides horticultural importance, these naturally occurring plant biodiversity of arid region could be the potential source ofr biotic and abiotic stress tolerant genes. Thus, the conservation of such unexploited arid flora is also to be taken as a priority area for future prospective.

Arid vegetable crops: Various arid vegetables, including those of Solanaceae, Leguminaceae and Cucurbitaceae families are also grown in arid and semi-arid regions of the country. The cluster bean, moth, Mathania chilli, thorny brinjal and Indian aloe are some widely grown vegetables of the arid region. The crops belonging to family Cucurbitaceae are generally known as 'Cucurbits'. It consists of a wide range of vegetables either used for salad (cucumber) or for cooking (all gourds) or as a dessert fruit (muskmelon and watermelon) or candied or preserved (ash gourd). The majority of cucurbits are characterized by presence of bitter principle i.e. cucurbitacin in some portions of plant and at some stages of stages of development. Cucurbitacins are tetracyclic triterpins having extensive oxidation levels. Fruit is essentially an inferior berry and is called as 'pepo' due to hard rind when mature. The family Cucurbitaceae includes about 118 genera and 825 species, many of which are economically important crops, notably those of the genera are *Cucumis*, *Cucurbita*, *Citrullus*, *Momordica*, *Lagenaria, Luffa,* etc. Among cucurbits, watermelon, muskmelon, round melon, bottle gourd, ridge gourd, *kachri*, longmelon, snapmelon, etc. are mainly grown in arid regions of India (Table 4).

Table 4. Economically important vegetable crops of arid region

S.No.	Common name	Botanical name	Chromosome number (2n)
1	Bitter apple	*Citrullus colocynthis*	22
2	Bottle gourd	*Lagenaria siceraria*	22
3	Kachri	*Cucumis callosus*	24
4	Long melon	*Cucumis melo var. utilissimus*	24
5	Muskmelon	*Cucumis melo* L.	24
6	Ridge gourd	*Luffa acutangula*	26
7	Round melon	*Pracitrullus fistulosus*	24
8	Snapmelon	*Cucumis melo* var. *momordica*	24

Germplasm Conservation and Utilization for Mitigating Climatic Change

Despite the presence of harsh climatic conditions, the desert region is endowed with valuable natural plant

genetic resources including fruit and vegetable crops. The ICAR-Central Institute for Arid Horticulture, Bikaner-334006, Rajasthan is conserving and maintaining the large number of germplasm of arid fruit and vegetables in National Field Repository of the institute (Table 5) and has credit to conserve highest germplasm of ber, bael, date palm, aonla, other minor fruits and arid vegetables in India. The institute is also DUS center for date palm, ber, aonla, bael, jamun, muskmelon and watermelon. These germplasm were also characterized and utilized further in crop improvement programmes.

The increased fruits and vegetable production in hot arid region can be achieved by developing drought hardy and high temperature tolerant varieties. Intensive breeding work on vegetable crops has been done at many research institutes, including ICAR-CIAH, Bikaner-334006, Rajasthan in the country which resulted in the release of several high yielding/disease resistant and abiotic stress tolerant varieties/hybrids. However, ICAR-CIAH, Bikaner is the only institute mainly working on arid fruits and vegetables and released several improved varieties suitable for arid environment (Saroj, 2017) [Table 6].

Besides, there are a large number of genetic materials of different vegetables have been identified which are tolerant to drought conditions (Table 7). Such genotypes can be utilized in crop improvement programme as well

Problems Associated with Arid Vegetables

The cultivated varieties are very much susceptible to certain diseases like powdery mildew, downy mildew, leaf curl, bud necrosis, mosaic, etc. and pests like fruit fly, shoot and fruit borer and root knot nematode. The prevailing high temperature leads to flower drop, late flowering, loss of tenderness in fruits, crookedness of fruits in cucurbits, increase in number of staminate flowers in cucurbits, loss of colour development in tomato, etc (Table 8). Keeping in view, the breeding programme must properly address these issues so as to develop biotic and abiotic stress resistant/tolerant varieties/hybrids coupled with better yield and quality characteristics.

Trait Specific Breeding Objectives

Fruit yield is not the only criterion to select a variety of any fruit crops but there are various considerations like plant architecture, early ripening, shape and size of fruits, colour, taste, softness, pulp recovery, storage life, processing quality, nutritional and medicinal attributes, resistant/ tolerant to different biotic and abiotic stresses etc. Similarly, vegetables are consumed in various ways

Table 5. Germplasm of fruit and vegetable crops conserved at ICAR-CIAH, Bikaner field gene bank

Common Name	Botanical Name	No.	Common Name	Botanical Name	No.
Fruits					
Ber	*Ziziphus spp.*	340	Wood apple	*Feronia limonia*	10
Pomegranate	*Punica granatum*	150	Mahua	*Madhuca latifolia*	50
Cactus pear	*Opuncia ficus-indica*	80	Chironji	*Buchanania lanzan*	30
Lasoda	*Cordia myxa*	66	*Khirni*	*Manilkara hexandra*	30
Date palm	*Phoenix dactylifera*	55	Custard apple	*Annona squamosa*	9
Aonla	*Emblica officinalis*	50	Sapota	*Achras zapota*	7
Ker	*Capparis decidua*	32	Jamun	*Syzigium cuminii*	50
Bael	*Aegle marmelos*	21	Tamarind	*Tamarindus indica*	25
Karonda	*Carissa carandus*	8	Fig	*Ficus carica*	3
Phalsa	*Grewia subinaequalis*	6	Marula nut	*Sclerocarya congesta*	1
Sweet orange	*Citrus sinensis*	3	Mango	*Mangifera indica*	52
Vegetable crops					
Kachri	*Cucumis melo var. callosus*	68	Drumstick	*Moringa oleifera*	10
Mateera/ Watermelon	*Citrulluslanatus*	46	Bottle gourd	*Lagenaria siceraria*	20
Snapmelon	*Cucumis melo var. momordica*	65	Bitter gourd	*Momordica charantia*	05
Chilli	*Capsicum annuum*	45	Ridge gourd	*Luffa acutangula*	20
Muskmelon	*Cucumis melo*	60	Sponge gourd	*Luffa cylindrica*	16
Kakdi	*Cucumis melo var. utilissimus*	18	Indian bean	*Lablab purpureus*	30
Pumpkin	*Cucurbita moschata*	04	Cluster bean	*Cyamopsis tetragonoloba*	02
Round melon	*Praecitrullus fistulosus*	10	*Khejri*	*Prosopis cineraria*	14
Brinjal	*Solanum melongena*	30	Indian Aloe	*Aloe barbadensis*	04
Amaranthus	*Amaranthus sp.*	02	Palak	*Spinacia oleracea*	01

Table 6. Varieties of arid horticultural crops adopted for mitigating ill impact of climate change

S.No.	Crop	Variety	Characteristics
Fruits			
1	Aonla	Goma Aishwariya	Early and drought tolerant.
2	Bael	Goma Yashi	It is a semi dwarf tree and suitable for dry land areas.
		Thar Divya	Precocious bearer and highly suitable for growing under dryland/rainfed hot semi-arid ecosystem. Drought tolerant, luxuriant growth and higher fruit yield under less precipitation and high temperature.
		Thar Neelkanth	Drought tolerant under aberrant agro-climatic conditions.
3	Ber	Thar Sevika and Thar Bhubhraj	Performing well under arid climate
		Thar Malti	Diseases and pest resistance
4	Jamun	Thar Kranti	Diseases and pest resistance
5	Pomegranate	Goma Khatta	Drought tolerant
6	Karonda	Thar Kamal	Moderately drought tolerant
7	Mulberry	Thar Lohit and Thar Harit	Frost (-2 ºC) and high temperature (49 ºC) tolerant
Vegetables			
1	*Kachri*	AHK-119 and AHK-200	Drought and heat tolerant
2	*Khejri*	Thar Shobha	Drought and high temperature tolerant, multipurpose variety
3	Snapmelon	AHS-10 and AHS- 82	Drought and high temperature tolerant.
4	Mateera	Thar Manak, AHW-19, AHW-65	Early maturingand hightemperature tolerant
5	Bottle gourd	Thar Samridhi	High temperature tolerant.
6	Ridge gourd	Thar Karni	Its fruit set at high temperature and resistant to mosaic disease and melon fruitfly under field condition.
7	Long melon	Thar Sheetal	Early and set fruits at high temperature during summer season under hot arid conditions.
8	Sponge gourd	Thar Tapish	Multiple-stress tolerant/ heat tolerant variety.
9	Cluster bean	Thar Bhadavi and Goma Manjri	Drought and high temperature tolerant
10	Drumstick	Thar Harsha	Tolerant to moisture and heat stress.
11	Brinjal	Thar Rachit	High yield under high temperature and abiotic stresses of hot arid environment.
12	Palak	Thar Hariparna	It tolerates high temperature conditions.

Table 7. Drought tolerant species and genotypes of vegetables

S.No.	Vegetables	Drought tolerant species/ genotypes	References
1	Brinjal	*Solanum microcarpon*, *S. gilo*, *S. macrosperma*, *S. integrifolium*, Bundelkhand Deshi.	Rai *et al.*, 2011
		S. sodomaeum syn. *S. linneanum*.	Toppino *et al.*, 2009
		SM- 1, SM- 19, SM- 30, Violette Round, Supreme.	Kumar and Singh, 2006
2	Chili	*Capsicum chinense*, *C. baccatum* var. *pendulum*, *C. eximium*, ArkaLohit, IIHR-Sel.-132	Singh, 2010
3	Melons	*Cucumis melo* subsp. *momordica* (Snapmelon): VRSM-58, AHS-10, AHS-82. *Cucumismelo* subsp. *callosus* (*Kachri*): AHK-119, AHK-200. *Cucumis melo* subsp. *chate*: *Arya*.	Pandey *et al.*, 2011; Kusvuran, 2012
4	Okra	*Abelmoschus caillei*, *A. rugosus*, *A. tuberosus*	Charrler, 1984
5	Onion	*Allium fistulosum*, *A. munzii*, Arka Kalyan, MST 42, MST 46	Singh, 2010
6	Potato	*Solanum acaule*, *S. demissum* and *S. stenotonum*, Alpha, Bintej	Arvin and Donnelly, 2008
		S. ajanhuiri, *S. curtilobum*, *S. xjuzepczukii*	Ross, 1986
		Kufri Sheetman, *S. chacoense*, Kufri Sindhuri).	Pandey *et al.*, 2007
7	Sweet potato	VLS6, IGSP 10, IGSP 14, Sree Bhadra	Singh, 2010
8	Tomato	*Solanum habrochaites* (EC- 520061), *S. pennelli* (IIHR 14-1, IIHR 146-2, IIHR 383, IIHR 553 , IIHR 555, K-14, EC-130042, EC-104395, Sel-28), *S. pimpinellifolium* (PI-205009, EC-65992, Pan American), *S. esculentum* var. *cerasiforme*, *S. hirsutum*, *S. cheesmanii*, *S. chilense*, *S. habrochaites*, *S. sitiens.*	Rai *et al.*, 2011
		Arka Vikas, RF-4A	Singh, 2010
		L. pennellii (LA0716), *L. chilense* (LA1958, LA1959, LA1972), *S. sitiens* (LA1974, LA2876, LA2877, LA2878, LA2885), *S. pimpinellifolium* (LA1579)	Symonds *et al.*, 2010
9	Wild watermelon	*Citrullus colocynthis* (L.) Schrad.	Dane and Liu, 2007

like salad, dessert, juice, etc., thus increased marketable yield alone will not be the sole breeding objective. Keeping in view, Ram (1997), Peter (1998), Peter *et al.* (2007), More and Khan (2009) and Prohens and Nuez (2009) suggested a number of breeding goals that will be taken into consideration during improvement programme of vegetable crops. Peter and Swamy (2006) also focused on the need of introduction of vegetable materials with specific traits. The traits of interest of different fruits and vegetables are given in Table 9.

Table 8. Limiting factors associated with crop production of arid vegetables

Group	Limiting factors
Cucurbits	Flower and fruit drop, late to produce pistillate flowers, loss of tenderness and early development of fibers, low female: male sex ratio due to high temperature, crookedness of fruits, high incidence of fruit fly, attack of powdery mildew, downy mildew, bud necrosis, shoe string virus, etc.
Beans and Pea	Low temperature injury, susceptibility to wilt, powdery mildew and bean mosaic virus, high loss due to pod borer.
Solanaceous crops	Flower and fruit drop, blossom end rot, fruit cracking, sun scald and improper colour development in tomato, damping off, blight, root knot nematode, fruit borer, shoot and fruit borer, thrips, leaf curl viruses, wilt and die back.
Bulb crops	Bolting, sprouting of bulbs, short shelf life, attack of purple blotch and Stemphylium blight, rotting in storage due to black mold, problem of thrips.
Okra	Flower and fruit drop, take more time for flowering, yellow vein mosaic virus, fruit borer.

Table 9. The germplasm of arid fruits and vegetables with trait of interest

Crop	Botanical name	Trait of interest
Fruits		
Date palm	*Phoenix dactylifera*	Early maturing to harvest at pind stage
Bael	*Aegle marmelos*	Cracking resistant
Aonla	*Emblica officinalis*	Frost tolerant
Mulberry	*Morus spp.*	High temperature tolerant
Lasoda	*Cordia myxa*	Frost tolerant
Citrus fruits	*Citrus spp.*	Drought, salinity and high temperature tolerant and free from viruses
Ber	*Ziziphus spp.*	Fruit fly resistant and frost tolerant
Pomegranate	*Punica granatum*	Drought tolerant and cracking resistant
Guava	*Psidium guajava*	Wilt resistant, tolerant to drought and sodic soil, dwarfing nature and nematode tolerant
Vegetables		
Khejri	*Prosopis cineraria*	Tingid bug and leaf, shoot and fruit gall resistant
Watermelon	*Citrullus lanatus*	Wilt and viruses resistant; yellow fleshed, less seeded, early, ice box type, good storage type, suitable for juice making, more seeded for oil purpose
Ridge gourd	*Luffa acutangula*	Fruit fly resistant
Sponge gourd	*Luffa cylindrica*	Fruit fly resistant
Bottle gourd	*Lagenaria siceraria*	Fruit fly resistant
Cucumber	*Cucumis sativus*	Biotic and abiotic stress resistant, gynoecious and parthenocarpic lines
Musk melon	*Cucumis melo*	Fruit fly and viruses resistant; good storage capacity, multiple fruiting, early lines, male sterile lines
Drumstick	*Moringa oleifera*	Leaf eating caterpillar resistant
Brinjal	*Solanum melongena*	High temperature tolerant, shoot and fruit borer resistant/tolerant
Chilli	*Capcicum spp.*	Hot type, heat tolerant lines, resistant to leaf curl virus
Tomato	*Solanum lycopersicum*	Biotic and abiotic stress resistant, long shelf life and good for paste
Onion	*Allium cepa*	Lines with high TSS and resistant to storage diseases
Garlic	*Allium sativum*	Lines with large bulb and clove

Research Strategy for Adaptation and Mitigation of Climate Change

Climate change has become one of the biggest challenges for the sustainable crop production. Prolonged droughts and desertification are the major issues faced by Indian hot arid zone where rural poor and small holders are most heavily affected. Therefore, the crops which can withstand to such conditions like drought, high temperatures and poor soils need more emphasis (Kumar *et al.*, 2019). Limited precipitation and low relative humidity are the characteristic features of arid regions of India resulting in the fair biodiversity of flora and fauna adapted over these harsh climatic conditions. In fact, arid horticultural crops have developed and/or modified their organs to perform certain vital physiological functions such as strong deep root system (ber, bael, aonla, wood apple, Jamun etc.),

synchronized their flowering and fruit development with the season of moisture availability (*ker*, *pilu*, lasoda, aonla etc.) and other xerophytic characters like leaf shedding in summer (ber), scanty foliage (*ker*), spiny cladode (cactus pear), mucilaginous sap in plant part (*ker*, lasoda, *pilu* bael etc.), sunken stomata and fur/hairiness and waxy coating on the leaf surface (phalsa, ber, lasoda fig etc.), thorny nature, and selective or reduces absorption of cation (Na^+) and anions (Cl^- and SO_4^-) for survival under adverse arid conditions. Thereby, arid horticulture fits well under such adversities. Adoption of approaches such as integrated farming systems developed for these regions like, fruit-based diversified cropping models, *khejri*-based farming systems, multi-storey cropping models, protected cultivation, low tunnel cultivation, fruits and vegetable forcing etc. will be very useful in resource poor situations and have a positive impact on adaptation and mitigating adverse effect of climate change in the arid ecosystem. In most arid regions of the country, fruits and vegetables are cultivated only in small holdings, as a component of the regular farming system. But with the adoption of the above mentioned approaches in the true sense, arid horticulture is gaining further momentum at commercial venture.

The changing pattern in the area and production of major arid fruit and vegetable crops in arid and semi-arid regions shows a continuous increase in the area and productionof these crops. This is mainly due to systematic research efforts on arid zone crops, as these crops are somewhat adapted to harsher climatic conditions and can face changing pattern of climate. On the other hand, development of new varieties, establishment of nurseries for supply of quality planting materials andgood management practices made upon these arid crops over the years are the other dimension of development of arid horticulture.Whereas, low infrastructure support for postharvest handling, processing and value addition, lack of cold storage facilities and lack of proper marketing of produce are some of the long standing addressable issues for making the arid horticulture further prosper in the arid region and semiarid regions.

Technological Interventions

Adoptions of fruit based diversified cropping models, multistorey cropping system and *khejri* based cropping models etc. in the arid ecosystem have potential to mitigate the adverse effects of climate change on fruit and vegetable crops by creating microclimate. A set of several combinations of above models (ber, aonla, bael based models etc.) have been well established at ICAR-CIAH, Bikaner and continuous field days/visits/exhibitions are being done to adapters, cultivators, nurserymen etc. for taking advantages of these cropping systems in hot arid regions (Anonymous, 2015). Selection of crop and variety is very much important while establishing such models. Selection of over, ground storey and inter crops are such that which do not have adverse effect with component crops but may have positive/synergistic effect.The agro-techniques developed/improved for maximizing returns per unit area in vegetables under environmentally stressed areas are related to site selection, field micro-climate management, seed treatment method and time of sowing, maintenance of plant population, soil-water conservation, irrigation systems and scheduling foliar feeding and crop protection measures. Besides, post-harvest management, on farm value additions, organic and hi-tech farming and marketing has also been taken up for remunerative cultivation of arid vegetables (Saroj and Choudhary, 2019). There are several advantages of growing arid fruits and vegetables through adoption of these cropping systems under changing scenario of the climate, a few of them are enlisted here below.

Tree based diversified cropping models: Mono-cropping is a risky proposition in hot arid region. Therefore, integrated farming system, including perennial trees, annual crops, animal component, etc. is a better approach for such environmentally fragile ecosystem. The work done at ICAR-CIAH, Bikaner suggested that the fruit based diversified cropping systems improve the overall growth of arid fruits under multiple cropping models, alleviate the risk of crop failure, enhance productivity and income per unit area/volume as a result of efficient use of natural resources and can mitigate the ill effects of hot arid climate on crops. Thus, the utilization of arid germplasm against changing climatic conditions can be adopted using such systems. Agri-horticultural combinations with legume intercrops such as mung bean, moth bean, cluster bean, and cowpea are beneficial. In the rainfed orchards of guava and ber, cluster bean, okra and cowpea in *kharif* proved good in the medium rainfall region of Gujarat. Under South Indian conditions of Hyderabad; cowpea, green gram, cluster bean and horse gram in ber orchards and bitter gourd, tomato and okra in acid lime orchards have been grown as intercrops. In areas where large livestock population exists, horti-pastoral system would be beneficial. In the

arid areas, the system could have combinations such as *khejri* (*Prosopis cineraria*) + ber + *dhaman* (*Cenchrus ciliaris*, *C. setigerus*) or *sewan* (*Laisuruss indicus*). In semi-arid areas, perennial trees (mango, tamarind and sapota,) could be grown with fodder crops.

Multi-storey combinations incorporating large trees, small trees, and ground crops can be used. In low rainfall (300-500 mm) zone, combinations such as *khejri* or ber + ber or drumstick + vegetables (legumes and cucurbits) in 500-700 mm rainfall zone, a combination of mango or ber or aonla or guava + pomegranate or sour lime or lemon or drumstick + solanaceous or leguminous or cucurbitaceous vegetables and in 700-1000 mm rainfall zone, a combination of mango or jackfruit/mahua/ tamarind/guava + sour lime or lemon or pomegranate or aonla + vegetables can be adopted. In the arid ecosystem, attempts have been made to develop models for crop diversification. It has been demonstrated that in ber based cropping system, cultivation of Indian aloe can be taken up as a remunerative intercrop (Saroj, *et al*., 2004). Similarly, in aonla based cropping system, it has been demonstrated that model consisting of aonla + ber along with moth bean or fenugreek can be adopted as a sustainable model for nutritional and income security of the inhabitants (Awasthi *et al*., 2007). Fruit based multistorey cropping system such as aonla-ber-brinjal-moth bean, aonla- drumstick-senna-moth bean-cumin can be profitably adopted by the farmers of arid region for better cash flow, nutritional and environmental security and sustainable livelihood. In areas where frost is severe, aonla-*khejri*-suaeda-moth bean and mustard can be another option (Awasthi *et al*., 2007).

A long-term investigation to understand soil fertility and scope of improvement in building-up of fertility and nutrient levels was carried-out adopting *khejri* based crop production site management approaches at ICAR-CIAH, Bikaner under hot arid agro-climate. A wide spectrum of varying land-use patterns (47 situations) were studied with or without *khejri* planting models. Results exhibited that the approach is effective in improving the organic carbon and nutrient status in sandy soils. The treatment code KS-39 (KM-11, field of *khejri* plantation of nine years age-group with cluster bean cultivation) exhibited more effectiveness for soil fertility build-up in comparison to different land-use patterns. Based on 6-year age-group, treatment code KS-13 (KM-1, field of 4m×4m khejri plantation with three cluster bean crops during the establishment period and normal field crop culture as organic plot) is found more effective for soil fertility build-up in comparison to other land-use patterns of the period (Samadia, 2014).

Protected cultivation: The desired environmental conditions can be simulated in protected structures not only to grow high value crops and mass multiplication of quality planting materials but also for the conservation genetic materials. High quality work has been done for the development of structural design, level of control system, selection of crops, management of crop and system, etc. specific attention is needed regarding structural design for arid ecosystem, where extremes of temperature and high wind velocity and dust storm are the common phenomena. Therefore, low cost and lesser height structures like a shade net and tunnel cultivation are gaining popularity in arid regions. In hot arid region, the cultivation of cucurbits in summer season gets affected by various environmental factors such as very high temperature, scorching sun, hot waves, scarcity of insect pollinators, etc. owing to very low yield of poor quality. Under such conditions, adopting low tunnel cultivation is the best option to get quality produce with low cost. The use of low tunnels with some modification becomes the reality of successful early season cultivation of cucurbits in arid regions (Choudhary and Saroj, 2018). This technology escapes the crop from low temperature during January-February and advances the crop by 45-50 days. It increases the concentration of carbon dioxide inside tunnels, thereby, enhance the photosynthetic activities and ultimately yield. The success of tunnel technology in the arid region includes selection of site, drip irrigation system, fertigation and integrated crop management (ICM) practices. The best time of sowing is the last week of December to first week of January in hot arid region. The poly-cover can be removed with the advancement of summer during February which leads quick flowering and fruiting. It was observed that tunnel cultivation of musk melon, long melon, watermelon, bottle gourd, ridge gourd, *tinda*, summer squash, *etc*. offers good opportunity for successful early season cultivation with B:C ratio of 2.21 to 2.43 (Choudhary and Saroj, 2019). This technology is spreading in arid regions at faster rate and within 5-6 years, more than 20,000 ha area has been covered in western Rajasthan under tunnel cultivation.

Drip technology: Availability of irrigation water is a major limiting input of crop production in arid regions, where not only rainfall is meager but underground water

is also brackish. *In-situ* moisture conservation and water harvesting and recycling is a very important aspect for arid horticulture. During the establishment phase of orchard, water supply through pitchers, double-wall pots or trickle units, depending on agro-climatic conditions of the location are considered better than by the conventional ring basin method of irrigation. In rainfed orchards, *ex situ* or *in situ* water harvesting to catch run-off and soil and plant moisture conservation methods help not only in the establishment of orchards but also in increasing fruit productivity. Water use efficiency can be improved by checking evaporation losses by use of mulches and by modifications in canopy environment. The time and frequency of water application depend upon critical growth and development stages in different horticultural crops, and the agro-climatic conditions. Water stress should not be allowed particularly during fruit set and fruit development stage. In general, frequent irrigations during the flowering period result in in flower and fruit drop in many arid fruits. Among the controlled irrigation systems, drip irrigation is the most suitable for cucurbitaceous crops under arid conditions. Single lateral lines with on-line drippers were found to be the most suitable for different cucurbitaceous vegetable crops like *kachri*, snapmelon, muskmelon, long melon, bottle gourd, ridge gourd and watermelon (*mateera*). Increased fruit yield of about 25-30 percent was obtained in these crops in comparison to the channel system of irrigation under arid conditions. Based on seasonal agro-climatic and weather situations, crop potentiality and available resources, a complete production technology, adopting drip irrigation have been developed and recommended for commercial cultivation of arid zone vegetables (More *et al.*, 2007). Drip irrigation or more broadly known as micro-irrigation saves 30-70 per cent irrigation water and increase yield by 25-80 per cent.

IPM strategies: Comparatively problem of pest and diseases are lesser in arid region compared to humid region, but the kind of pest and disease species surviving over the years in arid climate are more devastating and sometimes difficult to manage. Moreover, with the change in climatic conditions such as prolonged winter with cloudy weather are very congenial for incidence of the disease and pests. In general, incidence of pest and disease apparently depends upon the weather aberrations of a particular region. For example, if there is an increase in relative humidity in the environment during long period of time, there are more chances of occurrence of diseases of the crop plants. Similarly, it also favors for pest attack. For their management at the appropriate time, IPM strategies have been standardized in arid fruits and vegetable crops. Therefore, integrated pest management (IPM) practices should be followed to reduce load of insecticides. Alternatively, soil should be exposed to the sun during summer by deep ploughing to kill hibernating pupa of insects.Field sanitation and proper canopy architecture should also be maintained for perennial fruit trees in order to reduce pest/disease incidence and to produce quality fruits. In addition to this, commercially available Cue-lure traps 8-10 in one-hectare area should be installed to manage fruit fly (Haldhar *et al.*, 2014).

Opportunities in Arid Horticulture to Combat the Ill Impact of Climate Change

Bringing additional area under horticulture on good land is least possible, therefore the untapped potential of nontraditional areas like arid and semi-arid regions must be exploited. The arid region is endowed with vast land resource (about 12% of the geographical area of the country), hardy natural biodiversity, surplus family labourers, increasing canal command area, plenty of solar and wind energy, high animal population, etc. which offers great potential for successful utilization of wastelands for commercial cultivation of fruits, vegetables, seed spices, medicinal and aromatic plants, ornamental plants, tuber crops, etc.

In spite of, harsh conditions for life, the region is bestowed with rich biological diversity. The genetic diversity of arid ecosystem is of great significance because of its adaptability to various biotic and abiotic stresses. Perhaps, it is the storehouse of 'genes' of stress tolerance and represent germplasm which need to be collected and conserved for its utilization as donor in developing stress tolerant/resistant varieties or inducing tolerance in otherwise fragile but economically important crops including arid fruits and vegetables (Malik *et al.*, 2018).

Often, arid fruits and vegetables are being grown in resource poor environment, therefore, they possess a hardy nature against the climatic changes. They have numerous xerophytic characteristics which are helping in tolerating adverse climatic conditions of the arid region. The strong deep root system of ber, bael, aonla, wood apple, Jamun and wild watermelon (*Citrullus colosynthes*); synchronized their flowering and fruit

development with the season of moisture availability (*ker*, pilu, lasoda, aonla etc.) and other xerophytic characters like leaf shedding in summer (ber), scanty foliage (*ker*), spiny cladode (cactus pear), mucilaginous sap in plant part (*ker*, lasoda, *pilu*, bael etc.), sunken stomata and fur/hairiness and waxy coating on the leaf surface (phalsa, ber, lasoda fig etc.), thorny nature (ber, bael, karonda, *ker* etc.), and selective or reduces absorption of cation (Na^+) and anions (Cl^- and SO_4^-) are well known characteristic features of arid vegetation for survival under adverse arid conditions (Saroj, 2018).

The arid and semi-arid fruit such as ber, aonla, *ker*, lasoda, karonda, bael, *pilu*, phalsa, wood apple, chironji etc. have tremendous scope for mitigation of the ill impact of climate change. These fruits are nutritious and nutraceutically rich in numerous bioactive compounds and some of these are of high processing quality; besides several other uses. The demand for such fruits are growing tremendously in local as well as export market for processing purposes. These plant types are highly fit for diversification in agriculture, as they have unique resistant and tolerant traits to withstand against the global climatic changes (Saroj and Jatav, 2019).

In addition to this, physiological, biochemical and molecular understanding of the mechanisms of adaptive behavior of arid flora in extreme hot and dry environment is the future thrust area in arid biodiversity research. To conduct a high throughput research for developing tolerant varieties of arid fruits and vegetable crops against various biotic and abiotic stresses, needs more emphasis on genomic and biotechnological interventions for crop improvement point of view. The genome editing using high throughput technologies such as CRISPR/CAS9 may also be emphasized for genetic improvement of arid fruits and vegetables for desired traits (Tian *et al.*, 2017; Kurkute *et al.*, 2017).

Further, the need should be addressed through collection and evaluation of natural biodiversity of arid flora to develop a strong gene bank including cryopreservation for conserving indigenous germplasm and introduction of desired genotypes for breeding purpose against changing scenario of climate. *In situ* conservation of neglected and underutilized species, landraces of bael, jamun, *ker*, *phog*, *pilu*, *khejri,*etc. should be promoted to protect from disappearance. The development of high yielding, nutrient rich, short duration with desired branching habit, early flowering, less inter-nodal length, suitable for processing and export purpose need to be bred for supporting the livelihood of arid ecosystem. Emphasis must be given on exploration of heterosis breeding for desirable traits like earliness, preferred fruit size, extended harvesting, uniform quality coupled with high marketable yield. The multiple disease and pest resistant/tolerant varieties/hybrids of arid fruits and vegetables should be developed through use of molecular breeding tools such as marker assisted selection (MAS). The farmers' participatory breeding approach is another important aspect of crop improvement in arid ecosystems.

Advance production technologies suited to diverse socioeconomic conditions of arid ecosystem should be standardized. Focus on production of quality seeds and planting materials should also be given to increase productivity and quality. The technologies like *in-situ* orchard establishment, use of suitable rootstocks, proper canopy management, low cost protected cultivation, precision farming, organic cultivation, IPM, INM etc. should be given due consideration in order to address the climatic changes. The availability of quality irrigation water is a limiting factor for crop production in the arid zone. Therefore, emphasis should be given to conserve and enhance the water use efficiency to harvest more crops per drop of water.

The livestock component is an integral part of agriculture in arid regions; therefore, the sustainable development of arid ecosystem can be achieved only by diversification of arid horticulture with the integration of animal component, poultry, fishery, bee keeping, forestry, *etc*. Monocropping is often risky due to uncertainty of climatic conditions. Various fruit-based agroforestry systems have been standardized by integrating multiple compatible components which are practically feasible, economically viable and environmentally sustainable. The adoption of such systems will not only minimize the risk of crop failure due to adverse weather conditions but highly economical with multiple outputs.

The challenges which require strategic attention are insufficient trained human resource, sub-optimal use of resources, the unavailability of quality seeds and planting materials, unorganized and scattered areas of fruit and vegetable production, high post-harvest losses and minimum farm level processing, poor marketing infrastructure, weak linkage with agro-based industries, etc. which should be addressed by proper policy interventions at grass root level.

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Indian J. Plant Genet. Resour. 33(1): 32–33 (2020)
DOI 10.5958/0976-1926.2020.00004.2

MEETING REPORT

Expert Consultation Meeting on Global Crop Conservation Strategies

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An expert consultation meeting of conservation scientists was held at the Crop Trust office in Bonn, Germany during 14-15 October, 2019. The main objective of this meeting was to finalize the technical details for development of a comprehensive project on global conservation strategies. The meeting was attended by representatives from IPK, Germany; USDA ARS, USA; FAO, Italy; INIA, Chile; VIR, Russia; ECPGR, Italy; IITA, Nigeria; BGCI, UK and ICAR-NBPGR, New Delhi. The Crop Trust, over a period of past 10-12 years, has compiled 27 crop-specific documents in which, status and required strategies for conservation have been charted out. However, it is evident that the existing documents have been reduced to 'archives' and there is a need to revisit them and add new crops to the list, based on the global germplasm exchange and utilization priorities. The ITPGRFA secretariat was also involved in the current meeting and it was conveyed that the revised strategy documents will be utilized as a tool for consolidating and updating information on availability and access to plant genetic resources, as per the Treaty mandate. During the meeting an overview was made of the existing 27 strategies, and the diversity tree approach followed in the case of cassava conservation document was taken as the acceptable model for preparing the revised documents. A thorough discussion was held on the list of crops that were to be identified for the new documents. The selection criteria were primarily based on global germplasm demand and exchange data available in literature. Consequently, the following crops were finalized for preparation of the new conservation strategy documents–

1. Cucurbitaceous crops (cucumbers, watermelons, squashes, pumpkins as well as a number of 'minor' crops)
2. Citrus crops (oranges, lemons, grapefruit, limes as well as a number of 'minor' crops)

Participants of expert consultation meeting of conservation scientists held at Crop Trust in Bonn, Germany during 14-15 October 2019

3. Sunflower
4. Temperate forages (grass and legume species that originate from – and are used in – temperate and subtropical regions of the world)
5. Groundnut
6. Eggplant (cultivated species predominantly found in Africa and Asia)

For updating the existing strategies, potato, yams, sorghum and Vigna were identified.

With regard to the scope of the strategies, the group agreed that the new and revised strategies should include information on the following: - Economic, nutritional, agronomic value of crops; Eco-geographic information on the crops and their wild relatives; Molecular characterization data whenever available; Assessment of threats, vulnerability etc. both in situ and ex situ; Identification of gaps, completeness, representativeness, uniqueness of collections, using the diversity tree approach; Security aspect of collections (safety duplication status and approaches etc.); Structure and management of collections; Conservation standards for each crop (including descriptor); Priority conservation actions and targets (including consideration of population genetics parameters); Accessibility and availability of collections by diversity of users (including farmers, NGO's, breeders, scientists etc.); Information on holdings of genetic stocks, pre-bred materials and other types of 'Material under Development'; Information from private collections and 'non-traditional' collections holders, whenever possible; Research priorities for conservation; Phytosanitary issues and their impact on conservation and distribution (and how to overcome such barriers). It was decided that the meeting will be followed by crop-specific workshops, wherein further discussions will be held.

Indian J. Plant Genet. Resour. 33(1): 34–35 (2020)
DOI 10.5958/0976-1926.2020.00005.4

MEETING REPORT

Expert Consultation Workshop on "Global Conservation Strategy for Crops in the Cucurbitaceae Family"

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An expert consultation workshop on "Global Conservation Strategy for Crops in the Cucurbitaceae Family" was held at the World Vegetable Center, East and Southeast Asia, Research and Training station, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, Thailand during 11-13 December, 2019 with the following objectives:

- To consult experts to validate and contribute to a global conservation strategy for cucurbit crops.
- To prioritize actions to improve the conservation and use of the genetic resources of cucurbit crops.

The expert consultation was organised by Crop Trust (Germany) in collaboration with World Vegetable Center (World Veg), Taiwan. The workshop was attended by 19 participants from 13 countries including Bangladesh Agricultural Research Institute (BARI); Spanish National Research Council (CSIC); Crop Trust, Germany; Tropical Agricultural Research and Higher Education Center (CATIE), Costa Rica; University of KwaZulu-Natal (UKZN), Benin; United States Department of Agriculture (USDA); Chinese Academy of Agricultural Sciences (CAAS); ICAR-National Bureau of Plant Genetic Resources (NBPGR), India; Centre for Genetic Resources (CGN), Netherland; National Autonomous University of Mexico (UNAM); World Vegetable Center (World Veg), Taiwan; East and Southeast Asia, Research and Training Station, Thailand; Tropical Vegetable Research Center (TVRC), Kasetsart University, Thailand. The seed industry was represented by Rijk Zwaan-Spain, Chia Tai-Thailand and East West Seed-Philippines. The participants comprised of cucurbits crop conservation experts/genebank managers/breeders/researchers from public and private sector.

The workshop included Technical Session, Plenary Session, Working Group Discussion and visits to field and farm. The technical sessions focused on

1. Scope of global conservation strategies
2. Background on Cucurbitaceae crops (number of crops, uses, taxonomy, centers of origin/diversity eco-geographic information on the crop and their wild relatives
3. Report on online survey conducted in 28 Genebanks
4. Conservation status of Cucurbitaceae crop genetic resources (4 Speakers)
5. Status and future priorities for germplasm screening, characterization and evaluation, use perspective & update from cucurbit breeders (5 Speakers)
6. Working group discussion and presentation (4 Groups)
7. Plenary discussion on current status of conservation, diversity tree, gaps, vulnerability, threats to genetic diversity, data availability, accessibility and policy issues.

The workshop provided a wonderful platform for exchange of knowledge with respect to global genebank collections, conservation status, maintenance and management issues related to regeneration of cucurbit genetic resources. The meeting was much useful in prioritizing conservation actions and targets of genebanks; identifying the collection gaps; with priority for wild relatives, land races and primitive cultivars from the center of origin/primary region of diversity; collection from extreme environments; areas for pest and disease resistance; extending support to genebanks for regeneration/multiplication; improve science on seed conservation for *Cucurbita*– e.g. Resolve seed borne disease issues (major issue for USDA, World Veg Center); Safety duplication of important collections; Centralized information system for genebanks; Resolve the issues/challenges with respect to phytosanitary requirements and different policies at country level,

Participants of expert consultation workshop on "Global conservation strategy for crops in the Cucurbitaceae family" held at World Vegetable Center, East and Southeast Asia Office, Kasetsart University, Thailand

which restrict the exchange of germplasm; Seed indents to be made easier through online information systems. The participants of the workshop emphasized the need for more international cooperation to work across regions of diversity; develop conservation teams for exploration in these countries with the help of donors like USDA, Crop Trust, etc. This effort should aim at collection and evaluation in the host country and sharing the germplasm with the international community. Most of the participants were of the opinion that there is a need to strengthen the public-private partnership or collaboration in breeding/regeneration/research activities and also to establish storage facilities to maintain the genetic resources. It was decided that more meetings will be conducted for developing new conservation strategy not only in the Cucurbitaceae crops but also in *Brassica* crops, groundnuts, eggplants, Citrus, peppers/ chillies, sunflowers, peas and temperate forages. The development of new conservation strategy will act as living documents that will be actively used to guide conservation efforts by all relevant stakeholders.

Indian J. Plant Genet. Resour. 33(1): 36–42 (2020)
DOI 10.5958/0976-1926.2020.00006.6

RESEARCH ARTICLE

Development and Documentation of DUS Traits for *Melia dubia* Cav. Genetic Resources

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(Received: 03 August, 2017; Revised: 11 October, 2019; Accepted: 21 October 2019)

Melia dubia Cav. is a fast-growing, multi-purpose tree suitable for various wood-based industries. Several tree improvement programmes have been undertaken within the country and Tamil Nadu Agricultural University has played a significant role in varietal development of this species. In order to protect the genetic resources through the existing legal mechanism, there is a need to develop DUS traits for each germplasm. Under such criteria, attempts were made to characterize and document DUS traits for *Melia dubia* genetic resources which involved 30 improved genotypes. As of now, there is no systematic documentation of DUS traits. The present study deployed 30 *Melia dubia* genotypes and identified DUS traits for bark, branch and leaf characters. The DUS characterization was carried out by studying the morphological characters such as bark colour and texture, branch angle, leaf apex and base shape, leaf margin and leaf rachis colour as qualitative parameters. The lenticel characters like size, diameter, density and leaf characters like length and breadth are assessed as quantitative parameters. The study exhibited significant variations among the melia genotypes for various DUS traits

Key Words: *Melia dubia* –DUS Traits –Morphological characters–Bark, Branch, Leaf, Lenticel

Introduction

Melia dubia Cav. is an economically and industrially important fast-growing multipurpose tree distributed naturally in India, Sri Lanka, Malaysia, Bhutan, Burma, Australia and Africa. It is commonly known as Malabar neem and is a member of the family Meliaceae. It is a large, deciduous, perennial tree attaining height of 6 to 30 metres. Leaves are shed during (December-January) and new leaves appear in February-March followed by flowering. Fruit is a drupe, pulpy and yellowish on ripening with a sweet smell. Fruit ripens in winter season (October-February), with seeds enclosed in a stony endocarp.

Melia dubia with its multi-purpose uses like pulpwood, timber, fuel wood and plywood can be a suitable species for agro- and farm-forestry plantation programme. The wood is also used for making packing cases, ceiling planks, agricultural implements, pencils, match boxes, splints, furniture and also for building purposes. It is a good fuel wood and fodder yielding tree. It is also planted as an ornamental in avenues and also as shade tree in plantations. It grows rapidly and hence used as a fast-growing industrial agro-forestry species (Parthiban and Seenivasan, 2017).

In recent years, the species is becoming popular in plantation forestry in India due to its fast growth, coppicing ability and adaptability to variety of soil conditions. Large scale plantations of *Melia dubia* have been raised by the farmers, state forest departments and private entrepreneurs. Many tree improvement programmes are under way to develop varieties suitable for varied industrial utility. The species exhibits wide variability which needs to be documented in order to protect the Intellectual Property Rights (IPR) generated on this species. To distinguish the variety of this species, it is important to develop the descriptors so that these descriptors can be utilized as a reference and through this, protection of *Melia* variety can be achieved.

Protection of Plant Varieties and Farmers' Right Authority (PPV&FRA) insists on characterization and registration of extant, farmers and new varieties as a part of national and botanical asset. In order to implement the *sui generis* system for plant variety protection for granting Plant Breeder's Right (PBR) to a breeder or

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farmer or institution, DUS (Distinctiveness, Uniformity and Stability) testing is compulsory (PPV&FRA, 2001). A new variety shall be registered if it conforms to the criteria of novelty, distinctness, uniformity and stability and an extant variety, a variety about which there is a common knowledge shall also be registered within a specified period if it conforms such criteria as distinctness, uniformity and stability as shall be specified (Shobha *et al*., 2006). The grant of PBR under this Act entitles the breeder/his successor, agent, licensee to exclude others from producing, offering for sale, marketing, distributing, export or import of propagating material of the protected varieties for a period of 15 years for annuals and 18 years for vines and trees. The act provides all researchers the rights to use a protected variety as an initial source for creating another variety without prior approval of holder of PBR, provided that such use does not involve repeated use of the protected variety as a parental line or multiplication of its propagating material for commercial nature (Raghuvanshi *et al.,* 2014). Under such circumstances, it was planned to develop DUS traits for *Melia dubia* genetic resources in order to protect them through PPV&FRA.

Materials and Methods

The present study was conducted at the six-year-old progeny of *M. dubia* evaluation trial established at Forest College and Research Institute, Mettupalayam (11º19' N; 76º56' E; 300 MSL) developed in an evaluation trial. The experimental site experienced an annual rainfall of 922 mm. The mean maximum and minimum temperature of the location was 32.2 ºC and 23.2 ºC respectively. The soil is red sandy loam with pH 7.5.

The material for the present study consisted of 20 progenies of seed origin and within them 30 superior individual performers were selected based on growth and yield attributes amenable for varied industrial utility. These superior trees were felled and the bark, lenticels, branching and leaf characters were recorded and documented.

From the felled stumps, the coppice shoots were collected and rooted using apical shoot based clonal technology (Parthiban, 2017) and the trees multiplied through this technology are termed as clones. The clones were established in the clonal nursery in Randomized Block Design (RBD) at a spacing of 1.5m × 1.5m. Observations were taken for two years. The leaf characterization was done using lowermost leaves of the clones developed and the results are presented.

Data Collection and Analysis

Data was collected on morphological (both quantitative and qualitative) characters using character descriptors. The type of assessment of characteristics is followed as per the standard method prescribed by UPOV (International Union for the Protection of New Varieties of Plants) (1989):

- MG: Measurement by a single observation of a group of plants or parts of plants.
- MS: Measurement of a number of individual plants or parts of plants.
- VG: Visual assessment by a single observation of a group of plants or parts of plants.
- VS: Visual assessment by observation of number of individual plants or parts of plants

Descriptors

The requirement of distinctiveness, uniformity and stability were assessed on the basis of descriptors. The descriptors (a feature of whole plant or part of plant) were developed based on the phenotypic assessment of 30 *Melia dubia* genotypes. The observed and measured properties determined in the DUS testing procedure for a new variety shall be qualitative and quantitative.

The selection was made on phenotypic assessment of a character with distinctiveness *viz.,* bark, branch and leaf. A total 30 genotypes were focused for DUS characterization using morphological descriptors. The steps involved and the list of characters chosen for descriptor development are as follows:

i. Identification and screening of characters with distinctness based on the existing tree information followed by examination of screened characters for its uniformity and stability.

ii. Examination of specific time *i.e.* the time at which the most relevant characters can be assessed.

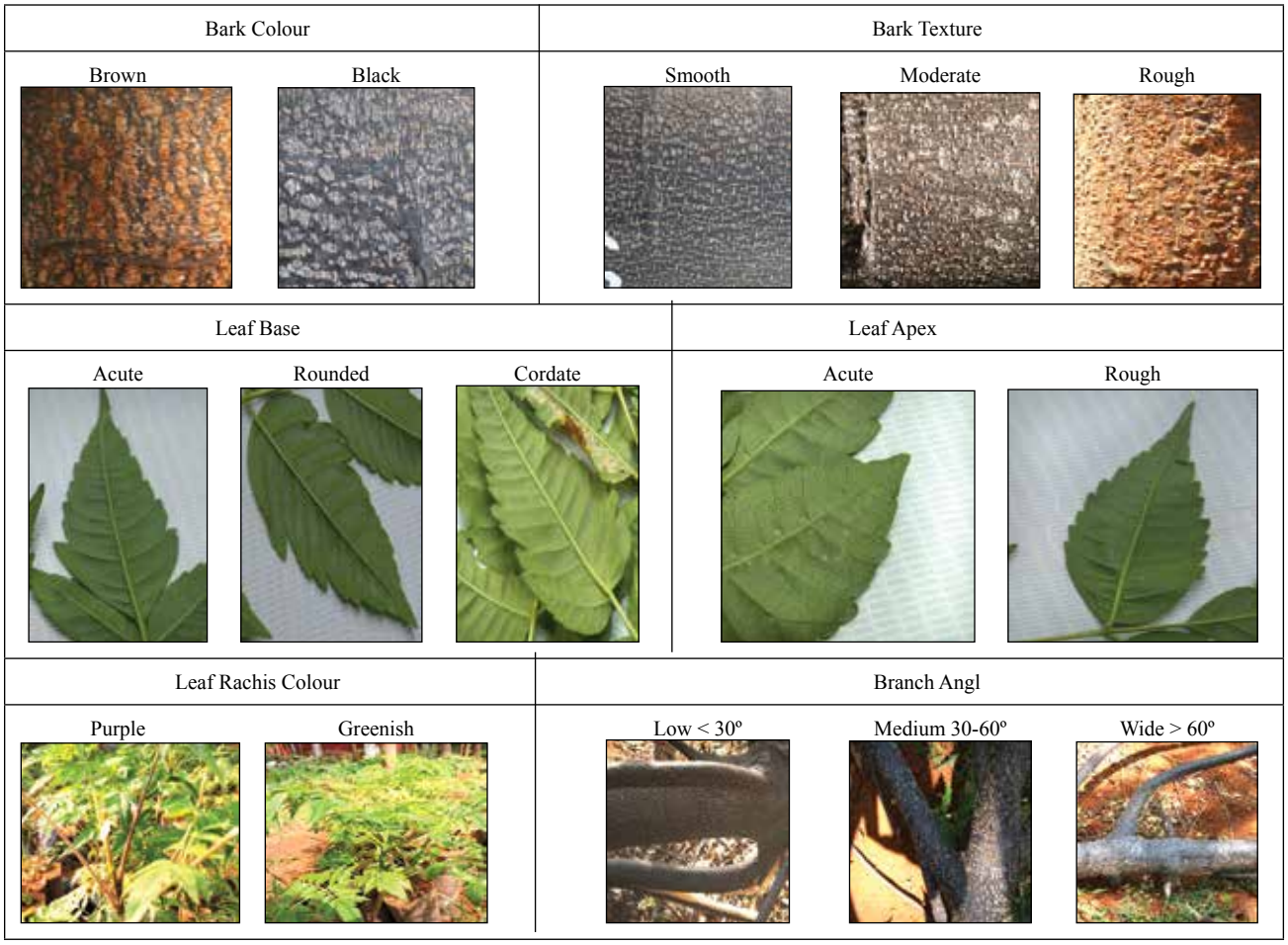
iii. Photographic documentation of visually assessed characters namely bark colour and texture, lenticel, branching pattern, leaf apex shape, leaf base shape, leaf serration and leaf rachis colour were done on site.

iv. Measurable characters *viz.,* leaf length, leaf breadth, lenticel size and lenticels density were assessed.

Qualitative Descriptors

Qualitative descriptors are those that are expressed in discontinuous state. These states are self-explanatory and independently meaningful. All states are necessary to describe the full range of the characteristics and every form of expression can be described by a single state. The qualitative descriptors studied and the classifications followed are furnished in Table 1.

Table 1. Qualitative Descriptors



Quantitative Descriptors

Quantitative descriptors are those where the expression covers the full range of variation from one extreme to other. The expression can be recorded on a one-dimensional, continuous or discrete and linear scale. The range of expression is divided into a number of states for the purpose of description. The division seeks to provide, as far as possible, an even distribution across the scale and the same is furnished in Table 2.

Table 2. Quantitative Descriptors

S. No.	Character	State	Scale
1.	Lenticel size	Small	1-3mm
		Medium	3-6mm
		Large	>6mm
2.	Lenticel no./density	Low	<30 / 10cm^2
		Medium	31-45 / 10cm^2
		High	>45 / 10cm^2
3.	Lenticel diameter	Small	< 5 mm
		Medium	5 – 7 mm
		Large	> 7mm
4.	Leaf length	Short	< 30 cm
		Medium	30 – 50 cm
		Long	> 50 cm
5.	Leaf breadth	Short	< 20 cm
		Intermediate	20 – 30 cm
		Wide	> 30 cm

Pseudo-Qualitative Characteristics

In case, the range of expression is at least partly continuous, but varies in more than one dimension and cannot be adequately described by just defining two

ends of a linear range, such characters are expressed in range. In a similar way the qualitative characteristics needs to be identified and to be adequately described the range of the characteristics (Table 1).

Results

DUS Traits for Bark Characteristics

The *Melia dubia* genetic resources exhibited two distinct bark colour *viz*., brown and black. The texture of bark exhibited three different types viz., smooth, moderate and rough. Based on bark colour and texture, the data characterized and tabulated are given in Table 3.

The stem of the *Melia dubia* genotype has been characterized based on the size and frequency of lenticels which provide a direct exchange of gases between internal plant tissue and atmosphere. Accordingly, the genetic resources have been grouped under three types based on lenticels type as small (1–3 mm), medium (3–6 mm) and large (above 6 mm). Through this characterization, the genetic resources MD 42 has been characterized under small, four genetic resources *viz*., MD 39, MD 40, MD 43 and MD 44 under medium type and the remaining resources under large category. Lenticels diameter exhibit variations among the genetic resources, they are grouped into Small (<5mm), Medium (5-7mm), Large (>7mm). Through this characterization the genetic resources MD 42 and MD 43 are grouped in to small, seven genetic resources *viz*. MD 2, MD 12, MD 14, MD 15, MD 25, MD 32 and MD 46 under large and remaining resources are in medium category (Table 3).

Lenticels help in transpiration and lenticular transpiration occurs when stomata closes. Thus, it helps to prevent the plant parts from heating up. The frequency of lenticels differed significantly among the genotypes. In 10cm^2 area, the number of lenticels varied among the genetic resources and are grouped in to Low (30 and less), Medium (31-45) and High (>45). With this characterization four genetic resources MD 12, MD 19, MD 26 and MD 29 are grouped in to low, five genetic resource *viz*. MD 2, MD 13, MD 15, MD 39 and MD 42 grouped in to high and the remaining are grouped in to Medium category. The lenticels diameter, frequency and the size expressed significant scope for confirming the DUS traits towards protection for IPR (Table 3).

Table 3. Characterization of DUS traits through bark characters

S.No.	Characteristics	State	Example source	Type of assessment
1	Bark colour	Brown	MD 1, MD 3, MD 4, MD 7, MD 12, MD 14, MD 15, MD 17, MD 23, MD 24, MD 26, MD 29, MD 32, MD 34, MD 39, MD 46	VS
		Black	MD 2, MD 5, MD 6, MD 11, MD 13, MD 19, MD 21, MD 22, MD 25, MD 30, MD 40, MD 42, MD 43, MD 44)	
2	Bark smoothness	Smooth	MD 3, MD 6, MD 7, MD 12, MD 19	VS
		Moderate	MD 1, MD 5, MD 11, MD 13, MD 14, MD 15, MD 17, MD 21, MD 22, MD 23, MD 24, MD 25, MD 29, MD 30, MD 39, MD 42, MD 43, MD 44, MD 46	
		Rough	MD 2, MD 4, MD 26, MD 32, MD 34, MD 40	
3	Lenticel size	Small (1-3 mm)	MD 42	MS
		Medium (3-6 mm)	MD 39, MD 40, MD 43, MD 44	
		Large (above 6 mm)	MD 1, MD 2, MD 3, MD 4, MD 5, MD 6, MD 7, MD 11, MD 12, MD 13, MD 14, MD 15, MD 17, MD 19, MD 21, MD 22, MD 23, MD 24, MD 25, MD 26, MD 29, MD 30, MD 32, MD 34, MD 46	
4	Lenticel diameter	Small (<5mm)	MD 42, MD 43	MS
		Medium (5-7mm)	MD 1, MD 3, MD 4, MD 5, MD 6, MD 7, MD 11, MD 13, MD 17, MD 19, MD 21, MD 22, MD 23, MD 24, MD 26, MD 29, MD 30, MD 34, MD 39, MD 40, MD 44)	
		Large (>7mm)	MD 2, MD 12, MD 14, MD 15, MD 25, MD 32, MD 46	
5	Lenticel no. (density)	Low (30 and less)	MD 12, MD 19, MD 26, MD 29	MS
		Medium (31-45)	MD 1, MD 3, MD 4, MD 5, MD 6, MD 7, MD 11, MD 14, MD 17, MD 21, MD 22, MD 23, MD 24, MD 25, MD 30, MD 32, MD 34, MD 40, MD 43, MD 44, MD 46	
		High (>45)	MD 2, MD 13, MD 15, MD 39, MD 42	

DUS Traits for Branch Characteristics

Melia dubia genetic resources expressed different branching patterns. They are characterized into three types based on the angle of branch *viz*., narrow (< 30°), intermediate (30-60°) and wide (>60°). Predominantly 16 genetic resources registered intermediate angle of branching whereas six genetic resources *viz.,* MD 6, MD 11, MD 13, MD 15, MD 29 and MD 31 registered wide angle of branching (Table 4).

Leaf Characteristics

Melia dubia leaves exhibited three different leaf base shapes *viz.,* acute, round and cordate. Among all, acute and round shapes are commonly occurring in the genetic resources. Cordate shape was observed in MD 5, MD 29 and MD 30. Leaf margin found to be serrate in all the 30 genetic resources. Apex shapes of the leaves were either acuminate or acute. The predominant apex shape was acuminate. Two genetic resource *viz.,* MD 22 and MD 29 showed acute shape at the apex (Table 5).

Leaf length was characterized into three categories *viz*., Short (<30 cm), Medium (30-50cm) and Long (> 50 cm). Two genetic resources *viz.,* MD 2 and MD 19 registered short type. Other resources registered medium (14 resources) as well as long type (14 resources). Leaf breadth was characterized to three types *viz*., Short (<20 cm), Intermediate (20-30 cm) and Wide (>30 cm). Three genetic resource *viz*., MD 2, MD 4 and MD 19 registered short leaf breadth whereas remaining falls under Intermediate (16 resources) and wide type (11 resources) (Table 5).

The *Melia dubia* genetic resources have also been characterized for leaf rachis colour which exhibited two major colours *viz.,* purple and green. 11 genetic resources *viz.,* MD 01, MD 02, MD 03, MD 06, MD 17, MD 29, MD 30, MD 32, MD 34, MD 39 and MD 46 recorded purple colour rachis and the remaining genetic resources expressed green colour leaf rachis which indicated the presence of significant variability in the genetic resources and extend greater scope for DUS trait registration towards IPR protection (Table 5).

Discussion

The principal objective of PVP & FRA 2001, is to stimulate both private and public investment in the plant breeding research and enhance the interest of plant breeders as well farmers or farmer's community in the development of outstanding varieties, by granting protections rights to plant variety. Considering this, the morphological traits were evaluated as per DUS guidelines, expressed variability within the *Melia dubia* genetic resources.

Bark has numerous functions during the lifespan of the plant, while it also changes with age. The outer bark is very diverse and can take characteristic shape in some species. Bark of *Melia dubia* showed variations in colour as well as in texture. Colour of the bark characterized into brown and black whereas bark texture is characterized into smooth, moderately smooth and rough. A similar type of description for stem colour *viz.,* light green, green, light grey, and grey have been reported in jatropha by George *et al.* (2016) and skin texture of *Solanum tuberosum* in to very rough, rough, intermediate, smooth and very smooth (Arslanoglu *et al*., 2011). Jaskani *et al*. (2006) reported a similar study where the branch angle of three citrus rootstocks was found to have wide angle. Similarly, George *et al.* (2016) reported branch angle variations in the jatropha which extend support for the current DUS trait characterization in *Melia dubia.*

Leaf apex and leaf base shows predominant variations in *Melia dubia*. Leaf margin found to be serrate in all genetic resource. It is parallel with the study by Jaskani *et al.* (2006) where leaf lamina shape was lanceolate and ovate in sweet orange and yuma citrange, respectively.

Table 4. DUS traits for branch characterization

S. No.	Characteristics	State	Example source	Type of Assessment
1	Branching angle	<30º Narrow	MD 2, MD 3, MD 4, MD 22, MD 24, MD 39, MD 42, MD 43	VS
		30º-60º intermediate	MD 1, MD 5, MD 7, MD 12, MD 14, MD 17, MD 19, MD 21, MD 23, MD 25, MD 26, MD 29, MD 32, MD 40, MD 44, MD 46	
		>60º Wide	MD 6, MD 11, MD 13, MD 15, MD 30, MD 34	

Table 5. DUS Trait through Leaf Characters

S.No.	Characteristics	State	Example source	Type of Assessment
1	Leaf base shape	Acute	MD 1, MD 2, MD 3, MD 5, MD 11, MD 12, MD 15, MD 17, MD 19, MD 21, MD 22, MD 24, MD 42, MD 46	VG
		Rounded	MD 4, MD 7, MD 13, MD 14, MD 23, MD 25, MD 26, MD 32, MD 34, MD 39, MD 40, MD 43, MD 44	
		Cordate	MD 6, MD 29, MD 30	
2	Leaf margin	Serrate	MD 1, MD 2, MD 3, MD 4, MD 5, MD 6, MD 7, MD 11, MD 12, MD 13, MD 14, MD 15, MD 17, MD 19, MD 21, MD 22, MD 23, MD 24, MD 25, MD 26, MD 29, MD 30, MD 32, MD 34, MD 39, MD 40, MD 42, MD 43, MD 44, MD 46	VG
3	Leaf apex shape	Acuminate	MD 1, MD 2, MD 3, MD 4, MD 5, MD 6, MD 7, MD 11, MD 12, MD 13, MD 14, MD 15, MD 17, MD 19, MD 21, MD 23, MD 24, MD 25, MD 26, MD 30, MD 32, MD 34, MD 39, MD 40, MD 42, MD 43, MD 44, MD 46	VG
		Acute	MD 22, MD 29	
4	Leaf length	Short (<30 cm)	MD 2, MD 19	MG
		Medium (30-50cm)	MD 1, MD 4, MD 5, MD 7, MD 12, MD 17, MD 22, MD 23, MD 24, MD 29, MD 30, MD 32, MD 39, MD 43	
		Long (>50 cm)	MD 3, MD 6, MD 11, MD 13, MD 14, MD 15, MD 21, MD 25, MD 26, MD 34, MD 40, MD 42, MD 44, MD 46	
5	Leaf breadth	Short (<20 cm)	MD 2, MD 4, MD 19	MG
		Intermediate (20-30cm)	MD 1, MD 5, MD 7, MD 11, MD 12, MD 13, MD 17, MD 22, MD 23, MD 24, MD 26, MD 30, MD 32, MD 39, MD 43, MD 46	
		Wide (>30 cm)	MD 3, MD 6, MD 14, MD 15, MD 21, MD 25, MD 29, MD 34, MD 40, MD 42, MD 44	
6	Leaf rachis colour	Purple	MD 1, MD 2, MD 3, MD 6, MD 17, MD 29, MD 30, MD 32, MD 34, MD 39, MD 46	VG
		Green	MD 4, MD 5, MD 7, MD 11, MD 12, MD 13, MD 14, MD 15, MD 19, MD 21, MD 22, MD 23, MD 24, MD 25, MD 26, MD 40, MD 42, MD 43, MD 44	

The sour orange and yuma citrange showed sinuate leaf lamina margin. Leaflet size and bristle number have frequently been used as descriptors of *Arachis pintoi* cultivars. The variability in bristle number in the different plant structures as well as in leaflet size permits the use of these traits in cultivar development (Argel and Villarreal, 1998). Leaves of sweet cherry, duke cherry and sour cherry were characterized into obovate elliptic, acuminate to elliptic acuminate. Leaf margin of sweet cherry was crenate serrated and with glandular teeth (Perez *et al.*, 2010). Leaf length and breadth also showed considerable variation in *Melia* genetic resource. Similar kind of variations were reported in neem (Gnanasekar *et al.,* 2014) and jatropha (George *et al.,* 2016). Leaf rachis colour variation might be due to the hereditary or geographical variations.

All the genetic resources have shown morphological differences which could be attributed to several factors including hereditary, differences in geographical and ecological adaptation to sites. A similar report has been observed in cashew, where variability was observed in nut, kernel characteristics and other traits (Felix *et al.,* 2009).

Conclusion

An attempt was made to identify and document DUS traits in *Melia dubia* based on morphological characters by developing DUS descriptors. Descriptors were developed based on the guidelines that are envisaged in PPV and FRA Act 2001. Accordingly, in the present study major focus was given to develop descriptors for bark, branch and leaf characters. Twelve DUS descriptors were developed for *Melia dubia* after selecting the 30 superior genetic resources. Among the 12 descriptors, five were quantitative (Lenticel size, Lenticel diameter, Lenticel no., Leaf length, Leaf breadth) and seven

were qualitative characters (Bark colour, Bark texture, Branch angle, Leaf apex shape, Leaf base shape, Leaf margin and Leaf rachis colour). Among the quantitative characters three were developed for bark character and two were developed for leaf characters. Whereas among the qualitative character two were developed for bark character, one was developed for branch and four for leaf characters. The DUS traits identified and documented in this manuscript will help the breeders and farmers to protect their variety developed in *Melia dubia* by deploying suitable traits.

Acknowledgement

The authors profusely thank the Indian Council of Agricultural Research (ICAR), New Delhi for having funded the research project entitled "Development of High Yielding Short Rotation Varieties for Industrial Agroforestry" through extramural research project wherein the current study formed a part of the objectives.

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Indian J. Plant Genet. Resour. 33(1): 43–51 (2020)
DOI 10.5958/0976-1926.2020.00007.8

RESEARCH ARTICLE

Survey of Major Ethnomedicinal Plants of District Kinnaur, Himachal Pradesh

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(Received: 27 February, 2018; Revised: 17 May, 2019; Accepted: 23 August, 2019)

This paper highlights the medicinal plant wealth and its gradual depletion in Kinnaur district of Himachal Pradesh, India. In most cases, the entire plant is dug out for their rhizomes or roots thereby reducing the chances of regeneration. Out of the forty one plants species in the study areas, 83% belong to herbs, 7% to shrubs and 10% to trees. Apiaceae and Asteraceae being the predominant families represented by 7 species each. Maximum utilisation (56%) of roots and rhizomes was observed followed by whole plant (12.2%), seeds (10%), leaf and flower (7.3%), fruits (5%), barks and leaf (2.4%), and bark, stem and flower (2.4%). Out of 41 plants recorded in the present study, 10 were reported to cure stomachache followed by rheumatism and fever (09), and 4 by anaemia and skin disease. Thirty-three plants species have been reported to have more than one therapeutic uses, whereas 17 species are reported to be used for single ailment.

Key Words: Central Himalaya, Cold desert; Depletion; Medicinal Plants; Traditional uses

Introduction

The Himalayan ranges is one of the most important gene rich centers in India holding a large number of useful plant species including 8000 angiosperms, 44 gymnosperms, 600 pteridophytes and 1159 lichens (Ambasta *et al*., 1992; Barthlott *et al*., 2005; Joshi, *et al*., 2016). Of the total phytodiversity, the Indian Himalayan region contains at least 1748 (23.2%) plant species of known medicinal value (Samant *et al*., 1998). Among the various eco-climatic zones in the region, the alpine flora has shown a particular interest for the phytogeographers and plant taxonomists (Kala and Rawat, 2004). These plant species, having slow growth rate, low population density and narrow geographic ranges (Kala 1998; Dhyani and Kala 2005; Kandari *et al*., 2012). Economic potential of medicinal plants growing in the Himalayan region is a vital area for contribution towards novel biomolecules for medicinal purposes which are already well documented (Dhawan, 1997; Kandari *et al*., 2012; Bisht *et al*., 2013). It is estimated that there are already more than 1000 species of diverse plants occurring between 3300 to 3600 m asl (Rau, 1975). Most existing high altitudinal medicinal plants of the region are habitat specific and their endemic nature makes them more prone to biotic and abiotic stress including climate change.

Sudden rise in global demand of herbal products has restricted in exploitation of plants from the wild. Further, the development of herbal based pharmaceutical companies in developing as well as developed countries has increased the demand of raw materials. As a result, the traders have started exploiting the resources indiscriminately thereby about 90% of raw material from the wild (Tandon, 1996; Ved *et al*., 2003). Declining number of the important medicinal plants in the wild due to over-exploitation has raised concern among various scientists, ecologists and conservationists (Dhar *et al*., 2000). Loss of species and habitat destruction worldwide has increased the risk of extinction of medicinal plants in India (Heywood and Iriondo, 2003; Hamilton, 2008)

Presently, India ranks at 6th place for having the largest number of threatened plant species in the wild (Badola and Pal, 2003). Among them, medicinal plant species are facing a drastic decline in their number, hence placed in Appendix I and II of CITES (Negi and Chauhan, 2009). Recognizing and the need for exploring the need for scientific data gathering and documentation

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in order to ensure appropriate conservation planning and action, the Government of Himachal Pradesh has initiated a project, entitled "Establishment of Forestry Herbarium Plan-7 (http://www.yspuniversity.ac.in).

It was aimed to preserve the genetic resource of forest and other MAPs of Himachal Pradesh. Under this project, various explorations were carried out to estimate the present status of available medicinal plant resources in Kinnaur district, which is a part of Himalayan cold desert. The activity also involved networking and liaising with the local forest administration as well as with several inhabitants of the region. (http://www.yspuniversity.ac.in/fp/fp-rese.htm). The present study largely, focuses on ethnobotany of threatened and endangered flora of the Kinnaur district at different altitudinal variations which can later serve as a base document for initiating restoration steps and suitable measures by various government organizations.

Methodology

Study area

The present study was conducted in Kinnaur district of Himachal Pradesh in Western Himalaya, India. The area lies between 31º 05′ 20′′ to 32º 05′ 15′′ N latitude and 77º 45′ 00′′to 79º 00′ 35′′ E longitudes (Fig. 1). It is bounded by Lahaul & Spiti in the north, Kullu in the northwest, Shimla in the southwest and Uttarakhand state in the south. It also shares an International border with China (Tibet) in the east having the three high mountains ranges i.e. Zanskar, Greater Himalaya and Dhauladhar, enclosing rivers of Sutlej, Spiti, Baspa and their tributaries.

Details of the collection site were attached to the specimens for record. Field characters were noted and later transferred to the field book and herbarium labels. For description of specimens, macroscopic characters of the gathered specimens and field observations were used. Nomenclature has been made up to date with the help of recent taxonomic literature (Collect, 1921; Polunin and Stainton, 1985; Nayar, 1996; Ved *et al*., 2003) and specimens were finally identified in Dr. YSP University of Horticulture and Forestry, Solan, H.P.

Ethnobotanical Survey

Help of the local populace of the district Kinnaur was taken for a detailed ethnobotanical survey which included collection of plants and their ethno medicinal (local) usage. A questionnaire approach was adopted for conducting the survey. Group participation in their local rituals and festivals (including fuliach-festival of flowers) was also carried out to identify and establish their deep association with plants.

Results and Discussion

Socio-economic setup

The people of district Kinnaur called "Kinnaura" belong to scheduled tribes and possess physical resemblance

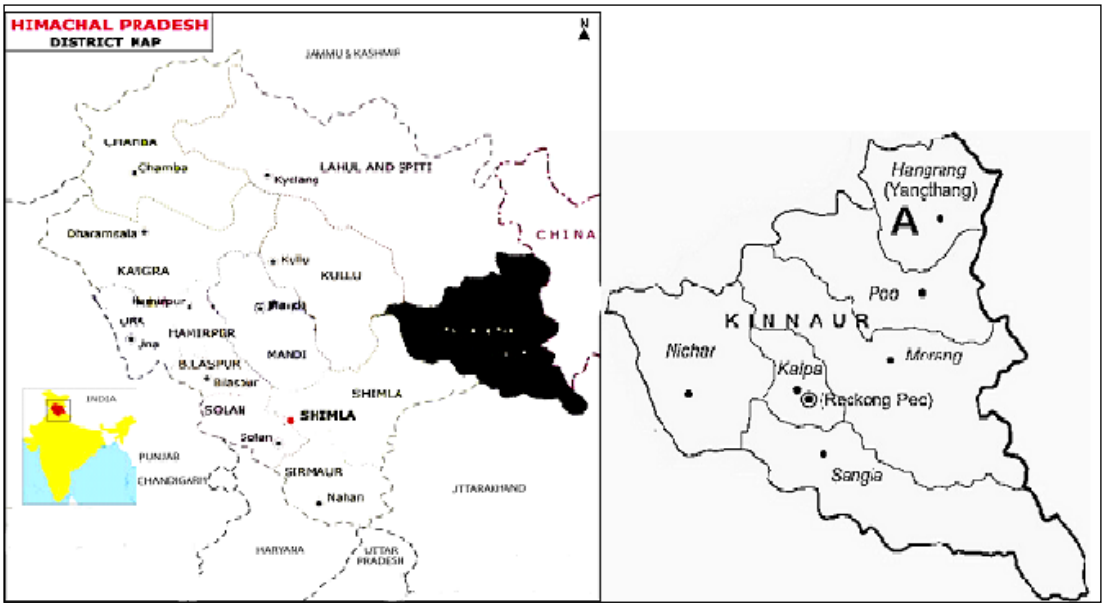

Fig. 1. Map of the study site

with the Mongoloid races (Chandel, 2015). They usually live in dwelling settlements which could be found even up to an elevation of 4300 m asl called "Kanda" area (Alpine zone) during summers. With the onset of winters, they return to their original houses in the lower reaches. Horticulture (cultivation of apple, pear and apricot) and animal husbandry remains most important activities followed by, dairy which are essentially needed. Due to long distance from district headquarters the inhabitants have developed their own system of healing and maintain a strong belief in this regard for immediate ailment relief. These people use locally available plants for traditional household remedies complemented by Vaids and Amchis (folk medicine practitioners) for the cure of minor to major diseases. These traditional medicinal practices adopted by them have been conserved for over decades which can serve as an effective basis for the discovery and development of many drugs. The study areas can be broadly divided into three major sub-divisions based on prevalent climatic conditions viz. upper Kinnaur; mid Kinnaur and lower Kinnaur. The distribution pattern of plant species under the study have been broadly shown by their presence in representative areas of sub divisions indicated in Table 1. Maximum numbers of plants (26) were found growing in Sangla (1500-2000 m asl) valley followed by Kalpa (23) and Morang (16) where conditions are ideal for their development. Lowest numbers of plants (9) were found growing in Yangthang, which is at a higher elevation (beyond 3000 m) and offered tough conditions for plant growth. The plant *Aconitum deinorrhizum* used for cold, fever and cough was found growing all over the Kinnaur area except Yangthang and widely used by locals.

Ethnobotanical study

A total of 41 plant species identified in the area were studied (Table 2). All the plant species belongs to high and medium conservation priority, which are included in some or the other form of near depletion status (Table 3). These species represent 20 families; among which the families' Apiaceae and Asteraceae are the predominant ones represented by seven genus each. The prominent angiosperm families are Asteraceae, Rosaceae, Poaceae, while many families are monotypic (Fig. 2a). Of the total plant species studied, herbs contributed to 83% followed by trees (10%) and only 7% by shrubs (Fig. 2b). However, 56% of the plants have their roots and rhizomes being extensively used followed by whole plant (12.2%), seeds (10%), leaf and flower (7.3%), fruits (5%), bark and leaf (2.4%), bark, stem and flower (2.4%) each (Fig. 3). The type of ailments that were treated by the traditional healers indicates that most of them are of common and simple ones. However, when a traditional healer finds that a particular patient is not responding to his treatment, he is always referred to modern system of medicine for further diagnosis and check-up.

Out of 41 plants recorded in the present study, 10 were reported to cure stomachache. Nine plants cure rheumatism and fever, and 4 could take care of anaemia and skin disease (Fig. 4). Area under commercial medicinal plants ie., *Arnebia benthamii, Dactylorhiza hatagirea, Polygonatum verticillatum* which are known for taking care of problems like baldness, sexual dysfunction and kidney trouble, need to be expanded for bringing in more income to the farmers. Many negative list of export plant species under the EXIM policy since March 1996 like. *Aconitum heterophyllum, A. violaceum, Podophyllum hexandrum, Dactylorhiza hatagirea, Picrorhiza kurroa* and *Jurinea dolomiaea* which are banned from extraction from Himachal Pradesh, are reported to be illegally extracted in abundance from the study area. *Dactylorhiza hatagirea* locally called hathpanja was reported to flourish well in Kalpa Kanda (alpine zone) and was even suggested to be declared as protected area for this particular species (Bhardwaj *et al*., 2013).

Traditional and Social Beliefs

The plant *Saussurea obvallata* called 'dongar' in Kinnaur is used during religious occasions during Fuliach festival (festival of flowers) in Sangla, Ropa and Kalpa Kanda along with the village priest. The study revealed that, priest is the only authorized person to pluck the flowers of this particular species for offering it to local deity and removal of even a small twig by any other person is a taboo. This social restriction was studied thoroughly and was found to be very successful in conservation of this endemic and endangered species in the region (Bhardwaj et al., 2011). *Betula utilis* locally called Bhuj was found in abundance in Chitkul area of Sangla valley, although most of the houses of that area were observed to be thatched using the bark of Bhuj. *Taxus baccata* was also reported to be flourishing well in Chitkul area abounding with *Abies pindrow* (Fir) forest. In Sangla region of the study area, local people have started cultivation of *Saussurea costus* (Kuth) in the alpine

Table 1. Species distribution in different parts of study area

S.No.	Species	Nichar	Morang	Kalpa	Sangla	**Poo**	**Yangthang**
1.	*Aconitum deinorrhizum* Stapf	+	-	-	-	-	-
2.	*Aconitum heterophyllum* Wall. Ex Royle	+	+	+	+	+	-
3.	*Aconitum violaceum* Jacq. ex Stapf.	+	+	+	+	-	-
4.	*Allium stracheyi* Baker Baker	-	+	-	-	+	+
5.	*Angelica glauca* Edgew.	-	-	+	+	-	-
6.	*Arnebia benthamii* (Wall. Ex G. Don)	-	+	-	+	+	+
7.	*Artemisia maritima* L.	-	+	+	-	+	+
8.	*Atropa belladonna* Linn	-	-	+	-	-	-
9.	*Bergenia stracheyi* (J.D. Hooker & Thomson) Engl.	+	-	+	+	+	_
10.	*Betula utilis* D. Don.	-	-	-	+	-	-
11.	*Bunium persicum* Jones Fedtsch	-	_	+	+	-	-
12.	*Carum carvi* Linn.	+	-	+	+	-	-
13.	*Chaerophyllum villosum* Wall. ex DC	+	-	+	+	-	-
14.	*Dactylorhiza hatagirea* (D. Don) Soo	+	+	+	-	-	-
15.	*Dioscorea deltoidea* (D. Don) S	+	+	+	+	_	_
16.	*Ephedra gerardiana* Wall. Ex Stapf.	-	+	-	-	+	+
17.	*Eremurus himalaicus*	-	-	-	-	+	+
18.	*Ferula jaeschkeana* Vatke	-	-	-	-	+	+
19.	*Fritillaria roylei* Hook.	+	-	-	-	-	-
20.	*Heracleum lanatum* Michx.	+	-	+	+	-	-
21.	*Hippophae rhamnoides* Linn.	-	-	+	+	-	-
22.	*Hyssopus heterodonta*	-	+	-	-	+	+
23.	*Hyoscyamus niger L.*	-	+	-	-	+	+
24.	*Inula racemosa* Hook. F	-	-	-	+	-	-
25.	*Jurinea dolomiaea* Boiss	-	+	-	-	+	+
26.	*Jurinea macrocephala* DC	-	+	-	-	+	-
27.	*Nardostachys grandiflora* DC.	-	-	+	+	-	-
28.	*Picrorhiza kurroa* Royle Ex Benth.	-	-	-	+	+	-
29.	*Pleurospermum brunonis* Benth. ex C.B. Clarke	+	-	+	+	-	-
30.	*Podophyllum hexandrum* Royle	-	+	+	+	-	-
31.	*Polygonatum verticillatum* L.	+	-	-	+	-	-
32.	*Rheum australe* D. Don	-	-	+	+	-	-
33.	*Rheum moorcroftianum* Royle	-	+	+	+	-	-
34.	*Rhododendron anthopogon* D. Don	+	-	-	+	-	
45.	*Rhododendron campanulaceae* D. Don	+	-	-	+	-	-
36.	*Rhododendron lepidotum* Wall. ex. D. Don	-	+	+	-	-	-
37.	*Saussurea costus* (Falc) Lipsch.	-	-	-	+	-	-
38.	*Saussurea gossypiphora* D. Don	-	-	+	+	-	-
39.	*Saussurea obvallata* (DC.) Edgew	-		+	+	+	-
40.	*Taxus baccata* Zucc.	-	-	+	+	-	-
41.	*Valeriana jatamansi* Jones	+	+	+		-	-

+ = Present - = Absent

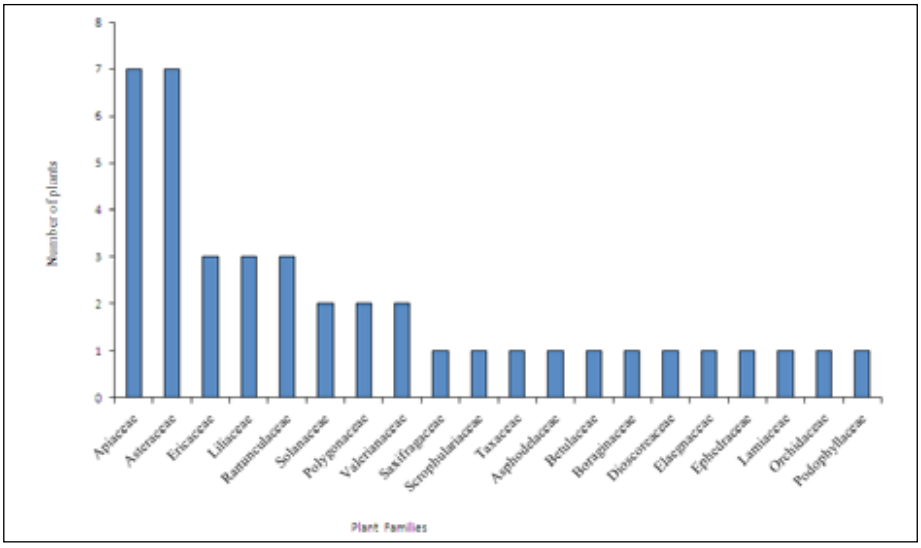

Fig. 2(a). Medicinal plants belongs to different families

pastures (Kanda areas) thereby improvement presently in the plant status. Many other crops viz. *Bunium persicum* (Siah zeera) and *Carum carvi* (Kala zeera) were also found to be under cultivation in the study area ie., The herb *Humulus lupulus* (Hops) was found cultivated in Batsei and Chitkul villages of the study area. A very aromatic herb *Hyssopus heterodonta* (Luffa), was noticed in completely arid region while moving towards Kanda area (alpine zone) which could cause giddiness due to its strong fragrance in oxygen deficit areas. The herb *Ephedra gerardiana* was also found in good number in arid Kinnaur. An important plant *Dioscorea deltoidea* called ratalu is heavily exploited in the study area not only for medicinal purpose but also for its saponin content, which is utilized for washing of woolen clothes by the inhabitants.

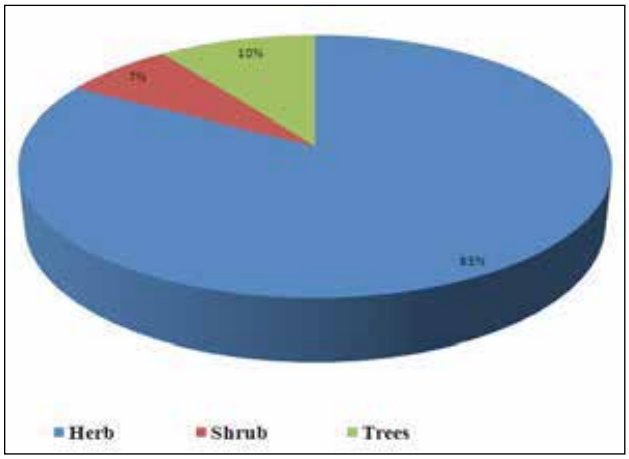

Fig. 2(b). Representation percentage of different life forms

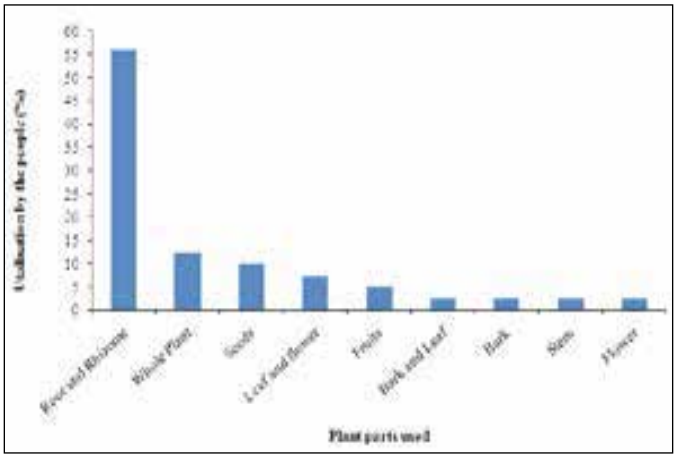

Fig. 3. Plants parts used by traditional communities

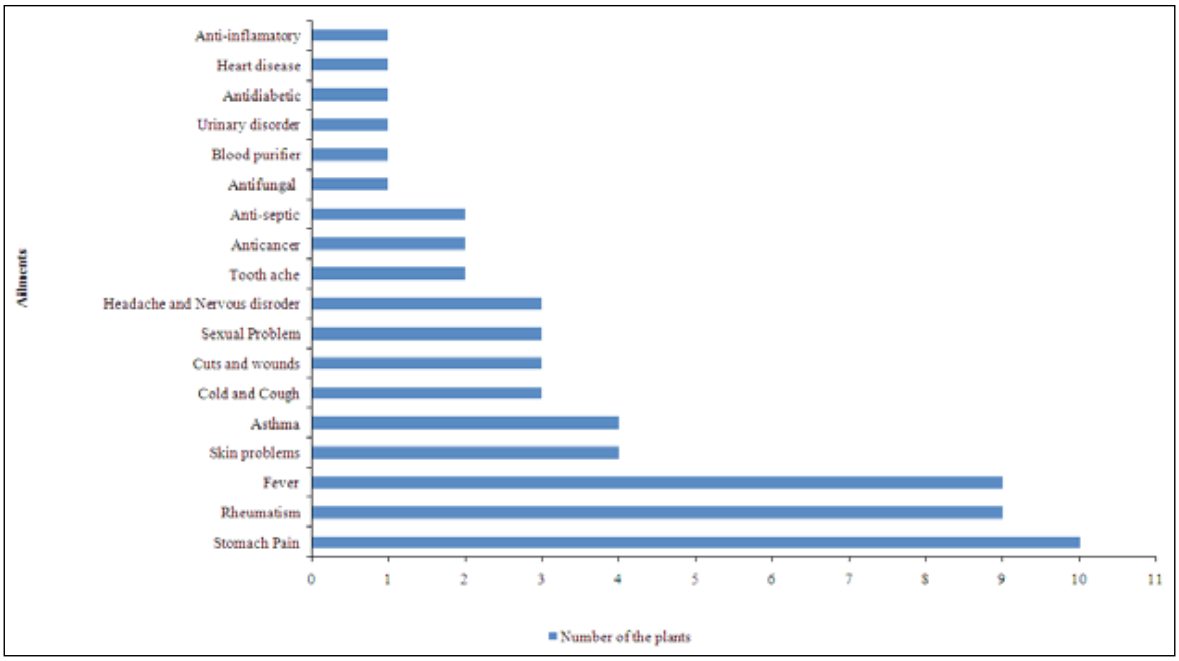

Fig. 4. Number of the plants having different pharamacological actions

This study further highlights the localized, patchy and habitat-specific distribution of the studied plants. Restricted distribution and heavy pressure in the form of grazing by sheep and goat have degraded their habitats further at many places. The habitat has also overlapped with the grazing sites due to easy availability to both livestock and human beings. Therefore, grazing has already been established to be one of the reasons for erosion of biodiversity (Pfister and Gardner, 1999). It was observed that, the species with high market demand

and prohibition for export are declining more rapidly (Table 4). According to an all-India trade survey of prioritized MAPs, demands for some of these species have increased by 50%, whereas availability has declined by 26% (Anonymous, 1976). It was also observed that, people used to collect these plant material for shorter

Table 2. Medicinal Plants resources Selected for population estimation from the wild in Kinnaur area

S. No.	Species	Local name	Field Book No.	Altitude (m asl)	Habitat	Ethnobotanical uses
1	*Aconitum deinorrhizum* Stapf	Mohra bish	10067	2800-3200	SH, AS	Neuralgia, paralysis and muscular rheumatism.
2	*Aconitum heterophyllum* Wall ex Royle	Atees	9817	2400–4000	F, SH, Ogs	Fever Cold, Cough
3	*Aconitum violaceum* Jacq. ex Stapf.	Mitha patish	10081	3200-4500	AS	Rheumatism
4	*Allium stracheyi* Baker	Jimbu	3969	3000–3500	RS, Ogs	Jaundice, cold, cough
5	*Angelica glauca* Edgew	Chora	9678	2200-3200	F	Stomach disorders, diarrhea, bronchitis
6	*Arnebia benthamii.* (Wall ex. G. Don)Johns	Khomae, Ratanjot	10002	3000–4300	OS, SH	Baldness
7	*Artemisia maritima* L.	Nurcha, Seinski	3987	2300-2700	OS	Stomach disorder, fever, jaundice
8	*Atropa belladonna* Linn	Sag-angur	3959	2100-2700	Mr	Spasmolytic
9	*Bergenia stracheyi* (J.D. Hooker & Thomson) Engl.	Ghee-pati	3928	2900–3400	AS	Stomach disorder, fever, Jaundice
10	*Betula utilis* D. Don	Shak-pang, Bhojpatr, Bhooj	9996	2900-3400	F	Rheumatism
11	*Bunium persicum* Jones Fedtsch	Siah jeera	3911	270-3200	Cul	Anti-oxidant
12	*Carum carvi* Linn	Jira	1073	2800-3200	Cul, Mr	Stomach problems, and sexual dysfunction
13	*Chaerophyllum villosum* Wall. ex DC	Ganjari	3913	2100-3600	SH, F	Antimicrobial, antioxidant, stimulant and expectorant.
14	*Dactylorhiza hatagirea* (D. Don) Soo	Hathpanja	10341	2500-4000	OS, Mr	Sexual dysfunction
15	*Dioscorea deltoidea* (D. Don) S	Ratalu	3957	2100-2400	F	Steroid, used I birth control pills cure gastric problems and bloody dysentery
16	*Ephedra gerardiana* Wall. ex stapf	Somlata, Khanta, Phok	3930	2500-4000	RS	Headache and rheumatism
17	*Eremurus himalaicus* Baker	Desert candle	10571	2400-3100	RS	Leaves as remedy for anemia
18	*Ferula jaeschkeana* Vatke	Jungli-hing, Kaith, Kaidmo	10096	2500-3500	RS	Treatment of tumors, chronic wounds and ulcers in man as well as in animals
19	*Fritillaria roylei* Hook	Kakoli	9870	2500-3500	As	Health tonic, member of ashtavarga group (a combination of eight rejuvenating drugs)
20	*Heracleum lanatum* Michx.	Poral ,Patrala	9758	3000-3600	F	Cures leukoderma and psoriasis
21	*Hippophae rhamnoides* L.	Charma, Seabuckthorn, Dhurchuk	3909	2000-3500	RS	Antioxidant, antiulcerogenic, radio protective effects
22	*Hyssopus heterodonta*	Luffa		3200-3800	RS	Stimulant, Carminative and cures digestive uterine and urinary disorders.
23	*Hyoscyamus niger* L.	Khurasani ajwain, Henbane	3929	2800-3900	RS	Analgesic
24	*Inula racemosaa* Hook. F	Pushkarmool	9963	2800-3200	F	Cardiotonic, anti-inflamatory, digestive and febrifuge
25	*Jurinea dolomiaea* Boiss	Dhoop	10001	2800-4000	Os	Antiseptic and for curing fever
26	*Jurinea macrocephala* DC	Dhup, Jari dhoop	9968	3000-4300	Os	Stimulant and applied to skin eruptions
27	*Nardostachys grandiflora* DC.	Bhutkesi	9453	3600-4800	RS	Antispasmodic and stimulant hence used in treatment of fits and heart palpitations
28	*Picrorhiza kurrooa* Royle ex Bent	Kutki	9818	3300-4300	RS	Stomach disorders
29	*Pleurospermum brunonis* C.B. Clarke	Nesar, Chicha	1006	3200-3900	F	Powdered flowering shoots used against fever.
30	*Podophyllum hexandrum* Royle	Bankakri	10016	2400-4500	F, Os	Antifungal also treat warts and timorous growth on the skin.
31	*Polygonatum verticillatum* (L.) All	Macheti	9690	1500-3200	SH	Kidney troubles
32	*Rheum australe* D. Don	Aarcha,Chikri, Revandchini	10006	3000–4200	RS	Antidiabetic, anti-inflammatory, antimicrobial, anticancer and hepatoprotective.
33	*Rheum moorcroftianum* Royle	chikri	11003	3100-3400	Os	Internal injury, cold and cough
34	*Rhododendron anthopogon* D. Don	Talashang, Morua	10026	3000-3400	AS	Leucorrhoea, gonorrhea and post delivery complications
35	*Rhododendron campanulacae* D. Don	Burans, Cherailu	10005	2900-3600	AS	Chronic fever and rheumatism
36	*Rhododendron lepidotum* Wall. ex. D. Don	Cherailu	9869	3100-3700	AS	The tea made from bark is purgative
37	*Saussurea costus* Falc.	Kuth	9834	2700-3100	Cul	Toothache, stomach disorder, asthma
38	*Saussurea gossypiphora* D. Don	Khasbal	10029	3400-3700	RS	Check bleeding from Cuts and wounds

Contd.

S. No.	Species	Local name	Field Book No.	Altitude (m asl)	Habitat	Ethnobotanical uses
39	*Saussurea obvallata* (DC.) Edgew	Dongar, Brahmkamal	9796	4400-4900	RS	Cuts and wounds, Rheumatism
40	*Taxus baccata* Zucc.	Yamdhal	10501	2400-3100	AS	Headache, rheumatism, Anticancerous
41	*Valeriana jatamansii* Jones	Mushkbala	10540	1900-2300	F	Sedative, antispasmodic, Stomachic, stimulant and cure nervous disorders

OS= Open Slopes; **SH**= Shrub Beries; **AS**= Alpine Slopes; **RS**= Rocky Slopes; **F**= Forest; **OGS**= Open grassy slopes; Mr= Marshland; **Cul**=cultivated

Table 3. Assessment of status/depletion level for selected species (based on different guidelines) from the study area with suggested conservation

Species	RDB	PN	CITES Anonymous, 2001	CAMP	IUCN (NW Himalaya)	Mode of propagation	Conservation priority
Aconitum deinorrhizum	-	-	-	CR	-	Seeds and vegetative	High
Aconitum heterophyllum	-	-ve	-	CR	CR, EN	Seeds and Tuber division	High
Aconitum violaceum	-	-	-	CR	CR, EN	Seeds	High
Allium strachei	-	-	-	VU		Seeds	Medium
Angelica glauca	-	-	-	CR		Seeds	High
Arnebia benthamii	-	–ve	-	CR	CR, EN	Seeds, Root cuttings	High
Artemisia maritime	-	-	-	VU	EN	Seeds	Medium
Atropa belladonna			-	CR		Seeds	High
Bergenia stracheyi	-	-	-	VU	VU	Seeds, Rhizome cuttings	Medium
Betula utilis	-	-		EN	EN	Seeds, Vegetatively through layering, grafting , budding	High
Bunium persicum	-	-	-	EN	NL	Seeds	High
Carum carvi	-	-	-	VU	-	Seeds	Medium
Chaerophyllum villosum	-	-	-	VU	-	Seeds	Medium
Dactylorrhiza hatagirea	-	-ve	-	CR	CR, EN	Seeds, Tuber division	High
Dioscorea deltoidea	-	-	CR* Appx. II	CR	-	Tubers	High
Ephedra gerardiana	-	-	-	EN	VU	Seeds	Medium
Eremus himalaicus	-	-	-	Vu	-	Seeds	Medium
Ferula jaeschkeana	-		-	VU	VU	Seeds	Medium
Fritillaria roylei	-	-	-	CR	CR, EN	Seeds	High
Heracleum lanatum	-	-	-	VU	-	Seeds	Medium
Hippaphae rhamnoides	-	-	-	VU	LR-ND	Seeds, Cuttings	Medium
Hyoscyamus niger	-	-	-	VU	LR-ND	Seeds	Medium
Hyossopus heterodonta	-	-	-	VU	NL	Seeds, Division of stem arising from rootstock.	Medium
Inula racemosa	-	-	-	CR	CR	Seeds, Root -stock	Medium
Jurinea dolomiaea	-	-	-	LR NT	NL	Seeds and divisions of rootstock at collar level.	Medium
Jurinea macrocephala	-	-ve	-	EN	-	Seeds	Medium
Nardostachys grandiflora	-	-ve	CR* Appx. II	CR	-	Seeds, Ramets	High
Picrorhiza kurroa	-	-ve	CR* Appx. II	EN	-	Root stolons	High
Pleurospermum brunonis	-	-	-	VU	-	Seeds	Medium
Podophyllum hexandrum	-	-ve	CR* Appx. II	CR	EN	Seeds, Rhizome splits	High
Polygonatum verticillatum	-	-	-	EN	VU	Seeds, Rhizome cuttings	Medium
Rheum austral	-	-ve	-	VU	-	Rhizome splits	Medium
Rheum moorcroftianum	-	-ve	-	VU	-	Rhizome splits	Medium
Rhododendron anthopogon	-	-	-	VU	-	Seeds	Medium
Rhododendron campanulaceae	-	-	-	VU	VU	Seeds	Medium
Rhododendron lepidotum	-	-	-	VU		Seeds	Medium
Saussurea costus	-	-	CR* Appx. I	CR	CR, EN	Seeds, Root cuttings	High
Saussurea gossypiphora	-	-	-	CR	EN	Seeds	High
Saussurea obvallata	-	-	-	EN	VU	Seeds	Medium
Taxus baccata	-	-	CR* Appx. II	CR	LR	Seeds, Shoot cuttings	High
Valeriana jatamansii	-	-	-	CR	-	Seeds	High

RDB= Red Data Book; **PN**= Public notice regarding negative list of export issued by Department of Commerce **CITES**=Convention on International Trade of Endangered Species of Fauna and Flora; **CAMP**= Conservation Assessment and Management Plan; **IUCN** International Union for Conservation of nature and natural resources;**CR**-Critically endangered, **EN**-Endangered, **VU**-Vulnerable, **LR-**Lower Risk**, E**-Endangered; **NL**-Not listed; **LR-NT**-low risk-near depletion.

period of two months (August-September) in earlier days which now has extended to five months (May–September) resulting in a negative effect on regeneration potential of these plants thereby contributing to the present status of these valuable resources. Among the studied species *Berberis aristata*, *Podophyllum hexandrum, Saussurea obvallata, Saussurea costus* and *Taxus baccata* are native to the Himalayan region and prefer to grow in this particular area only. This endemism and habitat specificity can also be considered as one of the major reason for their depletion. The rate and extent of human-mediated extinctions are debated, but there is a general agreement that extinction rates have soared over the past few years, largely because of accelerated habitat destruction. The species with high habitat specificity and/or low, population densities are more prone to extinction. Many policies governing the conservation of these plants have also been issued from time to time including both at National and International level including Convention of Biological Diversity (CBD), Trade-Related Aspects of Intellectual Property Rights (TRIPs) agreement, Biodiversity Act, 2002 and The Protection of Plant Variety and Farmers Right (PPV & FRA) Act, 2001 (Srivastava *et al*., 2011).

Table 4. Export Prohibited Medicinal Plants due to depletion

S. No	Botanical Names	Family
1	*Saussurea Species*	Asteraceae
2	*Podophyllum species*	Berberidaceae
3	*Dioscorea deltoidea*	Dioscoreaceae
4	*Taxus baccata*	Taxaceaee
5	*Aconitum species*	Ranunculaceae
6	*Picrorhiza kurroa*	Scrophulariaceae
7	*Gentiana kurroo*	Gentianaceae

Conclusion

The study analysed the medicinal and aromatic plants are uprooting for the uses of rhizomes or roots from the wild for their regeneration for the next coming growing year. It was found that certain locations, viz. Sangla Kanda, Kalpa Kanda, Ropa, Namgia, Batseri harbour a vast diversity of MAPs. Therefore, these places could be marked as control sites for future monitoring, to provide trends of population status and help in assessing the near future.

It was observed that the species with high market rates are declining more rapidly in their natural habitat and over exploiting. In the study area, few villagers have already started cultivation of important species such as *Saussurea costus*, *Bunium persicum* and *Carum carvi* due to their high economic return and spiritual or sacred values.

Few species *viz., Bupleurum falcatum, Pleurospermum candollei, Pinus gerardiana, Quercus baloot*, *Skimmia anquetilia* which are not considered threatened have been found to be in very small populations in the survey area thereby indicated the necessity of adopting immediate conservation measures for these species. Biotic interference in terms of increase and regular human interventions and unstopped grazing appears to be one of the major causes of declining population of these species in the region which needs to be curbed through village education.

Recommendations

- Protective measures for conservation of key species should be encouraged for conservation. It is suggested that, proper strategy and policy dealing with conservation management for prioritized communities and habitats should be formulated so that effective management of forests could be undertaken.
- Cultivation and conservation of medicinal plants should be promoted through village representatives and priests.
- Local people should be made aware of both *in-situ* and *ex-situ* conservation measures, which are essential to maintain the desired population status of this valuable gene pool.
- Curbing unwanted human intervention in the area.
- Bringing neglected uncultivated wasteland and dry land areas under cultivation of popular commercial medicinal plants.
- Opening up of state-level pharmacy within the district for capacity building and collection of plant material for elementary processing before being sent out of district for sale.
- Creation of plant nurseries facing depletion by forest department for sale/distribution people for planting in their vacant farm areas.

Acknowledgement

Authors are thankful to Government of Himachal Pradesh, Department of forest products, Dr. YSP University, Solan, HP for all needed facilities for this study. The help and cooperation rendered by the local

populace and Forest Department of Kinnaur district is highly acknowledged.

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Indian J. Plant Genet. Resour. 33(1): 52–59 (2020)
DOI 10.5958/0976-1926.2020.00008.X

RESEARCH ARTICLE

Genetic Diversity for Yield and Water Use Efficiency related Traits in Groundnut (*Arachis hypogaea* L.)

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(Received: 23 October, 2018; Revised: 28 September, 2019; Accepted: 30 September, 2019)

Cluster analysis using Mahalnobis D^2 was performed using 97 groundnut diverse genotypes for 14 yield contributing and water use efficiency related traits. The genotypes were grouped into twelve clusters based on D^2 statistic. Cluster II was the largest with 54 genotypes followed by cluster I with 33 genotypes and remaining ten clusters had one genotype each. The inter cluster D^2 values revealed maximum divergence between cluster VI and cluster III (1736), followed by cluster XII and cluster III (1622); cluster VI and cluster X11 (1389); cluster IX and cluster XI (1171) and cluster XI and cluster II (1041). It was observed that plant height was the largest contributor (65%) towards genetic divergence followed by days to maturity (10%) and secondary branches per plant (10%), SPAD Chlorophyll Meter Reading (SCMR; 4.3%) kernel length and hundred pod weight (1.2%) and Specific Leaf Area (SLA; 0.06%) contributed the least for divergence. Estimates of GCV and PCV were high for plant height, primary and secondary branches and pod yield per plant indicating higher genetic variation present in the genotypes studied. High heritability coupled with high genetic advance as per cent of mean was observed for days to fifty per cent flowering, secondary branches per plant, hundred pod and kernel weight, kernel length and, SCMR. SLA exhibited moderate estimates of heritability and genetic advance as per cent of mean.

Key Words: Divergence, Germplasm, Yield, Water use efficiency

Introduction

Groundnut is oilseed legume crop grown mainly by small and marginal farmers in arid and semi arid tropical areas. It covers an area of 53 lakh hectares and production of 91 lakh tonnes with productivity of 1731 kg/ha in India (FAOSTAT, 2017). In spite of having largest groundnut area in the world, its production and productivity levels are low in India because maximum area (75%) is rain fed condition. Hence, the crop is frequently subjected to drought stresses of different duration, intensities and timing.

Use of genetic resources has been limited in groundnut breeding programs, resulting in a narrow genetic base of cultivars (Upadhyaya *et al*., 2005). Characterising groundnut germplasm for agronomically superior traits is currently a major part of groundnut breeding efforts across the globe. Therefore identification of trait specific broad based germplasm and pyramiding of novel gene combinations in breeding population is important breeding strategy to address the complex nature of water deficit stresses. The Mahalanobis D^2 analysis followed by cluster analysis using Tocher's method is the rational criteria to assess the divergence and identifying diverse parents for hybridization. In the present study, efforts have been made to assess the genetic diversity in a set of 97 groundnut genotypes based on yield and surrogate traits of water use efficiency.

Materials and Methods

Ninety seven diverse groundnut genotypes consisting of released varieties of India and germplasm accessions obtained from Genetic Resources Section of ICAR-DGR, Junagadh (Table 1) including 4 checks were planted in the Randomized Complete Block Design (RCBD) with two replications at the Experimental plots of ICAR-Directorate of Groundnut Research (DGR) Station, Junagadh, Gujarat, India during *kharif*-2017. ICAR-DGR is situated between 21.49° N latitude and 70.44°E longitude at an elevation of 107 meters above mean sea level. Recommended agronomic practices were followed to raise crop. Each genotype was sown in a single row of 3m length and with a spacing of 60×10 cm. The observations on days to first flowering, days to 50% plants flowering, plant height, number of primary and secondary branches per plant, days to

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Table 1. List of 97 groundnut genotypes used for diversity study

S.No.	Genotype	Origin	S.No.	Genotype	Origin	S.No.	Genotype	Origin	S.No.	Genotype	Origin
1	NRCG 6780	AUSTRALIA	25	NRCG 14487	UNKNOWN	49	GG 2	INDIA	73	SB XI	INDIA
2	NRCG 17277	BRAZIL	26	NRCG 14412	USA	50	GG 3	INDIA	74	SG 99	INDIA
3	NRCG 14507	EQUDOR	27	NRCG 14386	CHINA	51	GG 6	INDIA	75	Spanish Improved	INDIA
4	Gangapuri	INDIA	28	NRCG 14309	HONDURAS	52	GG 8	INDIA	76	TAG 24	INDIA
5	NRCG 14345	INDONESIA	29	GG 12	INDIA	53	Girnar 1	INDIA	77	TG 38	INDIA
6	NRCG 14379	SUDAN	30	GJG 17	INDIA	54	Girnar 3	INDIA	78	TG 51	INDIA
7	NRCG 14435	USA	31	Kaushal	INDIA	55	GJG 9	INDIA	79	TLG 45	INDIA
8	NRCG 14491	CAMAROON	32	M 13	INDIA	56	GJG 31	INDIA	80	TMV 9	INDIA
9	GG 20	INDIA	33	NRCG 14467	INDIA	57	GPBD 4	INDIA	81	TPG 41	INDIA
10	Girnar 2	INDIA	34	Somnath	INDIA	58	ICGV 91114	INDIA	82	VRI (Gn)-6	INDIA
11	HNG 10	INDIA	35	NRCG 14475	UNKNOWN	59	J 11	INDIA	83	VRI 2	INDIA
12	HNG 69	INDIA	36	NRCG 734	USA	60	JGN 23	INDIA	84	VRI 3	INDIA
13	ICGS 76	INDIA	37	Sun oleic	USA	61	JGN 3	INDIA	85	NRCG 14477	INDONESIA
14	Kadiri 3	INDIA	38	NRCG 14368	ARG	62	JL 220	INDIA	86	NRCG 14456	TANZANIA
15	LGN 2	INDIA	39	NRCG 14472	BURMA	63	JL 24	INDIA	87	NRCG 1439	TAIWAN
16	M 522	INDIA	40	NRCG 10983	CENTRAL AFRICAN REPUBLIC	64	JL 501	INDIA	88	NRCG 14405	UNKNOWN
17	NRCG 14457	INDIA	41	NRCG 14485	CONGO	65	Kadiri 6	INDIA	89	NRCG 14326	UNKNOWN
18	NRCG 2615	INDIA	42	GG 7	INDIA	66	Kadiri 9	INDIA	90	NRCG 7627	UNKNOWN
19	R 8808	INDIA	43	TG 26	INDIA	67	NRCG 10620	INDIA	91	NRCG 8763	UNKNOWN
20	R 9251	INDIA	44	TG 37 A	INDIA	68	NRCG 14343	INDIA	92	NRCG 14336	USA
21	TG 39	INDIA	45	AK 159	INDIA	69	NRCG 14350	INDIA	93	NRCG 14501	USA
22	TGLPS 3	INDIA	46	AK-12-24	INDIA	70	NRCG 14474	INDIA	94	NRCG 14407	ZIM
23	NRCG 14463	KOREA	47	Dh 101	INDIA	71	R 2001-2	INDIA	95	NRCG 14424	ZIM
24	NRCG 12431	SENEGAL	48	DH 86	INDIA	72	S 206	INDIA	96	NRCG 14473	ZIM
									97	NRCG 17284	INDIA

maturity, hundred pod and kernel weight, kernel width, kernel length, pod yield per plant and late leaf spot incidence were recorded on a five random plants from each genotype.

The surrogate traits of water use efficiency, SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) were measured at 60 days after planting. SCMR was recorded at 60 days after sowing by collecting the second to third leaves from the top of the main stem of each plant and transported to a laboratory soon fresh weight was recorded. SCMR was measured immediately by a Minolta handheld portable SCMR meter (SPAD-502 plus Minolta, Tokyo, Japan), using four leaflets per sample and care was taken to ensure that the SPAD meter sensor fully covered the leaf lamina, avoiding any interference from veins and midribs. The same samples were further measured for leaf area, using a leaf area meter (LI 3100C Area meter, LI COR Inc., USA). The modified 1-9 point scale to late leaf spot as given by Subba Rao *et al.* (1990) was used for late leaf spot (LLS) screening under the natural condition. The analysis of genetic divergence was carried out using Mahalanobi's (1936) D^2 statistic and clustering of genotypes was done as per Tocher (Rao, 1952) using Indostat software package. Genotypic and phenotypic coefficients of variation were worked out as per the method suggested by Burton and De Vane (1953), heritability and genetic advance were calculated according to Johnson (1955) and Robinson *et al.* (1949).

Results and Discussion

Genetic improvement in groundnut crop depends on extent of genetic variability for yield and its components, resistance/tolerance to biotic and abiotic stresses. Judicious selection of parents for hybridization based on

genetic divergence between genotypes using D^2 statistics proves to be useful tool. The present investigation aims to determine the magnitude and extent of variability and extent of divergence among genotypes for 14 different traits including two surrogate traits of water use efficiency.

Variability and genetic parameters

The analysis of variance (Table 2) for different traits exhibited significant differences among the genotypes for all the traits studied which indicates that considerable genetic variability is available in the genotypes studied. This genetic variation enables selection of desired genotypes for improvement in desired direction. First flowering ranged from 21 to 33 days and 50 per cent flowering ranged from 23 to 37 days. Plant height was in the range of 25 to 69 cm. Primary and secondary branches per plant were between 3 to 8 and 1 to 24 respectively. Hundred pod weight ranged from 35 to 108 g and hundred kernel weight ranged from 15 to 48 g. Kernel shape which is decided by kernel length and kernel width ranged from 10 to 17 mm and 6 to 8 mm respectively. Pod yield per plant was as low as 2 g to as high as 18 g per plant (Table 3). The two surrogate traits of water use efficiency *viz.,* SPAD cholorophyll meter reading (SCMR) ranged between 19 and 39 and specific leaf area (SLA) ranged from 155 to 259 $cm^2\ g^{-1}$. Range of disease score for late leaf spot indicated that the genotypes fell between tolerance (recorded a disease score of 5) to susceptibility (recorded a disease score of 8). Most of the genotypes studied matured early (92 to 106 days) irrespective of botanical groups. It may be due to shortening of life cycle to escape end-of-season drought that prevailed during *kharif* 2017.

Selection efficiency mainly depends on the magnitude of genetic variability for quantitative traits. An assessment of heritable and non-heritable components of the total variability decide breeding procedure to be adopted. The nature and magnitude of variation for individual traits was assessed by phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (Table 3). High GCV and PCV estimates were observed for plant height, primary and secondary branches per plant and pod yield per plant indicating the higher genetic variation observed in the genotypes. Higher estimates of GCV and PCV for these traits were not uncommon in groundnut and have already been well documented (Sudha *et al.,* 2012; Sunday and Omalayo 2013).

Four other traits, days to first and fifty per cent flowering, kernel length, SPAD chlorophyll meter reading and reaction to late leaf spot incidence were exhibited moderate estimates of GCV and PCV. Moderate estimates for days to first flowering (Patel, 2017); days to fifty per cent flowering (Sunday and Omalayo, 2013); SCMR (Yamunara, 2015 and Savita, 2012) and reaction to late leaf spot incidence (Vishnuvardhan *et al.,* 2012) have already been reported in groundnut. Low GCV and PCV estimates were observed for days to maturity (Zaman *et al*., 2011) and kernel width which indicate the existence of low variability for these traits in the genotypes studied.

Table 2. Analysis of variance for yield and water use efficiency related traits in groundnut

S. No.	Character	Source of Variation (Mean sum of squares)			CV
		Replication (df=1)	Genotypes (df=96)	Error (df=96)	
1	Plant height (cm)	0.6237	198.49***	0.70	1.98
2	Primary branches per plant	0.0463	0.0463***	0.23	10.45
3	Secondary branches per plant	5.2783**	32.478***	0.74	16.6
4	Late leaf spot (LLS) incidence	1.3195*	1.6429***	0.21	6.3
5	Days to maturity	4.0412***	10.018***	0.29	0.5
6	Days to first flowering	1.4896	17.126***	3.45	7.3
7	Days to 50% flowering	0.3298	26.001***	4.75	7.8
8	SPAD chlorophyll meter reading	17.460*	39.686***	2.87	5.7
9	Specific leaf area ($cm^2\ g^{-1}$)	135.98	993.47***	337	9.0
10	Hundred pod weight (g)	791.73***	394.65***	55.8	10.7
11	Hundred kernel weight (g)	211.58***	70.582***	9.06	10.5
12	Kernel width (cm)	2.7505***	0.3997***	0.13	4.77
13	Kernel length (cm)	0.0561	5.4695***	0.76	6.47
14	Pod yield per plant (g)	15.164	28.708***	8.33	32.4

Table 3. Genetic parameters for yield and water use efficiency related traits in groundnut

S.No.	Particulars	Minimum	Maximum	Mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	$h^2_{(BS)}$	GA	GAM
1	Plant height (cm)	25	69.5	42.09	98.9	99.5	23.62	23.7	99.3	20.4	48.5
2	Primary branches per plant	3	8	4.62	1.04	1.27	22.1	24.45	81.7	1.9	41.2
3	Secondary branches per plant	1	24	5.14	15.87	16.6	77.44	79.21	95.6	8.0	155.9
4	Late leaf spot (LLS) incidence	5	8	7.16	0.719	0.92	11.83	13.41	77.8	1.5	21.5
5	Days to maturity	92	106	96.03	4.86	5.15	2.297	2.36	94.4	4.4	4.6
6	Days to first flowering	21	33	25.14	6.83	10.28	10.39	12.75	66.5	4.4	17.5
7	Days to 50% flowering	23	37	27.75	10.62	15.37	11.47	14.12	96.1	5.6	20.1
8	SPAD chlorophyll meter reading	19.3	40.0	29.58	18.4	21.27	14.5	15.95	86.5	8.2	27.8
9	Specific leaf area ($cm^2\ g^{-1}$)	155.5	259.4	202.60	328	665.4	8.937	12.73	49.3	26.2	12.9
10	Hundred pod weight (g)	35.5	108.6	69.60	196.4	225.2	18.67	21.73	75.2	23.3	33.4
11	Hundred kernel weight (g)	15.9	48.0	28.44	30.76	39.8	19.49	22.18	77.3	10.0	35.3
12	Kernel width (mm)	6.4	8.65	7.64	0.133	0.26	4.779	6.753	50.1	0.5	7.0
13	Kernel length (mm)	10.1	17.75	13.40	2.356	3.11	11.41	13.122	75.7	2.8	20.5
14	Pod yield per plant (g)	2.1	18.51	8.90	10.187	18.52	35.82	48.311	55	4.9	54.7

σ^2 g – Genetic variance | σ^2 p - Phenotypic variance | $h^2_{(BS)}$ - Heritability in broad sense
GCV (%) - Genotypic coefficient of variation | PCV (%) -Phenotypic coefficient of variation | GAM- Genetic advance as per cent of mean

Heritability estimates along with genetic advance estimates would be more useful in predicting effectiveness of selection. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, primary and secondary branches per plant, days to fifty per cent flowering, hundred pod and kernel weight, kernel length, SPAD chlorophyll meter reading and reaction to late leaf incidence suggesting role of additive gene effects and scope for simple phenotypic selection. Sudha *et al.* (2012), Vishnuvardhan *et al*. (2012), Rao *et al.* (2012) and Sunday and Omalayo (2013) have also advocated selection of these traits for genetic improvement. The traits *viz*., days to first flowering exhibited high heritability with moderate genetic advance as per cent of mean (Zongo *et al*., 2017). Specific leaf area (SLA) had moderate heritability and genetic advance as per cent of mean indicating role of environment in the inheritance of these traits. Pod yield per plant showed moderate heritability coupled with high genetic advance as per cent of mean. Two traits, kernel width (with moderate heritability and low genetic advance as per cent of mean) and days to maturity (high heritability with low genetic advance as per cent of mean) exhibited non-additive effects indicating less usefulness of these traits for direct selection. These results are in accordance with the findings of Vishnuvardhan *et al*. (2012) for days to maturity, Shreya *et al.* (2014) for specific leaf area and Kavera (2008) for pod yield per plant.

Correlation analysis

Days to first and fifty per cent flowering, hundred pod and kernel weight, kernel width and length and SPAD Chlorophyll meter reading (SCMR) were correlated significant positively with pod yield per plant, whereas the relationship of plant height and specific leaf area (SLA) with pod yield was negative and significant (Table 4). High SCMR indicates higher unit chlorophyll efficiency and higher photosynthesis rate and which in turn results in higher pod yield (Nageswara Rao *et al.,* 2001). The surrogate traits of water use efficiency, SPAD chlorophyll meter reading and specific leaf area correlated negatively to each other (Nageswara Rao *et al.,* 2001 and Upadhyaya, 2005). SPAD chlorophyll meter reading correlated positively with flowering and productive traits. Hence SCMR can be a more reliable trait for enhanced WUE and yield traits (Kalariya *et al.,* 2017).

Diversity analysis

The D^2 statistic is more useful tool to determine divergence among populations in terms of generalized group distance. Following the procedure of Tocher (Rao,1952) and by treating the estimated D^2 values as the square of the generalized distance, 97 genotypes studied were grouped into twelve clusters (Table 5, Fig. 1). Cluster II was the largest with 54 genotypes followed by cluster I with 33 genotypes. Remaining ten clusters had one genotype each. Interestingly it has been observed that the 13 genotypes in both the large clusters

Table 4. Phenotypic correlation coefficients of yield and water use efficiency related traits in groundnut

Trait	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1	-0.128	-0.179	-0.032	-0.143	-.312**	-.326**	-.417**	0.216*	-.207*	-.260*	-.226*	-.409**	-.331**
X2		1	0.196	-0.096	0.022	0.139	0.129	0.118	-0.18	0.037	0.028	0.148	0.094	0.188
X3			1	-.210*	0.250*	0.288**	.330**	0.134	-0.177	-0.176	-0.187	-0.047	0.008	0.085
X4				1	-0.175	-0.077	-0.058	.247*	-0.224*	0.13	0.186	0.029	0.109	0.169
X5					1	.201*	0.232*	0.007	0.032	-0.013	-0.071	-0.173	0.155	-0.024
X6						1	0.957**	0.439**	-0.355**	0.043	-0.029	-0.049	0.270**	0.287**
X7							1	0.445**	-0.370**	0.063	-0.023	-0.043	0.288**	0.290**
X8								1	-0.689**	0.347**	0.405**	0.343**	0.544**	0.536**
X9									1	-0.297**	-0.332**	-0.255*	-.383**	-0.409**
X10										1	0.890**	0.533**	0.734**	0.538**
X11											1	0.691**	0.692**	0.558**
X12												1	0.375**	0.467**
X13													1	0.559**
X14														1

*significance at 0.05%; ** Significance at 0.01%

X1- Plant height (cm) X2- Primary branches per plant X3- Secondary branches per plant X4-Late leaf spot incidence
X5- Days to maturity X6- Days to first flowering X7- Days to 50% flowering X8-SPAD chlorophyll meter reading
X9- Specific leaf area (cm^2 g^{-1}) X10- Hundred pod weight (g) X11- Hundred kernel weight (g) X12- Kernel width (mm)
X13- Kernel length (mm) X14- Pod yield per plant (g)

Table 5. Distribution of 97 genotypes of groundnut among the 12 clusters on the basis of D^2 analysis

Cluster	No. of genotypes	Grouped genotypes
I	33	AK 159, Dh 101, Gangapuri, Girnar 1, Girnar 2, Girnar 3, GJG 09, HNG 69, JGN 23, JL 220, JL 501, Kadiri 3, Kadiri 6, R 2001-2, Somnath, Spanish Improved, TG 38, TG 39, DH 86, TG 26, NRCG 10983, NRCG 12431, NRCG 14326, NRCG 14336, NRCG 14345, NRCG 14379, NRCG 14386, NRCG 14407, NRCG 14424, NRCG 14463, NRCG 14474, NRCG 14487, NRCG 14507
II	54	AK-12-24, GG 2, GG 3, GG 6, GG 8, GG 20, GJG 17, GPBD 4, HNG 10, ICGV 91114, J 11, JGN 3, JL 24, Kadiri 9, Kaushal, LGN 2, M 13, M 522, R 8808, S 206, SB XI, SG 99, Sun oleic, TG 51, TGLPS 3, TLG 45, TPG 41, VRI (Gn)-6, VRI 3, GG 7, TAG 24, TG 37 A, TMV 9, NRCG 734, NRCG 1439, NRCG 2615, NRCG 6780, NRCG 7627, NRCG 8763, NRCG 10620, NRCG 14309, NRCG 14368, NRCG 14405, NRCG 14412, NRCG 14435, NRCG 14456, NRCG 14457, NRCG 14467, NRCG 14473, NRCG 14477, NRCG 14485, NRCG 14501, NRCG 17277, NRCG 17284
III	1	VRI 2
IV	1	GG 12
V	1	R 9251
VI	1	NRCG 14472
VII	1	ICGS 76
VIII	1	NRCG 14491
IX	1	NRCG 14475
X	1	NRCG 14350
XI	1	NRCG 14343
XII	1	GJG 31

had either JL 24 or Robut 33-1 genetic background in their pedigree. Similarly genotypes M 13, TG 26, TAG 24, GAUG 10, J 11, Girnar 1, TMV 10 and BARC-1 have been used in the development of 22 genotypes in cluster I, II and VI. Four in each cluster of I and II were direct selections from local land races/germplasm.

D^2 values between clusters revealed maximum divergence between cluster VI and cluster III, followed by cluster XII and cluster-III; cluster VI and cluster X11; cluster IX and cluster XI and between cluster XI and cluster II (Table 6). Larger inter-cluster distance between these clusters suggests considerable diversity between genotypes of these clusters. The minimum divergence between cluster VIII and cluster V (12) followed by cluster V and cluster IV (42) indicates the close relationship among the genotypes included in these two clusters.

The per cent contribution of each character (Table 8**)** indicated that plant height was the largest contributor (65.98%) towards divergence. This is because the

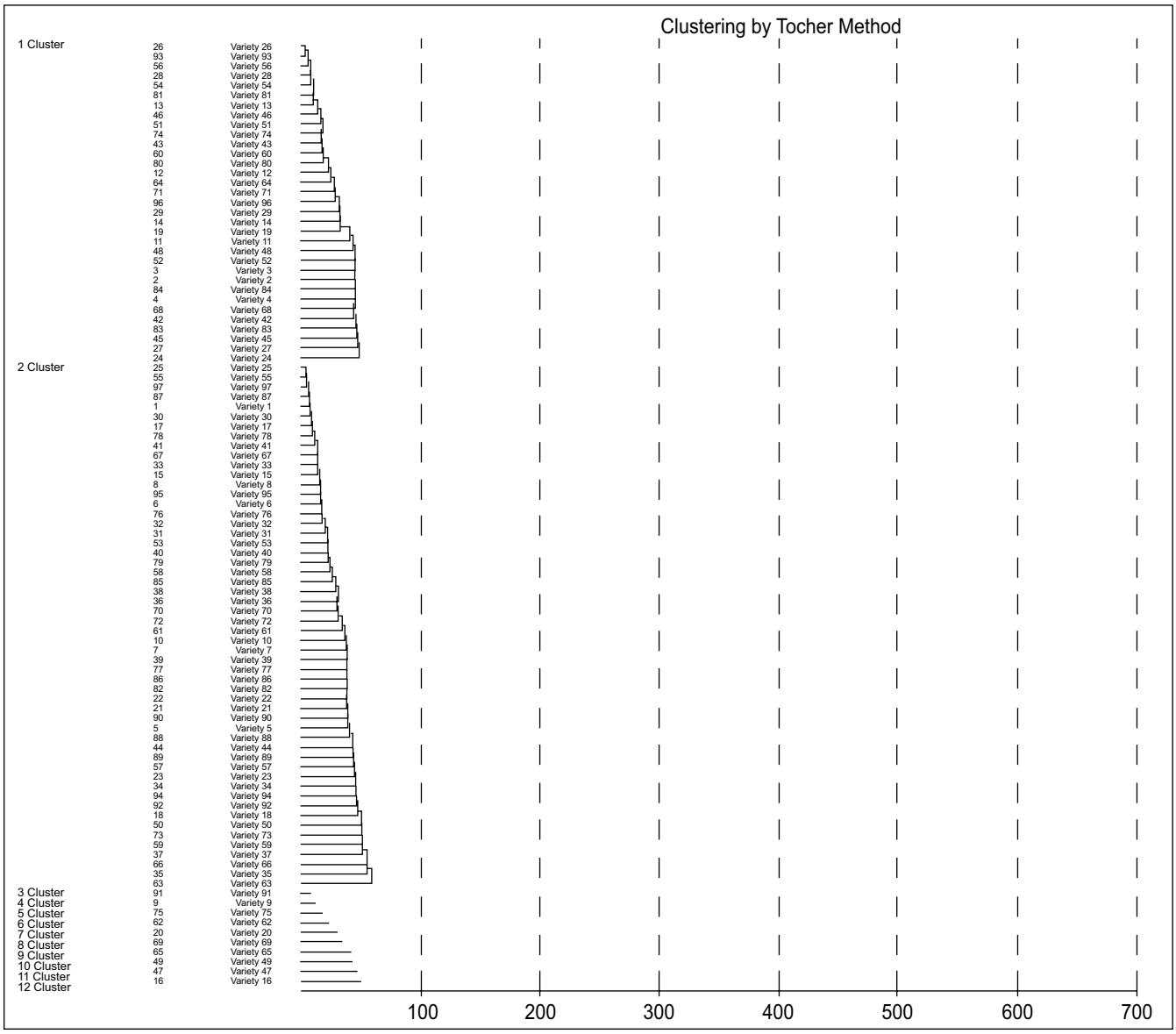

Fig. 1. Dendrogram showing 12 clusters of groundnut genotypes based on Tocher's method

Table 6. Intra and inter cluster distances among 12 clusters constructed based on Toucher's method

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	101.36											
II	320.41	105.41										
III	684.68	181.61	0.00									
IV	146.04	202.18	463.14	0.00								
V	216.01	203.32	447.09	42.48	0.00							
VI	332.84	1041.27	1736.22	568.03	713.84	0.00						
VII	304.67	368.53	711.18	133.76	77.18	729.37	0.00					
VIII	166.48	342.2	698.39	86.03	12.36	442.92	212.67	0.00				
IX	501.25	366.17	579.34	459.93	450.33	1171.21	626.48	619.7	0.00			
X	195.03	286.44	617.03	160.33	235.49	546.7	352.19	208.52	263.63	0.00		
XI	344.19	931.81	1622.04	473.28	578.74	182.03	585.51	431.72	702.5	358.72	0.00	
XII	636.84	384.84	577.65	395.03	325.28	1388.9	447.64	613.63	192.3	303.37	880.54	0.00

genotypes studied belonged to all the four botanical groups of groundnut which vary greatly in their heights. The other traits *viz.,* days to maturity (10.22%), secondary branches per plant (10.09 %), SPAD chlorophyll meter reading (4.3%), primary branches per plant, hundred kernel weight (1.57%), disease score of late leaf spot (1.16%), kernel length (1.18%), hundred pod weight (1.14%), pod yield per plant (0.34%), kernel width (0.34%) and days to fifty per cent flowering (0.6%) contributed less to the divergence.

It is observed that 97 genotypes from different geographical origin representing diverse agro-climatic conditions were distributed at random among the clusters formed based on their genetic distance. The absence of relationship between genetic diversity and geographical diversity may be attributed to forces other than geographical origin such as exchange of breeding material, genetic drift, variations, natural and artificial selection are responsible for diversity (Murthy and Arunachalam, 1966 and Sheriff and Shivashankar, 1992).The genotypes with high mean performances for different traits studied in diverse clusters (II, III, VI, VII and IX) may serve as potential donors in hybridization programme.

Table 7. Cluster means of twelve clusters for yield and water use efficiency related traits of groundnut

Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X 12	X 13	X 14
I	51.58	4.3	3.55	7.1	95.0	23.83	25.88	27.50	210.00	66.53	27.05	7.59	12.58	7.42
II	35.45	4.79	5.27	7.2	96.0	25.98	28.91	30.97	199.27	71.49	29.24	7.70	13.88	9.99
III	25.0	4.0	2.0	7.0	95.0	26.0	29.0	35.00	183.09	108.6	48.02	8.65	17.75	12.74
IV	45.5	4.0	4.5	7.5	100.0	22.5	26.0	33.50	160.35	108.4	42.30	8.10	15.40	15.93
V	43.5	4.5	5.0	8.0	102.0	21.5	24.0	28.05	211.05	71.31	33.54	7.55	14.80	4.83
VI	69.5	5.5	1.5	7.5	94.0	23.5	25.0	24.30	210.50	49.82	20.99	7.30	11.45	4.18
VII	47.0	4.5	4.5	5.5	106.0	24.5	26.5	26.15	236.68	39.13	18.18	7.10	11.80	5.90
VIII	49.5	4.0	3.5	7.5	99.0	24.0	25.0	23.55	213.13	94.24	27.45	6.35	16.55	2.97
IX	38.5	4.0	24.0	6.0	94.0	23.5	25.5	26.70	201.74	54.21	22.00	7.65	11.15	4.48
X	47.5	7.0	14.0	5.0	96.0	30.5	35.0	34.30	164.59	67.62	16.63	7.35	16.30	7.26
XI	65.5	4.0	15.0	7.0	97.0	25.5	30.5	26.65	208.35	54.90	21.11	7.20	10.25	3.40
XII	35.5	6.5	23.5	7.5	101.0	28.5	30.5	32.20	175.91	55.70	27.51	8.00	14.30	18.1

X1- Plant height (cm) X2- Primary branches per plant X3- Secondary branches per plant X4-Late leaf spot incidence
X5- Days to maturity X6- Days to first flowering X7- Days to 50% flowering X8-SPAD chlorophyll meter reading
X9- Specific leaf area (cm^2 g^{-1}) X10- Hundred pod weight (g) X11- Hundred kernel weight (g) X12- Kernel width (mm)
X13- Kernel length (mm) X14- Pod yield per plant (g)

Table 8. Relative contribution (%) of individual trait to the genetic divergence

S.No.	Source	Times ranked 1st	Contribution (%)
1	Plant height (cm)	3072	65.98
2	Primary branches per plant	139	2.99
3	Secondary branches per plant	470	10.09
4	Late leaf spot (LLS) incidence	54	1.16
5	Days to maturity	476	10.22
6	Days to first flowering	28	0.6
7	Days to 50% flowering	1	0.02
8	SPAD chlorophyll meter reading	200	4.3
9	Specific leaf area (cm^2 g^{-1})	3	0.06
10	Hundred pod weight (g)	53	1.14
11	Hundred kernel weight (g)	73	1.57
12	Kernel width (cm)	16	0.34
13	Kernel length (cm)	55	1.18
14	Pod yield per plant (g)	16	0.34

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Indian J. Plant Genet. Resour. 33(1): 60–67 (2020)
DOI 10.5958/0976-1926.2020.00009.1

RESEARCH ARTICLE

Evaluation of Teosinte derived Maize Lines for Drought Tolerance

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(Received: 18 December, 2018; Revised: 17 January, 2019; Accepted: 02 February 2019)

Maize plants grown in subtropical and temperate regions are often subjected to moisture stress. The wild progenitors of the crop species are the important source of genes of various abiotic and biotic stress tolerance. Teosinte (*Z. mays* ssp. *parviglumis*), the progenitor of maize possesses several important genes of agronomic importance, majority of which were lost during the process of domestication. In the present investigation, 203 modern maize BC_1F_2 introgressed lines (encoded as AM-1 to AM-203) were developed and evaluated under irrigated and moisture stressed environments. In order to introduce the genes of agronomic importance from the progenitor teosinte to modern maize, DI-103 inbred were crossed with teosinte. The present study involved evaluation of 203 lines (encoded as AM-1 to AM-203). These lines were grown in a single row in two environmental conditions i.e. irrigated and stress condition during *Rabi* 2016-17 for the phenotyping of morpho-physiological traits *viz*., anthesis silking interval (ASI), leaf rolling, leaf firing, canopy temperature depression (CTD), chlorophyll content, ear length, ear diameter, kernel rows/ear, kernels/row, tip filling, grain filling, grain yield per plants (g), and 1000-kernel weight and drought tolerance index, stress tolerance index, yield index associated with drought tolerance. Overall sum of rank scores over thirteen traits associated with drought tolerance revealed that AM-39 was the most drought tolerant line among all the 203 lines under study with a total score of one hundred eight, followed by AM-64, AM-16, AM-42, and AM-102, whereas, AM-116 was the most susceptible, with the least score of thirty-four.

Key Words: BC_1F_2, Drought, Maize, Morpho-physiological trait, Teosinte

Introduction

Maize (*Zea mays* L., 2n=20) is an important cereal crop belonging to tribe Maydeae, of the grass family, Poaceae. The centre of origin of maize has been recognized as the Meso-American region and about 9000 years ago domestication was started independently in regions of the South-West USA, including Mexico and in Central parts of America. Being C4 plant, it can capture energy efficiently and is capable of producing maximum food grains per unit area as compared to other cereals. Maize grain contains about 10% protein, 4% oil, 70% carbohydrate, 2.3% crude fiber, 10.4% albuminoides and 1.4% ash and sufficient quantities of carotenoids and other vitamins. Besides large number of commercial products it is used for diversified purposes like human food (25%), poultry feed (49%), animal feed (12%), industrial (starch) product (12%), beverages and seed (1% each) (Anonymous, 2014). Teosinte (*Z. mays* ssp. *parviglumis*; hereafter referred to as teosinte) is a wild progenitor of domesticated maize (*Z. mays* ssp. *mays*). Teosinte has greater genetic diversity than maize inbreds and landraces. Exploitation of teosinte as a genetic resource for biotic and abiotic stresses is becoming a burning area of research in the recent years, through wide hybridization. Breeders are also working on the dissection of domestication and evolution phenomena of cultivated maize from teosinte, to know the segregation distortion in maize × teosinte progenies. QTL controlling root aerenchyma formation in a maize × teosinte F_2 population have been identified (Mano *et al*., 2005a; 2007a, b). Teosinte was the donor of several QTLs associated with the increased capacity to form aerenchyma, thus confirming the potential of teosinte genes to develop improved maize germplasm (Qing *et al*., 2011). Thus, there is tremendous interest and demand for improving maize drought tolerance through biotechnology (Wang *et al.,* 2016) and utilization of wild relatives for the same**.** Since the broad utilization

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of single cross hybrids during the past century, maize genetic base gradually became narrower. The yield is considerably limited due to drought, together with heat, salinity, pests, and diseases. Like all other agricultural crops, the present-day cultivated maize varieties are characterized by narrow genetic composition and fixation of relatively few adapted genes and their allelic variations. Landraces and wild relatives are possible genetic reservoirs to get the genes for moisture stress tolerance and to incorporate them in modern cultivars to improve their status of drought tolerance and thus ensure stability w.r.t. yield potential. Therefore, breeders are in search of new genetic resource i.e. wild relatives to broaden the genetic base by introgression of the desirable genomic region into the inbred lines used in the commercial cultivation. *Zea mexicana, Tripsacum floridanum* and *Z. mays* ssp. *parviglumis*, which are wild relatives of maize, are tremendous sources of novel genes for improvement of tolerance against drought and other stresses (Singh, 2010). BC_1F_3 lines of three maize-teosinte crosses exhibited significant variance for most of the characters. Mean, range, PCV and GCV for different characters analyzed across the three populations indicated that teosinte derived lines were diversified probably because of the allelic reshuffling between maize and teosinte genome. Thus, teosinte can be used effectively for diversification as well as enhancement of maize germplasm. The genetic narrowing formed by domestication followed by selective breeding, can be broadened using teosinte (Singh *et al*., 2017).

Maize crop is more sensitive to abiotic stresses, particularly moisture stress (drought) and water logging stress during the growing season, especially the reproductive stage. During reproductive growth stage, 8–9 mm water is needed per day by a single plant. Four weeks are most crucial regarding water requirement which includes two weeks before and two weeks after pollination. Pollination is the most critical growth stage for water requirement and all leaves are kept unfolded and grain yield is also decided at this stage (Aslam *et al.,* 2015). Plant breeder exploits the term drought according to his objective. In a given region, there may not be drought over an entire growing season but a small spell of moisture stress during reproductive stage may lead to drought. Here, we define drought (also referred to as agricultural drought) as the time point when the amount of moisture in the soil no longer meets the needs of the crop (Mannocchi *et al.,* 2009). Drought is the single most common cause of severe reduction in crop production in developing countries like India, and high temperature is predicted to further exacerbate drought's impact. Therefore, there is a need of breed genotypes which are able to maintain a stable yield over a range of water supply. This apparently seems simple but it is not an easy task and has several reasons behind it. Drought tolerance is a very complex trait, affected by a wide range of mechanisms spanning both the time scale and their plant geometry. In this regard, crop phenology is considered a very important feature of drought tolerance (Passioura, 1996) and the plant adaptation will be effective where climate changes are slow and consistent over the time. It has been observed for many crops, that there is a low genetic correlation for yield in high- and low-productivity environments, indicating that different sets of genes may be important in regulating the yield in different environments (Johnson and Geadelmann, 1989; Atlin and Frey, 1990). Extensive genetic dissections of drought tolerance traits have been carried out in maize over the last decade. It leads to the identification of numerous QTLs involved in the determination of morphological traits and physiological traits imparting drought tolerance. But still we are not able to develop hybrids and other varieties to overcome problems of drought. Therefore we need to search new resources of genes or QTLs for drought tolerance which can be exploited in breeding program.

Keeping in view the changing scenario of water availability and erratic rainfall, present experiment has been designed to evaluate the BC_1F_2 teosinte derived maize lines using morpho-physiological traits and therefore, our hypothesis was to identify the teosinte derived drought tolerant lines with the help of rank score assigned on the basis of least reduction or positive increase between the performance of genotype in irrigated condition and drought condition.

Materials and Methods

The present investigation was conducted at N.E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The planting materials were developed by introgressing the genomic regions from wild progenitor teosinte (*Z. mays* ssp. *parviglumis*) to the genetic background of modern cultivable maize inbred line DI-103. Teosinte was used a pollen parent to pollinate the maize inbred line DI-103 in *Kharif* 2015, followed by one backcrossed

with DI-103 as a recurrent parent to develop BC_1F_1 lines. In *Kharif* 2016, BC_1F_1 plants were selfed to produce 203 BC_1F_2 lines (encoded as AM-1 to AM-203), which were evaluated in the *Rabi* season 2016-2017 for drought tolerance. The lines were grown as 2m single row with spacing of 75cm in two environmental conditions i.e. irrigated condition and moisture stress condition during *Rabi* 2016-17, for the phenotyping of morpho-physiological traits associated with drought tolerance. The lines were challenged with moisture stress before anthesis and silking stage. The rainfall data was recorded during the experiment period and data revealed that on 16th May there was rain of 29 mm.

Ten morpho-physiological traits *viz*., Anthesis-silking interval (ASI), days to 75 per cent senescence (D75S), canopy temperature depression (CTD), chlorophyll content (CC), ear length (EL), ear diameter (ED), kernel row per ear (KE), kernels per row (KR), grain yield per plant (GY) and 1000 kernel weight (KW) were recorded as per standard protocols. The average value of genotypes for all the characters were used for the statistical analysis and calculation of drought tolerance, stress tolerance and yield indices.

Drought tolerance index, stress tolerance index and yield index were calculated with following formulae;

Drought tolerance index (DI) $= \frac{Y_s \times \frac{Y_s}{Y_p}}{\bar{Y}_s} = \frac{Y_s \times \frac{Y_s}{Y_p}}{\bar{Y}_s}$ (Lan, 1998).

Yield index (YI) $= \frac{Y_s}{\bar{Y}_s} = \frac{Y_s}{\bar{Y}_s}$ (Gavuzzi *et al.,* 1997).

Stress tolerance index $= \frac{Y_s \times Y_p}{\bar{Y}_p^2} = \frac{Y_s \times Y_p}{\bar{Y}_p^2}$ (Fernandez, 1992)

Where, *Ys*, *Yp*, are the yield of each genotype in stress (drought) and irrigated conditions for each genotype, respectively; $\overline{Y}$ s and $\overline{Y}$ p are the mean yield in drought and irrigated condition, respectively.

In order to identify the tolerant genotypes for the trait, irrigated and stress conditions were compared for percentage change and the genotypes showing least changes in both the environment was given maximum rank in the ranking scale of 1to10. First twenty genotypes showing least changes were considered most tolerant and accorded the rank value 10. Next twenty lines were given 9 and subsequently, at last twenty-three lines were given rank value 1.

Results and Discussion

The mechanism of drought tolerance is complex in nature. Therefore, none of the traits evaluated under investigation can be solely called responsible for drought tolerance *in toto*. Accounting of all the traits which have contributed towards tolerance, would help to screen drought tolerant lines in a comprehensive manner. Considering the multi-traits associated with drought tolerance mechanism, each genotype was given a rank score for each of the 10 morpho-physiological traits and three indices. The basis of ranking was the least reduction or positive increase between the performance of genotype in irrigated condition and moisture stress condition. All the lines were given a rank score in decreasing order of their tolerance for each trait from 1 to 10. Higher score corresponded to higher tolerance of that line to water stress for respective drought associated traits.

The mean values of the trait along with respective mean deviation were presented in the Table 1. The highest mean value (in days) of ASI in normal and drought condition was reflected by AM-115(2.60), AM-92 (4.00) and the lowest value -1.80 (AM-100), AM-18 (-6.00) exhibited respectively. The maximum and minimum mean deviation was found for AM-92(3.67) and AM-18(-7.35) respectively. For anthesis silking interval in drought stress, maximum tolerance was registered in AM- 39 (10), AM-115(10), AM-83(10) and AM-18(10). The least tolerance was exhibited by AM-193(1), AM-92(1) and AM-53 (1) (Table 4). For 75 per cent days to senescence in normal and drought condition, the maximum mean value showed by AM-92 (131), AM-137 and AM-92 (119) and the minimum value of 120 days was observed in AM-16, AM-99; 104 days in AM-115, AM-83. The highest and lowest mean deviation was found for AM-193 (-4.99) and AM-83 (-17.20). For 75 per cent days to senescence the highest tolerance to drought was shown by line AM-193 (10), AM-116 (10) and AM-53 (10), while the lowest was found in AM-71(1), AM-83 (1), AM-115 (1) and AM-102 (1). The highest mean value of canopy temperature depression (CTD) in normal and drought condition was reflected by AM-16(5.90), AM-138 (10.00) and the lowest value of 0.40 in AM-137 and AM-184 (1.70). The maximum and minimum mean deviation was found for AM-138(8.80) and AM-18(-3.80) respectively. Similarly, genotype AM-138 (10) showed highest tolerance to physiological trait, CTD and, AM-16 and AM-18 found as least tolerant to the same (1). For chlorophyll content

Table 1. List of Mean (normal and stress), Mean Deviation (MD) of ten most tolerant and most susceptible teosinte derived BC_1F_2 lines

	Anthesis silking interval (ASI)			Days to 75% senescence(days)			Canopy temperature depression (CTD)			Chlorophyll content (SPAD unit)		
TL	M		MD	M		MD	M		MD	M		MD
	N	S		N	S		N	S		N	S	
AM-39	-0.40	-1.50	-1.10	127.80	117.50	-8.06	4.60	4.90	0.30	43.60	42.10	-3.44
AM-64	-0.40	1.20	1.60	123.40	112.60	-8.75	1.90	6.40	4.50	45.00	46.50	3.33
AM-16	-2.0	-1.0	1.00	120.00	111.60	-7.00	5.90	3.40	-2.50	46.00	47.20	2.61
AM-42	-0.40	0.00	0.40	127.00	113.00	-11.02	4.00	3.70	-0.30	53.50	46.00	-14.02
AM-102	0.60	0.86	0.26	125.00	105.66	-15.47	2.10	8.70	6.60	40.80	54.30	33.09
AM-178	0.20	1.34	1.14	124.00	114.00	-8.06	1.10	7.30	6.20	40.00	39.10	-2.25
AM-115	1.40	-0.50	-1.90	123.80	104.00	-15.99	2.20	6.20	4.00	38.60	37.40	-3.11
AM-138	0.75	1.20	0.45	121.75	108.80	-10.64	1.20	10.00	8.80	36.50	35.70	-2.19
AM-83	2.60	-1.00	-3.60	125.60	104.00	-17.20	2.10	5.60	3.50	45.60	45.80	0.44
AM-99	0.60	1.00	0.40	120.20	109.00	-9.32	3.20	8.60	5.40	44.00	44.80	1.82
SL												
AM-116	-1.00	0.83	1.83	123.80	116.33	-6.03	0.80	5.00	4.20	49.60	40.50	-18.35
AM-193	-0.40	2.50	2.90	124.20	118.00	-4.99	1.40	5.50	4.10	51.10	41.00	-19.77
AM-18	1.35	-6.00	-7.35	126.60	114.00	-9.95	6.40	2.60	-3.80	54.40	49.30	-9.38
AM-90	1.20	0.50	-0.70	127.00	113.25	-10.83	2.60	6.20	3.60	51.50	50.30	-2.33
AM-137	0.60	1.80	1.20	130.60	119.00	-8.88	0.40	3.90	3.50	40.70	40.20	-1.23
AM-100	-1.80	-1.75	0.05	126.40	114.00	-9.81	2.70	7.70	5.00	50.50	44.60	-11.68
AM-92	0.33	4.00	3.67	131.00	119.00	-9.16	2.20	8.40	6.20	46.00	38.40	-16.52
AM-71	-0.50	1.00	1.50	129.00	113.00	-12.40	2.10	7.60	5.50	47.60	39.80	-16.39
AM-184	0.40	1.84	1.44	127.40	115.00	-9.73	1.90	1.70	-0.20	47.40	43.00	-9.28
AM-53	-1.75	1.33	3.08	123.75	117.16	-5.33	3.40	5.20	1.80	41.00	42.20	2.93

TL: Tolerant line SL: Susceptible line N: Normal S: Stress

in normal and drought condition, the maximum mean value was shown by AM-18 (54.40), AM-102 (54.30) and the minimum value was observed as 36.50, 35.50 for AM-138. The highest and lowest mean deviation was found for AM-102 (33.09) and AM-116 (-18.35). Chlorophyll content is another physiological trait for which the most stress tolerant line AM-102 (10) was identified, whereas, least tolerance was found in AM-116 (2) and AM-193(2) (Table 1).

Among the yield contributing traits, the highest mean value of ear length in normal and drought condition was showed by AM-102 (13.00 cm,13.80 cm) and the lowest value 5-6.60 cm by AM-39, AM-16 and AM-42; 5.60 cm by AM-100. The maximum and minimum per cent mean deviation was found 90.91 (AM-42, AM-16) and AM-18(-61.67) respectively. For ear diameter the highest mean value was reflected by AM-100 (2.90 cm), AM-42 (3.80 cm) and the lowest value (1.00 cm) for AM-16 and AM-18 in normal and drought condition respectively. The maximum and minimum percent mean deviation was found in AM-16 (180.00) and AM-18 (-64.29) respectively. For ear length and ear diameter, highest tolerance was exhibited in AM-39 (10), AM-64 (10), AM-16 (10), AM-42 (10) for both the traits and AM-83 (10) and AM-99 (10) for ear length only and AM-102 (10) for ear diameter. The lowest tolerant lines were found AM-100 (1), AM-90 (1), AM-18 (1) for both the traits. Ear length alone contributed to drought tolerance in lines AM-92 (1) and AM-53 (1), whereas, AM-137(1) and AM-116 (1) were marked for ear diameter. The highest mean value of kernel row per ear in normal and drought condition was showed by AM-116(13.20 cm), AM-42 (13.33 cm) and the lowest value of 4.80 cm by AM-16, and 3.60 cm by AM-53, respectively. The maximum and minimum percent mean deviation was found to be 113.33 (AM-42) and -66.67 (AM-53) respectively. For kernels per row in normal and drought condition, the maximum mean value was shown by AM-102 (23.20 cm, 22.60 cm) in both conditions and the minimum value was observed as 5.20 cm (AM-16) in normal and 4.20 cm (AM-18) in drought condition. The highest and lowest percent mean deviation was found for AM-42

Table 2. List of Mean (normal and stress), Per cent Mean Deviation (PMD) of ten most tolerant and most susceptible teosinte derived BC_1F_2 lines

TL	Ear length (cm)			Ear diameter (cm)			Number of kernel row/ear			Number of kernel /row		
	M		PMD	M		PMD	M		PMD	M		PMD
	N	S		N	S		N	S		N	S	
AM-39	6.60	8.00	21.21	2.00	2.60	30.00	7.60	9.60	26.32	8.80	9.40	6.82
AM-64	8.80	11.66	32.50	2.00	3.00	50.00	9.60	10.50	9.38	11.20	20.00	78.57
AM-16	6.60	12.60	90.91	1.00	2.80	180.00	4.80	9.20	91.67	5.20	13.20	153.85
AM-42	6.60	12.60	90.91	2.00	3.80	90.00	6.00	12.80	113.33	6.20	20.80	235.48
AM-102	13.00	13.80	6.15	2.70	3.50	29.63	11.60	12.00	3.45	23.20	22.60	-2.59
AM-178	8.30	6.00	6.45	2.30	1.00	-9.38	6.20	6.00	-3.57	10.80	8.20	34.72
AM-115	11.40	12.40	8.77	2.70	3.30	22.22	9.60	10.00	4.17	18.80	17.20	-8.51
AM-138	11.80	11.00	-6.78	2.80	2.80	0.00	8.80	10.00	13.64	19.80	16.00	-19.19
AM-83	11.60	13.80	18.97	2.70	2.70	0.00	10.00	10.80	8.00	15.20	21.00	38.16
AM-99	7.60	9.00	18.42	2.20	2.80	27.27	10.00	9.60	-4.00	15.60	15.60	0.00
SL												
AM-116	11.20	8.50	-24.11	2.20	1.50	-31.82	13.20	6.50	-50.76	20.20	9.25	-54.21
AM-193	9.80	7.50	-23.47	2.80	2.00	-28.57	9.60	10.00	4.17	12.20	6.50	-46.72
AM-18	12.00	4.60	-61.67	2.80	1.00	-64.29	9.60	4.40	-54.17	16.80	4.20	-75.00
AM-90	11.40	7.20	-36.84	2.80	1.80	-35.71	9.60	5.20	-45.83	12.80	5.20	-59.38
AM-137	10.20	6.96	-31.76	2.20	1.50	-31.82	9.20	5.60	-39.13	13.60	5.00	-63.24
AM-100	12.20	5.60	-54.10	2.90	1.80	-37.93	8.80	5.20	-40.91	14.20	6.20	-56.34
AM-92	9.80	6.66	-32.04	2.50	2.16	-13.60	12.00	10.00	-16.67	17.00	9.66	-43.18
AM-71	10.60	8.20	-22.64	2.50	2.00	-20.00	11.20	6.80	-39.29	14.80	9.60	-35.14
AM-184	9.80	7.33	-25.20	2.20	2.00	-9.09	11.20	8.00	-28.57	16.20	7.66	-52.72
AM-53	10.20	6.00	-41.18	2.00	1.90	-5.00	10.80	3.60	-66.67	12.60	4.80	-61.90

TL: Tolerant line SL: Susceptible line N: Normal S: Stress

(235.48) and AM-18 (-75.00). For kernel row per ear and kernels per row the most tolerant lines were AM-16 (10) and AM- 42 (10), while, AM-64 (10), AM-178 (10), AM- 83 (10) were found tolerant for kernels per row. The maximum mean value of 1000 kernel weight reflected by AM-102 (211.05 g, 204.75 g) in both the condition respectively and the minimum value (124.00 g) for AM-64 and AM-100 (94.25 g) in normal and drought condition respectively. The highest and lowest percent mean deviation was found in AM-64 (30.56) and AM-100 (-37.70) respectively (Table 3). For 1000 kernel weight the maximum tolerance was observed in AM-64 (10) and AM-42 (10) and least tolerant was found in AM-193 (1), AM-100 (1) and AM-137 (1) (Table 4). For grain yield per plant in normal and drought condition, the maximum mean value was shown by AM-115 (96.00 g) and AM-178 (84.00 g) and the minimum value was observed as 24.00 g (AM-137) and 2.00 g (AM-193) respectively. The highest and lowest mean deviation was found for AM-16 (-6.00) AM-64, AM-16, AM-42, and AM-102. On other hand, AM-116 was found as the most susceptible with the and AM-193 (-93.75) respectively. The contribution of grain yield per plant in drought stress was highest in lines *viz*., AM-39, AM-64, AM-42, AM-16, AM-178 and AM-83, whereas, least in lines AM-116, AM-193, AM-71 and AM-184.

For drought tolerance index, all the tolerant lines exhibited high tolerance except AM-64 (1.13) and AM-99 (1.042), while none of the susceptible lines grouped as tolerant in drought tolerant index. For yield index and stress tolerance indexes the highest tolerant lines were AM-102, AM-178, AM-115 and AM-138; whereas, AM-42 was found tolerant for yield index and AM- 99 for stress tolerance index. The least tolerance for stress tolerance index was exhibited by lines AM-193 and AM-137 (Table 3).

Overall sum of rank scores over ten morpho-physiological traits and three indices associated with drought tolerance revealed that AM-39 was most drought tolerant genotype with a total score of 108, among all the two hundred and three lines, which is followed by

Table 3. List of Mean (normal and stress), per cent mean deviation (PMD) along with indexes of ten most tolerant and most susceptible teosinte derived BC_1F_2 lines

	1000 kernel weight (g)			Grain yield per plant (g)			Drought Tolerant Index (DTI)	Yield Index (YI)	Stress Tolerance Index (STI)
TL	**Mean**		**PMD**	**Mean**		**PMD**			
	N	S		N	S				
AM-39	138.70	143.80	3.68	52.00	46.00	-11.54	1.43	0.78	0.68
AM-64	124.00	161.90	30.56	40.00	36.00	-10.00	1.13	0.61	0.41
AM-16	199.00	191.70	-3.67	50.00	47.00	-6.00	1.547	0.794	0.670
AM-42	178.55	215.80	20.86	62.00	56.00	-9.68	1.772	0.946	0.990
AM-102	211.05	204.75	-2.99	92.00	70.00	-23.91	1.866	1.182	1.836
AM-178	161.00	156.10	-3.04	92.00	84.00	-8.70	2.686	1.418	2.204
AM-115	188.00	194.95	3.70	96.00	72.00	-25.00	1.891	1.216	1.971
AM-138	177.25	196.50	10.86	90.00	60.00	-33.33	1.401	1.013	1.540
AM-83	188.00	174.45	-7.21	52.00	48.00	-7.69	1.552	0.811	0.712
AM-99	171.85	144.70	-15.80	84.00	50.00	-40.48	1.042	0.844	1.198
SL									
AM-116	141.15	115.70	-18.03	80.00	6.00	-92.50	0.02	0.10	0.14
AM-193	171.85	125.90	-26.74	32.00	2.00	-93.75	0.004	0.034	0.018
AM-18	147.70	137.31	-7.03	40.00	10.00	-75.00	0.088	0.169	0.114
AM-90	150.40	119.35	-20.64	60.00	12.00	-80.00	0.084	0.203	0.205
AM-137	129.00	95.95	-25.62	24.00	12.00	-50.00	0.210	0.203	0.082
AM-100	151.20	94.20	-37.70	50.00	14.00	-72.00	0.137	0.236	0.200
AM-92	141.90	123.79	-12.76	46.67	10.00	-78.57	0.075	0.169	0.133
AM-71	153.00	150.00	-1.96	62.50	12.00	-80.80	0.081	0.203	0.214
AM-184	140.00	156.50	11.79	80.00	10.00	-87.50	0.044	0.169	0.228
AM-53	143.15	122.84	-14.19	48.00	10.00	-79.17	0.073	0.169	0.137

TL: Tolerant line SL: Susceptible line N: Normal S: Stress

least score of thirty-four. Our findings were also at par with the results of Shadakshari and Shantakumar (2014) who screened inbred lines under water stress condition. Fifteen inbreds viz., DMIL 101, DMIL103, DMIL112, DMIL117, DMIL122, DMIL125, DMIL129, DMIL130, DMIL136, DMIL140, DMIL145, DMIL147, DMIL150, DMIL152 and DMIL160 were exhibiting superior performance for various morpho-physiological traits and identified as drought tolerant inbreds, whereas, inbreds *viz*., DMIL480, DMIL492, DMIL493, DMIL510 and DMIL518 recorded the maximum ASI, drought susceptibility index and leaf senescence under water stress condition. Based on secondary traits and stress indices, the hybrids RML-4/RML-17, RML-32/RML-17, RML-8/RML-17, and RML-32/RL-111 were found to be more tolerant compared with other hybrids (Parajuli *et al*., 2018). The identification of promising drought tolerant line is an essence of a breeding program. We found several drought tolerant lines in our investigation and similar findings were reported by Wattoo *et al*. (2018) in his population and found significant variation in maize genotypes for drought tolerance.

Conclusion

Maize is highly cross pollinated crop Because of the monoecious plant habit and protandrous nature. It is more sensitive to abiotic stresses, particularly drought stress and water logging stress during the growing season, specific to the reproductive stage. Exploitation of teosinte as a genetic resource for biotic and abiotic stresses becoming a burning area of research in the recent years through wide hybridization. Therefore, teosinte derived maize lines were evaluated to identify the drought tolerant lines. It was found that for anthesis silking interval in moisture stress, maximum tolerance was registered in AM- 39, AM-115, AM-83 and AM-18. Whereas, the least tolerance was exhibited by AM-193 and AM-92. For 75 per cent days to senescence the highest tolerance to water stress was shown by line AM-193, AM-116 and AM-53, while, the lowest was

Table 4. Ranking of ten most tolerant and most susceptible lines of teosinte derived BC_1F_2 maize lines

Tolerant line	Anthesis silking interval (ASI)	Days to 75 per cent senescence	Canopy temperature depression (CTD)	Chlorophyll Content	Ear length (cm)	Ear diameter (cm)	Kernel row per ear	Kernels per row	Grain yield per Plant (g)	1000 kernel weight (g)	Drought tolerance index (DTI)	Yield index (YI)	Stress tolerance index (STI)	Total Score
AM-39	10	8	3	6	10	10	9	8	10	7	10	9	8	108
AM-64	4	7	6	8	10	10	8	10	10	10	9	8	6	106
AM-16	5	9	1	8	10	10	10	10	10	6	10	9	7	105
AM-42	7	3	2	3	10	10	10	10	10	10	10	10	9	104
AM-102	7	1	9	10	8	10	7	7	9	6	10	10	10	104
AM-178	5	8	8	7	8	5	6	10	10	6	10	10	10	103
AM-115	10	1	6	7	9	9	7	7	9	7	10	10	10	102
AM-138	7	4	10	7	6	7	9	6	8	8	10	10	10	102
AM-83	10	1	5	7	10	7	8	10	10	5	10	9	8	100
AM-99	7	6	8	8	10	9	6	8	7	3	9	9	10	100
Susceptible Line														
AM-116	3	10	6	2	3	1	1	1	1	2	1	1	2	34
AM-193	1	10	6	2	3	2	7	2	1	1	1	1	1	38
AM-18	10	5	1	5	1	1	1	1	2	5	2	2	2	38
AM-90	9	3	5	7	1	1	1	1	2	2	2	2	3	39
AM-137	5	6	5	7	2	1	1	1	5	1	3	2	1	40
AM-100	8	5	7	4	1	1	1	1	3	1	2	3	3	40
AM-92	1	6	9	3	1	4	3	2	2	4	2	1	2	40
AM-71	4	1	8	3	3	3	1	3	1	6	2	2	3	40
AM-184	4	5	2	5	2	5	2	1	1	9	1	1	3	41
AM-53	1	10	3	8	1	6	1	1	2	3	1	2	2	41

found in AM-71, AM-83, AM-115 and AM-102. Overall sum of rank scores over thirteen traits associated with drought tolerance revealed that AM-39 was most drought tolerant genotype among all the 203 lines under study with total score of one hundred eight, followed by AM-64, AM-16, AM-42, and AM-102, whereas, AM-116 was the most susceptible with the least score of thirty four. Adaptation of wild allele is important to combat the abiotic stresses in maize and these alleles can further help in broadening the genetic base.

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Indian J. Plant Genet. Resour. 33(1): 68–76 (2020)
DOI 10.5958/0976-1926.2020.00010.8

RESEARCH ARTICLE

Assessing Genetic Diversity of Newly Developed Winter Maize (*Zea mays* L.) Inbred Lines

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(Received: 21 December, 2018; Revised: 28 September 2019; Accepted: 17 December 2019)

Understanding the genetic diversity among the breeding materials is fundamental consideration for any crop improvement programme. Ninety seven newly developed winters maize inbred lines along with thirteen released inbreds were evaluated to assess the genetic diversity based on morphological traits. Analysis of variance revealed significant differences for 13 characters studied. All the inbred lines were grouped into fifteen clusters with ten solitary clusters. The D^2 statistics displayed that cluster I being largest group, with maximum inbred lines (37) followed by Cluster II (24), Cluster III (16) Cluster IV (14) and Cluster V (9). The maximum inter-cluster distance was observed between cluster V and cluster XV (26.96) followed by cluster IV and XV (26.12), cluster V and XII (24.55) suggesting higher probability of heterotic combinations if parents selected from these pairs of groups. Cluster IV has the highest intra-cluster distance (11.59). Maximum genetic divergence as per cent was contributed by 100 kernel weight (39.45) followed by days to anthesis (22.64), grain filling duration (10.31) and grain yield (10.50). On the basis of per se performance, intra and inter cluster distance, inbred lines IMLSB-2005, IMLSB-1000-2, IMLSB-182-1, IMLSB-719-1, IMLSB-164-1, IMLSB-457-2, IMLSB-2083, IMLSB-1298-2, IMLSB-1298-5 and IMLSB-246-2 were identified that might be used in maize improvement programme to develop superior hybrid combinations.

Key Words: Diversity, D^2 analysis, Inbred lines, Principal component analysis, Winter maize

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops of the world known as "Queen of Cereals" because of its highest yield potential and wider adaptability which plays a pivotal role in food security of many developing countries. Maize is currently produced on nearly 160 million hectares in 125 developing countries with a production of 850 million tonnes (Anonymous, 2016). In India, maize is emerging as third most important crop after rice and wheat. It is worldwide important crop used as a food, feed and as a source of raw material for several industries. This is also considered as a model genetic organism with immense genetic diversity (Prasanna, 2012). The introduction of new hybrids resilient to changing climates *viz*., low temperature during winter season, off-season disease and pests with high productivity has made maize a profitable alternative for small farmers in U.P., Bihar, Andhra Pradesh and Karnataka. In India, winter maize could help to meet the industrial requirements consistently throughout the year. Winter maize has emerged as an important crop in the non-traditional areas including major winter maize growing states *i.e.* Andhra Pradesh, Bihar, Tamil Nadu, Karnataka, Maharashtra and West Bengal. There is potential to increase the production of maize by increasing the area under winter maize in the coming years as winter maize has a higher yield at 4 MT/hectare as against 2.5MT/hectare for *Kharif* maize. Due to inbuilt tolerance for biotic and abiotic stresses under winter ecology the winter maize inbred lines with high yield potential can be utilised for developing more productive hybrids and provide more adaptability to different agro-climatic conditions. Since opportunities are limited for further expansion of maize area, future increases in maize supply will be achieved through the intensification and commercialization of current maize production systems (Krishnamoo and Mohan, 2017). Genetic improvement of a crop is pivoted on the strength of genetic diversity within the crop species.

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Assessing genetic diversity and relatedness among breeding materials has a preponderant role in a breeding program. Development of improved inbred lines and identifying suitable parental combinations to generate high performing hybrids is the leading task of maize breeders (Semagn *et al,* 2012). Morphological traits are the functional manifestation of underlying genetic constitution of an organism hence they constitute an important set of markers to assess the genetic diversity. Therefore, characterization of genetic diversity of maize germplasm or inbred lines is of great importance in hybrid maize breeding (Xia *et al.,* 2005). For effective management of genetic diversity, there is need of well-characterized germplasm and genetic pools classified into different clusters based on genetic diversity (Wende *et al,* 2013). Quantification of magnitude of genetic diversity among the germplasm has become possible with the help of advance biometrical technique; *viz*., multivariate analysis, based on D^2 statistics and principal component analysis (PCA). In view of the above, present investigation was conducted to assess the genetic diversity among newly developed inbred lines of winter maize based on morpho-physiological and yield traits using D^2 statistics and principal component analysis (PCA).

Material and Methods

Ninety seven new inbred lines of winter maize were developed through pedigree method from the diverse source of germplasm. These inbred lines along with thirteen released inbred lines (Table 1) were evaluated in randomized complete block design (RCBD) with three replications for morpho-physiological and yield traits during winter season of 2014-15 and 2015-16 at Regional Maize Research and Seed Production Centre, (ICAR-IIMR), Begusarai-851129 (Bihar). Each inbred line was sown in a single row of 4 m spaced at 60 cm with interplant distance of 25 cm. All recommended agronomic practices were followed to raise a good crop. Observations were recorded on thirteen morpho-physiological and yield characters**.** In each line, five plants were randomly selected for recording observations on plant height, ear height, ear length, ear girth, kernel rows per ear, kernels per row and 100-kernel weight. Observations on days to anthesis, days to silk, anthesis–silking interval (days), grain filling duration (days) and days to maturity were recorded on plot basis. The period after pollination to 75 per cent dry husk maturity was considered as grain filling duration. Observations were also recorded on three qualitative traits i.e. kernel colour (Y= yellow, O= orange, LY= light yellow, W= white, CW= creamy white), kernel type (D= dent, F= flint, SF= semi-flint, SD= semi-dent) and kernel size (S= small, M= medium, B= bold). Pooled mean over years was utilized for analysis of variance (ANOVA) and used to quantify the genetic differences among the genotypes. Data were subjected to Mahalanobis (1936) D^2 statistical analysis extended by Rao (1952) and Principal Component Analysis (Pearson*,* 1901*)*. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985) using INDOSTAT software and significant means were compared using significant differences at P 0.05 and 0.01.

Results and Discussion

A significant variability was exhibited among the inbred lines for morphological characters as well as yield components. Variability for grain type (flint, semi dent, dent), grain colour (white, creamy white, yellow and orange), kernel size (small to very bold) and 100 kernel weight (14.73-38.27g) was exhibited by the genotypes under study which play a key role for targeted trait improvement. The analysis of variance (Table 2) revealed the significant differences among the genotypes for all the characters studied indicating that the experimental materials were genetically divergent to each other. This shows that there is sufficient scope for selection of lines with specific traits amongst the available inbred lines aimed to enhance the genetic potential of maize.

All the inbred lines were grouped into fifteen (Table 3) clusters having variable number of entries. Cluster I with 37 genotypes had the maximum number of genotypes followed by cluster II with 24, cluster III with 16, cluster IV with 14 and cluster V with 9 genotypes while rests of the clusters were solitary entry clusters demonstrating the impact of selection presence in increasing the genetic diversity. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/ human selection for diverse adaptive complexes. The clustering pattern of inbred lines revealed that the inbred lines had significant genetic divergence among themselves. Similar results were reported by Bhusal *et al*. (2016) and Ranawat *et al.* (2013). In a similar study, Shrestha (2016) grouped sixty maize inbreds into six major groups through cluster and principal component analysis and concluded that the presence of high level of diversity among the inbred lines grouped

Table 1. Detail of winter maize inbred lines, source of germplasm and kernel characters

S. No.	Name of Inbred line	Source of germplasm	Institute of source germplasm	Kernel colour	Kernel type	Kernel size	S. No.	Name of Inbred line	Source of germplasm	Institute of source germplasm	Kernel colour	Kernel type	Kernel size
1	IMLBG-3-1	VH1266	CIMMYT	O	F	M	56	IMLBG-763-1	HQPM-1F2	IIMR	O	F	M
2	IMLBG-13-1	VH112935	CIMMYT	LY	SD	S	57	IMLBG-800-1	Pro4794F2	IIMR	O	SF	M
3	IMLBG-16-1	VH112940	CIMMYT	W	F	M	58	IMLBG-801-2	Bio-9681F2	IIMR	O	SF	M
4	IMLBG-22-1	ZH114207	CIMMYT	O	SF	S	59	IMLBG-814-2	Bio-9681F2	IIMR	O	SD	B
5	IMLBG-23-2	VH112922	CIMMYT	O	F	M	60	IMLBG-825-2	Bio-9681F2	IIMR	O	SF	M
6	IMLBG-43-2	ZH112700	CIMMYT	O	F	B	61	IMLBG-961-1	NK6240F2	IIMR	O	SF	M
7	IMLBG-46-1	VH101421	CIMMYT	O	SD	M	62	IMLBG-975-2	NK6240F2	IIMR	O	F	M
8	IMLBG-49-2	VH112450	CIMMYT	O	D	M	63	IMLBG-976-2	P3522F2-1	IIMR	O	F	M
9	IMLBG-55-2	VH112934	CIMMYT	Y	F	VS	64	IMLBG-1000-2	P3522F2	IIMR	O	F	B
10	IMLBG-58-1	VH112948	CIMMYT	O	F	M	65	IMLBG-1052-1	NQPM-Pool	IIMR	O	F	M
11	IMLBG-66-1	ZH111659	CIMMYT	O	F	S	66	IMLBG-1333	WNC18242	IIMR	O	SF	B
12	IMLBG-81-1	ZH112645	CIMMYT	O	F	B	67	IMLBG-1334	WNC18261	IIMR	O	SF	M
13	IMLBG-91-2	ZH112606	CIMMYT	O	F	B	68	IMLBG-1364	WNC19053	IIMR	O	SF	S
14	IMLBG-93-2	VH112933	CIMMYT	Y	F	M	69	IMLBG-1382	WNC19207	IIMR	Y	SD	B
15	IMLBG-100-1	VH11152	CIMMYT	Y	F	M	70	IMLBG-2005	ZL11258	CIMMYT	Y	SD	B
16	IMLBG-103-1	ZH112656	CIMMYT	Y	SF	M	71	IMLBG-2025	VL054794	CIMMYT	W	SD	B
17	IMLBG-106A-2	ZH116117	CIMMYT	Y	F	M	72	IMLBG-2032	VL05616	CIMMYT	W	SF	M
18	IMLBG-114-1	VH1275	CIMMYT	O	SD	B	73	IMLBG-2039	VL108305	CIMMYT	Y	SF	M
19	IMLBG-123-1	VH101429	CIMMYT	O	F	B	74	IMLBG-2045	VL105544	CIMMYT	Y	SD	B
20	IMLBG-141-2	ZH111929	CIMMYT	O	F	M	75	IMLBG-2051	VL108880	CIMMYT	O	F	M
21	IMLBG-147-1	ZH111450	CIMMYT	O	D	B	76	IMLBG-2077	VL108727	CIMMYT	Y	SF	B
22	IMLBG-156-2	ZH12421	CIMMYT	O	D	B	77	IMLBG-2083	VL1018391	CIMMYT	O	SF	M
23	IMLBG-164-1	ZH111948	CIMMYT	Y	SD	B	78	IMLBG-2086	VL0512418	CIMMYT	O	SF	M
24	IMLBG-173-2	ZH111948	CIMMYT	O	F	B	79	IMLBG-2092	ZL11884	CIMMYT	O	F	M
25	IMLBG-182-1	VH112552	CIMMYT	O	F	B	80	IMLBG-2093	ZL124332	CIMMYT	LY	SD	B
26	IMLBG-183-1	VH12280	CIMMYT	O	F	M	81	IMLBG-2094	ZL124478	CIMMYT	O	F	M
27	IMLBG-197-1	VH121028	CIMMYT	Y	SF	S	82	IMLBG-2096	ZL124351	CIMMYT	O	F	M
28	IMLBG-201-1	VH121038	CIMMYT	O	F	M	83	IMLBG-2097	ZL124430	CIMMYT	Y	SD	M
29	IMLBG-210-2	VH101411	CIMMYT	O	F	M	84	IMLBG-2102	ZL124372	CIMMYT	Y	SF	M
30	IMLBG-219-2	VH112650	CIMMYT	Y	F	B	85	IMLBG-2103	ZL124384	CIMMYT	O	F	B
31	IMLBG-231-1	ZH116132	CIMMYT	Y	W	M	86	IMLBG-2108	ZL124485	CIMMYT	O	F	M
32	IMLBG-246-2	VH113021	CIMMYT	O	D	B	87	IMLBG-2115	ZL124382	CIMMYT	Y	F	S
33	IMLBG-254-1	VH112906	CIMMYT	Y	SD	M	88	IMLBG-2128	ZL11863	CIMMYT	W	SD	M
34	IMLBG-269-1	VH112993	CIMMYT	O	F	B	89	IMLBG-2132	ZL11589	CIMMYT	W	SD	M
35	IMLBG-274-1	VH1279	CIMMYT	Y	F	M	90	IMLBG-2135	ZL126611	CIMMYT	W	SD	M
36	IMLBG-282-2	VH121043	CIMMYT	Y	F	M	91	IMLBG-2145	ZL114846	CIMMYT	W	SD	M
37	IMLBG-285-2	VH121055	CIMMYT	O	F	B	92	IMLBG-2147	ZL113897	CIMMYT	W	SF	S
38	IMLBG-301-2	VH12157	CIMMYT	O	F	S	93	IMLBG-2150	ZL113672	CIMMYT	W	SD	M
39	IMLBG-306-2	VH121082	CIMMYT	O	D	B	94	IMLBG-2152	ZL113792	CIMMYT	W	SF	M
40	IMLBG-310-1	AH1222	CIMMYT	O	F	B	95	IMLBG-2166	VL109126	CIMMYT	O	D	B
41	IMLBG-310-2	AH1222	CIMMYT	O	SD	M	96	IMLBG-1298-2	900MF2	IIMR	Y	SD	M
42	IMLBG-334B-1	Check4	CIMMYT	O	F	M	97	IMLBG-1298-5	900MF2	IIMR	O	SD	B
43	IMLBG-343-2	VH126	CIMMYT	Y	F	M	98	HKI-193-1	HKI-193-1	HAU	Y	F	m
44	IMLBG-406-1	VH112650	CIMMYT	O	SD	B	99	HKI-163	HKI-163	HAU	O	SD	M
45	IMLBG-406-2	VH112650	CIMMYT	O	SD	B	100	BML-6	BML-6	ANGRAU	Y	SD	M
46	IMLBG-428-2	VH1293	CIMMYT	Y	SD	B	101	BML-7	BML-7	ANGRAU	O	SD	B
47	IMLBG-457-2	ZH111688	CIMMYT	y	SD	B	102	LM-16	LM-16	PAU	O	SD	B
48	IMLBG-481-2	VH1277	CIMMYT	O	F	M	103	LM-13	LM-13	PAU	O	SD	B
49	IMLBG-507-1	VH11124	CIMMYT	O	D	M	104	LM-14	LM-14	PAU	O	F	S
50	IMLBG-592-2	ZH112687	CIMMYT	O	F	B	105	HKI-1105	HKI-1105	HAU	Y	SF	M
51	IMLBG-617-1	CP838F2	IIMR	O	SF	M	106	HKI-1128	HKI-1128	HAU	Y	SF	M
52	IMLBG-667-1	S 900MF2	IIMR	Y	S	M	107	UMI-1200	UMI-1200	TNAU	Y	SF	M
53	IMLBG-678	Bio-9637F2	IIMR	Y	SF	B	108	UMI-1201	UMI-1201	TNAU	Y	D	B
54	IMLBG-719-1	DKC9081F2	IIMR	O	D	B	109	UMI-1210	UMI-1210	TNAU	O	SD	M
55	IMLBG-722-1	DKC9081F2	IIMR	O	F	M	110	BML-15	BML-15	ANGRAU	O	SF	M

Table 2. Analysis of variance for maturity and yield traits in winter maize inbred lines

Source of Variation	df	Mean Squares												
		DOA	DOS	ASI	DM	GFD	PH	EH	EL	EG	KR	K/R	100KW	GY(q/h)
Replicate	2	0.039	1.973	2.239	6.221	3.648	61.131	0.820	2.036	1.330	2.583	15.626	0.094	53.135
Treatments	109	81.625**	84.327**	3.613**	102.390**	95.847**	1461.872**	370.505**	10.280**	3.634**	6.601**	56.162**	67.601**	98.118**
Error	218	1.226	2.025	0.872	3.928	5.349	79.266	31.505	1.770	0.861	1.674	5.730	0.781	3.434

*Significant at 5% level, ** Significant at 1% level
DOA= Days to anthesis, DOS= Days to silk, ASI=Anthesis-Silking interval, GFP= Grain filling duration, DM= Days to maturity, PH= Plant height, EH= Ear height, EL= Ear length, EG= Ear girth KR=kernel rows per ear, K/R= Kernels per row, 100kw= 100 kernel weight, GY(q/h)= Grain yield q/h,

Table 3. Distribution of 110 maize inbred lines in 15 different clusters

Name of Cluster	No. of inbred lines	Name of inbred lines present in a cluster
I	37	IMLSB-173-2, IMLSB-231-1, IMLSB-667-1, IMLSB-269-1, IMLSB-2115, IMLSB-2094, IMLSB-800-1, IMLSB-976-2, IMLSB-310-1, IMLSB-2039, IMLSB-507-1,IMLSB-274-1, IMLSB-201-1, IMLSB-678, IMLSB-2103, IMLSB-722-1, IMLSB-2102, IMLSB-2093, IMLSB-975-2, IMLSB-814-2, IMLSB-49-2, IMLSB-2032, IMLSB-43-2, IMLSB-2147, IMLSB-23-2, IMLSB-343-2, IMLSB-1052-1, BML-6, IMLSB-428-2, IMLSB-2135, IMLSB-763-1, BML-7, IMLSB-254-1, IMLSB-825-2, IMLSB-592-2, IMLSB-2086, IMLSB-2145
II	24	IMLSB-197-1, IMLSB-2150, IMLSB-1334, IMLSB-961-1, IMLSB-100-1, IMLSB-481-2, IMLSB-22-1, IMLSB-16-1, IMLSB-81-1, IMLSB-617-1, LM-16, IMLSB-13-1, IMLSB-2108, IMLSB-147-1, IMLSB-103-1, IMLSB-114-1, IMLSB-2152, IMLSB-58-1, IMLSB-91-2, IMLSB-2045, IMLSB-106A-2, IMLSB-46-1, IMLSB-156-2, HKI-193-1
III	16	IMLSB-801-2, IMLSB-2132, IMLSB-2096, IMLSB-334B-1, IMLSB-1333, IMLSB-219-2, IMLSB-210-2, IMLSB-306-2, IMLSB-2097, IMLSB-2166, IMLSB-310-2, IMLSB-1382, IMLSB-2092, IMLSB-183-1, IMLSB-141-2, IMLSB-282-2
IV	14	IMLSB-2051, IMLSB-2077, IMLSB-406-2, IMLSB-406-1, IMLSB-2083, IMLSB-164-1, IMLSB-457-2, IMLSB-246-2, IMLSB-1298-5, IMLSB-1298-2, IMLSB-301-2, IMLSB-2128, IMLSB-285-2, IMLSB-93-2
V	9	UMI-1201, UMI-1210, LM-13, UMI-1200, BML-15, HKI-163, HKI-1128, HKI-1105, LM-14
VI	1	IMLSB-182-1
VII	1	IMLSB-719-1
VIII	1	IMLSB-123-1
IX	1	IMLSB-1000-2
X	1	IMLSB-3-1
XI	1	IMLSB-2025
XII	1	IMLSB-55-2
XIII	1	IMLSB-2005
XIV	1	IMLSB-66-1
XV	1	IMLSB-1364

into divergent clusters. The clustering pattern (Fig. 1) revealed that some genotypes that originated from the source germplasm of different geographical regions had been grouped into the same cluster. On the other hand, the genotypes that originated in one region had been distributed into different clusters, indicating that genotypes with same geographic source germplasm could have undergone change for different characters under selection. This could be due to selection pressure, genetic drift and environment, which created greater diversity rather than genetic distance during the developmental phase (Marsan *et al*, 1998; Senior *et al*, 1998; Wende *et al*, 2013). Discrepancies in classification of germplasm based on pedigree relatedness were earlier reported by Dhliwayo *et al* (2009) and Yang *et al.* (2011). These might resulted due to the fact that majority of the inbred lines involved in the current study were developed from maize germplasm obtained from CIMMYT. Therefore, there might be exchange of breeding materials among different CIMMYT breeding programs, justifying the alignment of some inbred lines from different origin in the same clusters.

The intra and inter-cluster distance ($D = \sqrt{D^2}$) values were worked out from divergence analysis and are listed in Table 4. It revealed that the highest inter cluster distance was observed between cluster V and cluster XV (26.96) followed by cluster IV and XV (26.12), V and XII (24.55) indicating more diverse genetic makeup of the inbred lines included in the respective pairs of clusters. The genotypes in cluster V and XV were more diverse for days to maturity and genotypes in cluster IV for days to anthesis and days to silking whereas, genotypes in cluster V and XII were more diverse for 100 kernel weight. Therefore, parents of these clusters

Table 4. Average intra-cluster (diagonal bold) and inter- cluster distances (d values above diagonal) and D^2 values (below diagonal) among newly developed winter maize inbred lines

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	8.41	11.40	11.74	13.23	14.87	14.39	9.85	15.13	10.10	11.73	10.14	19.05	13.89	18.22	20.95
II	129.96	8.71	16.60	15.09	17.57	17.02	12.00	16.33	11.23	15.03	13.36	13.41	17.62	12.53	15.36
III	137.83	275.56	9.66	18.00	17.29	13.19	13.03	16.10	14.30	12.12	12.13	25.75	14.67	23.21	25.33
IV	175.03	227.71	324.00	11.59	15.74	22.87	16.47	23.28	16.40	14.61	16.06	20.97	20.98	19.38	26.12
V	221.12	308.70	298.94	247.75	10.25	23.00	15.98	23.75	19.30	18.17	15.51	24.55	19.62	21.51	26.96
VI	207.07	289.68	173.98	523.04	529.00	0.00	13.10	5.53	10.18	16.85	13.51	22.79	10.28	24.52	20.12
VII	97.02	144.00	169.78	271.26	255.36	171.61	0.00	12.70	9.92	17.33	12.76	18.31	10.94	19.81	18.80
VIII	228.92	266.67	259.21	541.96	564.06	30.58	161.29	0.00	8.56	19.36	13.93	19.63	9.91	23.78	16.84
IX	102.01	126.11	204.49	268.96	372.49	103.63	98.41	73.27	0.00	14.47	10.63	15.25	11.16	18.96	16.63
X	137.59	225.90	146.89	213.45	330.15	283.92	300.33	374.81	209.38	0.00	12.57	24.08	20.12	19.82	25.63
XI	102.82	178.49	147.14	257.92	240.56	182.52	162.82	194.04	113.00	158.00	0.00	19.92	12.70	19.54	20.31
XII	362.90	179.83	663.06	439.74	602.70	519.38	335.26	385.34	232.56	579.85	396.81	0.00	22.30	14.26	10.91
XIII	192.93	310.46	215.21	440.16	384.94	105.68	119.68	98.21	124.55	404.81	161.29	497.29	0.00	25.35	21.78
XIV	331.97	157.00	538.70	375.58	462.68	601.23	392.44	565.49	359.48	392.83	381.81	203.35	642.62	0.00	15.15
XV	438.90	235.93	641.61	682.25	726.84	404.81	353.44	283.59	276.56	656.90	412.50	119.03	474.37	229.52	0.00

can be chosen for hybridization programme. Cluster IV has the highest intra-cluster distance (11.59). The inbred lines belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates and to obtain high heterosis. The distance between the clusters VI and VIII was lowest (5.53) followed by the distance between the clusters I and VII (9.85) indicating that the inbred lines belonging to these clusters were comparatively less diverse. This is probably because genotypes in these clusters may possess common alleles governing the characters.

The genetic differences between clusters were reflected in their cluster means. Cluster mean values for 13 morphological and yield related characters are presented in Table 5. The cluster means of inbred lines revealed that the highest mean value for days to anthesis and days to silking were reported in cluster IV. Required minimum days to anthesis, silking and high grain yield were observed in cluster VIII indicating the early inbreds with high yield in this group. Zaman and Alam (2013) also reported genotypes ranking first in a cluster for early days to maturity, days to 50% silking, and tasseling, The solitary cluster XI revealed the highest cluster mean for plant height, ear height and ASI and low mean for grain yield which indicated the usefulness of inbred line for fodder yield instead of grain yield, whereas lowest mean for ASI was reported by cluster XIV which is desirable trait for high seed setting to enhance the grain yield and such material may be tested under drought and water logging stress. The cluster XIII reported the highest mean for ear girth, kernel rows per ear and kernels per row which are desirable trait for grain yield. Similarly, cluster IX reported highest mean for ear length and grain yield. Shazia *et al.* (2017) also reported genotypes with highest grain yield in one cluster while grouping of 47 maize genotypes. Highest cluster mean for 100 kernel weight was revealed by the cluster III whereas, solitary cluster VII reported highest mean for grain filling duration. The lowest maturity duration was reported by solitary cluster VI which also reported third rank for mean grain yield among the clusters. The results of the study showed that desirable genotypes may be selected from the respective cluster for utilization in breeding programme and improvement of the specific trait. Similar results have also been reported by Shrestha (2016) Bhusal *et al.* (2016), Shazia *et al.* (2017) *and* Suryanarayana *et al.* (2017). The clusters contributing maximum to D^2 values are to be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization. The cluster means and characters contributing towards genetic divergence (Table 5) showed that maximum genetic divergence in percent was contributed by 100 kernel weight (39.45) followed by days to anthesis (22.64), grain filling duration (10.31) and grain yield (10.50). In a similar study Suryanarayana *et al.* (2017) also reported that grain yield was one of the major component traits for contributing towards genetic divergence. The least and negligible contribution towards divergence was observed by ear girth (0.55%).

Principal Component Analysis (PCA) used to visualize genetic distance and relatedness between

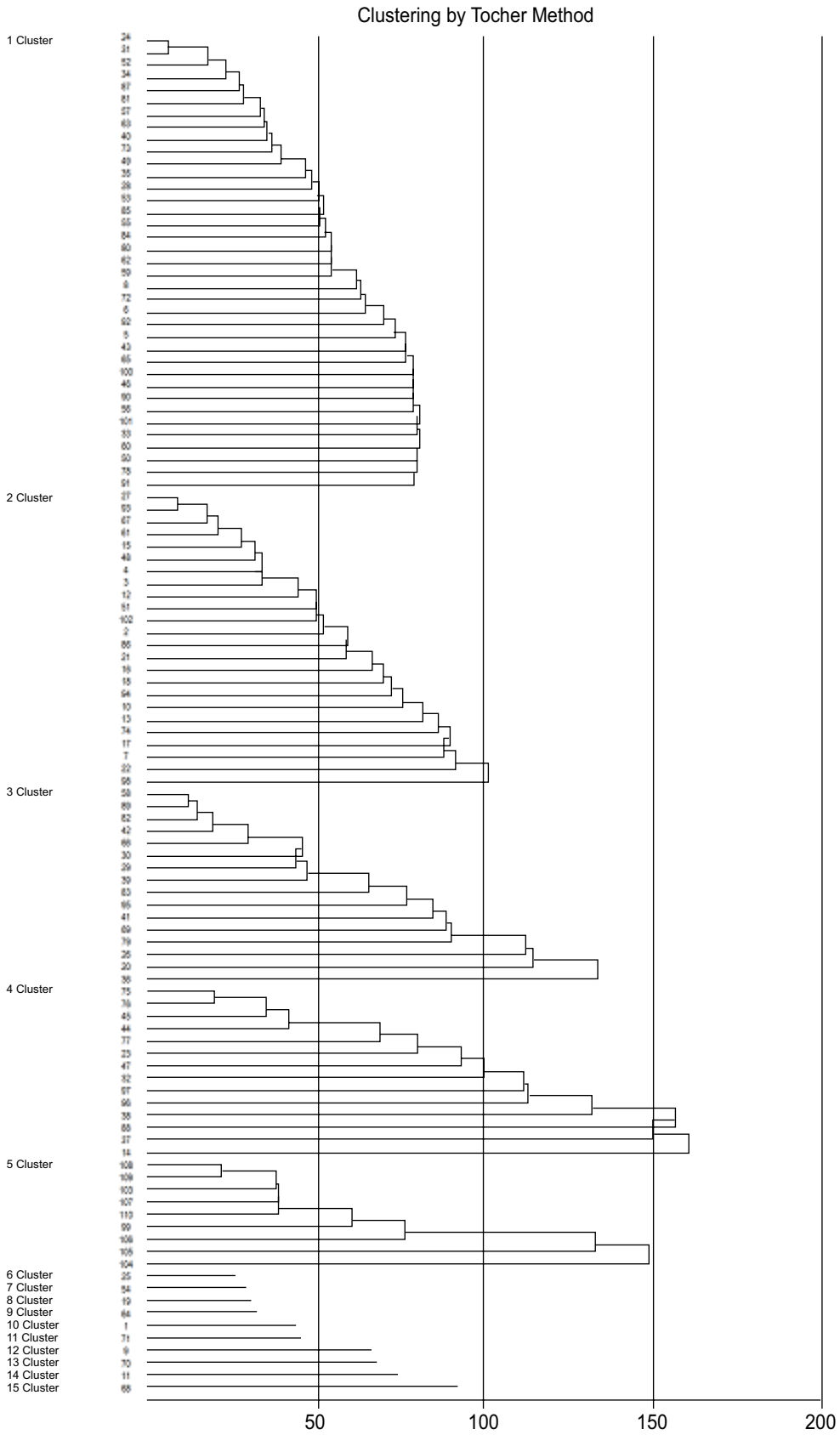

Fig. 1. Clustering of winter maize inbred lines by Tocher's method

Table 5. Cluster means and per cent contribution of characters towards divergence in newly developed winter maize inbred lines

Character	Clusters															Per cent contribution
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	
Days to anthesis	105.72	102.83	105.96	112.98	110.00	96.33	99.00	93.33	100.67	112.67	105.67	97.00	97.33	104.33	90.33	22.64
Days to silking	109.67	106.76	109.40	116.74	115.52	99.00	102.67	97.67	104.33	115.33	111.33	101.00	102.33	106.33	94.67	2.3
Anthesis-silking interval	3.95	3.93	3.44	3.76	5.52	2.67	3.67	4.33	3.67	2.67	5.67	4.00	5.00	2.00	4.33	2.1
Days to maturity	151.25	147.46	150.19	154.86	161.41	139.67	156.00	140.00	142.00	141.00	151.33	146.00	153.33	146.33	140.67	4.27
Grain filling duration	41.59	40.88	40.79	38.33	51.41	40.67	53.33	42.33	37.67	25.67	40.00	45.00	51.00	40.00	46.00	10.31
Plant height (cm)	106.19	80.18	100.56	112.37	118.67	111.33	82.00	125.00	123.23	110.57	151.10	100.23	141.67	57.77	78.33	5.2
Ear height (cm)	38.16	29.92	36.54	38.63	47.41	44.90	26.43	44.00	42.90	37.77	70.57	41.67	57.23	20.77	32.00	0.67
Ear length (cm)	9.94	8.65	9.25	10.48	10.22	9.27	12.23	11.00	13.20	6.30	9.93	10.00	12.77	7.23	8.67	0.58
Ear girth (cm)	12.24	11.41	12.43	12.25	12.07	12.73	13.93	12.67	12.40	10.30	11.40	10.40	15.00	8.23	10.50	0.55
Kernel rows per ear	12.08	11.93	11.97	12.66	11.04	13.07	11.87	12.67	12.33	11.07	11.53	14.00	14.00	8.90	10.67	0.27
Kernels per rows	17.00	14.58	15.20	18.55	13.48	21.27	18.50	22.33	22.87	10.77	10.97	18.00	31.43	12.33	13.33	1.53
100 kernel weight (gm)	27.45	22.46	33.77	23.08	26.56	33.47	28.00	30.33	26.33	29.43	28.13	14.73	31.40	17.53	18.73	39.45
Grain yield (q/h)	28.01	23.88	26.67	29.67	20.71	30.09	31.40	30.33	31.51	25.87	19.72	24.85	28.81	9.83	15.40	10.13

populations. The Principal component analysis can be used to uncover similarities between variables (Venujayakanth *et al*, 2017). In the present study principle component (PC) analysis partitioned the total variance (Table 6) into 5 PCs contributing maximum to the total diversity among the genotypes due to various traits. In PC analysis, first 3 PCs were found to contribute 75.89% of the total variation. The traits contributing most heavily to variation in PCI were 100 kernel weight (-0.976), plant height (-133) and ear girth (-0.121) with negative loading similarly traits, days to 50 per cent anthesis (0.830), days to maturity (0.421) and grain filling duration (0.296) with positive loading and ear height (-0.144) with negative loading contributed significantly towards total variation in PCII. In PCIII, grain yield (-0.649), plant height (-0.340), days to maturity (-0.320), ear length (-0.298), ear girth (-0.269) with negative loadings and days to anthesis (0.276) with positive loading were causing variability among genotypes. Therefore, the results showed that traits like days to anthesis, days to maturity, 100 kernel weight, grain filling duration ear length, grain yield as whole contributed most strongly towards variability among genotypes, indicating that more emphasis should pay

Table 6. Principal component analysis for morphological traits in winter maize inbreds

Characters	PCI	PCII	PCIII	PCIV	PCV
Days to anthesis	0.014	0.830	0.276	0.378	0.201
Days to silking	0.014	0.060	-0.097	-0.135	0.014
Anthesis-silking interval	0.000	0.000	0.000	0.000	0.000
Days to maturity	-0.058	0.421	-0.320	-0.346	-0.161
Grain filling duration	-0.026	0.296	-0.187	-0.630	-0.095
Plant height (cm)	-0.133	0.016	-0.340	0.049	0.770
Ear height (cm)	-0.005	-0.144	-0.077	-0.051	0.348
Ear length (cm)	-0.028	-0.059	-0.298	0.000	0.114
Ear girth (cm)	-0.121	-0.007	-0.269	-0.068	0.157
Kernel rows per ear	0.063	-0.091	-0.020	0.192	0.062
Kernels per rows	-0.026	0.069	-0.208	0.046	0.026
100 kernel weight (gm)	-0.976	-0.032	0.171	0.011	-0.079
Grain yield (q/h)	-0.078	0.062	-0.649	0.524	-0.403
Canonical roots	3510.198	3112.714	1277.573	1040.338	543.505
Percent of Variance	33.718	29.900	12.272	9.993	5.221
Cumulative proportion of Variance	33.718	63.617	75.889	85.882	91.103

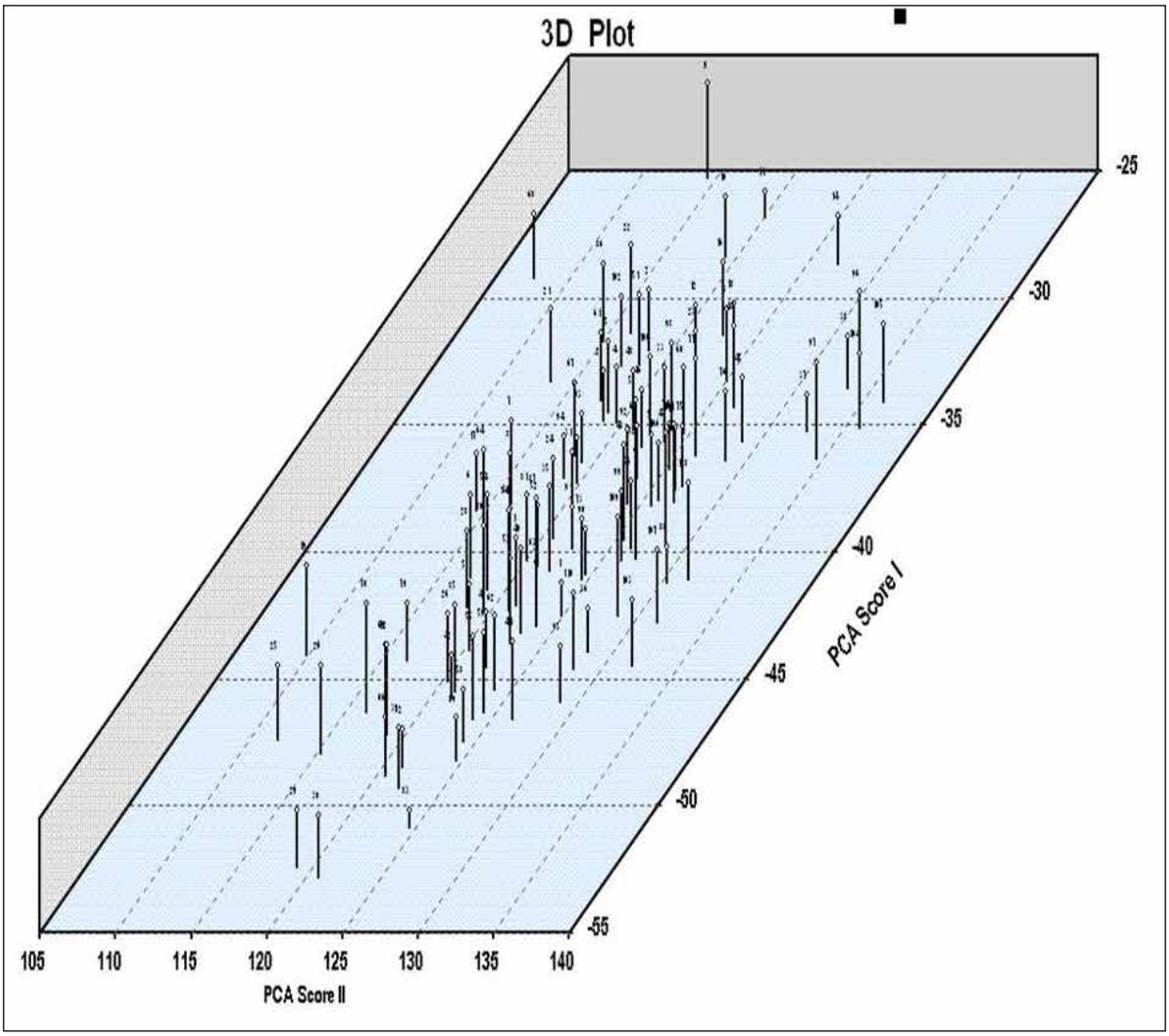

Fig. 2. 3D plot diagram showing Principle Component Analysis score of newly developed winter maize inbred lines.

on these traits while selecting the inbreds lines for their further use in breeding programme. The 3D bi-plot representation of PCI score and PCII score showed the genotypes falling in same cluster were present closer to each other in diagrams. The inbred lines in solitary clusters were present distantly from the other genotypes which have desirable mean value for traits i.e. IMLSB-3-1 (least grain filling duration), IMLSB-66.1(low plant height), IMLSB-182-1 (high plant height a desirable trait for forage), similarly lines with high intra cluster mean and with desirable mean value i.e. IMLSB-49-2 (high grain yield), IMLSB-93-2 (least grain filling duration). IMLSB-183-1(higher grain yield and 100 kernel weight) and IMLSB-975-2 (higher grain yield and 100 kernel weight indicating their usefulness in breeding programmes. Hafiz *et al.* (2015), Shazia *et al.* (2017) and Suryanarayana *et al.* (2017) also reported similar results and highlighted the usefulness of PCA in selection of maize genotypes *via* choosing of traits that strongly contributed in genetic variation of maize germplasm.

Conclusion

Selection of contrasting inbred lines for hybridization as reflected from D^2 statistics and principal component analysis (PCA) would ensure greater chances of obtaining high heterotic hybrids. The results of the present investigation will be very handy in the selection of genetically diverse and agronomically superior inbreds for hybridization programme. The genetic divergence of

parental varieties defines the manifestation of heterosis, and the heterotic pattern is determined by the genetic divergence of 2 parental lines. Therefore, crossing schemes comprising the more distant maize genotypes might allow for greater success in the production of genetic variability and thus might maximize the exploitation of heterosis and segregation (Molin *et al*, 2013). On the basis of inter cluster distances and *per se* performance, inbred line IMLSB-2005, IMLSB-1000-2, IMLSB-182-1, IMLSB-719-1, listed in solitary cluster XIII, IX, VI and Cluster VII could be used for developing hybrids. Similarly, on the basis of *per se* performance and intra cluster distance inbred line of cluster IV *viz*. IMLSB-164-1, IMLSB-457-2, IMLSB-2083, IMLSB-1298-2, IMLSB-1298-5 and IMLSB-246-2 may be used for developing new material. Inter-crossing of divergent groups would lead to greater opportunity for crossing over, which may release hidden variability by breaking linkage. Progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability. Hence, hybridization of inbred lines from cluster IV with Cluster III, IX and XIII might be used in single as well as multiple crossing programmes for development of better hybrids and populations.

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Indian J. Plant Genet. Resour. 33(1): 77–84 (2020)
DOI 10.5958/0976-1926.2020.00011.X

RESEARCH ARTICLE

Notes on Diversity Distribution and Systematics Study of *Abelmoschus tuberculatus* Pal & Har B. Singh: A Close Wild Relative of Okra from India

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(Received: 04 February 2019; Revised: 24 May 2019; Accepted: 24 May, 2019)

Germplasm of *Abelmoschus tuberculatus* Pal & Har B. Singh, a close wild relative of okra {*A. esculentus* (L.) Moench}was collected during an exploration undertaken to western Uttar Pradesh, adjoining areas of Haryana and Uttarakhand. The locality reported in Haryana indicates a new record of distribution of *A. tuberculatus* for the state. Field observations on plant habit, capsule and seed characters were compared with accessions from Rajasthan and characters delimitation at varietal level were identified. Gap analysis was presented here to find out target areas for future collection.

Key Words: *Abelmoschus tuberculatus,* Crop wild relative, Germplasm, Morphology, Wild okra

Introduction

The Indian sub-continent is a center of diversity for the genus *Abelmoschus* with a number of wild and semi-wild species growing in diverse habitats. Different species of *Abelmoschus*, *A. esculentus*, *A. caillei* (A. Chev.) Stevels, *A. manihot* (L.) Medik and *A. moschatus* (L.) Medik are reported for edible fruits and other uses (Mishra *et al*., 2000; Velayudhan *et al*., 2007; Pandit *et al.,* 2012). In genus *Abelmoschus,* taxonomic confusion is compounded due to the lack of consistent criteria within current taxonomic treatments pertaining to species identification, differentiation, and phylogeny. Studies to understand centers of origin of cultivated okra (Joshi and Hardas, 1956; Joshi *et al*., 1974; Bhat, 1996), cytological evidences and crossability studies between *A. esculentus* and *A. tuberculatus* (Joshi and Hardas, 1956; Joshi *et al*., 1974) have suggested that one of the parents of *A. esculentus* should have been *A. tuberculatus*. Redefining the genepool of *Abelmoschus* through the genetic diversity and the systematics study may facilitate in addressing the centre of origin of okra (Ramya and Bhat, 2012; Yuan *et al*., 2015; Werner *et al*., 2016; Ravishankar *et al.,* 2017).

Systematics studies on the complex group of cultivated, wild, semi-wild forms and putative progenitors with wide number of accessions from entire distribution range of the taxon help to fully understand relationships among species (Rana *et al*., 1991, 1994; Bisht and Bhat, 2006). In cultivated okra, some major problems of disease and pest being faced are yellow vein mosaic disease (YVMD) in the wet zone (Samarajeewa and Rathnayaka 2004; Kumar and Reddy 2015); and shoot and fruit borer and leaf hopper in north-western India (Dhankar and Mishra 2004, 2005). *A. tuberculatus* an endemic species and a wild relative of cultivated okra (*A. esculentus*), shows infraspecific variation in populations occurring in the semi-arid tracts of northern and north-western India (Sharma and Sanjappa, 1993; Kumar *et al*., 2010). Under National Exploration Plan (2018-19) of ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi an exploration for collection *A. tuberculatus* with other wild relatives of okra was planned in the unexplored regions to collect germplasm under the threat of extinction due to fast replacement of populations and also to study its potential in okra breeding programme. This study was undertaken with an objective to: report new distributional record and field study on capsule and seed characters of *Abelmoschus tuberculatus* and to identify the gaps in germplasm collection. Since this species is less-known, the botanical description and comparison with other taxonomic varieties is also included to facilitate field identification and collection of germplasm.

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Materials and Methods

An exploration was undertaken in parts of Uttar Pradesh and adjoining areas of Haryana and Uttarakhand during November, 2018. The germplasm from healthy plants was collected and processed. Capsules and seeds of ten plants from each accession were randomly selected for recording data on visual observations [comparison was drawn including 'type specimen' available in the National Herbarium of Cultivated Plants (NHCP)]. For taxonomic identification and data recording, ICAR-NBPGR Minimal Descriptor (Mahajan *et al*., 2000); IBPGR Descriptor List, Charrier (1984) and guidelines of PPV&FRA (2001) were used.

Comparative study was undertaken using accessions collected from Rajasthan and characters were validated using herbarium material at NHCP and on-line herbaria of London (BM), Edinburgh (E), Kew (K), Paris (P) and Beijing (PE)] and the global databases viz. NGB, GBIF, USDA/GRIN, Kew Catalogue, etc. for eco-geographic records. Observations were validated and supplemented with relevant literature.

Eco-geographic distributional records of the species were used to identify gaps and map was drawn using GIS software (DIVAGIS7.5) indicating areas of future germplasm collection and availability of species (Fig. 1). Herbarium vouchers (HS23146, 23147, 23150) were prepared as per standard methods and deposited in the National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi. Germplasm material was sent for seed multiplication at ICAR-IIVR, Varanasi, Uttar Pradesh, India for long-term conservation and use in the National Genebank (NGB) at the ICAR-NBPGR, New Delhi.

Result and Discussion

Germplasm of wild *Abelmoschus* collected from parts of Uttar Pradesh (Saharanpur) and adjoining states (Uttarakhand and Haryana) (with average altitude 242 MSL) during November 19-26, 2018 in habitats like open fields, fallow lands and farmers' fields that were thoroughly surveyed for occurrence of wild *Abelmoschus* species.

New distribution record for A. tuberculatus

A population was observed on fallow, open grassland near the road side (reported now; Fig. 1). After critical morphological observations, comparison with the herbarium specimens preserved in NHCP, New Delhi and validation from relevant literature, the identity of species was confirmed as *Abelmoschus tuberculatus* Pal & Har B. Singh. The species was recorded by the authors in present locality during field survey and germplasm collection of wild *Abelmoschus* species. Upon critical study of literature, the species and the areas mentioned as 'new collection site' was not documented in recent literature (Pradheep *et al*., 2014; Yadav *et al*., 2014; *https://sites.google.com/site/efloraofindia/...z/.../abelmoschus/abelmoschus-tuberculatu*).

The present report is the first occurrence record of *A. tuberculatus* in Haryana. *A. tuberculatus* was first collected and described by HB Singh (HS5277, Saharanpur; Pal *et al*., 1952). Collected germplasm (collector no. IW130, IW130-A) from original locality was raised in the field of Plant Introduction Division, Indian Agricultural Research Institute (IARI), New Delhi, (now ICAR-NBPGR), New Delhi.

Report on occurrence of *A. tuberculatus* in 2010 and subsequently from Panipat (Haryana) was thought to be doubtful (*https://sites.google.com/site/efloraofindia/species/m--z/m/malvaceae/abelmoschus/abelmoschus-tuberculatus*).

Botanical description: *Abelmoschus tuberculatus* Pal & Har B. Singh, Bot. Gaz. 113:458, 1952; Raizada, Suppl. F1. Upper Gang. Pl. 25. 1976.

Annual, upto 5.5 m tall herbs. Stems strigose with simple hairs, glabrescent, hollow at maturity. Internodal length 2-3.5 cm. Leaves 4-12 × 6-15 cm, lower and middle leaves 5-7 lobed, 8-12 × 10-15 cm, palmilobed to palmatisect lobes, ovate-oblong with 2-3 lobules in each, upper leaves 3-5 lobed, palmatisect, 4-6 × 6-8 cm; petiole 2-15 cm long. Stipules 3-8 mm long. Pedicel 4-8 mm long, accrescent upto 1.5 cm. Epicalyx segments 9-12, each c.1 cm long. Calyx lobes 1.0-2.5 × 1 cm. Corolla whitish-yellow with deep purple blotches; petals 1.5-3.5 × 1.0-1.5 cm. Fruit capsule 4.3-6.2 × 1.8-2.1 cm (terminal smaller 2.5 × 1.5 cm), densely tuberculate pericarp, narrowly oblong with tapering blunt tip. Seeds 3 mm in diameter, glabrous (not villous), black-darkest brown, hilum dark brown-black, glabrous; number of seeds per capsule 40-55.

Specimens examined: HB Singh1950, October 1946; (Holotype, NHCP); locality: Saharanpur, Uttar Pradesh; HS5278, 5280, 5277, 5279.

Fig. 1. ***Abelmoschus tuberculatus*** **var.** ***tuberculatus*****: a. flower showing unique blotches inside the petal base; b. tuberculated pericarp of immature fruit; c. plant growing in the newly reported location (village Sewah, district Panipat, Haryana); d. mature capsules and seeds (left-var.** ***tuberculatus*** **from collection site; right-var.** ***deltoidefolius*** **from Rajasthan; e. herbarium raised from seeds of accession IW130 (HS5277; 15/12/1946, HB Singh)**

Distribution reported (now): details of the distribution site of collected germplasm are as follows: collector no. ANV/18-1143, village Sewah (latitude: 29º36' N; longitude: 76º99' E; altitude: 235 m), Panipat district, Haryana, India; Date of collection: November 19, 2018; flowering and fruiting in October-November.

Ecology: plants reported were growing in the open grassy fallow land with associated flora– *Cichorium intybus* L., *Peristrophe bicalyculata* (Retz.) Nees, *Cynodon dactylon* (L.) Pers., *Calotropis procera* (Aiton) W.T. Aiton, *Cassia occidentalis* (L.) Link and *Chenopodium album* L. and *Achyranthus aspera* L.

Use: no recorded use was noted in the area of collection; the species was unfamiliar to local people where a most popular wild, semi-domesticated or cultivated taxon, *A. manihot* subsp. *tetraphyllus* (locally called '*Sukrali'*, '*Sukhlai'*) was in use as clearant in local jaggery production.

Notes: plants in newly recorded location were very rare in occurrence. The species was identified with the most striking character of tuberculate, cylindrical capsules borne on erect and less-branched stem. Flower with aesthetically designed blotches on corolla centre is one of the most striking characters of this taxon distinct from all other *Abelmoschus* species. The characters of plant matched with the 'holotype description' and therefore identified as *A. tuberculatus* var. *tuberculatus*. The seed size varied from 3-3.5mm and testa glabrous/semi-glabrous and tomentose. Co-occurrence of *A. ficulneus* was noted in three locations, out of seven (confirmed from Rajasthan; pers. comn. Dr K Pradheep, ICAR-NBPGR).

Distribution of Diversity and Germplasm Collection

The global germplasm resource databases (NGB, GBIF, GRIN/USDA) do not record locality information on occurrence of this species from the Uttar Pradesh, Uttarakhand and from the new reported area (now) (Pal *et al*., 1952, Arora and Nayar, 1984; Pradheep *et al*., 2014; https://www.ars-grin.gov/cgi-bin/npgsold/swish/accboth?query=Abelmoschus%20tuberculatus&sort=swishrank&si=0&si=1&start=75; https://www.ars-grin.gov/). Velayudhan *et al.* (1996) while collecting okra genetic resources in India have indicated rare occurrence of *A. tuberculatus* within the northern parts of the country.

Abelmoschus tuberculatus Pal & Har B. Singh is endemic to semi-arid regions of states – Uttar Pradesh, Madhya Pradesh, Rajasthan, Gujarat, Maharashtra, Haryana, Uttarakhand and Andhra Pradesh; sporadic in field margins; rare in Gujarat, India (Fig. 2). There are two distinct taxonomic varieties that are endemic in scrub forest areas upto 900 m; var. *deltoidefolius* T.K. Paul & M.P. Nayar occurs in Madhya Pradesh, Rajasthan and Gujarat and var. *tuberculatus* in Uttar Pradesh, Madhya Pradesh and Rajasthan (Sharma and Sanjappa, 1993). During the survey and exploration, over 110 locations including 15 farmers' fields, 10 abandoned areas and over 70 sites (10 in Haryana and 53 in Uttar Pradesh, 7 Uttarakhand) were explored. Of these only in seven sites, Haryana (one), Uttar Pradesh (three) and Uttarakhand (three) the plant populations of *A. tuberculatus* were recorded (Fig. 1, 2). Over 45 farmers/informants of Haryana, Uttar Pradesh and Uttarakhand were contacted and feedback was sought on knowledge on occurrence of the species, common names, uses, etc. The distribution was determined as rare occurrence. Three sites were disturbed, open grassy fallow land and two sites were under constant threat of grazing or lopped for fodder. Site 2 and 3 were disturbed fallow land under construction in Shamli district of Uttar Pradesh; in fourth site only two plants were growing in abandoned plot along with *Ziziphus mauritiana* Lam. shrubs on roadside in highly-disturbed area. Site 5, 6 and 7 were located in nearby area but the habitats were very different, grassy open plot to highly disturbed construction area on roadside. A few plants in segregating population were found in undisturbed abandoned grassy land in Rehmadpur, Roorkee in Uttarakhand. These observations probably support very high niche specificity of the species. In previous multi-crop explorations undertaken to the parts of Uttar Pradesh and foothills of Uttarakhand for collection of germplasm of crop wild relatives, the first author did not locate any population that probably indicated its un-common status (Pandey *et al*., 2016).

As compared to this, the related taxon, *Abelmoschus manihot* (L.) Medik. subsp. *tetraphyllus* (Roxb. ex Hornem.) Borss. Waalk., which is very tall, branched, robust, and remained standing in fields even after maturity and widely distributed in area of survey. The mature plants of *A. tuberculatus* were very fragile, brittle hollow stem that tends to break at maturity and rare and habitat specific. In none of the visited locality *A. tuberculatus* populations were found to co-occur with *A. manihot* subsp. *tetraphyllus*, despite occurrence in nearby areas.

The area under study did not show plant populations in flowering; rather the fruits were well matured and shattering was frequent. This indicated that the period in the areas for flowering was late September to mid-October; and fruiting in October-November onwards. As per the earlier collections made from Rajasthan and Madhya Pradesh, the authors observed end of October-January for fruiting in some areas. This was in contrast to the phenology described in 'holotype' where the reported period was October-January (Pal *et al*., 1952).

Taxonomic and Genetic Resource Study

Abelmoschus tuberculatus belongs to closer genepool of cultivated okra [*A. esculentus* (L.) Moench], sometimes considered as its wild form. *A. tuberculatus* has been grouped as a synonym of *A. esculentus* (http://www.theplantlist.org/tpl1.1/record/kew-2609634; The Plant List Ver. 1.1). Bates (1968) has suggested that *A. tuberculatus* should be included under *A. esculentus* Its morphological similarity with okra at vegetative as well as reproductive characters but differs from it by having smaller flowers, profuse fruiting,

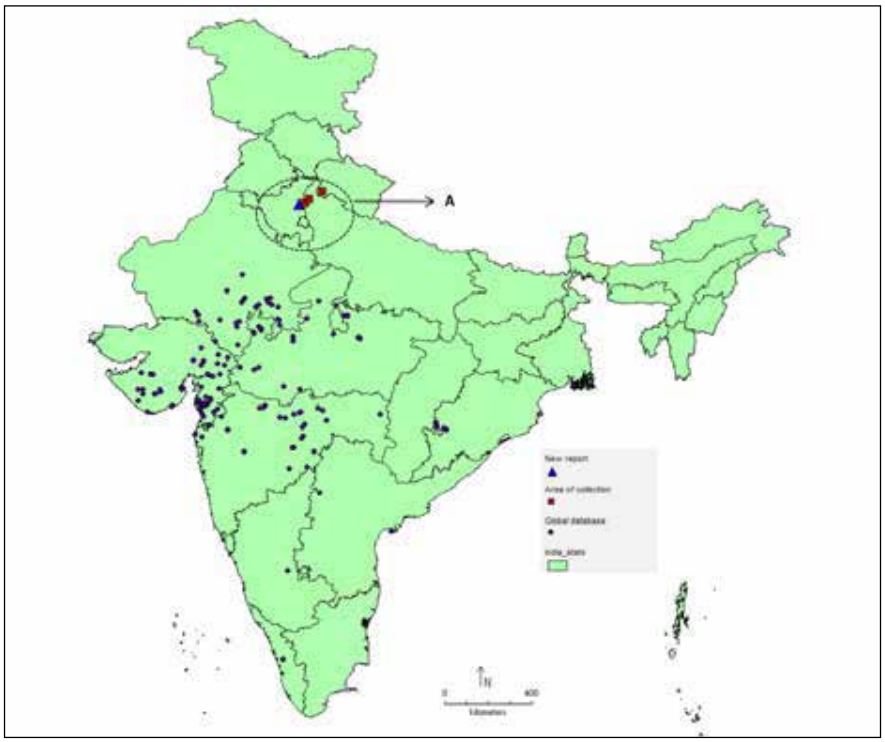

Fig. 2. Distribution of *Abelmoschus tuberculatus* in India: 'A': occurrence of *A. tuberculatus* var. *tuberculatus*; germplasm records in global databases (NGB, GBIF, GRIN) (shown with black dots); areas of collection in present study (red square); new site of collection (blue triangle)

and smaller capsules and dense tubercles on fruit pericarp (Sharma and Sanjappa, 1993) deserve a mention. *A. tuberculatus* has already been recognized as a distinct species by Pal *et al.* (1952). Distinctiveness as two different biological species was evidence through sterility of direct and reciprocal F_1 hybrids between *A. esculentus* and *A. tuberculatus* (Kuwada, 1966). Distinct species status of *A. tuberculatus* has been confirmed through sequence information data on internal transcribed spacer (ITS) gene (Patil *et al*., 2015; data unpublished; Ramya and Bhat 2012).

Two controversial hypotheses have been suggested for geographical origin of cultivated okra (*A. esculentus*): Ethiopian origin (Vavilov 1926) and Asian origin (Joshi *et al*., 1974) but supportive evidences for former are still awaited. Occurrence of *A. tuberculatus* with *A. ficulneus* in India may be an argument for an Asian origin of *A. esculentus* (Rana *et al*., 1991). Grouping of *A. tuberculatus* alongwith *A. manihot* revealed a close relationship between data on phenology and geographical origin (Bisht and Bhat, 2006).

Seed macro- and micro-morphological characters, including shape/size, seed coat sculpture and trichome density/structure provide stable and diagnostic characters for many morphologically closely related taxa of *Abelmoschus* in solving systematics problems and management of *Abelmoschus* genetic resources (Patil *et al*., 2015). During present study accessions (coll. No. ANV/1147 and ANV/1178) from Uttar Pradesh had capsules with more prominent erect hairs and brownish-black seeds with moderate hairy testa and when compared with the material from Rajasthan, this character was very prominently distinct (Table 1). Characterization through biochemical and morphological means have supported screening of germplasm for resistance in okra (Singh *et al*., 1988; Singh *et al*., 2006 and Kumar and Reddy, 2015). Singh *et al.* (1988) have reported the hair density on leaf surface of okra and incidence of leaf hopper to be negatively correlated.

Studies undertaken on okra improvement programmes evidently supported *Abelmoschus tuberculatus* as an important source of heavy fruit bearing (Pal *et al*., 1952), resistance to shoot borer (Mishra *et al.*, 2000), tolerance to *Bhendi yellow vein mosaic virus* (BYVMV) and crossability with other related taxa viz. *A. caillei* and *A. ficulneus* (NBPGR Ann. Rep. 2009-10, 2010-11).

Table 1. Qualitative and quantitative characters of capsule and seed of A. *tuberculatus* as recorded in field

S. No.	Collector no.	Capsule size (cm) L×B; ridges	Pedicel size (cm)	Capsule hairiness	Seed colour, shape	Seeds/ capsule	Seed diameter (cm)	Seed hairiness	100 seed weight (g)
1.	ANV/1143	5.7×1.57; very prominent	1.80×0.32	Sparse erect hairs	Black, round	40	0.32	Absent	21.74
2.	ANV/1146	5.2×1.8; not very prominent	1.74×0.22	Appressed hairs	Blackish-brown; round	38	0.30	Absent	22.80
3.	ANV/1147	5.7×1.54; prominent	2.46×0.31	Prominent erect hairs	Brownish-black; perfect round	47	0.27	Present (sparse)	20.80
4.	ANV/1150	6.24×1.68; very prominent	2.3×0.33	Appressed hairs; more visible	Grey; round	49	0.31	Absent	24.40
5.	ANV/1178	4.6×1.7; Not very prominent	2.0×0.28	Erect hairs; more prominent	Brownish black; round	36	0.34	Present (sparse)	22.40
6.	ANV/1180	4.0×1.8; prominent	1.8×0.27	Erect hairs; more prominent	Black brown; round	33	0.30	Absent	25.20
7.	ANV/1182	5.2 ×1.86; prominent	2.14×0.31	Sparse appressed more visible	Grey; perfect round	40	0.30	Absent	22.20
8	NNK-18	6.22×0.82; shallow	2.66×0.42	Prominent, erect hairs visible	Brown, round	43	0.43	Present (dense)	42.80
9	PKM-T-1	4.3×1.42; shallow	1.24×0.38	Erect hairs; more prominent (3 mm)	Brown, hairy, round-angled	34	0.31	Present (dense)	27.7
10	AP-T-1	5.9×1.58; shallow	2.4×0.41	Erect hairs; more prominent	Brown, hairy; round-angled	46	0.38	Present (dense)	23.20

In earlier genetic resource programmes for exploration and collection of okra and its wild relatives, areas of South Asia were explored under the International Plant Genetic Resource Institute/ IPGRI (now Bioversity International) during 1989-92 and over 150 accessions of *A. tuberculatus* were collected. The material was subsequently characterized and evaluated at the ICAR-NBPGR Regional Station, Akola, Maharashtra (Bisht *et al*., 1997). Currently the germplasm at National Genebank at ICAR-NBPGR, New Delhi mainly consists of material from north-western parts mainly Maharashtra, Madhya Pradesh, Gujarat and Rajasthan.

Genetic diversity study of 49 accessions represented from Gujarat, Madhya Pradesh, Maharashtra, and Rajasthan revealed no relationship between geographic origin and genetic diversity (Bisht *et al*., 1997). Evaluation studies proved resistance to shoot and fruit borer and leaf hopper in *Abelmoschus tuberculatus* (Gangopadhyay *et al*., 2017). Variability study in 58 accessions from North Western, Central India and its adjoining regions for agro-morphological traits supported that Maharashtra, Gujarat and Madhya Pradesh are diversity rich pockets (Chand *et al*., 2018).

A total of seven accessions of *A. tuberculatus* were studied for 10 morphological characters (data presented in Table 1): capsule characters (length 4.0-6.24 cm and breadth 1.42-1.86 cm); pedicel length (2.66-1.24 cm); seed diameter (0.27-0.3 cm); 100 seed weight (21.74-25.20 g); and capsule hairiness (sparse and prominent). Accession PKM-T-1 showed prominent hairiness with hair length 3 mm in comparison to others. Seed colour ranged from black-grey-brown black; seed shape from perfect round to slightly angular; number of seeds/ capsule from 33-49.2; and seed hairiness- absent-sparsely present. Character of fruit and seed: non-hairy testa, black colour was in conformity with 'type collection' available in the NHCP. Field guide generated through study on genus *Abelmoschus* reported that A. tuberculatus subsp. deltoidefolius is distinguishable from subsp. tuberculatus by deltoideform leaves (vs. palmilobed to palmatisect) and villous seeds (vs glabrous) (Yadav *et al*., 2014). These accessions of *A. tuberculatus* including a newly reported accession forms a new addition to the germplasm holdings of wild *Abelmoschus* species in the NGB, ICAR-NBPGR, New Delhi. Exploratory studies are likely to add new potential germplasm in plant genetic resources, especially in the crop wild relatives (Pandey *et al*., 2016).

Conclusions

The present study adds to our understanding on new distributional record, and systematics of *Abelmoschus tuberculatus* especially for var. *tuberculatus*. The two taxonomic varieties of *A. tuberculatus* geographically distinct with variation in characters need further study. The use of advanced molecular techniques could generate large amounts of data representing variability at interspecific levels. The main aspects that need attention are:

- Fine grid survey and collection of germplasm from parts of Uttarakhand, Haryana and adjoining areas
- Taxonomic and phylogenetic study on taxa related to *A. tuberculatus*
- Crossability and cytogenetic studies through inter-specific hybridization among *A. esculentus* and wild relatives including *A. tuberculatus* and *A. ficulneus*.

Acknowledgements

Authors are thankful to the Director, ICAR-NBPGR, Pusa Campus, New Delhi for the facilities rendered during the course of study and ICAR-IIVR, Varanasi, Uttar Pradesh for facilitation, active collaboration in the collection programme and facilitating field and seed multiplication studies. We are grateful to the Head, Division of Plant Exploration and Germplasm Collection for logistic support and to the curators of various herbaria for study of the herbarium specimens. Critical suggestions on this paper by anonymous reviewers are greatly acknowledged.

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Indian J. Plant Genet. Resour. 33(1): 85–89 (2020)
DOI 10.5958/0976-1926.2020.00012.1

SHORT COMMUNICATION

Exploiting Genetic Diversity for Identification of Protein Dense Seed Parent in Pearl Millet

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(Received: 03 January, 2018; Revised: 27 September, 2019; Accepted: 14 October 2019)

The present study was carried out to identify the protein dense pearl millet parental lines amongst 46 advanced inbred lines and designated B-lines (counterpart of CMS lines) during kharif 2013 & 14. Analysis of variance indicated significant differences between the tested genotypes during both the seasons. Protein content of these inbred lines varied from 8.62 (TPBL-11-109) to 16.03% (HBL-0620) with an average value of 11.38% and 9.92% (HBL-94/54-1) to 15.38% (HBL-0620), while designated B-line ranged from 11.09 % (HMS 26B) to 18.75% (HMS 18B) with an average value of 14.56% and 11.07% (HMS 33B) to 17.89% (HMS 18B) with an average value of 12.00% grown during *kharif-2013 & 14* respectively. On the basis of two years mean performance, four inbred lines and 11 designated B-lines were selected as potential parental lines with ≥13% protein content, for development of protein rich pearl millet hybrids or composites.

Key Words: Pearl millet, Inbreds, CMS lines, Protein content

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important food and fodder crop and is the life line of animal husbandry dominated farmer's economy of dry land areas in India and Africa. In India, it is grown over an area of 7.90 million hectares with total production of 9.20 million tones and productivity of 1161 kg/ha (Anonymous, 2013). The major pearl millet growing states in order of area are Rajasthan, Maharasthra, Gujarat, Uttar Pradesh and Haryana. These states account for 87% of the total area under cultivation. In Haryana, area under this crop during *kharif-2013-14* was 4.04 lakh hectare, with total production of 8.31 lakh tonnes and productivity of 2057 kg/ha (Anonymous, 2014).

Higher protein content with good proportion of essential amino acids and lipid content greatly enhances the nutritional value of pearl millet food and feed stuff (Sullivan *et al.,* 1990) and it also show very good antioxidant potential (Berwal *et al*., 2016). In high protein lines starch and soluble sugars decreased by 40% and fat content by 20%. The total amino acid composition of high protein lines remained normal except for a 16% decrease in lysine. However, the high protein lines gave a high value for utilizable protein but low digestible energy which may be due to high dietary fibre fraction (10%) (Singh *et al*., 1987). The cultivars developed for high protein content showed increase in prolamine content which resulted in lower proportions of glutalin, albumin and globulin fractions (Jambunathan and Subramanian, 1988). Thus the high protein varieties should be preferred from a nutritional point of view compared to low protein varieties, in spite of negative correlation between protein content and protein quality. However, information about status of protein content in inbred lines, designated B-lines, high-yielding hybrids and populations will be helpful for breeding high protein pearl millet hybrid. Cultivars of high-protein content could be potential sources for the development of protein dense pearl millet hybrids/ composites.

Materials and Methods

The present study was carried out to observe the variability for protein content in advanced inbred lines and designated B-line (counterpart of CMS lines) developed at CCS HAU, Hisar and ICRISAT, Hyderabad. A total number of 92 genotypes including 46 each of inbred lines and designated B line were grown in randomized

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block design with two replications and 10 cm intra-row and 45 cm inter-row spacing at Research Farm of CCS HAU, Hisar during *kharif*-2013 and selected 33 lines during kharif-2014 as well. Grain samples were taken from each entry in both the replications and analyzed for protein content according to micro-Kjeldahl method (AOAC 1990) and for converting the N% in protein % a crop specific conversion factor 5.7 was used. Analysis of variance for randomized block design was carried out for protein content according to as described Panse and Sukhatame (1957). To assure the data quality w.r.t. recovery % and repeatability for quality control, two released hybrid variety samples were used as positive control.

Results and Discussions

Data presented in Table 1, 2, 3 and 4 showed a statistically significant and marked variation in protein content of the genotypes of each group (inbreds and designated B-lines). protein content of inbred lines grown during *kharif-2013* varied from 8.62 to 16.03% with an average value of 11.38%. HBL 0620 (16.03%), HTP 94/54 (13.59%), HBL 0902-5 (13.11%), HBL 72 (13.11%) and HBL 0843-4 (12.90%) were identified as the promising inbreds for protein content (Table 1). During *Kharif*-2014, protein content of the selected lines varied from 9.92% to 15.38% with an average value of 12%. Except HBL 0843-4, (Table 3) whose protein content showed a difference of more than 2%, all other selected lines for other characters showed similar protein content as was observed during *Kharif*-2013. Thus on the basis of two years mean performance, four inbreds (with protein content > 13%) have been finally selected for high protein content viz. HBL 0620 (15.70 %), HTP 94/54 (13.31%), H 77/833-2-202 (13.38%) and HBL 0809 (13.38%). Protein content in designated B-line ranged from 10.11% (HMS 26B) to 16.68% (HMS 18B) with an average value of 13.24% grown during *Kharif*-2013 (Table 2). A total number of 17 designated B-line viz. HMS 16B, HMS 18B, HMS 20B, HMS 39B, HMS 40B, HMS 41B, HMS 42B, HMS 44B, HMS 45B, HMS 46B, HMS 49B, HMS 55B, HMS 56B, HMS 57B, HMS 58B, HMS 60B and ICMA 95222 exhibited significantly higher protein content than released hybrids

Table 1. Protein content (%) of pearl millet inbreds grown during *kharif*-2013

S.No.	Pedigree	Protein (%)	S.No.	Pedigree	Protein (%)
1	B08/2013	11.52^{de}	24	HBL-0854	11.80^{d}
2	Brs-10-2	12.60^{c}	25	HBL-0902-1	12.09^{cd}
3	Brs-10-6	12.01^{cd}	26	HBL-0902-5	13.11^{bc}
4	Brs-10-7	11.69^{de}	27	HBL-0904-1	9.43^{fg}
5	DPHBL-11-123	12.24^{c}	28	HBL-0904-2	10.90^{e}
6	EBLT-11-101	10.31^{f}	29	HBL-0906-2	12.66^{c}
7	EBLT-11-114	9.07^{g}	30	HBL-0906-3	11.37^{de}
8	HBL- 0703	11.64^{de}	31	HBL-1108	8.92^{g}
9	HBL-0508	10.48^{ef}	32	HBL-112/H12/1011	11.60^{de}
10	HBL-0510-2	10.19^{f}	33	HBL-1120	10.85^{e}
11	HBL-0547	10.10^{f}	34	HBL-34	10.82^{e}
12	HBL-0561	11.20^{e}	35	HBL-72	13.11^{b}
13	HBL-0620	16.03^{a}	36	HBL-828-1	10.19^{f}
14	HBL-0706	12.85^{bc}	37	ICMB-88006	11.90^{d}
15	HBL-0802	11.29^{de}	38	LPBL-10/112	9.06^{g}
16	HBL-0809	12.87^{bc}	39	LPBL-10/120	11.10^{e}
17	HBL-0825-1	10.78^{e}	40	TPBL-11-109	8.62^{g}
18	H-1305	10.75^{e}	41	94/54-1	10.08^{f}
19	HBL-0828-2	10.40^{ef}	42	G-73/107	10.53^{ef}
20	HBL-0832	12.87^{bc}	43	HTP-94/54	13.59^{b}
21	HBL-0843-2	11.82^{de}	44	HBL-11	11.64^{de}
22	HBL-0843-4	12.90^{bc}	45	H-77/833-2-202	13.42^{b}
23	HBL-0847-3	9.59^{fg}	46	78/711	11.56^{de}
	C.D. ($p < 0.05$)	0.79		C.D. ($p < 0.05$)	0.79
	SE(d)	0.39		SE(d)	0.39
	C.V. (%)	2.44		C.V. (%)	2.44

Table 2. Protein content pearl millet designated B-lines (CMS lines) grown during *kharif* 2013

S.No.	Pedigree	Protein (%)	S.No.	Pedigree	Protein (%)
1	HMS 7B	13.15^{g}	24	HMS 42B	14.78^{d}
2	HMS 7B-1	14.66^{d}	25	HMS 44B	16.08^{b}
3	HMS 13B	13.10^{gh}	26	HMS 45B	14.14^{e}
4	HMS 14B	13.17^{g}	27	HMS 46B	16.08^{b}
5	HMS 16B	14.22^{e}	28	HMS 49B	13.71^{f}
6	HMS 18B	16.68^{a}	29	HMS 50B	12.94^{gh}
7	HMS 20B	14.08^{e}	30	HMS 51B	11.80 ^{jk}
8	HMS 21B	11.18^{l}	31	HMS 52B	11.75 ^{jk}
9	HMS 22B	11.64^{jk}	32	HMS 53B	13.04^{gh}
10	HMS 23B	10.92^{l}	33	HMS 55B	14.04^{e}
11	HMS 26B	10.11^{m}	34	HMS 56B	13.95^{ef}
12	HMS 28B	11.06^{l}	35	HMS 57B	15.03^{cd}
13	HMS 29B	11.43^{k}	36	HMS 58B	13.95^{e}
14	HMS 30B	11.85 ^{j}	37	HMS 59B	13.10^{gh}
15	HMS 32B	13.25^{fg}	38	HMS 60B	14.08^{e}
16	HMS 33B	12.53^{i}	39	HMS 61B	13.59^{fg}
17	HMS 34B	13.53^{f}	40	ICMB-843-22	13.32^{g}
18	HMS 36B	12.68^{i}	41	ICMB-89111	12.64^{i}
19	HMS 37B	11.92^{k}	42	ICMB-95222	13.34^{g}
20	HMS 38B	13.04^{gh}	43	ICMB-97111	12.13^{j}
21	HMS 39B	14.27^{e}	44	ICMB-94555	14.22^{e}
22	HMS 40B	13.78^{f}	45	ICMB-94222	10.40^{m}
23	HMS 41B	15.31^{c}	46	ICMB-843-22	13.32^{g}
	C.D.	0.39		C.D.	0.39
	SE(d)	0.19		SE(d)	0.19
	C.V.	1.47		C.V.	1.47

Table 3. Protein content of selected pearl millet inbreds grown during *kharif-2013* and *kharif-2014*

S.No.	Pedigree	Protein (%)		
		Kharif-2013	Kharif-2014	Mean
1	HBL-0620	16.03	15.38	15.70
2	HTP-94/54	13.59	13.02	13.31
3	H-77/833-2-202	13.42	13.34	13.38
4	HBL-0843-4	12.90	10.97	11.94
5	HBL-0809	12.87	13.24	13.06
6	HBL-0706	12.85	12.98	12.91
7	DPHBL-11-123	12.24	11.06	11.65
8	HBL-11	11.64	12.38	12.01
9	HBL-112/H12/1011	11.60	10.53	11.07
10	LPBL-10/120	11.10	10.27	10.68
11	H-1305	10.75	12.55	11.65
12	G-73/107	10.53	10.62	10.58
13	94/54-1	10.08	9.92	10.00
14	LPBL-10/112	9.06	11.76	10.41
	C.D. ($p < 0.05$)		0.62	
	SE(d)		0.30	
	C.V. (%)		2.47	

and composites. Designated B-line exhibited very high protein viz., HMS 18B (16.68%) followed by HMS 44B (16.08%) and HMS 46B (16.08%). A total of 19 designated B-lines were selected for low and high protein content and grown during kharif 2014. Results of *Kharif-2014* presented in Table 4, showed that except HMS 39B (12.63%) and HMS 32B (11.06%), all other selected lined were comparable for protein content with *Kharif-2013* results. It varied from 10.10% (HMS 33B) to 16.32% (HMS 18B) with an average value of 12.34%. The average protein content of both the season for respective lines confirms the selection of promising CMS lines for protein content. Thus, on the basis of protein content recorded in grains produced during *Kharif*-2013 & 2014 both the seasons HMS 18B (16.50%), HMS 46B (16.08%), HMS 7B-1(14.15%), HMS 39B (14.27%), HMS 16B (13.61%), HMS 40B (14.63%), HMS 14B (13.26%), HMS 13B (13.12%), HMS 59B (13.34%), and HMS 53B (13.32%) are high protein designated B-lines. Large variations in protein content, from 6 to 21 percent, have also been observed

Table:4. Protein content (%) of Selected designated B-lines (CMS lines) of pearl millet grown during kharif 2013 and kharif 2014

S.No.	Pedigree	Protein %		
		Kharif-2013	Kharif-2014	Mean
1	HMS 18B	16.68	16.32	16.50
2	HMS 7B-1	14.66	13.63	14.15
3	HMS 39B	14.27	12.63	13.45
4	HMS 16B	14.22	13.00	13.61
5	HMS 40B	13.78	12.90	13.34
6	HMS 32B	13.25	11.06	12.16
7	HMS 14B	13.17	13.34	13.26
8	HMS 7B	13.15	12.50	12.83
9	HMS 13B	13.10	13.15	13.12
10	HMS 59B	13.10	13.59	13.34
11	HMS 38B	13.04	12.76	12.90
12	HMS 53B	13.04	13.61	13.32
13	HMS 36B	12.68	10.99	11.83
14	ICMA89111	12.64	10.62	11.63
15	HMS 33B	12.53	10.10	11.31
16	HMS 52B	11.75	10.27	11.01
17	HMS 21B	11.18	11.14	11.16
18	HMS 26B	10.11	10.44	10.28
	C.D.		0.62	
	SE(d)		0.30	
	C.V.		2.47	

earlier (Sawhney and Naik 1969; Uprety and Austin 1972). On the contrary, a lower variation in protein content (9-15%) in pearl millet genotypes was also reported Goswami *et al.* (1969; 1970). Grain protein content of pearl millet hybrids and varieties released in India ranges between 8.00 to 13.00 % (Berwal *et al.,* 2017).

Analysis of variance presented in Table 1 to 4 indicated significant differences between the tested genotypes. The inbred lines and CMS lines of these B-lines may extensively be used in development of high protein hybrids or composite seed of high protein B-line lines and following the random mating in isolation to form the high protein population and further improve the per se performance following recurrent selection. Pearl millet hybrids and population developed at CCS HAU, Hisar possessed the maximum protein content 12.85 % and 13.89 %, respectively. There is possibility to develop hybrid with more than 15% protein by extensively utilizing the CMS possessing more than 15% protein content. Further germplasm accession should be screened to identify the restorer with high protein content. Correlation of grain yield with protein is generally negative, but certain genotypes in specific combinations may give high yield and high protein (Dua and Kapoor, 1982). Therefore, it is possible to breed pearl millet hybrids with availability of high protein inbreds and CMS lines. High heterosis has been reported for protein content using CMS lines (Kumar *et al.,* 2003).

Conclusion

The inbred lines (HBL 0620, HTP 94/54, H 77/833-2-202, and HBL 0809) and designated B-lines (HMS 18B, HMS 46B, HMS 7B-1, HMS 39B, HMS 16B, HMS 40B, HMS 14B, HMS 13B, HMS 59B, HMS 38B, and HMS 53B) sowed consistently more than 13% average protein content, which could be potential parental lines for development of protein dense pearl millet hybrids/ composites.

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Indian J. Plant Genet. Resour. 33(1): 90–93 (2020)
DOI 10.5958/0976-1926.2020.00013.3

SHORT COMMUNICATION

Studies on Reproductive Behavior of Fifteen Elite Wheat Genotypes in Relation to Hybrid Development

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(Received: 05 January, 2018; Revised: 14 October, 2019; Accepted: 14 October 2019)

Fifteen elite wheat genotypes viz. WH 147, WH 542, HD 2967, CBW 38, DBW 31, DBW 39, KRL 99, KRL 284, HD 2964, NIAW 1188, MP 1194, LB-PY 05-02, LBPY 05-04, RWP 206-33 and DBW 50 were screened for variation in floral characteristics viz., glume opening angle, anther size, pollen viability, filament length, and anther extrusion percentage, related to out crossing of wheat. In present study, on the basis of floral characteristics, WH 147 was identified as best pollen parent followed by DBW 50, CBW 38 and NIAW 1188.

Key Words: Allogamy, Anther extrusion, Floral traits, Hybrid wheat, Pollen dispersal, Pollen viability

It is a well-known fact that in wheat hybrid seed production, use of cytoplasmic genetic male sterility (CGMS) lines had always remained a very challenging task to accomplish. To address the problem it was concluded that hybrid wheat requires a transformation in flower behavior from self to cross-fertilization. Wilson (1968) suggested that the nature of flowering in wheat indicates that adaptation to cross-pollination was prevalent in its ancestors and may still be operating in present day cultivated forms. Singh (1992) stated that a good pollinator for hybrid wheat production should possess high pollen productivity and ability to extrude anthers in addition to favourable combining ability. The best male parents were those, which extruded their anthers from the florets for effective cross pollination. Chowdhry *et al*. (1994) stated that selection for long anthers and high rate of anther extrusion should be effective in promoting natural cross pollination. Several researchers worked on this aspect to transform the nature of pollination in wheat. Important floral characteristics leading to increase in out-crossing ability of wheat had been identified and subjected to their genetic improvement in CGMS lines by Wilson (1968); Singh (1992); Sethi & Chhabra (1990) and Singh (2007). For hybrid seed production in wheat, allogamy related floral traits such as glume opening in the A lines are essential part of hybrid breeding programme. For this purpose, it is first needed to identify potential donors. A good pollinator for hybrid wheat production should possess high pollen productivity and dispersal of pollen.

The experiment aimed at studying floral characteristics of the male parents was carried out at the experimental farm area of CCS Haryana Agricultural University, Hisar (29.1700° N, 75.7200° E), Haryana, India, under normally grown, irrigated conditions, during November 2011-April, 2012. Fifteen elite wheat cultivars studied for the floral traits were WH 147, WH 542, HD 2967, CBW 38, DBW 31, DBW 39, KRL 99, KRL 284, HD 2964, NIAW 1188, MP 1194, LB-PY 05-02, LBPY 05-04, RWP 206-33 and DBW 50. The elite lines were grown in randomized block design with three replications, in normal environment. Each genotype was grown in a plot of two meter long in single row. The row was spaced 30 cm apart keeping 10 cm plant to plant distance. The other packages of practices were the same as recommended for normal environment.

Observations on the floral traits related to outcrossing abilities of wheat were recorded on five spikes (one main and four side tillers) per plant for five randomly selected plants, for glume opening angle (degree), anther size (mm^2), filament length (mm), pollen viability (%) and anther extrusion (%). Pollen viability percentage was determined as the number of pollen grains stained red per hundred, when stained with 2% aceto-carmine,

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and observed under light microscope, at 10x and 40x resolution. Anther extrusion percentage was calculated as the number of florets with extruded anthers per hundred florets. The mean values for these observations in each replication were calculated and subjected to analysis of variance under Randomized Block Design by using statistical software OPSTAT developed by Dr. O.P. Sheoran, CCS HAU, Hisar (Anonymous, 2017). For the purpose of suitability of applying ANOVA, to the percentage data, square root transformation and arc sine transformation was applied. Genetic variability for floral characteristics were worked out in terms of range, mean, genotypic and phenotypic coefficient of variation (GCV and PCV), broad sense heritability, genetic advance under selection and genetic advance under selection as percentage of character mean. Data recorded for floral traits of male parents are represented in Table 1. Sum of square values from the analysis of variance for the floral traits of male parents are presented in Table 2, which clearly revealed that all these characters varied significantly among these elite lines. Genotypic differences were significant for glumes opening angle (degree), anther size (mm^2), filament length (mm), pollen viability (%) and anther extrusion (%) among the elite lines.

In the present study, all the floral traits, *viz.,* glume opening angle, anther size, pollen viability (%), filament length (mm) and anther extrusion (%) studied in fifteen elite lines of wheat showed significant amount of variability as detected by F test for each traits. Among all fifteen elite lines studied, WH 147 was found to be the best performer for pollen viability (%) and anther extrusion (%), while DBW 50 was found to produce largest anther size and longest filament. Comparison of relative performances of all lines for these allogamy related floral traits (Fig. 1) led to identification of WH 147 as the best performer, followed by DBW 50. These lines can be used as pollen donor in hybrid seed production programme. Besides, these lines can also be used as effective donor for these traits to transform reproductive behavior of A lines from autogamy to allogamy, through repeated back-cross breeding. Among other lines evaluated, WH 542, CBW 38 and NIAW 1188 are worth mentioning as WH 542 produced widest open glumes; CBW 38 produces inflorescence with wider glume opening angle, long filament length, and higher anther extrusion percentage; while NIAW 1188 produces inflorescence with larger anther size, longer filament length and higher anther extrusion percentage (Fig. 2). Above findings were in line with the observation of Arya and Sethi (2005).

Literature references from several research workers were found to be in agreement with the result of the present investigation. High rate of anther extrusion, 97% in wheat, was reported by Sethi and Chhabra (1990). Wilson and Ross (1962) observed that the tightness of the spikelet influences the width of separation of glume opening angle. Akhmedov (1983) found that sufficient degree of open flowering in male sterile lines allowed adequate hybrid seed set. Singh *et al*. (2007) studied

Table 1. Mean performance of allogamy related floral traits of elite lines of wheat

Pollen Parents	Glume opening angle (°)	Anther size (mm^2)	Pollen viability (%)	Filament length (mm)	Anther extrusion (%)
WH 147	11	4.26	96.87	14.55	81.44
WH 542	13.8	1.31	96.07	12.28	73.48
HD 2967	8.27	1.31	93.47	12.75	75.02
CBW 38	10.93	2.39	83.33	14.04	78.86
DBW 31	7.67	5.60	92.4	7.16	80.11
DBW 39	11.87	3.72	92.53	9.28	65.13
KRL 99	10.4	4.39	94.93	9.73	63.54
KRL 284	7.27	4.99	93.73	13.73	70.38
HD 2964	5.6	2.04	93.40	9.27	68.90
NIAW 1188	9.93	5.88	92.20	12.99	76.74
MP 1194	8.67	5.69	96.07	12.24	72.48
LB-PY 05-02	10.4	5.19	95.67	11.01	65.63
LBPY 05-04	8.53	3.55	95.80	9.29	53.89
RWP 206-33	8.73	4.66	93.80	12.98	63.54
DBW 50	7.53	6.41	96.60	14.78	73.48
Grand mean	9.37	4.09	93.79	11.48	70.84
Range	5.6-13.8	1.31-6.41	83.33-96.87	7.16-14.78	53.89-81.44
CD at 5%	0.54	0.30	1.17	0.06	4.62

Table 2. Variability of floral traits in 15 elite lines of wheat

Variability parameters	Glume opening angle (°)	Anther size (mm^2)	Pollen viability (%)	Filament length (mm)	Anther extrusion (%)
Mean	9.37	4.09	93.79	11.74	70.84
Range	5.6-13.8	1.31-6.41	83.33-96.87	7.16-14.78	53.89-81.44
GCV	22.21	40.64	3.49	18.66	10.36
PCV	22.46	40.86	3.57	18.66	11.06
Broad sense heritability (%)	97.74	98.93	95.62	99.97	87.71
GA at 1% selection intensity	5.43	4.36	8.45	5.78	18.14
GA at 5% selection intensity	4.24	3.41	6.59	4.51	14.15
GA as per cent of mean at 1% selection intensity	57.96	106.71	9.01	49.25	25.61
GA as per cent of mean at 5% selection intensity	45.23	83.27	7.029	38.43	19.98

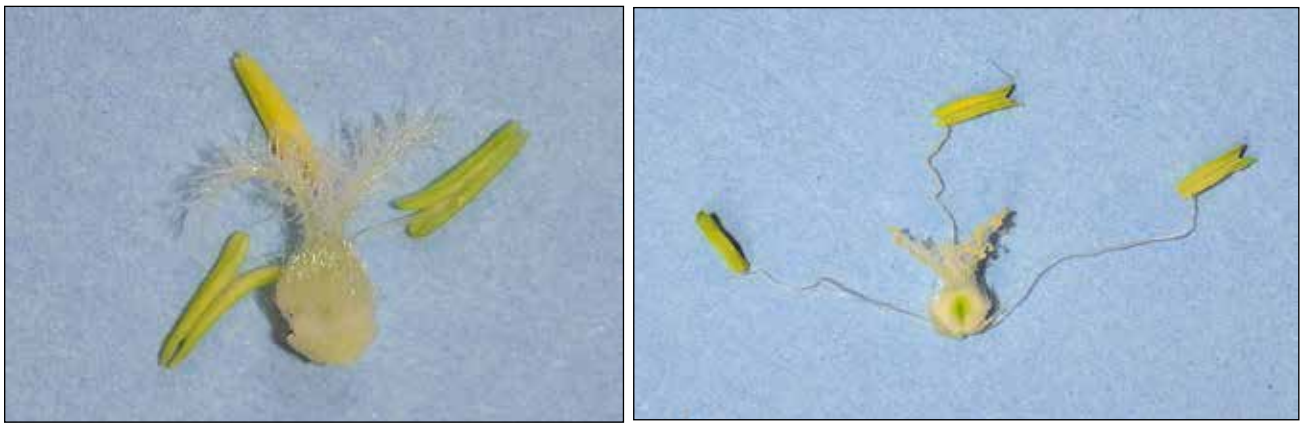

Fig. 1. Comparison of longest and shortest filament length among pollen parents studied.
A: Shortest filament length was observed in pollen parent DBW 31. B: Longest filament length was observed in DBW 50.

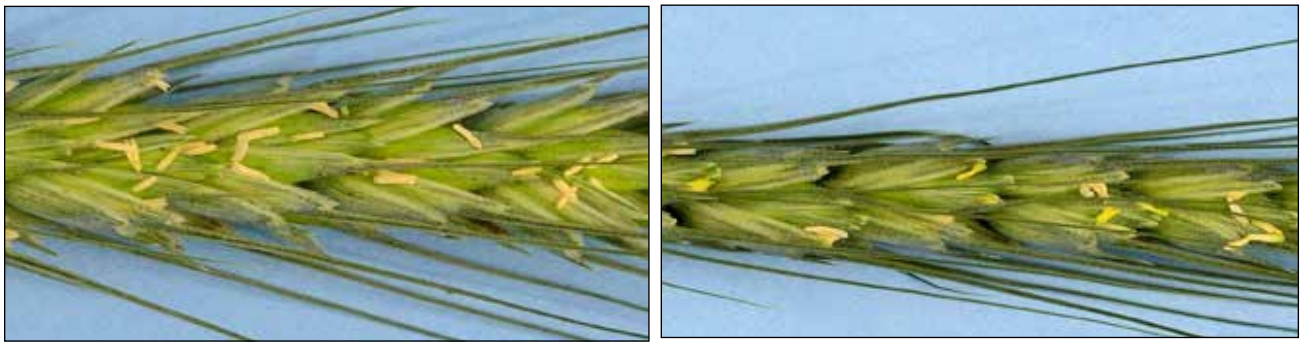

Fig. 2. Comparison of maximum and minimum glume opening angle in pollen parents A: Maximum glume opening angle was observed in pollen parent WH 542. B: Minimum glume opening angle was observed in pollen parent HD 2964.

degree of open flowering in male sterile lines allowed adequate hybrid seed set. Singh *et al*. (2007) studied floral characteristics of spring wheat in Indo-Gangetic plains of north India and reported existence of significant quantitative variation among indigenous, exotic and adapted wheat germplasm. Genetic variability among these fifteen elite lines of wheat were explored in terms of range, mean, genotypic and phenotypic coefficients of variation, broad sense heritability, genetic advance and genetic advance as percentage of character mean, and represented in Table 2. For all the floral characters studied, phenotypic co-efficient of variation was more than genotypic co-efficient of variation, although the differences were very small

and thus broad sense heritability was very high. This clearly indicates higher degree of genotypic control for expression of these traits, and provides strong hint that phenotypic expression will not be influenced greatly under various environmental conditions. Besides, there is scope for further improvement of these traits, as indicated by high values of genetic advance under selection and genetic advance under selection expressed as per cent of character mean.

Conclusion

On the bases of allogamy related floral traits, WH 147 and DBW 50 can be used as pollen donor in hybrid seed production. Besides, these lines can also be used as effective donor for these traits to transform reproductive behavior of A lines from autogamy to allogamy, through repeated back-cross breeding. Moreover, WH 542 produced widest open glumes; CBW 38 produces inflorescence with wider glume opening angle, long filament length, and higher anther extrusion percentage; while NIAW 1188 produces inflorescence with larger anther size, longer filament length and higher anther extrusion percentage. The higher degree of genotypic control for expression of these traits, and phenotypic expression will not be influenced greatly under various environmental conditions. Besides, there is a scope of further improvement for these traits, as indicated by high values of genetic advance under selection and genetic advance under selection expressed as per cent of character mean. Observations reported here are being utilized in the ongoing hybrid wheat development programme at the HAU.

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Indian J. Plant Genet. Resour. 33(1): 94–97 (2020)
DOI 10.5958/0976-1926.2020.00014.5

SHORT COMMUNICATION

Collection and Evaluation of Henna (*Lawsonia inermis* L.) Germplasm from South India

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(Received: 31 March, 2018; Revised: 11 November, 2019; Accepted: 19 December 2019)

An extensive germplasm exploration survey of *Lawsonia inermis* was undertaken to identify superior germplasm. Morphometric evaluation showed significant (P<0.001) variation for leaf morphometric traits and lawsone content. Total leaf dry weight (99.76 g), lawsone content (21.5 mg^{-1} g dw) and lawsone yield/tree (2.14 g) were maximum in candidate elite plant 16, thus selected as 'elite' germplasm of *L. inermis*.

Key Words: Elite germplasm, *Lawsonia inermis*, Lawsone content, Morphological evaluation, Variability

Lawsonia inermis L. (syn: *L. alba* Lam., common name: Henna), the only species under the genus *Lawsonia* L. belonging to the family Lythraceae, is a small tree growing up to 12 m high. The colouring principle present in henna is lawsone (2-hydroxy-1,4 naphthoquinone), which occurs in quantities of 0.5-1.5% in dried leaf (Singh *et al*., 2014); its concentration varies in relation to environmental factors. Lawsone has proved as a non-toxic natural dye reported to have hepatoprotective, antioxidant and antimicrobial activities. This species is native of North Africa and South West Asia, and cultivated widely for the commercial production of henna leaf powder. The recent market trend indicates that the demand of henna leaf powder is increasing worldwide, thus people in many parts of India ventured commercial cultivation of *L. inermis*. However, in Kerala, the southernmost state of India, though the plant is naturalized and distributed throughout, organized cultivation is not yet initiated. It is mainly due to the poor market system coupled with the availability of comparatively low-priced products emerging from northern India. Market potential of henna largely depends on lawsone content of the leaf powder. Thus efforts to screen the germplasm having high content of lawsone coupled with other quality attributes deserve due attention. In this direction, selection of candidate elite plants (CEPs) and their morphological characterization, estimation of lawsone and analyzing correlation between growth characters will be a useful approach.

To achieve this goal, an extensive germplasm exploration survey of *L. inermis* was undertaken in different locations of Kerala and Tamilnadu states of India during 2012. To compare various yield characteristics, at first, 108 plants were randomly sampled in the study area with two prime quantitative parameters, viz., number of fresh leaves weighing 1 g and lawsone content (Dhiman *et al*., 2012). Mean value of these parameters in 108 samples was determined. Among 108 samples, 20 plants which showed 50% less number of leaf weighing 1 g than mean value and 50% higher lawsone content than mean of 108 plants were further selected for the detailed examination through single location selection programmes. These 20 plants were designated as CEPs and were subjected to detailed yield evaluation based on various quantitative traits. Collection details such as locality, latitude and longitude of 20 CEPs are as follows; CEP1 (Kariavattom, 8º33.539"N; 76º53.113"E), CEP2 (Kariavattom, 8º33.534"N; 76º55.106"E), CEP3 (Palarivattom, 10º00.128"N; 76º18.807"E), CEP4 (Poovaloor, 10º01.926"N; 76º42.407"E), CEP5 (Ayakkad, 10º36.208"N; 76º28.487"E), CEP6 (Kaapistore, 10º13.272"N; 77º08.132"E), CEP7 (Paisa Nagar, 10º14.388"N; 77º11.041"E), CEP8 (Kambiline, 10º02.255"N; 77º00.768"E), CEP9 (Kaithakkal, 11º45.600"N; 76º04.81"E), CEP10 (Devagiri 11º28.647"N; 76º21.184"E), CEP11

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(Kaithkuzhi, 11º28.205”N; 76º23.520”E), CEP12 (Devala, 11º28.526”N; 76º22.478”E), CEP13 (Korachal, 11º31.297”N;.106 ”E), CEP 14 (Kayyunni, 11º32.660”N; 76º15.660”E), CEP15 (Parashuramapuram, 10º09.820”N; 77˚43.301”E), CEP16 (Parashuramapuram, 10º09.820”N; 77º43.301”E), CEP17 (Parashuramapuram, 10º09.820”N; 77º43.301”E) CEP18 (Kovilkadavu, 10º15.224”N; 77º10.083 ”E), CEP19 (Sattur, 9º21.457”N; 77º54.939”E), CEP20 (Kalthmmuri, 9º28.738N; 76º20.192”E).

To compare yield of 20 CEPs at a single location, the branch cuttings (approx. 40 cm) were collected from these plants during monsoon season (Mid May-August 2012) and were planted in experimental plot at 1.5 × 1.5 m spacing in the Department Garden, Department of Botany, University of Kerala, Kariavattom (8º34’02.77”N; 76º53’13.42”E; altitude 42 m asl). Area receives an annual rainfall of 1500 mm, mainly through southwest monsoon during June to September. Mean monthly temperature varies between 22ºC in January and 33ºC in April. For each CEP, six cuttings were successfully established in the garden. After three years of planting, metric morphological traits of each CEP were determined and were continued for the next two successive years. Mature leaves from each CEP were collected and labeled properly. The leaves were shade-dried for one week and powdered (5 g) followed by subjected to soxhlet extraction (48 h; 37ºC) using 40 ml methanol (AR Grade, SISCO, Mumbai, India) as solvent. Quantitative estimation of lawsone (Dhiman *et al*., 2012) in air dried extract was carried out by using UV Vis spectrophotometer (Shimadzu, Japan, Model Name: UV-1700 Pharma Spec, Model No. 1700) at 452 nm, based on lawsone standard (Sigma Chemical Co., St. Louis, USA). Lawsone quantification was repeated three times for all the randomly sampled trees and 20 CEPs. For yield traits, ten replications per trait per plant were carried out. CEPs established in the experimental garden were scored during hot summer season (March-April). Scored data were subjected to one-way analysis of variance (ANOVA) and mean separation was performed using Duncan’s New Multiple Range Test ($P<0.05$). Spearman rank correlation coefficients were performed to determine the relationship between leaf yield traits as well as lawsone content (SPSS package version 22, IBM Corp. Released 2013, IBM SPSS Statistics for Windows, Armonk, NY, USA) to find P value of less than 0.05 as threshold for statistical significance.

Genetic improvement of a crop, by trait specific selection can be achieved through morphometric and biochemical traits. In order to meet the ultimate goal of high yield of the plant, evaluation of morphometric variability and selection of superior gemplasm will be beneficial. In the present study, total lawsone yield is considered as the prioritized goal in *L. inermis* for selection of superior germplasm for future breeding programmes. Mean number of leaves (61.8) weighing 1 g and mean lawsone content (10.32 mg g^{-1} dw) were estimated among 108 collections and found that 20 plants are superior for both the evaluated traits, and were therefore compared further through one site yield trials. Metric characters revealed significant differences among 20 CEPs of *L. inermis* (Table 1). Leaf morphometric traits among CEPs such as length of leaf, width of leaf, length of petiole, leaf area showed significant ($P<0.001$) variation (Table 1). This significant variation might explain the genetic divergence of the germplasm originally collected from different agro-climatic regions of South India.

In the present study, morphological traits were used for characterization of different collections of *L. inermis*. In the previous studies also, such a wide range of variability in different accessions of *L. inermis* was reported (Singh *et al*., 2008). Number of leaves weighed 1 g was least in CEP6 where 15.3 freshly collected leaves constituted 1 g, substantiating large-sized leaves in this collection (Table 1). Maximum number of leaves (30.4 nos.) was required to weigh 1 g in CEP 18, characterized by narrow long leaves (Table 1). Total leaf dry weight data of 20 CEPs scored during three successive years showed highest dry weight in CEP16 (99.76 g dw). As per morphometric traits recorded, CEP6 showed some desired traits such as highest leaf length (5.38 cm) and leaf area (11.36 cm^2). However, superiority in leaf length and area estimates is not enough to elevate a CEP to elite category. The spectrophotometric determination of lawsone content in 20 collections of *L. inermis* showed significant ($P<0.001$) variation among collections which was planted in same climatic conditions (Table 1). The lawsone content in selected CEPs varied from 15.4 to 23.1 mg^{-1} g dw. Highest amount of lawsone was estimated in CEP15 (23.1 mg^{-1} g dw). The CEP6 recorded least (15.4 mg^{-1} g dw) lawsone content. Our findings on lawsone content of *L. inermis* suggest that a comparable range of lawsone is present in most of the CEPs studied with that of northern arid zone accessions

Table 1. Leaf morphometric traits of different candidate elite plants (CEPs) of *L. inermis* planted in the experimental plot.

Collection Code	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Leaf area (cm^2)	Total no. of main branches/ plant	Mean no. of leaves /sub-branch	No. of leaf weighing 1 g	Total leaf dry weight (g)	Lawsone content (mg^{-1} g dw)	Total lawsone yield/tree (g)
CEP1	3.87gh	1.51ij	0.55e	5.85m	12.4d	14.3b	28.2c	51.43gh	21.2de	1.09f
CEP2	3.84g	1.51ij	0.57cd	5.83m	14.0bc	12.7c	30.3a	29.56k	21.4d	0.63j
CEP3	4.31f	1.46j	0.50f	6.15j	13.1c	12.2c	26.2c	57.35f	21.2de	1.22e
CEP4	3.74hi	1.57hi	0.46gh	5.97l	14.1bc	14.5b	22.4d	75.09d	18.4g	1.38d
CEP5	4.32d	1.71ef	0.47gh	7.15g	13.2c	10.5d	29.1bc	38.56j	17.1h	0.66j
CEP6	5.38a	2.11ab	0.72b	11.36a	11.9d	14.4b	15.3e	92.80b	15.4j	1.43d
CEP7	3.48j	1.52ij	0.45h	5.35n	13.3c	12.3c	30.1a	43.10i	22.8ab	0.98g
CEP8	2.89k	1.45j	0.31k	4.18o	13.1c	14.8b	26.2c	45.00i	21.3de	0.96g
CEP9	3.82gh	1.61gh	0.34j	6.08k	12.2d	10.5d	27.5c	49.26h	16.8i	0.83h
CEP10	4.06f	1.46j	0.46gh	5.85m	13.8bc	12.2c	19.7de	34.66j	18.4g	0.64j
CEP11	3.94fg	1.78de	0.47fgh	7.03i	15.0ab	10.4d	21.1d	62.86e	22.2bc	1.39d
CEP12	4.73c	2.15a	0.67c	10.05d	12.2d	12.7c	21.2d	43.42i	20.4f	0.89hh
CEP13	3.70i	1.56hi	0.72b	5.87m	12.4d	10.2d	18.1de	49.27h	21.2de	1.04fg
CEP14	5.16c	2.11ab	0.93a	10.57b	13.2cd	12.7c	19.0d	52.00gh	17.3h	0.99g
CEP15	4.12f	2.05b	0.41i	8.49e	14.1b	14.8b	21.2d	86.66c	23.1a	2.01b
CEP16	4.37d	1.67fg	0.65c	7.33f	16.2a	14.3b	17.0e	99.76a	21.5cd	2.14a
CEP17	3.82gh	1.86c	0.48fg	7.13g	15.1a	10.2d	22.2d	53.18fg	18.5g	0.98g
CEP18	3.83g	1.85cd	0.47fgh	7.06h	14.9a	12.4c	30.4a	34.80j	20.6ef	0.72i
CEP19	3.72i	1.68fg	0.48fg	6.26i	16.1a	16.2a	19.3de	87.57c	20.7def	1.81c
CEP20	4.72c	2.17a	0.59d	10.22c	12.8c	10.3d	22.2d	46.09i	16.2i	0.75i
F value DF (n-1)= 19	453***	101***	339***	783.8***	114***	87.0***	76.3***	184.7***	90.8***	46.5***

***Significant at P<0.001 level; Means within column followed by same letter are not significantly (P<0.05) different as determined by Duncan's New Multiple Range test (DNMRT).

(Singh *et al*., 2008), where mean content among selected accessions was 19.8 mg^{-1} g dw (1.98%). In the present study, mean lawsone content of 108 randomly sampled individuals was 10.32 mg^{-1} g dw and best selected one (CEP16) had 21.5 mg^{-1} g dw lawsone content, which is 100% higher than the mean. Present finding is in agreement with previous report that leaf size and lawsone contents varied significantly among sampled accessions of *L. inermis* (Singh *et al*., 2008). Possibly, differences in regulation of synthesis of phytochemicals due to varying activity of regulating enzymes explained genetic differences of the plant.

Spearman rank correlation coefficients among the ten quantitative traits showed significant inter correlation of four traits with lawsone yield. Yield characters such as mean number of leaf/sub-branch (r=0.610), no. of leaf weighing 1 g (r=0.488) and total leaf biomass of plant (r=0.940) showed significant positive correlation with total lawsone yield of the plant. The leaf length was highly positively correlated with the leaf width (r=0.716) and leaf area (r=0.926), and negatively correlated with lawsone content (r=-0.574). Correlated quantitative traits are of major interest in crop improvement programme, as the improvement of one character may cause simultaneous changes in other characters. As long as the genes governing the characters are not combined at random, characters may show some correlation. If the observed correlation is due to multiple effects of a same gene, the selection for one character will affect other characters. Hence, correlation among the traits influences effectiveness of selection. Among various morphometric traits and lawsone yield, the lawsone yield was considered as the most prioritized trait which showed strong relationship with biomass and lawsone content. The tree having highest lawsone yield, which is a direct product of leaf biomass and lawsone content, was screened as "elite". Yield characters such as mean number of leaf/sub-branch (r=0.610) and total biomass of leaf per plant (r=0.79) showed significant positive correlation with total lawsone yield of the plant. Based on highest leaf dry biomass and maximum lawsone yield (2.14 g), CEP16 was selected as elite or plus tree. The selected CEP showed 100% higher lawsone content (21.5 mg^{-1} g dw) than mean content of 108 randomly sampled individuals. Thus best selected accession CEP16 can further be used for the clonal propagation both through

conventional and biotechnological tools and in breeding programmes.

Acknowledgment

The authors thank Dr. Suhara Beevy S, Professor and Head, Department of Botany, University of Kerala, for providing research facilities. PCS thank Kerala State Welfare Board (Govt. of Kerala, India) for providing research grant (B3-14931/06/11/2014) in the form of Senior Research Fellowship.

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Indian J. Plant Genet. Resour. 33(1): 98–101 (2020)
DOI 10.5958/0976-1926.2020.00015.7

SHORT COMMUNICATION

Variability in Fruit and Seed Parameters of *Manilkara hexandra* (Roxb.) Dubard in Rajasthan

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(Received: 25 August, 2018; Revised: 06 January, 2019; Accepted: 15 February, 2019)

Exploration trips were conducted in different villages of Pali district in Rajasthan for germplasm collection of *Manilkara hexandra* (Roxb.) Dubard. All the parameters i.e., fruit length, fruit width, fruit weight, pulp weight, seed length and seed width varied significantly ($p<0.001$) except for seed weight ($p=0.087$). Highest coefficient of variation (CV) was recorded for pulp weight (43.54%), followed by fruit weight (33.49%) and seed length (19.48%). Among the germplasm collected, the one from U1 (Utharan) area was found to be good in terms of all fruit parameters.

Key Words: Co-efficient of variation, Correlation, Germplasm collection, Khirni, Pali district

Manilkara hexandra (Roxb.) Dubard is an indigenous underutilized fruit tree belonging to the family Sapotaecae. It is locally known as 'khirni' or 'rayan' and is generally distributed in states such as Rajasthan, Gujarat, Madhya Pradesh and Maharashtra (Malik *et al*., 2010). In wild condition, it is found in dry deciduous forests of western and central India. The tree is adapted to semi-arid regions and drought conditions and also thrives well on rocky, saline and sodic soils. It is widely used as rootstock for grafting of sapota plants. Seed is also good source of edible oil which contains about 24.6% oil. The tree bears attractive golden yellow fruit with pulp which is soft and sweet in taste which possesses high nutritive value. Fruit is milky, sweet, sour, cooling, aphrodisiac, appetizer, emollient and used as tonic and a good source of minerals, sugars, protein, carbohydrates, vitamin-A and C (Pareek *et al*., 1998). Fresh or dried fruits are sweet; consumed raw as well as after drying by local inhabitants/tribal people (Malik *et al.,* 2010, 2012). Fruit serves as 'Vitamin A capsule' especially for nutritionally deficient tribal women and children. Mashed fruits are taken to cure diseases like arthritis, jaundice, and also for heat burning, deworming, for blood purification.

Germplasm collection is an indispensable component for tree improvement programme ensuring quick genetic gain of superior genotypes. The tree exhibits a wide range of variation due to heterozygous and cross-pollinated nature, which aids in selection of superior genotypes. It is essential to determine extent, cause and nature of variation present in the species which is also the first step towards improvement work. Owing to its economic importance as fruit, documentation of genetic variation of this species is needed for selection and improvement programme. Despite its ability to withstand adverse climatic conditions, there are no varieties or cultivars available for Rajasthan conditions. Locally grown trees in farmer's field show variation from tree to tree for fruit size, shape and pulp content. Therefore, an attempt has been made to document variability existing in khirni germplasm collection for fruit and seed characteristics.

With this background, a survey for khirni population was made during the fruit ripening stage in the month of May 2017 in the Pali and Sumerpur blocks of Pali district, Rajasthan. The average annual rainfall of the study area ranged from about 420mm in Pali to 550 mm in Sumerpur. The collections were made on random sampling method and the latitude, longitude and elevations details were recorded with GPS during collection (Table 1). A total of ten-germplasm collections were made (one from Pali and remaining nine from Sumerpur). Large populations were found in Santarao areas of Sumerpur. The defect-, insect and disease-free trees were selected falling in the age group of 25-80 years. The tree starts bearing fruit from 10th year onwards. Discussions were made with farmers and local people, and information on harvesting and mode of marketing were also gathered.

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Table 1. Details of collection localities of *Manilkara hexandra*

Location	Latitude (N°)	Longitude (E°)	Elevation (m)
Pali - P	25.46407	73.20199	217
Sumerpur – S1	25.06332	72.98021	281
Sumerpur – S2	25.06332	72.98021	281
Sumerpur – S3	25.06332	72.98021	281
Santaro – SA1	25.04265	72.98234	289
Santaro – SA2	25.04212	72.98212	277
Utharan – U1	25.15063	73.05064	285
Utharan – U2	25.03053	72.96573	285
Korta - K	25.1764	72.97547	245
Chandana - C	25.15044	73.05029	277

Matured fruits were collected from different parts of the crown as they may differ genetically, as khirni is insect-pollinated. In some of the collections, fruits fallen on the ground were also collected. Nearly 300 fruits were augmented for each germplasm collection, 25 fruits were randomly chosen from the lot and data were recorded for fruit and seed parameters. Analysis was made using SPSS (17) software for mean, standard error, coefficient of variation and analysis of variance at 95% level (ANOVA). Variations in fruit size were also noticed at the time of collection. Pearson method of correlation was used to find the correlation among the fruit and seed traits. The locations were named as P for Pali, S1, S2, and S3 for Sumerpur, SA 1 and SA 2 for Santarao, U1and U2 for Utharan, K for Korta and C for Chandana. (Table 1).

The trees surveyed were in the height range between 8 and 12 m and diameter at breast height (DBH) of 85 cm to 210 cm approximately. All the collections were characterized for fruit and seed characters. The fruit length varied from 1.45 to 2.24 cm (SA 1) with average of 1.80 cm. All the parameters i.e., fruit length, fruit width, fruit weight, pulp weight, seed length and seed width varied significantly (ANOVA p value <0.001) except for seed weight (p=0.087). Fruit width ranged from 0.79 (S2) to 1.33 cm (U1) with average of 1.06 cm. U1 collection recorded the highest fruit weight (2.39g), while the over all mean was 1.38 g. Lowest fruit weight was recorded for S2 (Table 2). The pulp weight ranged from 0.49 to 2.19g. Similar findings were reported by Malik *et al.* (2012) for *Manilkara hexandra* which were collected from Madhya Pradesh, Gujarat and parts of Rajasthan. The pulp weight from Sirohi (IC no. 546121 and 546123) germplasm collection recorded the lowest pulp weight (0.83g and 0.81g) (Malik *et al.,* 2012), whereas in the present study the highest pulp weight (g) is from U1 collection i.e., 2.19. The result indicates that, there exist chances for better germplasm in Rajasthan. The fruit also showed variation in size and shape in all the germplasm collections.

During the survey and exploration, it was also noticed that, some of the fruit contains two seeds per fruit. The seed length ranged from 0.80 (S-2) to 1.50 cm (SA-2) with average of 1.20 cm respectively. The seed width does not record much difference among the collections. The highest seed width was recorded from K collection i.e., 0.66 cm and the lowest from P collection 0.55cm with average of 0.62cm. Non-significant differences were observed for seed weight (p< 0.087) (Table 2). Seed colour also varied from light brown to dark brown in different germplasm. Almost, similar germplasm collection study revealed seed weight with average of 0.18g (Malik *et al.*, 2012). In the present study, the

Table 2. Variation in fruit and seed parameters of *Manilkara hexandra* in Pali district of Rajasthan

Location	Fruit			Pulp weight (g)	Seed		
	Length (cm)	Width (cm)	Weight (g)		Length (cm)	Width (cm)	Weight (g)
P	1.45±0.02	1.07±0.01	1.22±0.02	1.01±0.03	1.13±0.01	0.55±0.005	0.20±0.05
S 1	1.69±0.02	1.03±0.01	1.25±0.03	1.00±0.02	0.95±0.01	0.63±0.006	0.17±0.01
S 2	1.53±0.01	0.79±0.008	0.64±0.01	0.49±0.01	0.80±0.01	0.58±0.003	0.17±0.04
S 3	1.76±0.02	1.04±0.01	1.33±0.03	1.13±0.02	1.00±0.02	0.65±0.006	0.16±0.002
SA 1	2.24±0.04	1.06±0.02	1.58±0.08	1.26±0.06	1.47±0.01	0.63±0.008	0.18±0.004
SA 2	2.11±0.03	1.10±0.02	1.61±0.08	1.30±0.06	1.50±0.01	0.61±0.008	0.18±0.003
U 1	2.02±0.04	1.33±0.02	2.39±0.08	2.19±0.07	1.33±0.01	0.64±0.006	0.17±0.003
U 2	1.90±0.025	1.07±0.01	1.44±0.06	1.06±0.03	1.42±0.01	0.64±0.005	0.18±0.003
K	1.73±0.02	1.14±0.01	1.43±0.04	1.15±0.03	1.18±0.02	0.66±0.005	0.15±0.003
C	1.53±0.02	0.98±0.02	0.92±0.04	0.75±0.01	1.20±0.01	0.63±0.006	0.15
AVG	1.80±0.01	1.06±0.01	1.38±0.03	1.16±0.03	1.20±0.01	0.62±0.002	0.17±0.007
SD	0.27	0.13	0.46	0.50	0.23	0.04	0.02
CV (%)	14.79	12.60	33.49	43.54	19.48	5.73	9.30
p value of ANOVA	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.087

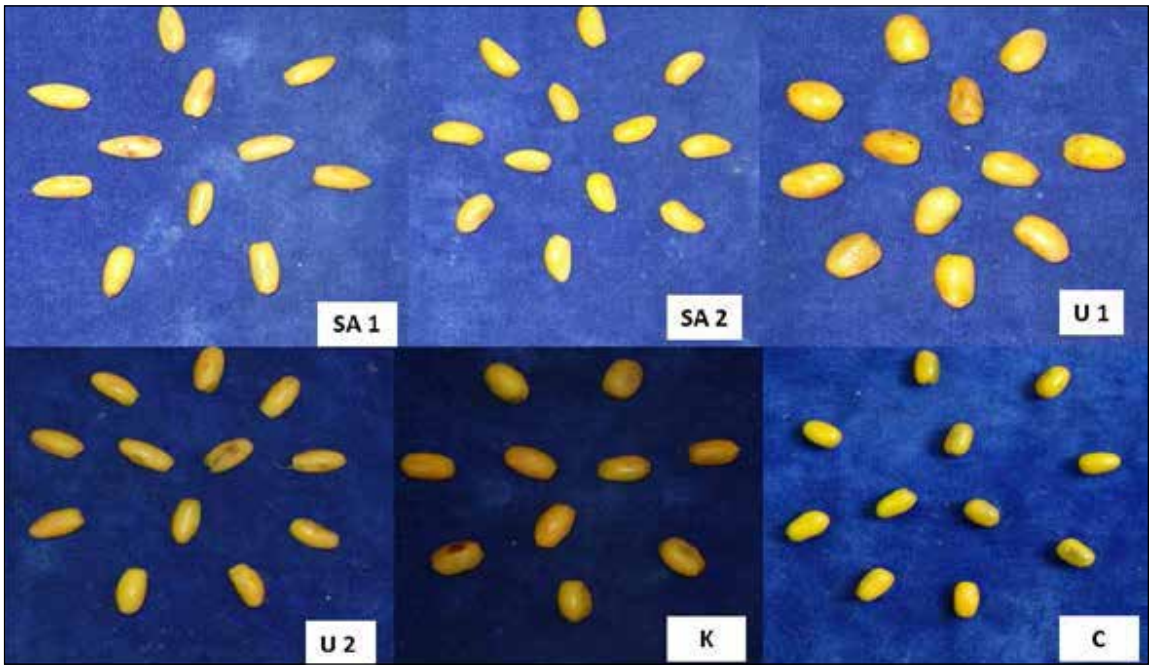

Fig. 1. Variation in fruit of *Manilkara hexandra* germplasm

average seed weight recorded was also 0.17g. Singh *et al*. (2006) also recorded variation in fruit and seed parameters in germplasm collection from candidate plus trees collected from Gujarat.

Among the morphological characters studied, the highest CV were recorded for pulp weight (43.54%), fruit weight (33.49%) followed by seed length (19.48%) (Table 2). The variability present in phenotypic characters may be due to heterozygous and cross pollinated nature of the tree. Thus, the variability existing in germplasm collection may guide in selection of superior performing genotypes having desirable traits. Gill and Navprem (2015) also observed highest co-efficient of variation in mango for fruit yield (19.63%) followed by fruit weight (17.28%). Besides this, variation in fruit and seed parameters has also been reported by Keerthika *et al.* (2017) in *Balanites roxburghii* and Meena *et al*. (2015) in *Tecomella undulata.*

Correlation is an important tool which measures degree and magnitude of association between various traits. In this study, pulp weight was significantly correlated with weight, length and width of fruit and length and width of seed. However, seed weight was not significantly correlated. Correlation coefficient of pulp weight was the highest with fruit weight (r = 0.916) and width (r =0.839). It indicated that higher the weight and width of fruit, higher the pulp content while seed weight have negligible effect on pulp content. Similar correlation study among fruit and seed parameters has been reported by many workers (Mkwezalamba *et al.,* 2015 and Dev *et al*., 2017). Mkwezalamba *et al.* (2015) reported strong relationship (r= 0.987) between fruit weight and pulp weight among provenances of *Sclerocarya birrea*. Variation in reproductive traits and economic traits among genotypes is useful for further selection and development of species for better utilization. This study indicated that selecting trees with higher fruit weight is a reliable indicator for pulp weight. This approach may have advantage of selecting improved germplasm.

It was also noticed that there were no new plantation and only sparse regeneration observed in this tree. It might be due to non-orthodox behaviour of seed and poor germination (Malik *et al.* 2012). Despite its demand as minor fruit tree species, a very few efforts have been taken for selection of suitable germplasm and popularization of this tree in the region. Almost all the trees in the surveyed region were found to be old, so it is need of the hour to give emphasis on establishing new plantations for conservation and utilization.

In this study, *Manilkara hexandra* germplasm showed significant variation in all the quantitative traits of fruits and seeds. Among ten collections, the U1 collection showed better for fruit width, fruit weight and pulp weight. Significant correlation was observed

in fruit and pulp weight, therefore, fruit weight may be a reliable indicator of pulp weight. Thus, these traits may be given importance in selection, improvement and breeding programme. Moreover, the genetic variability of this fruit species is under threat due to the large-scale urbanization, developmental activities and need for agriculture land. Hence, it is pertinent to collect, characterize and document the germplasm for future conservation and utilization programme.

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Indian J. Plant Genet. Resour. 33(1): 102–105 (2020)
DOI 10.5958/0976-1926.2020.00016.9

SHORT COMMUNICATION

Diversity in Seed Characters for Morphological Characterization of Date Palm (*Phoenix dactylifera* L.) Varieties

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(Received: 14 September, 2018; Revised: 28 September, 2019; Accepted: 11 October, 2019)

Date palm (*Phoenix dactylifera* L.; Family: Arecaceae) is a fruit tree suitable for dry and hot climatic conditions. The ripe fruits (*doka* or *khalal*) are used for fresh consumption and value addition. In India, date palm fruits are harvested during mid June to July at *doka* or *khalal* stage (hard ripe yellow, red or dark red colour) of maturity because of early rains. In many date growing countries, seed is an agricultural waste and used for several purposes. Besides raising saplings, its seed are used as feed additive for African catfish, oil extraction, cattle's feed and porus carbon preparation. Date fruit seeds comprise 6-12 per cent of total weight in *Tamer* stage fruit depending upon variety and quality grade. The plants are raised through suckers, seeds, and tissue culture in date palm and variations in seeds (stones) were observed. The diversity with respect to stone weight, size, shape, colour and presence of ridges and groove were observed in date palm seeds. The seeds were collected at *doka s*tage of maturity of fruits during 2016 from date palm germplasm repository for study. In general large, medium and small size seeds were grouped in date palm genotypes. Variation in groove like shallow, medium and deep was also noticed. In some cultivars, ridges on the seeds were also present. A significant difference in weight and size of seeds were observed in date palm genotypes. The study revealed that genetic diversity exit in seeds of date palm. A wide range of diversity was observed in seeds for morphological characterization of date palm genotypes.

Key Words: Date palm, Diversity, Genotypes, *Phoenix dactylifera*, Seed

Introduction

Date palm (*Phoenix dactylifera* L.; family-Arecaceae) is one of the most important fruit tree for semi arid and hot arid regions of the world. It is an ancient fruit and is believed to be indigenous to countries around Persian Gulf. It is commercially grown in many countries of the world (Zaid, 1999). Date palm groves in coastal belt of Kachchh from Anjar to Mandvi have developed naturally through seeds, which probably brought by Turk settlers, Traders, gardeners and Haj pilgrims. The seedlings are very old in Kachchh region and seedling populations are not found in other parts of country. The ripe fruits (*doka* or *khalal)* are used for fresh consumption and processing (Pareek and Sodagar, 1986). Every part of the date palm plant is useful since its history of cultivation and utilization (Chao and Krueger, 2007). Sawaya *et al. (*1984) reported that date palm seeds are nutritious in mineral constituents. Besides raising saplings, its seed are used as feed addditive for Juvenile African Catfish (Sotulu *et al.,* 2014) and as animal feed (Habibi *et al*., 2011) and seed characters for biochar preparation (Mahdi *et al.,* 2015). The agricultural waste like datepalm seeds is suitable for preparation of porus carbon (Reddy *et al.,* 2015). The significant difference in seed characters have been reported in date varieties and it may further serve as important constituents of functional foods (Habib and Ibrahim, 2009). Date palm seed is also used for several medicinal purposes. Date palm seeds contain 10-12% oil in different varieties and its oil could be used in cosmetics, pharmaceuticals and food products (Beabes *et al.,* 2004). Date fruit seeds comprise 6-12 per cent of total weight at full ripe (*Tamer)* stage fruit depending upon varieties and quality grade. It is also used for extraction of oil (Zaid, 1999). It has high market potential since the production of soft dates (*Pind Khajoor*) and dry dates (*Chhuhara*) in our country is very less (Singh and Dhandar, 2007). Presently, India imports about 3, 11 575 MT dates every year from Gulf and other countries (FAO database, 2013) to meet out the domestic requirement. At present, about 17,658 ha area is under date palm cultivation in the

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coastal region of Kachchh with estimated annual fruit production 16,5632 MT. Variability in date palm exists throughout Kachchh region because the date groves have originated from seeds. Date palm is a dioecious and monocotyledonous single stem plant. All the fruit from Kachchh palms are harvested during mid June to July at *doka* or khalal stage (hard ripe yellow, red or dark red colour) of maturity because of early rains. (Muralidharan *et al.*, 2008). Limited work is reported on morphological characterization of date palm seed in the literature. Keeping it in view, the present study was carried out on morphological characterization of date palm varieties/genotypes seeds to assess genetic diversity under hot arid environment.

Materials and Methods

The study was carried out at ICAR-CIAH, Bikaner during the year 2016 on morphological characters of seeds of date palm varieties/genotypes. The fruits of varieties /genotypes were collected from date palm field during July-August month and seeds of 30 genotypes were extracted from fruits at *doka* stage of maturity. For seeds of Saggai and Zamli variety, mature fruit samples were collected from Centre of Excellence on Date palm, Bhojka, Jaisalmer during August, 2016. The freshly harvested *doka* fruits of different varieties were used to extract seed for study. The seeds were cleaned with tap water and dried under ambient condition in lab. Morphological parameters of five seeds sample were taken in each replication. Size was recorded with help of digital verneer caliper. The weight of five seed was taken to calculate average weight of seed. The seed groove, apex colour and presence of ridges were noted on visual observations. The data were subjected for statistical analysis in Completely Randomized Design (CRD) to see the level of significance of characters at 5%.

Results and Discussion

The morphological characters of seeds were observed in terms of average weight and length and breadth of seed/stone. The apex of seed was also noted in terms of acute and obtuse/round shape. The colour of seeds was noted after extraction of seed from fruit. Groove in seed were also present and categorize in three group *viz.* shallow, medium and deep groove. Likewise ridges were also present in few varieties seeds. During record of observations, in few date palm seeds, a seed out growth like two seed were also noted. The apex in stone was almost round and angular in all germplasm. The colours of seeds were observed as dark grey and white during record of observation.

The data on physical characters of seed weight, size, surface texture and groove is given in Table 1.

Seed weight: Analysis of data in Table 1 reveals that weight of seed significantly differed among date palm germplasm. The maximum seed weight was observed in cv. Nagal Hillali (1.72 g), Medjool (1.54 g) followed by Sewi (1.29 g) and Saggai (1.24 g). However, minimum weight of seed was in cv. Barhee (0.53 g) followed by Khunezi (0.63 g). Variation in seed weight was observed from 0.53 to 1.72 g. Fruit and stone characters vary greatly depending on variety, environmental conditions and technical care given like pollination, etc. (Zaid, 1999). The variation in physical properties (weight, length, and density) were determined by Habib and Ibrahim (2009) in eighteen date varieties. Stone/seed weight and size is governed by genetic makeup of the cultivars besides growing sites.

Size of stone: The stone size (length and breadth) differed significantly among germplasm studied. The maximum length of seed was observed in Nagal Hilali (2.78 cm) followed by Saggaai (2.38 cm) and Hamara (2.37cm). Significantly higher seed length was observed in many germplasm like Kotho, Shamran, Dayari and Punjab red. However, breadth of seed differed significantly among the germplasm. The lower breadth of seed was observed in cvs. Halawy (0.73 mm) Barhee (0.74 mm.), Khairpur Pakistan (70 mm) and Khuneizi (0.63 mm.). The finding is similar to the earlier reports on stone: pulp ratio (Zaid,1999).

Seed surface, ridges and apex

In date seeds, the surface was found both smooth and rough type. In some varieties ridges were also present in stones. On visual observation, smooth and rough type seeds were characterized among the germplasm. In maximum seeds of date varieties, surface was smooth and ridges were absent. The seed apex was angular and round in most of germplasm except in few pointed apex.

Stone groove: The date palm seeds were also characterised on the basis of deep, shallow and moderate groove in stone. In maximum date palm varieties, shallow groove were present. In few varieties groove were broader. Variation in groove in stone may be due to genetic makeup of germplasm. The observation on variation in groove is similar to earlier findings (Chao and Krueger, 2007) while study on date fruits.

Table 1. Morphological characterization of seeds of date palm genotypes/varieties.

S.No.	Name of cultivars/ genotypes	Weight (g.)	Length (cm)	Breadth (mm)	Seed apex	Groove	Ridges	Surface of stone
1	Halawy	1.05	2.19	0.73	Angular	D	A	smooth
2	Khalas	0.82	2.15	0.76	Angular	S	A	smooth
3	Khadrawy	0.98	2.14	0.97	round	S	At	smooth
4	Shamran	1.07	2.34	1.07	round	S	P	rough
5	Zahidi	0.91	1.95	0.80	round	S	P	rough
6	Braim	0.97	1.62	1.01	round	D	P	rough
7	Chip-chap	1.03	2.26	1.03	Angular	S	P	smooth
8	Sewi	1.29	1.98	1.29	Angular	S	A	smooth
9	Khuneizi	0.63	1.82	0.63	round	S	A	smooth
10	Binte-a-isha	0.92	1.99	0.92	Angular	D	A	rough
11	Nagal Hilali	1.72	2.78	1.75	Angular	S	A	smooth
12	Medjool	1.54	2.23	1.54	Angular	S	A	smooth
13	Hamara	0.98	2.37	0.98	Angular	D	P	rough
14	Tayar	0.82	2.05	0.81	Angular	S	P	rough
15	Sayar	1.21	2.18	1.21	Angular	S	P	rough
16	Hayani	1.12	2.21	1.09	Angular	S	Pt	rough
17	Dayari	1.23	2.31	1.23	round	S	A	smooth
18	Suriya	1.18	2.00	1.18	round	S	A	smooth
19	Khoto	0.94	2.25	0.94	Angular	D	P	rough
20	Khairpur Pakisthan	0.70	1.62	0.70	round	S	A	smooth
21	Sabiah	0.79	1.96	0.79	Angular	M	P	rough
22	Saddmi	1.04	1.87	1.04	round	D	A	smooth
23	Gulchari	0.90	1.69	0.90	round	S	P	rough
24	Muscat	1.14	2.30	1.14	Angular	D	P	rough
25	Medini	1.19	2.13	1.19	round	S	A	rough
26	Javantri	1.04	1.79	1.04	round	S	A	smooth
27	Umshok	0.76	1.72	0.76	Angular	S	P	rough
28	Punjab red	1.14	2.17	1.14	Angular	S	P	rough
29	Saggai	1.24	2.38	1.21	Pointed	M	A	smooth
30	Bikaner Local	0.96	2.06	0.97	round	S	P	rough
31	Zamli	1.24	1.75	0.91	round	S	P	rough
32	Barhee	0.53	1.64	0.75	round	M	P	rough
SEm+		0.058	0.079	0.053	–	–	–	–
C.D. at 5%		0.164	0.225	0.150	–	–	–	–

1. Ridges: P =present, A=absent 2. Groove D= Deep S= Shallow M=Medium

Conclusion

The seed of date palm may be an approach for identifying the variety since a lot of variation is available among germplasm. Looking to the scarcity of planting material, it can be used for raising saplings for creation of variability and also as forest plantation. Date palm stone is not a waste material it can be utilized in several ways for animal feed, oil extraction, biochar preparation, etc. The study will help for proper utilization of date seeds to the growers/ researchers.

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Indian J. Plant Genet. Resour. 33(1): 106–108 (2020)
DOI 10.5958/0976-1926.2020.00017.0

PGR NOTE

Larnoo Purple: A High Yielding, Early Maturing, Cold Tolerant Maize Line with High Carotenoid and Protein Content

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(Received: 16 January, 2018; Revised: 29 September, 2019; Accepted: 05 October 2019)

The present study pertains to the development of new maize line Larnoo Purple possessing high yield, early maturity, disease resistance and cold tolerance. Larnoo Purple revealed an average yield performance of 5.6 t ha^{-1} in station trials that is almost similar to the commercial check variety Shalimar Maize Composite-3. The genotype revealed complete resistance to *Turcicum* leaf blight, common rust and stem borers. However for cutworms, the variety was found to be moderately resistant. Larnoo Purple due to its tolerance for drought and low temperature stresses, fits well under high altitude rainfed conditions of Jammu and Kashmir. The cob of Larnoo Purple is conical, semi-flint and purple in colour, possessing good grain characteristics. Biochemical profiling of Larnoo Purple revealed that the genotype contains elevated levels of carotenoids, protein, starch and oil over the commercial check variety Shalimar Maize Composite-3. Larnoo Purple has potential to improve the socio-economic conditions of small and marginal farmers in high altitude rainfed temperate agro-ecologies, besides improving their health and nutritional status.

Key Words: Early maturity, High carotenoid, High yield, Larnoo Purple, Protein content, Stress tolerance

Maize (*Zea mays* L.) is the third most important cereal crop in India grown over an area of about 9.1 million hectares with the production of around 22.75 million tons. In the state of Jammu and Kashmir, maize is the most important crop in terms of acreage and is being cultivated over an area of 0.31 million hectares with the annual production of 0.48 million tons (GoI, 2017). Kashmir valley (longitude 73.0-74.2°E and latitude 33-34°N) is agro-climatically a typical temperate region, where maize is being cultivated at an altitude of 1850-2500 m above mean sea level (amsl). Maize in Jammu and Kashmir is grown as *Kharif* season crop, mostly on marginal lands of hilly terrains and about 85% of the cropped area is rainfed. The average productivity of this crop in the state is significantly low (1.2 t ha^{-1}) when compared to the national productivity of 2.5 tons ha^{-1} (GoI, 2017). Cultivation of low yielding local land races followed by frequent incidence of various biotic and abiotic stresses act as the main limiting factors for maize production in the valley. Growing of high yielding stress tolerant varieties can serve as the most coherent approach to ensure high maize productivity under these conditions.

In addition to high yield, the demand for quality maize is continuously increasing primarily due to diversification in food habits, change in consumer preferences and improvement in standard of living. This entails the incorporation of desirable quality traits in maize, as the most important objective, next only to yield enhancement. Nowadays, pigmented maize has received increased attention from a nutraceutical quality perspective as it contains several bioactive phytochemicals such as carotenoids, tocopherols, phytic acid and phenolic compounds (Ibrahim and Juvik, 2009; Hu and Xu, 2011). Although these compounds are considered to be non-nutritive, the interest in their antioxidant and bioactive properties has been increased due to their potential health benefits (Okarter and Liu, 2010).

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Larnoo Purple is an early maturing, disease resistant, cold tolerant selection of maize possessing high carotenoid, protein and oil content. It has been developed by mass selection from early maturing, purple maize genotypes collected from higher altitudes (2000 to 2500 m amsl) of Kashmir valley. Initially, 200 plants were selected and equal quantity of seeds from these plants was composited and allowed to random mate in isolation. This was followed by three cycles of recombination and selection (half-sib) for high yield, early maturity, quality protein, disease resistance and cold tolerance in the target environment. The selected genotype (Larnoo Purple) was evaluated for yield and other agro-morphological attributes during the *Kharif* seasons of 2015-17 under station trials at Mountain Crop Research Station Larnoo (SKUAST-K) situated at an altitude of 2290 m amsl. The genotype was evaluated under various agronomic management practices *viz*., different fertilizer doses and spacing levels to devise the most effective combination for optimum yield returns. The genotype was also screened for resistance to prevailing diseases and pests following the Standard Evaluation System of CIMMYT (Mugo *et al*., 2001; Shekhar and Kumar, 2012). The quality analysis for protein, tryptophan, carotenoids, sugar, starch and oil was carried out at biochemistry laboratory of ICAR- Indian Institute of Maize Research (IIMR, Ludhiana). The maize line has been submitted to the National Genebank at ICAR-National Bureau of Plant genetic Resources under the accession number IC624629.

Larnoo Purple revealed an average yield performance of 5.6 t ha^{-1} in station trials that is almost similar to the commercial check variety Shalimar Maize Composite-3 (Table 1). The results of agronomic manipulations for the test genotype showed maximum yield potential at the spacing of 60 × 20 cm with 100% recommended fertilizer dose (60, 40 and 20 kg of N, P_2O_5 and K_2O ha^{-1}) along with the application of 15 t ha^{-1}of FYM. Similarly, maximum response to yield was observed when the crop was sown in between second to last week of April at the seed rate of 20 kg ha^{-1} for line sowing and 30 kg ha^{-1} for broadcasting. Moreover, biotic stresses like *Turcicum* leaf blight, common rust and insect pests (*viz*., cutworms and stem borers) are the major threats to maize cultivation under high altitude conditions of Kashmir valley. Larnoo Purple has shown complete resistance to *Turcicum* leaf blight (TLB), common rust and stem borers. However for cutworms, the variety was found to be moderately resistant (Table 2). Among the abiotic stresses, the major challenges for maize crop under temperate conditions of Kashmir valley are recurrent occurrence of droughts and cold spells. These abiotic stresses have devastating effects especially at sowing and flowering stages. Larnoo purple has tolerance to drought and low temperature stresses, and thus fits well under high altitude rainfed conditions of Jammu and Kashmir.

The cob of Larnoo Purple is conical, semi-flint and purple in colour, possessing good grain characteristics (Fig. 1). The plant height is about 235 cm with cob placement at around 105 cm from the ground level. The genotype matures within 130 to 135 days at an altitude range of 1800-2000 m amsl and 145-150 days at 2000-2250 m amsl. Biochemical profiling of Larnoo Purple, carried out at ICAR-IIMR Ludhiana, revealed that the genotype contains elevated levels of carotenoids, protein, sugar, starch and oil over the commercial check variety Shalimar Maize Composite-3 (Table 2). High-performance liquid chromatography (HPLC) was used for the estimation of carotenoids, sugar and starch. Protein content was determined using micro-kjeldal method and oil content was appraised using Nuclear magnetic resonance spectrometer (NMR).

To summarise, Larnoo Purple possesses high yield potential, early maturity, resistance to biotic and abiotic stresses along with elevated levels of carotenoid,

Table 1. Grain yield performance of Larnoo Purple in station trials over years.

Cultivar	Grain yield (t ha^{-1})		
	2015	2016	Average
Larnoo Purple	5.92	5.28	5.60*
Shalimar Maize Composite-3 (check)	6.17	5.55	5.86*
Larnoo Local	3.40	3.72	3.56

'*' indicates that the grain yield of Larnoo Purple is significantly higher over Larnoo Local and is at par with the check variety (SMC-3) at level p = 0.05.

Table 2. Disease and pest resistace reaction of Larnoo Purple over the check variety.

Cultivar	Disease Intensity		Pest infestation		
	TLB	common rust	cutworms	borers	Aphids
Larnoo Purple	10.3 (1)	9.4 (1)	13.4 (2)	7.0 (1)	5.8 (1)
Shalimar Maize Composite-3 (check)	15.6 (2)	18.0 (2)	27.3 (3)	9.7 (1)	7.2 (1)

Figures in parentheses indicate disease/pest scores. 1-5 scale was used for scoring the disease and pest reaction.
1= Resistant; 2= Moderately resistant; 3= Moderately susceptible; 4= Susceptible; 5= Highly susceptible

Table 3. Grain quality features (biochemical profile) of Larnoo Purple over the check variety.

Variety	Protein (%)	Tryptophan in protein (%)	Total carotenoids (µg/g)	Sugar (%)	Starch (%)	Oil (%)
Larnoo Purple	9.12	0.63	29.6	3.75	71.02	5.04
Shalimar Maize Composite-3 (check)	8.06	0.66	6.4	4.48	64.12	4.78
% improvement over the check	13*	-	362.5*	-	10.76*	6.06*

'*' indicates significant improvement in the trait at level, p = 0.05.

Fig. 1. Morphological features of Larnoo Purple

protein and oil content. The genotype can thus be used as a parent in breeding programmes for accumulation of favourable genes in elite cultivars (Harjes *et al.*, 2008). The development of high yielding maize genotypes possessing early maturity, cold tolerance and resistance to various biotic stresses in addition to high content of micronutrients can improve the socio-economic conditions of small and marginal farmers in high altitude rainfed temperate agro-ecologies, besides improving their health and nutritional status.

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Indian J. Plant Genet. Resour. 33(1): 109–114 (2020)
DOI 10.5958/0976-1926.2020.00018.2

PGR NOTE

Empowering Ethnic Groups through Farmers' Variety Protection by NBPGR: Success Story from Telangana State

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(Received: 27 November, 2018; Revised: 24 August, 2019; Accepted: 25 August, 2019)

The Protection of Plant Variety and Farmers' Rights (PPV&FR) Act. 2001 facilitates protection of rights of farmers and plant breeders in India. With the initiative of NBPGR Regional Station, Hyderabad, a total of three registrations in pigeon pea (*Erramachcha kandi*- 65/ 2015) and sorghum (*Pelala jonna*- 30/ 2016 and *Vayunowka jonna*- 32/ 2016) were accomplished from the state of Telangana for getting intellectual and ownership rights on the farmer's varieties. Distinct characters and speciality of these three farmer's varieties from Telangana are highlighted.

Key Words: DUS testing, Farmers' Varieties, PPVFRA, Telangana

Farmers' Variety Registration under PPV & FRA from the State of Telangana

In order to create intellectual protection, value enhancement and benefit sharing to the farming communities, diversity rich elite landraces/ farmers' varieties were identified in endemic native crops from Agri-biodiversity of Telangana (Pandravada *et al*., 2015 & 2017d) which include green gram (Pandravada *et al*., 2017e), dolichos bean, pigeon pea and sorghum (Pandravada *et al*., 2013; Sivaraj *et al*., 2012) for promoting for PPVFRA registration. In this regard, NBPGR Regional Station, Hyderabad identified potential farmers' varieties for evaluation for DUS characters for two seasons and filing of applications on behalf of the Biodiversity Management Committees (BMCs) from Adilabad with PPV & FR Authorty. Out of five farmer varietal registration proposals submitted, for three, one in pigeon pea (*Erramachcha kandi*) and two in sorghum (*Pelala jonna* and *Vayunowka jonna*), procedures completed and registration numbers were allotted/ certificates sent which are as follows:

Pigeon pea (*Erramachcha kandi*/ Reg. No. 65/ 2015)

This farmers' variety is under continuous cultivation by the local farming communities mainly in the mandals of Bejjur, Dahegaon, Kerameri and Sirpur (T) of Komaram Bheem and Bheemini of Mancherial districts. The ethnic community Gond is mainly associated with the cultivation, patronage and sustaining this variety *on-farm*. The pigeon pea farmer's variety (*Erramachcha kandi*) was evaluated for DUS characters during *kharif* season of 2011 and 2012 at NBPGR Regional Station, Rajendranagar, Hyderabad, Telangana. The major distinguishing traits including DUS characteristics of registered pigeon pea farmers' variety (*Erramachcha kandi*) are given in Table 1. This variety is promising with very tall (235.0 cm) plant habit, medium maturity, heavy bearing (269 pods/ plant), long green pods (9.4 cm/ 5-7 seeds/ pod) with brown streaks, seed large, cream with reddish-brown mottles/ speckles having high grain weight (18.0 g), protein (19.5%), dietary fibre (8.1%) and anti-oxidants (2.0%) (Fig. 1).

The application for this farmer variety was filed through BMC Jhari, Kerameri Mandal, Komaram Bheem District, Telangana (Fig. 1) on 1st April, 2013 which has become the 'Right Holder' of this farmers' variety from 5th of February, 2015 the date of grant. As per the legal provisions (PPVFRA, 2001 under section 47), the period of registration is initially for a period of six years and renewable up to 4th February, 2030 with an exclusive right to produce, sell, market, distribute, import or export the registered variety. The pigeon pea farmers' variety (*Erramachcha kandi*) which completed registration process and awarded a certificate (65/ 2015) became the first farmers' variety for Telangana state and third in the country for pigeon pea that have been registered (Pandravada *et al*., 2017a). The general recommended

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Fig. 1. Pigeon pea farmers' variety *Erramachcha kandi* (65/ 2015) registered with PPVFRA

Fig. 2. Sorghum farmers' variety *Pelala jonna* (30/ 2016) registered with PPVFRA

Fig. 3. Sorghum farmers' variety *Vayunowka jonna* (32/ 2016) registered with PPVFRA

package of practices for pigeon pea could be followed for cultivation of this particular farmers' variety as well.

Indigenous Traditional Knowledge

Seed size is large with high grain weight, protein, dietary fiber and anti-oxidants. The split *dal* cooks very fast with good taste and long keeping quality. It is consumed as *dal*/ *pappu* as such, mixed with bottle gourd/ ridged gourd/ *gutti beera* or *sambhar* is prepared.

Sorghum (*Pelala jonna/* Reg. No. 30/ 2016)

This farmers' variety is under continuous cultivation by the local farming communities mainly in the mandals of Boath, Indravelli, Narnoor, Talamadugu and Utnoor of Adilabad, Jainur, Kerameri, Sirpur (U) and Tiryani of Komaram Bheem and Khanapur, Sarangapur and Tanoor of Nirmal districts. The ethnic communities Gond and Kolam are mainly associated with the cultivation, patronage and sustaining this variety *on-farm*. The sorghum farmer's variety (*Pelala jonna*) was evaluated for DUS characters during *rabi* season of 2011-12 and 2012-13 at NBPGR Regional Station, Rajendranagar, Hyderabad, Telangana. The major distinguishing traits including DUS characteristics of registered sorghum farmers' variety (*Pelala jonna*) are given in Table 2. This variety is characterized by good initial establishment, tall plant habit (182.5 cm), early flowering, medium maturity (112.5 days), very loose panicles and small and chalky-white seed amenable for popping (Fig. 2). A dual purpose type useful as food and fodder and dependable in subsistence farming.

The application for this farmer variety was filed through BMC Gourapur, Indravelly Mandal, Adilabad District, Telangana on 28th March, 2014 which has become the 'Right Holder' of this Farmers' Variety from 15th of January, 2016 the date of grant. As per the legal provisions (PPVFRA, 2001 under section 47), the period of registration is initially for a period of six

years and renewable up to 14th January, 2031 with an exclusive right to produce, sell, market, distribute, import or export the registered variety. The sorghum farmers' variety (*Pelala jonna*) which completed registration process and awarded a certificate (30/ 2016) became the second farmers' variety for Telangana state and second in the country for sorghum that have been registered (Pandravada *et al*., 2017b). The general recommended package of practices for sorghum could be followed for cultivation of this particular farmers' variety as well.

Indigenous Traditional Knowledge

Seed unique as amenable for popping and preparation of popped flakes (*Jonna pelalu*) which are mixed with jaggery to prepare round ball like sweets (*Pelala vundalu*). Popped flakes (*Jonna pelalu*) and sweets made of them (*Pelala vundalu*) are offered to Gods during poojas/ festivals especially on *Vugadi* day and during *Vata Savithri Vratam* compulsorily to Goddess Devi/ Banyan tree as naivaidyam. During *Nagula Panchami* festival, used invariably along with milk for offering to Snake God and on *Polala Amavasya* day while doing pooja in the fields, compulsorily offered as naivaidyam to Goddess Parvati Devi. Popped flakes (*Jonna pelalu*) also used in pooja during *Nagula chavithi* (Fourth day after *Deepavali*) to worship the Snake God and sprinkle on the Snake mounds and to offer as naivaidyam. Popped sweets (*Pelala vundalu*) are consumed while on fasting during poojas/ festivals. Seed flour added to butter milk and kept for fermentation and consumed after two - three days in the mornings for cooling/ invigorating before going for field work. Seed flour mixed with curd, onion and chillies and made in to small thin round disks and dried in the sun for consumption directly or after frying in oil as a snack. Also used to prepare dosa, vada and paapad etc.

Sorghum (*Vayunowka jonna/* Reg. No. 32/ 2016)

This farmers' variety is under continuous cultivation by the local farming communities mainly in the mandals of Bela and Narnoor of Adilabad, Jainur, Sirpur (U) and Tiryani of Komaram Bheem, Kasipet of Mancheriyal and Sarangapur of Nirmal districts. The ethnic communities Gond, Kolam and Raj Gond are mainly associated with the cultivation, patronage and sustaining this variety *on-farm*. The sorghum farmer's variety (*Vayunowka jonna*) was evaluated for DUS characters during *rabi* season of 2011-12 and 2012-13 at NBPGR Regional Station, Rajendranagar, Hyderabad, Telangana. The major distinguishing traits including DUS characteristics of registered sorghum farmers' variety (*Vayunowka jonna*) are given in Table 3. This variety is characterized by good early plant vigour, tall plant habit (156.2 cm), medium maturity (108 days), semi-compact panicles, medium non-lustrous yellow seed, high antioxidants (3.8%) and protein (13.7%) and low carbohydrates (58.4%) (Fig. 3). A dual purpose and subsistence landrace useful as food and fodder.

Table 1. Major distinguishing traits including DUS characters of registered pigeon pea farmers' variety (*Erramachcha kandi*)

Trait	Distinctness	Trait	Distinctness
Plant growth habit	Determinate	Pod surface stickiness	Present
Branching pattern	Semi-spreading	Pods/ plant (no)	More/ Up to 269
Plant height (cm)	Tall - Very tall/ 150.0 - 235.0	Seeds/ pod (no)	5- 7
Stem colour	Green	Pod borer incidence	Present
Leaflet shape	Oblong	Pod size (Length/ Width (cm))	Long/ 9.4/ 1.1
Leaf pubescence	Pubescent	Seed colour (immature stage)	Light green with brown mottles/ speckles
Flower colour of base of petal (standard)	Light yellow	Seed colour (mature stage)	Cream with reddish-brown mottles/ speckles
Wing petal colour	Greenish-yellow	Seed colour pattern	Mottled and speckled
Keel petal colour	Greenish-yellow	Seed shape	Elongate
Pattern of streaks on petal (standard)	Dense	Seed size	Large
Flowering pattern/ Days to flowering	Determinate/ 107	100 seed weight (g)	18.0
Pod colour (Immature stage)	Green with brown streaks	Protein (%)	19.5
Pod colour (Mature stage)	Creamish-brown	Dietary fiber (%)	8.1
Pod form	Cylindrical	Anti-oxidants (%)	2.0
Pod constriction	Prominent	Cooking quality	Dal cooks very fast
Pod pubescence	Pubescent	Taste	Very good with longer keeping quality
Pod waxiness	Present		

Table 2. Major distinguishing traits including DUS characters of registered sorghum farmers' variety (*Pelala jonna*)

Trait	Distinctness	Trait	Distinctness
Early plant vigour	Good	Panicle shape	Very lax/ Pyramidal
Stem colour	Green	Glume colour	Straw-brown
Stem diameter (cm)	Small/ 1.3	Glume covering	One fourth grain covered
Internode length (cm)	25.7	Glume length	Very short (25% grain covered)
Leaf midrib colour	White	Plant height (cm)	Medium/ 182.5
Flag leaf yellow colouration of midrib	Absent	Grain colour	Greyed-white
Leaf colour	Dark green	Grain luster	Non-lustrous
Leaf orientation	Drooping	Grain size	Very small
Leaf length(cm)	Medium/ 46.1	Grain shape	Narrow-elliptic
Leaf width (cm)	Medium/ 4.9	Grain threshability	Freely threshable
Total leaves (no)	7.4	Days to 50% flowering/ Time to panicle emergence	Medium/ 75.0
Panicle compactness/ density	Very loose drooping	Days to maturity	112.5
Panicle length (cm)	Medium/ 27.2	100 Seed weight (g)	3.0
Panicle width (cm)	7.1	Yield/ plant (g)	25.6
Neck of panicle (cm)	Long (15.1-20.0)	Brix %	14.6

The application for this farmer variety was filed through BMC Goyagoan, Kerameri Mandal, Komaram Bheem District, Telangana on 28th March, 2014 which has become the 'Right Holder' of this farmers' variety from 15th of January, 2016 the date of grant. As per the legal provisions (PPVFRA, 2001 under section 47), the period of registration is initially for a period of six years and renewable up to 14th January, 2031 with an exclusive right to produce, sell, market, distribute, import or export the registered variety. The sorghum farmer's variety (*Vayunowka jonna*) which completed registration process and awarded a certificate (32/2016) became the third farmers' variety for Telangana state and third in the country for sorghum that have been registered (Pandravada *et al*., 2017c). The general recommended package of practices for sorghum could be followed for cultivation of this particular farmers' variety as well.

Indigenous Traditional Knowledge

Seed flour of this farmers' variety is used to prepare offerings (*Kudumulu*) during festivals/poojas and hence it is well known and hence under the continuous patronage of the farming community and cultivated at least in the backyards. This variety has high antioxidants (3.8%), protein (13.7%) and low carbohydrates (58.4%) and hence most suitable for diabetics for consumption.

NBPGR Regional Station, Hyderabad strived hard for registration of these farmers' varieties creating

Table 3. Major distinguishing traits including DUS characters of registered sorghum farmers' variety (*Vayunowka jonna*)

Trait	Distinctness	Trait	Distinctness
Early plant vigour	Very good	Glume covering	Three fourths grain covered
Stem colour	Green	Glume length	Medium/ 75% grain covered
Stem diameter (cm)	Small/ 1.2	Plant height (cm)	Medium/ 156.2
Internode length (cm)	20.4	Grain colour	Grayed-yellow
Leaf midrib colour	White	Grain luster	Non-lustrous
Flag leaf yellow colouration of midrib	Absent	Grain size	Medium
Leaf colour	Green	Grain shape	Circular
Leaf orientation	Drooping	Grain threshability	Freely threshable
Leaf length(cm)	59.9	Days to 50% flowering/ Time to panicle emergence	Medium/ 72.0
Leaf width (cm)	5.9	Days to maturity	108.0
Total leaves (no)	9.6	100 Seed weight (g)	Low/ 3.1
Panicle compactness/ density	Semi-compact	Yield/ plant (g)	89.5
Panicle length (cm)	Short/ 18.8	Starch (%)	58.4
Panicle width (cm)	7.1	Protein (%)	13.7
Neck of panicle (cm)	Medium (10.1-15.0)	Sugar (%)	7.6
Panicle shape	Elliptical	Brix (%)	13.5
Glume colour	Grey-red	Antioxidants (%)	3.8

awareness among the ethnic groups. All the concerned government organizations need to come together to educate/help/protect the farming community regarding their ownership rights on the variety, modalities for marketing and access and benefit sharing mechanism etc. Efforts are also being made to form cooperatives by the respective BMCs for production, marketing and creation of a value chain of these farmers' varieties which are having huge demand.

Acknowledgements

The authors thankfully acknowledge the association and cooperation of Telangana State Biodiversity Board, State Agricultural University and the tribal farmers belonging to *Gond, Kolam* and *Raj Gond* groups for liberally sparing their farmers' varieties and indigenous traditional knowledge which facilitated registration with PPVFRA for intellectual property rights and access and benefit sharing.

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Indian J. Plant Genet. Resour. 33(1): 115–118 (2020)
DOI 10.5958/0976-1926.2020.00019.4

PGR NOTE

Tubocapsicum anomalum (Franch. & Sav.) Makino: A New Record to the Flora of Arunachal Pradesh, India

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Tubocapsicum anomalum (Franch. & Sav.) Makino (Solanaceae) is reported as a new record for the flora of Arunachal Pradesh, India. Plants of this species were found wild in East Kameng and Upper Siang districts of Arunachal Pradesh, India. Its prolific fruit-bearing nature, high seed number per fruit and fruit flavour like chilli deserve further study as a potential genetic resource in India. A detailed description of the species along with distribution has been provided to facilitate identification and collection.

Key Words: New distribution record, North-eastern India, Plant genetic resources, *Tubocapsicum anomalum*

Introduction

Tubocapsicum anomalum (Franch. & Savat.) Makino (Solanaceae), commonly called as 'wild Japanese pepper', is native to tropical and temperate Asia (Makino, 1908) and widely distributed in southern China, Japan, Korea, Taiwan and the Philippines (Olmstead *et al.,* 1999). The genus *Tubocapsicum* Makino was formerly included in the genus *Capsicum* L. but it is taxonomically distinct and appears more closely related to the genera – *Aureliana* Lafit. ex Catesby and *Withania* Pauquy (Bosland and Votava, 2000). Phytochemical investigations have also proven its medicinal value due to presence of withanolides and withanolide glycosides in fruits (Kenji *et al.,* 1988 and Hsieh *et al.,* 2007).

North-eastern India is considered as one of the hot-spots of biodiversity including wild and cultivated plants of family Solanaceae. In an exploration conducted for multi-crop germplasm collection in Upper Siang district of Arunachal Pradesh during December 2018, the first and sixth authors came across with a few wild plants apparently resembling to 'chilli plant' in some localities. The fourth author has also observed the occurrence of *T. anomalum* in East Kameng district of Arunachal Pradesh during June 2015 but could not collect herbarium specimen and seed material as the plants were in vegetative stage. However, plants laden with fruits were located in Chiyang Taja Forest (27º40'21.8" N, 93º09'39.4" E, 2003 m) of East Kameng district of Arunachal Pradesh during November 2018. This species was also spotted by the fifth author in the mountainous slopes near Railing (28°09.203' N 96°31.149'E, 809 m) in the Metengliang block of Anjaw district of this state during October 2016. Information on morphological description and distribution is provided with photographs to facilitate the identification.

For confirming the identity, the plant characters were matched with digital images of herbarium available at online Herbarium, National Taiwan University, Taiwan (TAI; accessible through http://tai2.ntu.edu.tw) – herbarium nos. 098445, 196603, 250465 and 152453. After critical examination of the plant characters, herbarium specimens as well as through consultation with experts, the species was confirmed as *Tubocapsicum anomalum.* The Indian herbaria (Botanical Survey of India, Kolkata; National Herbarium of Cultivated Plants, ICAR-National Bureau of Plant Genetic Resources, New Delhi), floras of adjacent countries (Makino, 1963; Franchet and Savatier, 1878-1879; Wu and Raven, 1998) were also consulted for the confirmation of the identity. None of the Indian floras has reported the occurrence of *T. anomalum* in Arunachal Pradesh,

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hence the taxon is reported here as a new record for Arunachal Pradesh. Though, D'Arcy *et al.* (2001) has mentioned its occurrence from Assam, north-eastern region of India, herbarium specimen could not be traced out in any of the herbarium of the region by the authors.

Materials and Methods

An exploration was undertaken by the first and fifth authors in remote localities of Upper Siang district of Arunachal Pradesh for multi-crop germplasm collection as per National Exploration Plan 2018-19. During exploration, plants with matured fruits were seen to occur on the roadsides along the forest margin around Janbo village in Upper Siang district of Arunachal Pradesh, India. The matured fruits were harvested for conservation and herbarium specimen of fruiting twig was prepared as per standard procedure (Jain and Rao, 1977). The passport data along with coordinates of collecting site and taxonomic observations of collected specimens were recorded. Seed material was conserved in the National Genebank (IC0630421) while herbarium specimens were deposited in the National Herbarium of Cultivated Plants (NHCP) at ICAR-NBPGR, New Delhi and BSI, Itanagar Centre (Fig.1f).

***Details of herbarium specimens*:** India, Arunachal Pradesh, Upper Siang district, Jengging Circle, road side along forest margins near Janbo village, 22.12.2018, coll. RS Rathi and NS Panwar (NHCP23695) (Fig.1e); East Kameng district, Chiyang Taja Forest, 15.11.2018, coll. UK Tiwari (ARUN47143).

Results and Discussion

Tubocapsicum anomalum (Franch. & Savat.) Makino. Bot. Mag. Tokyo 22: 19. 1908; Basionym *Capsicum anomalum* Franch. & Savat., Enum. Pl. Jap. 2: 452. 1878 (1879). Lectotype: Japan, Leg. *Savatier* (P00279723). Syn. *Solanum anodontum* H.Lev. & Vaniot Monde Pl. sér. 2, 10: 37. 1908. Holotype: Korea, *U.J. Faurie* 776 (E00109636) [family Solanaceae].

A perennial herb, glabrous, height up to 2 m; stem stout, erect, sub-angular to-terete, sparingly pubescent, dichotomously branched with straight internodes. Leaf petiolate, ovate-elliptic or ovate-lanceolate, 5-15 x 3-6 cm, papery, base obtuse, margin subentire, apex acuminate. Flowers small, axillary, 2-5 flowers per cluster, calyx cup-shaped, 2-2.5×3 mm, truncate on margin, green; receptacle widely enlarged. Corolla yellow, short, campanulate, 5-8×6-8 mm; lobes

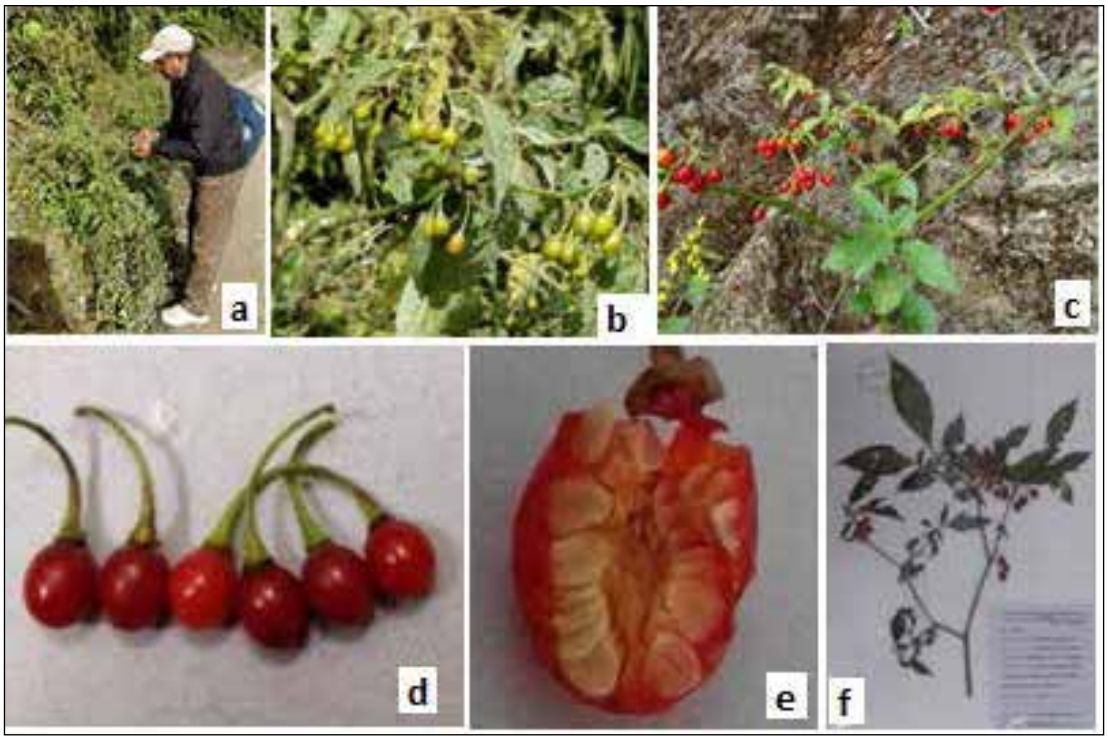

Fig. 1. (a) Collecting site and habitat of *Tubocapsicum anomalum*; (b) unripe berries; (c) mature berries; (d) mature berries with long pedicel; (e) longitudinal section of berry; (f) herbarium specimen.

Fig. 2. Distribution range of *T. anomalum* shown in green colour (historical distribution) and collection sites in Arunachal Pradesh, India (shown in black dots).

reflexed, ovate-deltoid. Stamens 5, somewhat exserted, erect, glabrous, adnate to the upper portion of corolla-tube base. Ovary depressed-globose, glabrous, 2-locular, style erect, terete-filiform, nearly equalling the stamens in height. Fruiting calyx not enlarged. Fruit a berry, juicy, bright red, shiny on ripening, 8-12 mm, persists for more than a month, wrinkles and shrivels at later stage. Seeds pale-yellow, 0.5-1.5 mm across, sub-orbiculate, laterally compressed and have a cavernulous reticulate surface.

Flowering during the month of August-October; and fruiting during October-January (in Arunachal Pradesh); flowers remain open during day and night (which is an unusual character of Solanaceae family). According to Makino (1908) flowering and fruiting occur during August-October in Japan.

***Field Observations*:** The first and sixth authors have observed only four plants in the collection site within 2 km^2 range, which is an indicative of poor regeneration ability. However, individual plants were growing luxuriantly under shade in moist forests. The associated floral elements around the site were *Hedychium spicatum* Sm., *Hyptis suaveolens* (L.) Poit., *Bidens pilosa* L., and *Solanum violaceum* Ortega. The plants were found with scarlet red berries, with 120-135 seeds/berry. The taste of berry was slightly bitter with little pungency and an aroma like chilli, with capsaicin value being 0.483 µg/g. Walsh and Hoot (2001) also reported pungency in fruits.

The map (Fig. 2) shows occurrence of the species in areas experiencing moderate temperatures (4-21ºC in winter and 13-39ºC in summer) and mild-moist climate. Collected sites are located at 28.35° N latitude and 94.37º E longitude at an elevation of 929-1000 m in mountain slopes. It was observed that *T. anomalum* requires abundant moisture; same observation was also reported by Proctor and Lack (1996). Merrill (1923) recorded its occurrence in the Philippines in mossy forest at an elevation of 1800–2000 m along streams in shaded ravines at low and medium altitudes in mesophytic sites in forests or open places.

Conclusion

Tubocapsicum anomalum is reported here as a new distribution record to the state of Arunachal Pradesh, India. Considering its potential as a genetic resource, effort should be made for germplasm collection for *ex-situ* conservation, biochemical characterization and utilization in crop improvement programmes.

Acknowledgements

Authors express their sincere thanks to the Director, ICAR-NBPGR, New Delhi for guidance as well as

help rendered during the course of study. Authors also express appreciation to the curators of various herbaria (National Taiwan University, Taiwan; Central National Herbarium, BSI, Kolkata, India) for providing herbarium images of investigated specimens, which enabled to infer the distributional range of this species. Thanks are also due to Mr. Shashi Kant Sharma for preparing the distribution map.

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GUIDELINES TO AUTHORS

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Indian Journal of Plant Genetic Resources (IJPGR) is the official publication of the Indian Society of Plant Genetic Resources. Aim of the Journal is to disseminate knowledge on plant genetic resources (PGR) research and application. Being the only journal in the area of PGR, the journal aims to provide a forum for discussion and debate on current issues of PGR. 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. Review articles (with prior consent or invitation only) summarizing the existing state of knowledge in topics related to plant genetic resources 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.

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- Policy research on access and benefit sharing; IPRs
- Status reports on ecology, conservation, traditional knowledge and use of PGR

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Pusa Campus, New Delhi–110012, India
E-mail:*ispgr2015@gmail.com*
Publisher website: *www.nbpgr.ernet.in/ispgr*
Journal hosting and online submission of manuscript: *www.indianjournals.com*

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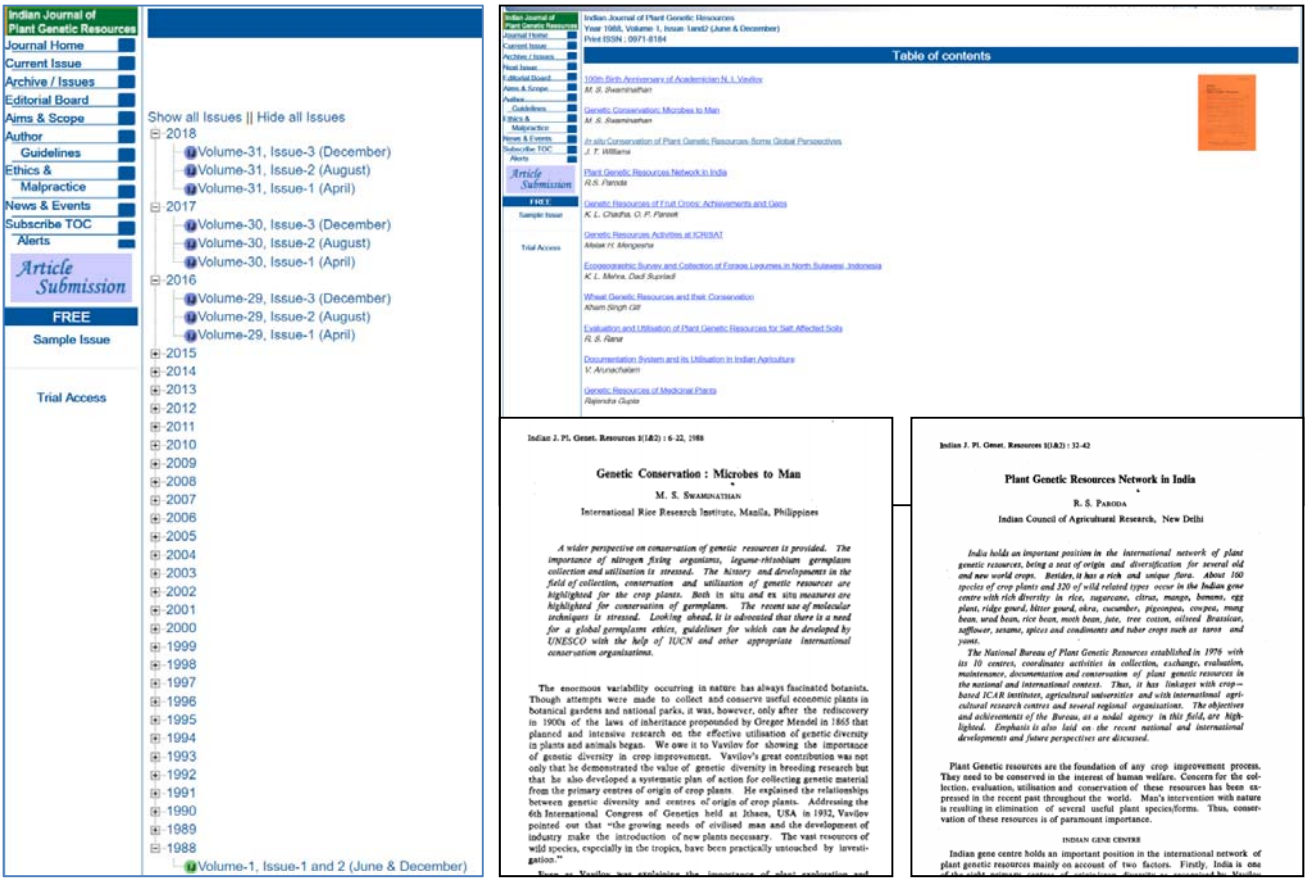

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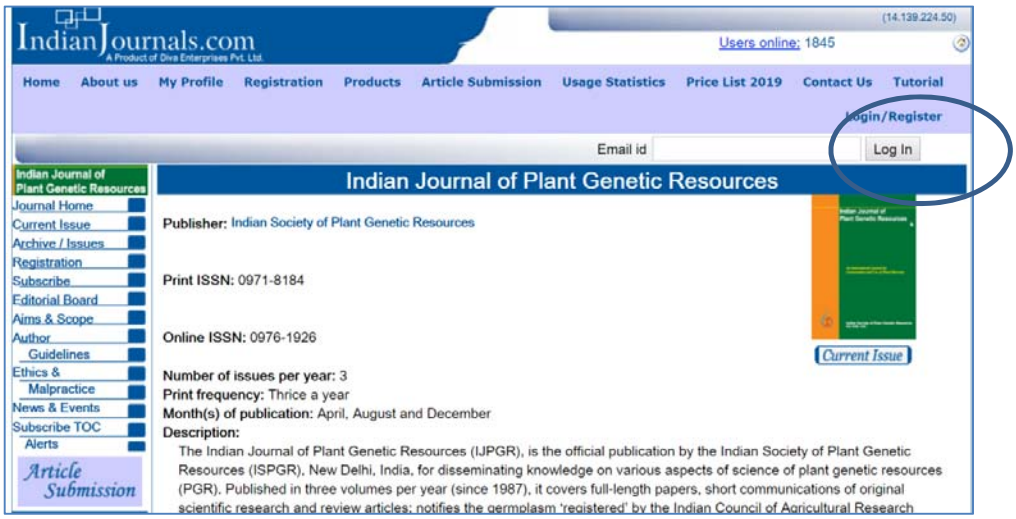

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Print ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

Vol. 33 No. 1 2020

CONTENTS

Commentary

COVID19: The Pandemic of Neglected Biodiversity 1
Prof SK Sharma

Special Article

Managing Agrobiodiversity of Indian Drylands for Climate-Change Adaptation 3
OP Yadav, JP Singh, RK Kakani, HR Mahla, MP Rajora, Akath Singh, PR Meghwal and Archana Verma

Review Article

Arid Horticultural Crops: Status and Opportunities under Changing Climatic Conditions 17
PL Saroj, Chet Ram and Kamlesh Kumar

Meeting Report

Expert Consultation Meeting on Global Crop Conservation Strategies 32
Sherry Rachel Jacob

Expert Consultation Workshop on "Global Conservation Strategy for Crops in the *Cucurbitaceae* Family" 34
Chithra Devi Pandey

Research Article

Development and Documentation of DUS Traits for *Melia dubia* Cav. Genetic Resources 36
TM Akhilraj and KT Parthiban

Survey of Major Ethnomedicinal Plants of District Kinnaur, Himachal Pradesh 43
Meenakshi Bhardwaj, LS Kandari and Tripti Negi

Genetic Diversity for Yield and Water Use Efficiency related Traits in Groundnut (*Arachis hypogaea* L.) 52
K Gangadhara, AL Rathnakumar, PP Thirumalaisamy, BC Ajay and HK Gor

Evaluation of Teosinte derived Maize Lines for Drought Tolerance 60
Amarjeet Kumar, NK Singh, AS Jeena, JP Jaiswal and SS Verma

Assessing Genetic Diversity of Newly Developed Winter Maize (*Zea mays* L.) Inbred Lines 68
SB Singh, RK Kasana, Santosh Kumar and Ramesh Kumar

Notes on Diversity Distribution and Systematics Study of *Abelmoschus tuberculatus* Pal & Singh: A Close Wild Relative of\ Okra from India 77
Anjula Pandey, S Nivedhitha, Vidya Sagar, Pavan K Malav, Shashikant Sharma and SP Ahlawat

Short Communication

Exploiting Genetic Diversity for Identification of Protein Dense Seed Parent in Pearl Millet 85
Mukesh K Berwal, Preeti Goyal, LK Chugh, Ramesh Kumar and Dev Vart

Studies on Reproductive Behavior of Fifteen Elite Wheat Genotypes in Relation to Hybrid Development 90
Krishnendu Guin, Sudhir Kumar Sethi and Rajesh Kumar Arya

Collection and Evaluation of Henna (*Lawsonia inermis* L.) Germplasm from South India 94
PC Shiji and EA Siril

Variability in Fruit and Seed Parameter of *Manilkara hexandra* (Roxb.) Dubard in Rajasthan 98
Keerthika A, AK Shukla, DK Gupta, MB Noor Mohamed, BL Jangid and Mahendra Singh

Diversity in Seed Characters for Morphological Characterization of Date Palm (*Phoenix dactylifera* L.) Varieties 102
RS Singh, R Bhargava and BD Sharma

PGR Note

Larnoo Purple: A High Yielding, Early Maturing, Cold Tolerant Maize Line with High Carotenoid and Protein Content 106
M Ashraf Ahangar, ZA Dar, Showkat A Waza, Asif B Shikari, FA Sheikh, S Sapna, NA Teeli and Ajaz A Lone

Empowering Ethnic Groups through Farmers' Variety Protection by NBPGR: Success Story from Telangana State 109
SR Pandravada, N Sivaraj, V Kamala, M Swapna and B Sarath Babu

Tubocapsicum anomalum (Franch. & Sav.) Makino: A New Record to the Flora of Arunachal Pradesh, India 115
RS Rathi, KC Bhatt, Anjula Pandey, UK Tiwari, K Pradheep, NS Panwar and SP Ahlawat

Referees for Volume 32 (1, 2 & 3) 2019 119

Guidelines to Authors 122

Published by the *General Secretary,* Indian Society of Plant Genetic Resources, NBPGR Campus, New Delhi-110012 and printed at *Angkor Publishers (P) Ltd.,* B-66, Sector 6, NOIDA. Mobile: 9910161199, E-mail: angkor@rediffmail.com.