Vol. 34 No. 1 2021

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

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(Registration No. S/18336)

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ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

Vol. 34 No.1 2021

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

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Indian J. Plant Genet. Resour. 34(1): 1–4 (2021)
DOI 10.5958/0976-1926.2021.00001.2

PGR NOTE

First Report of a Novel Multi-flowering Germplasm with Fasciated Stem in Lentil (*Lens culinaris* Medik.)

Kuldeep Tripathi[1]*, Gyan P Mishra[2], Gayacharan[1], Dileep Tripathi[1], Harsh Kumar Dikshit[2], Reena Mehra[3], Ashok Kumar[1], Ashutosh Sarker[3] and Kuldeep Singh[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi -110012, India*
[2]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi -110012, India*
[3]*International Center for Agricultural Research in the Dry Areas (ICARDA)-Food Legume Research Platform, Amalaha-466113, Madhya Pradesh, India*

(Received: 07 April, 2021; Revised: 09 April, 2021; Accepted: 16 April, 2021)

The mining of entire lentil accessions (2,324) of Indian genebank, ICAR-NBPGR, New Delhi led to the identification of a unique multi-flowering germplasm accession, IC241473, in cultivated lentil (*Lens culinaris* Medik.), forming up to 16 flowers per peduncle at multiple flowering node. Besides, this accession was also having a fasciation of the main stem. The multi-flowering expression was observed under field conditions at ICAR-NBPGR, New Delhi, India, consecutively during the winter seasons of year 2017-18, 2018-19, 2019-20 and was validated at NBPGR, New Delhi and ICARDA, Amlaha (Madhya Pradesh) during 2020–2021. Unlike earlier reported fasciated accessions in legumes, this fasciated accession showed stable multi-flowering expression over the years and locations and was also found fertile with fully developed reproductive organs. This unique and novel germplasm accession can be utilized for genetic studies to identify the locus regulating the multi-flowering trait in lentil and its association with environmental factors.

Key Words: Fasciation, Germplasm, Multi-flowering Lentil, Node

Lentil (*Lens culinaris* Medik.) is a cool-season self-pollinated pulse crop with genome size of 4.3 Gb (Bett *et al*., 2016). It is listed as one of the potential future smart food in South and Southeast Asia (Li and Siddique, 2018). It is native to the Near Eastern region and mainly cultivated in South Asia, North America and West Asia (Tripathi *et al*., 2019). During 2019, the world produced 5.73 million tonnes of lentil from 4.8 million ha of area, led by Canada (2.16 million tonnes) followed by India (1.23 million tonnes), collectively amounting to nearly 60% of the total production (FAOSTAT, 2021). Canada also ranks first (1.48 million ha) in acreage under the lentil, followed by India (1.36 million ha). Lentil is mainly grown in the central and eastern part of India, primarily as a rainfed crop. The average productivity of India is lower (901 kg ha^{-1}) than the world (1,194 kg ha^{-1}) (FAOSTAT, 2021).

Previous researchers studied the inflorescence morphology of diverse legumes such as garden pea, chickpea and lentils (Gaur and Gour, 2002; Sandhu and Singh, 2007; Devi *et al*., 2018; Mishra *et al*., 2020). Furthermore, the genetic basis of flowering patterns in any crop is of enormous practical significance for the crop researchers aiming to breed high-yielding cultivars (Sinjushin and Liberzon, 2015). The flowering characters in pulses, such as the number of flowering nodes per plant, the number of flowers per peduncle (FPP), and the number of flowers per plant, seems variable, as these traits directly influence productivity. Multi-flowering (MF) accessions can be identified with an expression of three or more flowers at one or multiple flowering nodes (Gaur and Gour, 2002; Benlloch *et al*., 2015; Sanwal *et al*., 2016; Devi *et al*., 2018). Multi-flowering clusters have been documented for a few flowering nodes in *Pisum sativum* (up to five FPP) (Devi *et al*., 2018), chickpea (upto nine FPP) (Gaur and Gour, 2002), lentil (upto seven FPP) (Mishra *et al*., 2020), having different mechanisms of MF expression (Gaur and Gour, 2002). Generally, lentils have two to four flowers in the axillary racemes on short and very thin peduncles (Muehlbauer *et al*., 1985; Sandhu and Singh, 2007). At the upper nodes, a more significant number of single and double flower clusters have been reported. Utilization of MF in lentil having fasciated stem for yield improvement

*Email: kuldeep.tripathi@icar.gov.in

is not yet explored. To date, we have not found any report highlighting the MF expression to the tune of 16 FPP in any cultivated lentil genotype. Stem fasciation is known to be the heritable trait, and spontaneous fasciation mutants have been reported in crops like soybean (Takagi, 1970), pigeon pea (Bhatnagar *et al*., 1967) and lupin (Blixt and Gottschalk, 1975).

However, the economic importance of this trait was recognized only in the recent past, when fasciation was induced in legumes using mutation (Tyagi and Gupta, 1991). A fasciated mutant of soybean and pea was used for producing a variety of valuable recombinants. The increase in yield of fasciated plants is often associated with an increased number of flowers and pods being formed in the upper nodes of plant.

In 2017-2018, this unique accession with MF expression was noticed for the first time during characterization of entire germplasm (2,324 accessions) conserved in NBPGR genebank, which was then re-evaluated in 2018-2019 and 2019-2020. During 2020–2021, this accession, along with checks IPL220, L4727, L4729 and RVL31, was again validated for the descriptor traits and MF associated traits such as number of Flowers Per Peduncle (FPP), Peduncle Length (PL), Pods Per Peduncle (PPP) and Stem Width (SW) at New Area Farm, NBPGR, New Delhi (28 º64′66″N, 77º15′08″ E) and ICARDA, FLRP, Amlaha India (23 º12′39″N, 76 º90′29″ E). The row-to-row and plant-to-plant spacing was 30×5 cm, and the row length was three-meter with each row containing nearly 60 plants. The mean environmental temperature was mostly in the range of 12–18 ºC during flowering time.

IC241473 is a vigorously growing genotype having dark green leaves with slight pubescence, days to 50% flowering ranged between 90-95 days, flowers are light purple, plant height ranged between 39.5-45.7 cm, pods per plant ranged between 296-397, the number of secondary branches were recorded from 14-24, peduncle length varied between 4.2-4.5 cm, and the stem width recorded was in the range of 5.08-5.28 mm. The inflorescence in lentil is racemose, with usually one to three flowers per peduncle. MF expression to the tune of 5-FPP has been reported in cultivated lentil (Mishra *et al.*, 2020) and some wild Lens accessions like *L. tomentosus*, *L. orientalis*, and *L. ervoides* (Sharma, 2009). However, in cultivated lentils, MF expression was also reported in some induced mutants. Still, the mutant lines exhibited sterility and did not show stability for subsequent generations' MF trait (Sharma and Kharkwal, 1983). Similarly, occasional expression of a maximum of 7-FPP (Saxena, 2009) and 6-PPP (Malhotra *et al*., 1974) was also reported in lentils. For the first time, this investigation reports the MF expression to the tune of 16 FPP (on 14th node) in cultivated lentil genotype IC241473 (Fig. 1).

The lentil germplasm IC241473 obtained from the Indian national genebank was uniform for various morphological traits, including MF. We have used single plant selection method (SPS) to maintain the purity of the germplasm. Previous researchers reported an array of genetic architectures underlying the multi flowering or multi-podding characters in *Pisum* (Hole and Hardwick, 1976; Devi *et al*., 2018). Lamprecht (1947) and Singer *et al*. (1999) reported two polymeric flower number genes (FN and FNA) and Neptune genes (nep-1 and nep-2), respectively.

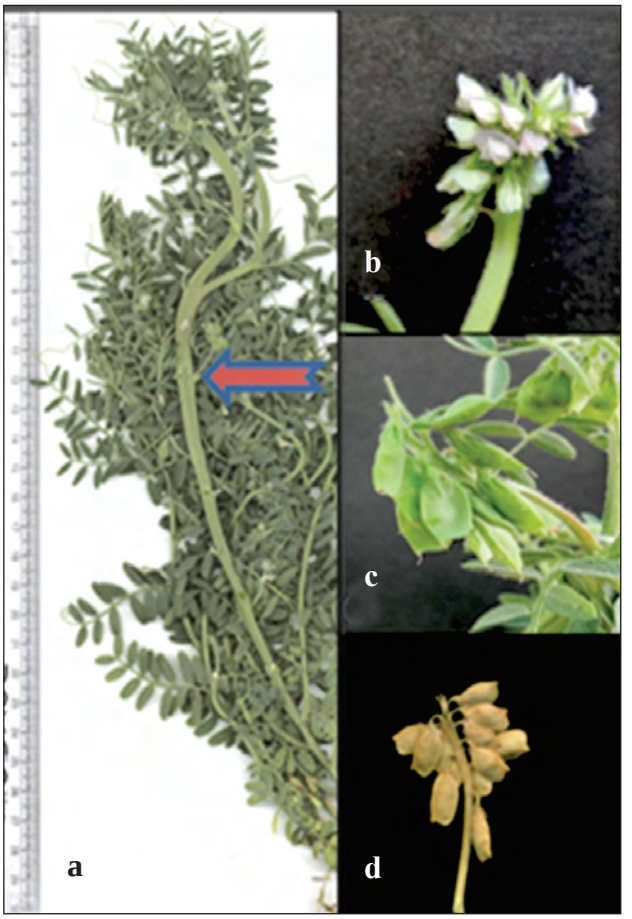

Fig. 1. Multi-flowering (MF) germplasm accession, IC241473 a. fasciated main stem; b. MF accession forming up to 16 FPP; c. MF accession at pod formation stage; d. MF accession at pod maturity stage.

On a similar note, in the lentil also, the 16-FPP expressed on the upper nodes (14th node), suggesting the probable occurrence of an Lf-like locus (late flowering) in this germplasm accession. This necessitates in-depth studies exploring the possibility of linkage between MF genes and late-flowering genes as reported in the case of other pulse crops such as pea and chickpea (Devi *et al*., 2018). Since lentil is global crop and often exchanged among countries for research purpose, many ecotypes developed due to selection, where trait like flowering is dependent upon the temperature and the photoperiod both (Erskine *et al*., 1994). In the present study, the lentil genotypes were found initially producing two FPP, followed by the increasing number of FPP upto 16, and again there is a gradual decrease in the number of FPP at the upper nodes. Similarly, Sharma (2009) also reported that MF expression was dependent upon plant age and the environment. MF was one of the most neglected characters to study because of its unstable expression, environmental influence, and poor conversion ratio of flowers to pods (Sharma, 2009). Among various environmental factors, the ambient temperature (11–20°C) during flowering was found to regulate FPP in peas (Hole and Hardwick, 1976; Murfet, 1985; Singer *et al*., 1999; Devi *et al*., 2018).

The abortion of flowers is frequent in MF accessions due to numerous factors, *viz.* genetic architecture, plant nutrition, and other environmental factors (Hole and Hardwick, 1976). In many pulse genera like *Cicer* and *Pisum*, the conversion of flower to pods is not always cent percent. Further, pea plants with 3-FPP usually develop 2-PPP (Srinivasan *et al*., 2006), whereas chickpea produces 9-FPP and not more than 4- or 5-PPP (Gaur and Gour, 2002; Srinivasan *et al*., 2006). After analyzing seed traits of MF accession, no change in seed size was observed. Moreover, in chickpea and garden pea (Devi *et al*., 2018), a positive correlation was observed between MF and yield traits in the study of Rubio *et al*. (2004). Globally, the lack of MF genetic resources and meagre studies of this complex trait in lentil limits the utilization of MF traits for yield improvement. Although various lentil genotypes producing 2- to 4-FPP have been reported worldwide (Sandhu and Singh, 2007), this present study is the first global report in cultivated lentil bearing up to 16-FPP as well as 13-PPP. Therefore, the identified MF germplasm accession has a tremendous potential as a promising donor for lentil breeding programs.

Acknowledgements

The authors acknowledge the Director, ICAR-NBPGR, New Delhi, for his valuable support in conducting the research.

Funding Information

The financial support received from ICAR-NBPGR, New Delhi and ICAR-ICARDA Research Program, ICARDA Agreement No. 200091, BUS No. 200284, is duly acknowledged.

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Indian J. Plant Genet. Resour. 34(1): 5–12 (2021)
DOI 10.5958/0976-1926.2021.00002.4

PGR NOTE

Our Trees, Our Heritage: Perennial Plant Species at the ICAR-National Bureau of Plant Genetic Resources, New Delhi

Anjula Pandey*, Rita Gupta, NS Panwar, RS Rathi and SP Ahlawat
ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India

(Received: 03 March, 2020; Revised: 18 August, 2020; Accepted: 20 August, 2020)

The trees and other perennial plant species in the campus of the ICAR-National Bureau of Plant Genetic Resources, New Delhi were documented in the form of a check-list. A total of 107 species (trees/shrubs and others) representing 85 genera and 46 families are listed here with information on botanical name, family, common name/local name, distribution, uses and planting location in the ICAR-NBPGR Campus.

Introduction

The trees provide environmental investment in an area additional to adding beauty, and reduce pollution and temperatures under abrupt weather conditions and thereby helping it to keep the area/locality green and cool. The activities of planting the trees provide multiple benefits including multi-disciplinary learning by involving the students, researchers, administrators, and others.

In various fora on the biodiversity conservation, it was felt that the thrust on planting trees would be laid through developing interest of masses towards our green heritage in the form of plants around us. Preliminary efforts were made to identify plants in both, the new and old campus of ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi and to document the plant wealth in the institute surroundings. It was decided to prepare a ready reckoner with plant name, family, common/local name and use and source if known on the one hand and to create awareness and fascination towards or green wealth among the new generation on the other hand. The record of the diversity of perennials in the ICAR-NBPGR campus would facilitate the inventory of plants in the form of check-list with the botanical name and detailed notes, besides sensitizing staff, students and visitors.

The area of the ICAR-NBPGR campus (old and new) was surveyed and presence of the perennials/trees was recorded as botanical name/common name and family name. Identity was revalidated using the appropriate identification aids. The check-list was prepared as per the data available on nativity, distribution and economic value, and present location in ICAR-NBPGR. This was mainly based on data drawn from various information sources.

To facilitate placement of the species, some landmarks have been provided. Some of the common ornamentals have been excluded from the list. Herbarium specimens of each plant /perennial have been added in the National Herbarium of Cultivated Plants (NHCP). Some of the significant photographs are also provided (Fig. 1, 2).

In botanical gardens of many institutions, the well labelled species are available for public use. The survey and physical verification of trees and perennial species in the both the campuses of the ICAR-NBPGR during 2019-2020 resulted in recording of the botanical and other data.

The ICAR-NBPGR has a plant biodiversity garden founded by Dr RS Paroda, the then Secretary DARE and DG, ICAR, on August 7, 2000. Since its foundation, a large number species have been added, or replaced by new ones due to changes in the layout, establishment, shifting, etc. The area was further expanded and the plant wealth is maintained from the time being. In the present holdings of tree/perennial species, some significant gymnosperms as *Pinus roxburghi*, *Cycas revoluta* and *Thuja occidentalis* have been included. *Musa* garden, plant nursery, net-houses having many species of experimental value have not been added as a part of this document many common ornamentals are also excluded.

During survey on trees in the ICAR-NBPGR, over more than a dozen of trees that were unique having

*Email: anjula.pandey@icar.gov.in

species brought from far distances and planted during earlier time were noted in the old campus. The details of the present holdings of the perennial species (check-list, and Table 1) are given below:

Table 1. Details of the perennial species

S. No.	Item	Details
1.	Life form	Trees (73), shrubs (26), perennial herbs (8)
2.	Botanical description	Species (107), Genera (85), Family (46)
3.	Location	Old campus (17), New campus (52), both campuses (38)

Check-list of Species

Acacia nilotica (L.) Delile (=*Vachellia nilotica* (L.) PJH Hurter & Mabb. subsp. *nilotica*)**:** (Mimosaceae) Gum Arabic tree, babul. Native-Africa, Asia-Temperate, Asia-Tropical. Use: source of gum arabic, medicinal. **Loc.** Biodiversity garden, New Campus.

Achras sapota L. (=*Manilkara zapota* (L.) P. Royen): (Sapotaceae) Sapota, chikku. Native-Northern America, Southern America. Use: Fruits edible. **Loc.** Biodiversity garden, new campus.

Aegle marmelos (L.) Correa (Rutaceae) Bengal quince, bael. Native - Asia-Tropical. India, Nepal. Use: Fruits edible, medicinal. **Loc.** Old and New Campus.

Ailanthus excelsa **Roxb.**: (Simaroubaceae) Tree of Heaven, mahanimb, urlu. Native - Asia-Tropical India, Andaman and Nicobar Islands, Sri Lanka, Indo-china. Use: Avenue tree, medicinal. **Loc.** old campus.

Aloe vera **(L.) Burm.f**.: (Liliaceae) Aloe, ghrita-kumari. Native - Africa, widely cultivated. Use: medicinal. **Loc.** old and new campus.

Alstonia scholaris **(L.) R. Br**.: (Apocynaceae) Devil's tree, scholar tree, saptaparni. Native - Asia-Temperate, Asia-Tropical region, Bangladesh, Bhutan, India, Nepal, Pakistan, Sri Lanka. Use: avenue tree, ornamental, medicinal. **Loc.** old campus.

Artocarpus heterophyllus **Lam.**: (Moraceae) Jackfruit, kathal. Native - Asia-Tropical, India (possibly indigenous in Western Ghats region). Use: human food. **Loc.** old and new campus.

Artocarpus altilis **(Parkinson) Fosberg**: (Moraceae) Breadfruit. Native - Asia-Tropical, Pacific, cultivated throughout tropics. Use: human food. **Loc.** old campus.

Artocarpus lacucha **Buch.-Ham.** (=*Artocarpus lakoocha* Roxb.): (Moraceae) Monkeyjack, barhal. Native - Asia-Temperate, Asia-Tropical, India, Laos, Myanmar, Thailand, Vietnam. Use: human food, medicine. **Loc.** old campus.

Azadirachta indica **A. Juss.**: (Meliaceae) Margosa tree, neem. Native - Asia-Tropical. Bangladesh, India, Myanmar. Use: medicinal. **Loc.** old and new campus.

Bambusa vulgaris **Schrad.ex J. C. Wendl.**: (Poaceae) Bamboo, bans. Native - Asia-Temperate, China. Use: medicine. **Loc.** Old and New Campus.

Bauhinia purpurea **L.**: (Caesalpiniaceae) Kachnar. Native - Asia-Tropical, Bhutan, India, Nepal, Pakistan, Sri Lanka, Myanmar, Thailand. Use: vegetable, medicinal, ornamental. **Loc.** old campus.

Bauhinia tomentosa **L.**: (Caesalpiniaceae) Yellow bell orchid tee, kanchan. Native - Africa, Asia-Temperate, Asia-Tropical, India. Use: vegetable, medicinal, ornamental. **Loc.** old and new campus.

Bauhinia variegata **L.**: (Caesalpiniaceae/ Fabaceae) Mountain ebony, kachnar. Native - Asia-Temperate, Asia-Tropical Bhutan, India, Nepal, Pakistan. Use: vegetable, medicinal, ornamental. **Loc.** old campus.

Bougainvillea spectabilis **Willd.**: (Nyctaginaceae) *Bougainvillea*. Native - Southern America. Use: ornamental. **Loc.** old campus.

Caesalpinia bonducella **(L.) Fleming**: (Caesalpiniaceae/ Fabaceae) Nicker bean, kankarej. Native - Africa, Asia-Temperate, Asia-Tropical Sri Lanka, Northern America, Pacific, Southern America. Use: medicinal. **Loc.** Biodiversity garden, new campus.

Calliandra haematocephala **Hassk.**: (Mimosaceae/ Fabaceae) Red powder puff. Native - Southern America. Use: ornamental, medicinal. **Loc.** old and new campus.

Callistemon lanceolatus **(Sm.) Sweet**: (Myrtaceae) Bottle brush. Native - Australia. Use: ornamental. **Loc.** old and new campus.

Canna indica **L.**: (Cannaceae) Indian shot, sarvajjaya. Native - Northern America, Southern America, Naturalized Africa, Asia-Temperate, Asia-Tropical, India, Nepal, Sri Lanka, Australia, Europe, Northern America, Pacific. Use: ornamental, medicinal. **Loc.** new campus.

***Carica papaya* L.**: (Caricaceae) Papaya, papita. Native - Northern America, Southern America. Use: medicinal. **Loc.** new campus.

***Carissa carandus* L.**: (Apocynaceae) Bengal currant, karanda. Native - Asia-Tropical Bangladesh, India. Use: vegetable, medicinal. **Loc.** old and new campus.

***Carissa macrocarpa* (Eckl.) A. DC.**: (Apocynaceae) Natal plum. Native - Africa. Use: ornamental, human food. **Loc.** Biodiversity garden, new campus.

***Cassia fistula* L.**: (Caesalpiniaceae/Fabaceae) Golden shower, amaltas. Native - Cultivated (naturalized in tropics). Use: ornamental, medsicinal, insect repellent. **Loc.** old and new campus.

***Casurina equisetifolia* L.**: (Casuarinaceae) Whistling pine, jangali saru. Native - Asia-Tropical India. Use: ornamental. **Loc.** old campus.

***Cayrota urens* L.**: (Arecaceae) Fishtail palm, mohakarin. Native - Asia-Tropical, India, Sri Lanka. Use: ornamental. **Loc.** old and new Campus.

***Ceiba pentandra* (L.) Gaertn.**: (Malvaceae) White silk-cotton tree, safed semal. Native - Africa, Northern America, Southern America, cultivated in Asia-Tropical, India. Use: ornamental, medicinal. **Loc.** old and new campus.

***Citrus aurantifolia* (Christm.) Swingle**: (Rutaceae) Lime, kaghzi nimbu. Use: edible, medicinal. **Loc.** old campus.

***Citrus* × *limon* (L.) Osbeck**: (Rutaceae) Lemon, nimbu. Native - cultivated widely cult. in tropics & subtropics. Use: edible, medicinal. **Loc.** old campus.

***Citrus jambhiri* Lush.**: (Rutaceae) Rough lemon. Native - Asia-Tropical. Use: edible, medicinal. **Loc.** old and new campus.

***Citrus japonica* Thunb.**: (Rutaceae) Kumquat. Native - Asia-Tropical. Use: fruit edible, essential oil, medicinal. **Loc.** old and new campus.

***Citrus maxima* (Burm.) Merr.**: (Rutaceae) Pummelo, chakotra. Native - Asia-Tropical, Indonesia, Malaysia; Cultivated (widely cult. in tropics & subtropics). Use: medicinal. **Loc.** new campus.

***Citrus medica* L.**: (Rutaceae) Citron, bara nimbu. Native - Asia-Tropical, India Cultivated in Asia-Temperate, China, Europe. Use: fruit edible, medicinal, ornamental. **Loc.** old campus.

***Citrus reticulata* Blanco**: (Rutaceae) Mandarin orange, santara. Native - Asia-Tropical, Indo-China-Vietnam, cultivated (widely cultivated in tropics & subtropics). Use: medicinal. **Loc.** new campus.

***Citrus* × *sinensis* (L.) Osbeck.**: (Rutaceae) Navel orange, malta. *Native - c*ultivated in tropics & subtropics. Use: medicinal. **Loc.** new campus.

***Cordia rothii* Roem. & Schult.** (=*Cordia sinensis* Lam.): (Boraginaceae) Indian cherry, lasoda. Native - Africa, Asia-Temperate, Asia-Tropical, India, Pakistan, Sri Lanka. Use: vegetable, medicinal. **Loc.** in the backside of herbarium lawns, old campus and new campus.

***Cycas revoluta* Thunb.: (Cycadaceae)** Sago palm, pahadi supari. Native - Japan, South China. Use: ornamental. **Loc.** old and new campus.

***Dalbergia sissoo* Roxb.**: (Fabaceae) Indian rosewood, shisham. Native - Asia-Temperate, Asia-Tropical, Bangladesh, Bhutan, India, Nepal, Pakistan. Use: avenue, timber, medicinal and environmental. **Loc.** old building entrance, Biodiversity garden, new campus.

***Ervatamia coronaria* (Jacq.) Stapf** (=*Tabernaemontana divaricata* (L.) Burkill): (Apocynaceae) Crepe jasmine, chandni. Use: ornamental. **Loc.** old and new campus.

***Feronia limonia* Swingle (=*Limonia acidissima* L.)**: (Rutaceae) Wood apple, kowit, kaith. Native - Asia-Tropical, India, Pakistan, Sri Lanka. Use: medicinal. **Loc.** new campus.

***Ficus benghalensis* L.**: (Moraceae) Banyan tree, barh. Native - Asia-Tropical, India, Pakistan. Use: avenue, medicinal. **Loc.** old and new campus.

***Ficus benjamina* L.**: (Moraceae) Weeping fig, pukar. Native - Asia and Australia. Use: ornamental. **Loc.** old and new campus.

***Ficus elastic*a Roxb. ex Hornem.**: (Moraceae) Indian rubber tree. Native - tropical Asia, India, and Malaysia. Use: ornamental. **Loc.** old and new campus.

***Ficus glomerata* Roxb. (=*Ficus racemosa* L.)**: (Moraceae) Cluster fig, gular. Native - Australia, Malaysia, Indo-China. Use: medicinal and ornamental. **Loc.** old and new campus.

***Ficus infectoria* Willd. (=*Ficus virens* Aiton)**: (Moraceae) White fig, pilkhan, pakhad. Native - Asia-Temperate, Asia-Tropical, Bhutan, India, Nepal, Sri Lanka. Use: ornamental, hedge plant. **Loc.** old and new campus.

Ficus panda: (Moraceae) Ficus. Native - primarily to tropical areas of East Asia, distributed throughout tropics. Use: ornamental**. Loc.** new campus.

***Ficus palmata* Forssk.**: (Moraceae) Punjab fig, bedu, jangali anjiri. Native - Africa, Asia-Temperate, Asia-Tropical, India. Use: fruits edible. **Loc.** old campus

***Ficus religiosa* L.**: (Moraceae) Sacred fig, peepal. Native - Asia-Tropical, Bangladesh, India, Nepal, Pakistan. Use: avenue tree, ornamental, medicinal. **Loc.** old and new campus.

***Grevillea robusta* A. Cunn. ex R. Br.**: (Proteaceae) Southern silky oak. Native - Australasia. Use: ornamental**. Loc.** old campus

***Hibiscus rosa-sinensis* L.**: (Malvaceae) China rose, gurhal. Native - probable tropical Asia. Use: ornamental, medicinal**. Loc.** old and new campus.

***Holoptelea integrifolia* (Roxb.) Planch**.: (Ulmaceae) Indian Elm, papdi. Native - Asia-Tropical, India, Nepal, Sri Lanka. Use: medicinal. **Loc.** old campus.

***Jatropha glandulifera* Roxb.**: (Euphorbiaceae) Glandular jatropha, jangli erandi. Native - Mexico, South America, India and the Caribbean Islands. Use: medicinal**. Loc.** Biodivrsity garden, new campus.

***Jatropha integrimma* Jacq.**: (Euphorbiaceae) Peregrina, spicy jatropha. Native - Cuba and Hispaniola. Use: ornamental**. Loc.** Biodivrsity garden, new campus.

***Juniperus communis* L.**: (Cupressaceae) Common Juniper, aaraar, haubera, abhal. Native -Africa, Asia-Temperate, Asia-Tropical, India, Nepal, Pakistan, Europe and North America. Use: medicinal and ornamental. **Loc.** Biodivrsity garden, new campus.

Kigelia pinnata (Jacq.) DC. (=*Kigelia africana* (Lam.) Benth.): (Bignoniaceae) Sausage tree. Native - Africa. Use: ornamental. **Loc.** Biodivrsity garden, new campus.

***Lagerstroemia speciosa* (L.) Pers.**: (Lythraceae) Pride of India, jarul**.** Native - Asia-Tropical, India, Sri Lanka. Use: ornamental. **Loc.** new campus.

Leucaena leucocephala Lam. De Wit.: (Mimosaceae) White lead tree, subabul. Native - Northern America, Southern America. Use: hedge plant, bio-energy. **Loc.** new campus.

***Livistona chinensis* (Jacq.) R. Br. ex Mart.**: (Arecaceae) Fan palm. Native - Asia-Temperate, China. Use: ornamental**. Loc.** old and new campus.

***Madhuca longifolia* (J. Konig) J.F. Macbr.**: (Sapotaceae) Mahuwa. Native - Asia-Tropical. Use: fruit edible, industrial and medicinal. **Loc.** old campus.

Malvaviscus conzattii Greenman (=*Malvaviscus arboreus* Cav. var. *arboreus*): (Malvaceae) Turk's cap mallow. Native - Northern-America, Southern-America. Use: ornamental. **Loc.** new campus.

***Mangifera indica* L.**: (Anacardiaceae) Mango, aam**.** Native - Asia-Tropical India. Use: human food, ornamental and medicinal**. Loc.** old and new campus.

***Manilkara hexandra* (Roxb.) Dub.**: (Sapotaceae) Ceylon Iron Wood, khirni. Native - Asia-Temperate**,** Asia-Tropical, Bangladesh, India, Sri Lanka. Use: human food. **Loc.** Biodiversity garden, new campus.

***Mimusops elengi* L.**: (Sapotaceae) Spanish cherry, maulsari**.** Native - Asia-Tropical, India, Sri Lanka. Use: ornamental and medicinal**. Loc.** old and new campus.

***Morinda citrifolia* L.**: (Rubiaceae) Indian mulberry, noni. Native - Asia-Temperate, Asia-Tropical, Bangladesh, India, Sri Lanka, India**,** Indochina, Thailand. Use: ornamental and medicinal**. Loc.** new campus.

***Moringa oleifera* Lam.**: (Moringaceae) Drumstick tree, sahajan. Native - Asia-Tropical, India. Use: vegetable, ornamental and medicinal**. Loc.** old and new campus.

***Morus alba* L.**: (Moraceae) Mulberry, shahtoot. Native - Asia-Temperate, Asia-Tropical, India. Use: human food, ornamental and medicinal**. Loc.** old and new campus.

***Murraya koenigii* (L.) Spreng.** (=*Bergera koenigii* L.)**:** (Rutaceae) Curry leaf, kari patta. Native - Asia-Temperate, Asia-Tropical, Bangladesh, Bhutan, India**,** Nepal, Pakistan**,** Sri Lanka, Andaman and Nicobar Islands, Laos, Myanmar, Thailand**,** Vietnam**.** Use: ornamental and medicinal**. Loc.** old and new campus.

***Murraya paniculata* (L.) Jack**: (Rutaceae) Orange jasmine, kamini. Native - Asia-Temperate**,** Asia-Tropical, Vietnam. Use: ornamental. **Loc.** old and new campus.

***Musa acuminata* Colla**: (Musaceae) Banana, kela. Native - Asia-Temperate, Asia-Tropical, India, Sri Lanka. Use: human food, medicinal. **Loc.** old and new campus.

***Musa balbisiana* Colla**: (Musaceae) Plantain banana. Native - Asia-Temperate, Asia-Tropical, India. Use: ornamental, food. **Loc.** old and new campus.

***Nerium indicum* Mill.** (=*Nerium oleander* L.): (Apocynaceae) Indian oleander, kaner. Native - Africa, Asia-Temperate, Asia-Tropical, India**.** Use: ornamental. **Loc.** new campus.

***Nyctanthes arbour-tristis* L.**: (Oleaceae) Night jasmine, harsingar. Native - Asia-Tropical, India**,** Nepal, Pakistan. Use: ornamental and medicinal. **Loc.** old campus.

***Pachira glabra* Pasq.**: (Malvaceae) Guinea peanut, french peanut. Native - Brazil. Use: seeds/nuts edible, ornamental**.** **Loc.** old campus.

Pandanus odorifer (Forssk.) Kuntze: (Pandanaceae) Seashore Pandan, kewda. Native - Polynesia, Australia, South Asia, Andaman Islands, and the Philippines, wild in southern India and Burma. Use: medicinal and aromatic**.** **Loc.** old and new campus.

Phoenix dacylifera L.: (Arecaceae) Date palm, khajur. Native -Probably Asia-Temperate. Use: human food, medicinal**.** **Loc.** Biodiversity garden, new campus and old campus.

Phyllanthus emblica L.: (Euphorbiaceae/Phyllanthaceae) Indian gooseberry, amla. Native - Asia-Temperate**,** Asia-Tropical, Bangladesh, Bhutan, India, Nepal, Pakistan, Sri Lanka. Use: fruits edible, medicinal. **Loc.** Biodiversity garden, new campus.

***Pinus roxburghii* Sarg.**: (Pinaceae) Chir pine tree, chir. Native - Asia-Temperate**,** Asia-Tropical, Bhutan, India, Nepal. Use: ornamental, timber. **Loc.** Biodiversity garden, new campus.

***Pithecellobium dulce* (Roxb.) Benth.**: (Caesalpiniaceae/ Fabaceae) Manilla tamarind, jangal jalebi. Native - Northern America, Southern America. Use: human food**,** wood**,** medicinal**.** **Loc.** Biodiversity garden, new campus.

***Plumeria rubra* L.**: (Apocynaceae) Red frangipani, champa. Native - Northern America, Southern America. Use: ornamental. **Loc.** old and new campus.

***Polyalthia longifolia* (Sonn.) Thwaites**: (Annonaceae) Indian fir tree, Ashoka tree, debdaru**.** Native - Asia-Tropical, India, Sri Lanka. Use: ornamental. **Loc.** old and new campus.

***Pongamia pinnata* (L.) Pierre** (=*Millettia pinnata* (L.) Panigrahi): (Fabaceae) Pongam tree, karanj**.** Native - Asia-Temperate, Asia-Tropical, Bangladesh, India, Sri Lanka. Use: medicinal and environmental. **Loc.** new campus.

***Prosopis cineraria* (L.) Druce:** (Mimosaceae) Khejri, shami. Native - arid portions of Western Asia and the Indian subcontinent including Afghanistan, Bahrain, Iran, India, Oman, Pakistan, Saudi Arabia, the United Arab Emirates and Yemen, state tree of Rajasthan. Use: medicinal, fodder, wood and environmental. **Loc.** Biodiversiy garden, new campus.

***Pterospermum acerifolium* (L.) Willd.**: (Malvaceae) Karnikara tree, kanakchampa. Native - Asia-Temperate**,** Asia-Tropical, Bangladesh, Bhutan, India, Nepal. Use: ornamental, mdicinal. **Loc.** opposite gate no. 1, new campus.

***Pseuderanthemum carruthersii* (Seem.) Guillaumin:** (Acanthaceae) Purple false eranthemum, Carruthers' falseface**.** Native - Pacific, widely cultivated in tropics. Use: ornamental. **Loc.** new campus.

***Pseuderanthemum reticulatum* (Hort. ex Hook. fil.) Radlk.**: (Acanthaceae) Yellow-vein eranthemum, golden net-bush. Native - the open forests of Polynesia and Melanesia. Use: ornamental. **Loc.** new campus.

***Psidium guajava* L.**: (Myrtaceae) Guava, amrood. Native - Northern America, Mexico Southern America. Use: human food, medicinal. **Loc.** old campus.

***Punica granatum* L.**: (Punicaceae) Pomegranate, anar. Native - Asia-Temperate**,** Asia-Tropical, India. Use: human food, medicinal and ornamental. **Loc.** Biodiversity garden, new campus.

Rauvolfia tetraphylla L.: (Apocynaceae) Devil pepper, barachandrika**.** Native - Northern America, Southern America. Use: medicinal. **Loc.** Biodiversity garden, new campus.

***Rondeletia odorata* Jacq.**: (Rubiaceae) Fragrant panama-rose**.** Native - Southern America. Use: ornamental. **Loc.** old campus.

***Schleichera oleosa* (Lour.) Oken**: (Sapindaceae) Gum lac tree, kusum. Native - Asia-Tropical, India, Nepal, Sri Lanka. Use: human food, medicinal, house of Lac insect**.** **Loc.** old campus.

***Simarouba glauca* DC.**: (Simaroubaceae) Paradise-tree, dysentery-bark, bitterwood and Lakshmi Taru. Native-Florida, South America. Use: edible oil from seeds. **Loc.** New campus (Biodiversity Garden).

***Spathodia campanulata* P. Beauv.**: (Bignoniaceae) African tulip tree, rudrapalash, rugtoora. Native: Angola, Ethiopia, Ghana, Kenya, Sudan, Tanzania, Uganda,

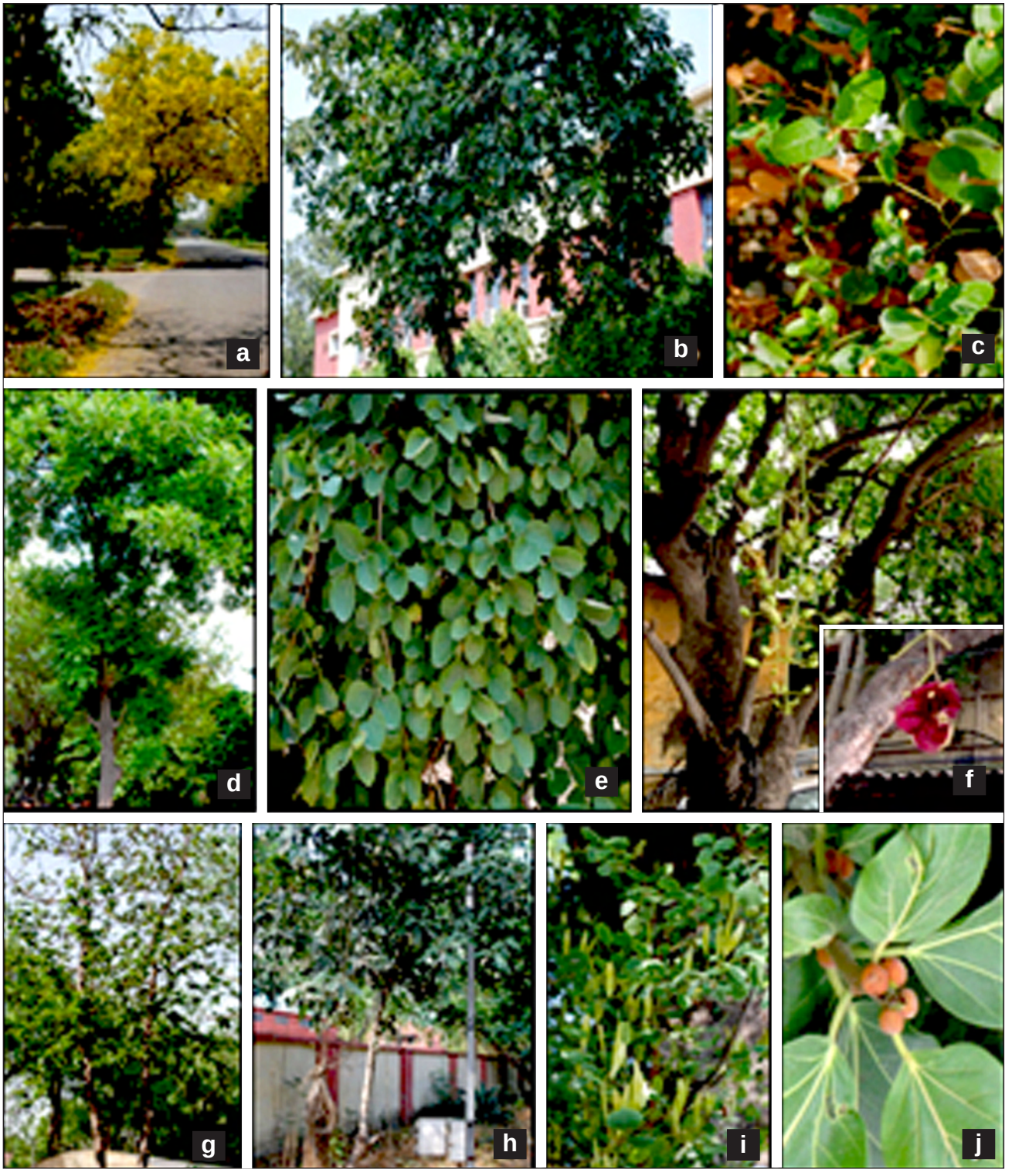

Fig. 1. (a) *Cassia fistula* L, (b) *Pachira glabra* Pasq., (c) *Carissa carandus* L., (d) *Simmarouba glauca*, (e) *Cordia rothii* Roem. & Schult., (f) *Kigelia pinnata* (Jacq.) DC., (g) *Artocarpus lacucha* Buch.-Ham., (h) *Manilkara hexandra* (Roxb.) Dub, (i) *Dalbergia sissoo* Roxb., (j) *Ficus benghalensis* L.

Fig.2. (a) *Phoenix dacylifera* L., (b) *Rondeletia odorata* Jacq., (c) *Ceiba pentandra* (L.) Gaertn., (d) *Pterospermum acerifolium* (L.) Willd., (e) *Alstonia scholaris* (L.) R. Br., (f) *Zamia furfuracea* L.f., (g) *Hibiscus rosa-sinensis* L., (h) *Tectona grandis* L.f., (i) *Citrus japonica* Thunb., (j) *Callistemon lanceolatus* (Sm.) Sweet, (k) *Emblica officinalis*

Zambia Use: ornamental, medicinal. **Loc.** Biodiversiy garden, new campus.

***Syzygium cumini* (L.) Skeels**: (Myrtaceae) Black plum, jamun, jambolan. Native - Africa, Asia-Temperate, Asia-Tropical, India. Use: ornamental, human food and medicinal. **Loc.** old and new campus.

***Tamarindus indicus* L.**: (Caesalpiniaceae) Tamarind, imli. Native - Africa, Asia-Temperate. Use: avenue, medicinal and human food. **Loc.** Biodiversity garden, new campus.

***Tecoma stans* (L.) Juss. ex Kunth**: (Bignoniaceae) Yellow bells, peeliya. Native - Northern America, Southern America. Use: ornamental. **Loc.** Biodiversity garden, new campus.

***Tecomella undulata* (Sm.) Seem.**: (Bignoniaceae) Desert teak, rohida. Native - Asia-Temperate, Asia-Tropical,

India**,** Pakistan. Use: ornamental. **Loc.** Biodiversity garden, new campus.

***Tectona grandis* L.f.** (Lamiaceae) Teak. Native to south and southeast Asia, Use: Furniture wood, avenue. **Loc. o**ld campus.

***Terminalia arjuna* (Roxb. ex DC.) Wight & Arn.**: (Combretaceae) Arjun, arjun. Native -Asia-Tropical, India, Sri Lanka. Use: avenue, medicinal. **Loc. o**ld and new campus.

***Terminalia catappa* L.**: (Combretaceae) Indian almond, jangali badam. Native - Africa, Asia-Temperate, Asia-Tropical, India. Use: ornamental and medicinal. **Loc.** old and new campus.

Thevetia neriifolia Juss. ex Steud. (=*Thevetia peruviana* (Pers.) K. Schum.): (Apocynaceae) Yellow oleander, kaner. Native - Northern America, Southern America. Use: ornamental. **Loc.** new campus.

***Thuja occidentalis* L.**: (Cupressaceae) Northern white-cedar, thuja. Native - Northern America. Use: ornamental and medicinal. **Loc.** old and new campus.

***Tinospora cordifolia* (Willd.) Miers**: (Menispermaceae) Heart-leaved moon seed, amrita, giloe. Native - Asia-Tropical, Bangladesh, India**,** Sri Lanka. Use: medicinal. **Loc.** old and new campus.

***Tylophora asthmatica* (L.f.) Wight & Arn.** (=*Tylophora indica* (Burm. f.) Merr.): (Apocynaceae) Indian ipecacuanha, arkparni. Native - Asia-Tropical, India**,** Sri Lanka. Use: medicinal. **Loc.** old and new campus.

***Vernonia amygdalina* Delile** (=*Gymnanthemum amygdalinum* (Delile) Sch. Bip.): (Asteraceae) African bitter leaf. Native- Africa, Asia-Temperate. Use: ornamental and medicinal. **Loc.** old and new campus.

***Vitex negundo* L.**: (Verbenaceae/Lamiaceae) Chinese chaste tree, nirgundi. Native - Africa, Asia-Temperate, Asia-Tropical, Bangladesh, Bhutan, India, Nepal, Pakistan, Sri Lanka. Use: ornamental, medicinal, insect repellent plant. **Loc.** Biodiversity garden, new campus.

***Volkameria inermis* L.** [=*Clerodendrum inerme* (L.) Gaertn.]: (Verbenaceae) Glory bower, wild jasmine. Native - Asia-Temperate, Asia-Tropical, Bangladesh, India, Sri Lanka, Australasia, Pacific. Use: hedge, medicinal. **Loc.** old and new campus.

***Withania somnifera* (L.) Dunal**: (Solanaceae) Indian ginseng, ashwagandha. Native - Africa, Asia-Temperate, Asia-Tropical, India, Pakistan, Sri Lanka**,** Europe. Use: medicinal. **Loc.** Biodiversity garden, new campus.

***Zamia furfuracea* L.f.**: (Arecaceae/Zamiaceae) Cardboard palm. Native - Northern America. Use: ornamental. **Loc.** new campus.

***Ziziphus mauritiana* Lam.**: (Rhamnaceae) Indian jujube, ber. Native - Asia-Temperate, Asia-Tropical, Bhutan, India (possibly native)**,** Nepal. Use: avenue tree/hedge, medicinal and human food. **Loc.** old and new campus.

The check-list will be updated with addition of new plants and the data with soft images would be uploaded on the ICAR-NBPGR web-page for the wider use and enhancing the knowledge. All readers are requested to visit http://www.nbpgr.ernet.in/ for comments on the contents of this paper for improvement.

Acknowledgements

Authors are grateful to the Director, ICAR-NBPGR for encouraging for documenting, and naming of the trees/ perennials planted in both the campuses of the institute. Help provided by the staff of the ICAR-NBPGR in different ways is acknowledged.

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Indian J. Plant Genet. Resour. 34(1): 13–24 (2021)
DOI 10.5958/0976-1926.2021.00003.6

DEBATE

Highway Genebank: An Ideation for Plant Genetic Resources Conservation on the Highway Margins

KP Mohapatra[1], Puran Chandra[1], S.P. Ahlawat[1], Ashok Kumar[1], Veena Gupta[1], Rashmi Yadav[1], Shubhendu Shekkhar Awasthi[2], Sunil Archak[1], Devashree Nayak[3], SK Dhyani[3], Javed Rizvi[3] and Kuldeep Singh[1]*

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*
[2]*Grey 2 Greens Foundation, A-9, Saraswati Vihar, Pitampura, New Delhi-110034, India*
[3]*World Agroforestry, ICRAF South Asia Regional Program, New Delhi-110012, India*

(Received: 27 March, 2021; Revised: 26 May, 2021; Accepted: 28 May, 2021)

India is an ecologically and culturally diverse country. Every region of this country has a plethora of woody perennials that have the potential to provide food, fibre, fodder, fuel, nutrition, and livelihood to the local population. Promoting access to this wide diversity of multipurpose trees can extensively address the problem of malnutrition and poverty in rural India. Therefore, these valuable biological resources should be conserved for posterity and promoted vigorously to make them accessible to the common citizen. Conservation of these valuable genetic resources and their germplasm in field genebanks is a common practice followed across the globe. But, every country including India faces severe constraint of land resources to upscale such efforts leading to assemblage of proportionately very less number of germplasm in the field genebanks. A massive highway development programme of nearly 69432 km length is being undertaken in India. These highway projects are being planted with tree species to make them green. With an appropriate policy convergence and coordination with various plantation and livelihood schemes, such plantations can conserve thousands of genetically diverse accessions available in the woody perennial while dispensing other benefits that had been stipulated in the plantation programme of the country. A conservative estimate projects that the express highways alone an accommodate nearly 20 million trees. Additionally, such plantations can serve as a platform for advancement of research on woody perennials for students, academicians, social scientists, conservationists etc.

Key Words: *ex situ* conservation, Field genebank, Genetic diversity, Green Highway Policy, MGNREGA, Roadside plantation

Background

Biological Diversity as the cradle of human survival has now been proven beyond doubt. The irony is, those who are well fed in the world give little thought to the challenges which the current food production system is facing. About 3,00,000 species on the earth are edible but only 200 are consumed in a more regular manner. Commercial diversity of food has increased many folds in the recent decades, but diversity in food grains consumption has become abysmally low. Only three crops i.e. rice, maize, and wheat contribute 60% of the energy in human diet leading to deficiency of many essential minerals and vitamins in the global population. Around two billion people in the world are deficient in one or more micronutrients. In India, around one in each 200 total mortality in 2016 was because of deficiency in micronutrients such as Iron, Zinc, Vitamin A etc. (Gonmei and Toteja, 2018). Forty one percent of pre-schoolers, 24% of school-age children and 28% of adolescents are anaemic. Iron deficiency (low serum ferritin) in pre-schoolers, school going children and adolescents is 32%, 17% and 22%, respectively. Female adolescents has a higher prevalence of iron deficiency (31%). In case of Vitamin A, the deficiency is 18%, 22% and 16 % among pre-school, school-age children and adolescents, respectively. Nearly 19% of pre-school children, 17% of school-age children and 32% of adolescents have zinc deficiency. It is important to note that the children and adolescents in urban areas have a higher prevalence of iron deficiency compared to their rural counterparts (MoHFW, 2019). It is also more pervasive in areas that are most productive in the world such as the Indian states of Punjab, Haryana, and Western Uttar Pradesh. These areas also have higher

*Email: Kuldeep.Singh4@icar.gov.in

average per capita income than rest of the country. This could be primarily due to the shrinkage of food diversity in the daily platter and non-availability of nutritionally rich fruit trees in the surroundings. Shrinkage in food diversity has become much narrower during the last half a century. Our ancestors probably had much more diverse and nutritionally rich food basket than the present generations. For example some bread like products, prepared from club-rush tubers (*Bolboschoenus glaucus*) and seeds of wild einkorn (*Triticum boeoticum*) (one of the ancestors of today's wheat), were used as a food in South-West Asia 14,400 years ago, much before the Fertile Crescent, where agriculture was believed to have been originated 10,000 years ago (Arranz-Otaegui *et al*., 2018; Voss-Fels *et al*., 2019). Ancient texts from across the world such as Greeks, Romans, Mesoptamian, Indus valley, Chinese, etc. had highlighted use of wild plant species for many nutritional and medicinal uses. Indian civilization, traditionally being a knowledge society, has accumulated a plethora of information compiled in valuable texts like Ayurveda, Siddha, Unani, Sowa Rigpa and other folk medicines. Apart from herbs and shrubs many medicinal trees like *Bahera* (*Terminalia belerica*), *Haridra* (*Terminalia chebula*), *Arjun* (*Terminalia arjuna*), *Neem* (*Azadirachta indica*), *Karanj* (*Pongamia glabra*), *Khirni* (*Manilkara hexandra*), *Junipers, Rhododendrons, Taxus,* etc. are extensively used in a wide range of herbal formulations. Demand for these plant based medicines is increasing both nationally and globally. Total consumption of herbal raw drug in India for the year 2014-15 has been estimated at 5,12,000 MT with a corresponding trade value of INR 55 billion (NMPB, 2020). Fruits are rich source of vitamins, minerals, anti-oxidants and many other secondary metabolites required for human health. Fruits like *Karonda* (*Carissa carandas*), *Ber* (*Ziziphus mauritiana*), *Phalsa* (*Grewia asiatica*), *Jamun* (*Syzygium cuminii*), *Lasoda* (*Cordia myxa*), *Sohiong* (*Prunus nepalesnsis*), *Wood Apple* (*Limonia acidissima*), *Star Fruit* (*Averrhoa carambola*), etc. are rich in vitamins and minerals, but are not utilized to their fullest potential in India. Bioavailability of the vitamins and minerals from these fruits is very high and sustainable as compared to the commercially available allopathic capsules and syrups. For example, one single fruit of *Aonla* can provide as much as 8 times vitamin C required by an adult per day. Leaves of *Moringa oleifera* is rich in protein (29.4% dry weight basis), provides 10 times more vitamin A than carrots, 17 times more calcium than milk, 15 times more potassium than bananas, 25 times more iron than spinach and 7 times more vitamin C than oranges (Rockwood *et al*., 2013; Gopalakrishnan *et al*., 2016). Fruits like *Phalsa* and *Karonda* are very rich in Calcium, Iron and Vitamin C. These fruit trees do not require the best fertile soils and can survive well on the marginal lands without any extra care. One or two such fruits in a day can substantially address the issue of anaemia, enhance immunity, bone development, and many other forms of malnutrition in the growing children of our country. Till few decades ago, plenty of such trees were available in the countryside, on community and waste lands which have depleted drastically due to urbanization, habitat loss, deforestation etc. Tree genetic resources also play an important role in livelihood support system in many rural areas. *Gum, resin* and damar yielding trees like *Kusum* (*Schleichera oliosa*), *Palas* (*Butea frondosa*) (for lac culture), *Sal* (*Shorea robusta*), *Chir pine* (*Pinus roxburghii*), etc are economically important trees supporting the livelihood of populations in the rural India. *Neem,* a wonder tree endemic to India, had been used since time immemorial in many traditional medicines, insect repellent etc. New policy of the Government of India to use neem coated urea in urea fertilizer to increase nitrogen use efficiency has increased the demand for neem oil. *Azadirachtin,* an active compound of neem oil, is the primary ingredient used for insect pest control in organic/natural farming, an emerging farming practice to produce green and safe food. Demand for all these plant derived products will increase with the increase in population, standard of living and awareness about using green products.

Threat to the Biological Diversity and the Need for Conservation

Development, urbanization and rampant consumerism of the 21st century have led to devastation of the valuable treasure of plant genetic resources conserved by the earlier generations. According to the Global Forest Resources Assessment 2020, the global rate of net forest loss in 2010–2020 was 7 million ha per year. Every day the world is losing few hundred species i.e. they are becoming extinct thereby pushing the survival of humanity to the brink. More than 32,000 plant species are threatened with extinction (IUCN, 2020); approximately 20,339 trees have been included in the red list of threatened plants. CITES listings of tree species have surged in recent years; more than 900 tree species are now included in CITES appendices and have their trade regulated

(FAO and UNEP, 2020). Rapid urbanization, mining, construction of mega-hydroelectricity projects, road constructions, railway lines, high tension transmission lines and other such anthropogenic interference are the major contributors to deforestation and habitat loss of many valuable species, landraces and ecotypes. Road construction has contributed significantly in depleting the tree vegetation along the road margins. In one of the impact assessment studies undertaken by the National Highways Authority of India (NHAI), it was reported that widening of about 403 km stretch of highway between Agra and Dhanbad demanded to remove approximately 48419 trees. The species included many valuable tree species such as Shisham (*Dalbergia sissoo*), Teak (*Tectona grandis*), Neem (*Azadirachta indica*), Arjun (*Terminalia arjuna*), Jamun (*Syzygium cuminii*), Mango (*Mangifera indica*) etc. (NHAI document E432 volume 17 www.nbrienvis.nic.in/WriteReadData/CMS/Tree%20Plantation%20Strategy%20%20GTR(1).pdf). The scenario is similar in all other road development projects undertaken in the country during the last 10-15 years. Genes of desirable traits present in these valuable species, their wild relatives and land races have tremendously contributed to the survival and productivity of many commercial cultivars. For example the resistance genes $v_{f,}$ $v_{m,}$ $v_{r,}$ $v_{bj,}$ against apple scab, a serious disease hampering apple production across the world, are found in small fruited apple *Malus floribunda*, *M. micromalus*, *M. pumila* and *M. bacata* Jackii, respectively; resistance source of pine wilt disease for Japanese pine (*Pinus pandorosa*) were reported in *P. thunburghii*, *P. luchuensis* and *P.massonianathe* (Nose and Shiraisi, 2008); *Mmd1* gene, resistant against Melamspora leaf rust in *Populus deltoides,* is found in *P.trichocarpa* (Jorge *et al*., 2005); citrus tristeza resistance gene was identified in the citrus relative *Poncirus trifoliata* (Mestre *et al*., 1997). The entire rice crop of Indonesia was threatened some decades ago by a growth-stunting virus. A gene transferred from *Oryza nivara* from Odisha saved rice crop against the virus. The muskmelon crop in the United States was saved from huge loss by transferring a single gene from the Indian germplasm having resistance to downy mildew. Another gene from the Indian genetic resources provided resistance to greenbug insect in sorghum providing millions of dollars of annual benefit to the American farmers. Dr. William Saunders of Canada used wheat variety Hard Red Calcutta and released new series of wheat later called Marquis A and B which were resistant to rusts. Recently in rice, Sub1A (from FR13A) and PSTOL1 (from Kasalath) are being used globally to save rice from losses due to flooding and improving P use efficiency (Singh *et al*., 2021). The genetic resources not only possess the genes and traits for biotic stress but also genes for abiotic stress and adaptive traits relevant to the changing climatic scenarios. Climate change is now a reality; issues of adaptation of a species to climatic aberrations, ecological shifts are likely to put more challenges on the future availability of these valuable forest resources. In India, altitudinal shift of apple in Himachal Pradesh and Uttarakhand, drying of *Parkia roxburghii* in Manipur and Nagaland are few such examples. New plant types, varieties or species are required to fill this gap. Undoubtedly, these precious wealth of genetic resources or germplasm which *Mother Nature* has bestowed upon us, has ample capacity to provide novel genes, traits, plant types or recombinants to face the aforementioned emerging challenges. The invaluable importance of genetic resources can be realized from the supreme sacrifice made by the scientists of All-Union Institute of Plant Industry, later named as Vavilov Institute of Plant Industry, in Russia, during the siege of Leningrad in the Second World War. Scientist like D.S. Ivanov, a rice specialist, M. Shcheglov, G. Kovalevsky, N. Leontjevsky, A. Malygina, A. Korzun and many others had slowly starved to death because of shortage of food but refused to eat the seeds from any of their collection containers of rice, peas, corn and wheat. They chose torment and death in order to preserve their valuable genebank (Krivchenko, 1991; Loskutov, 1999). Therefore, the available biological diversity must be conserved on priority to secure the existence of both the present and future generations.

Conservation of Genetic Resources – Global and National Efforts

In situ conservation of biological resources is considered to be the most ideal conservation strategy for all the biological diversity as it allows the evolutionary, and inter and intra ecosystem interactions to shape the quality and quantity of the natural variation. Accordingly, many biodiversity rich areas, unique habitats, representative ecosystems, gene sanctuaries, biosphere reserves etc. (collectively called as protected areas), have been established across the globe to conserve the biological diversity including plant genetic resources. There are about 257,817 protected areas (including terrestrial ecosystem, ocean and other water bodies) spread over 245 countries in the world (WDPA, 2021). Aichi Biodiversity

Table 1. Protected Areas established in India (As on December, 2019)

Protected Areas	No.	Total Area (km^2)	Coverage % of Country
National Parks (NPs)	101	40,564.03	1.23
Wildlife Sanctuaries (WLSs)	553	119,756.97	3.64
Conservation Reserves (CRs)	86	3,858.25	0.12
Community Reserves	163	833.34	0.03
Protected Areas (PAs)	903	1,65,012.59	5.02

(Source: http://www.wiienvis.nic.in/Database/Protected_Area_854.aspx)

Target 11 of the Strategic Plan for Biodiversity 2010-2020 had set a target of achieving at least 17 per cent of terrestrial and inland water areas under protected areas and other effective area-based conservation by 2020. In India, a good network of national parks, sanctuaries, biosphere reserves also have been established (Table 1). However, *in situ* conservation of plant genetic resources in these protected areas has certain limitations as many natural habitats are becoming vulnerable to destruction by anthropogenic misuse of the natural resources. An analysis by Lewis *et al.* (2019) reported that about 1.1 million km^2 area (both land and water) is being removed annually from the protected areas between 2006-2018. Therefore, *in situ* conservation efforts are supplemented by *ex situ* conservation measures in specially constructed genebanks having long term storage (LTS) and medium term storage (MTS) facilities, Cryo banks, *in vitro* cultures and DNA banks. Species which are difficult to store (recalcitrant seeds, vegetative propagules like Banana or species having long gestation period) are conserved in field genebanks.

Globally, nearly 5.7 million accessions of plant species and their wild relatives covering 7420 genera and 54305 species are being maintained in the LTS, MTS, field genebanks and cryo facilities of 831 genebanks located in 114 countries (WIEWS, 2021). More than 0.8 million accessions from over 600 genera are being maintained in 11 genebanks of Consultative Group on International Agricultural Research (CGIAR) and World Vegetable Centre. A good number of collections are being conserved *ex situ* in the 3400 botanical gardens located in different parts of the world (Bélanger and Pilling, 2019). A special permafrost facility to accommodate safety duplicates has been established deep inside a mountain on a remote island in the Svalbard archipelago, halfway between mainland Norway and the North Pole. This facility, popularly called as "Svalbard Global Seed Vault", has a capacity to store 4.5 million accessions. At present 1,074,537 samples of many unique crops and their land races have been stored in this facility (https://www.croptrust.org/our-work/svalbard-global-seed-vault).

In India, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), a national facility for conservation of Plant Genetic Resources, was established in 1976 to undertake exploration, collection, characterization, conservation, import and export of germplasm, phyto-sanitary and quarantine of plant genetic resources in India. Now it is one of the leading plant genetic resources organization in the world and the National Genebank ranks 2nd in the world with respect to plant genetic resources conservation. It has a capacity to conserve about one million germplasm in the form of seeds and is currently conserving about 0.45 million accessions belonging to nearly 2,000 species. In cryo-conservation facilities 11,932 accessions, and 1915 accessions *in vitro* have been conserved (*www.nbpgr.ernet.in*). But many of the forest and horticultural tree species cannot be conserved as seeds in seed genebanks due to recalcitrant/intermediate seed storage behaviour. Unlike annual field crops such as cereals, pulses, and vegetables seeds of tree crops are not easy to multiply because of the sole constraint of gestation period.

Additionally conservation of germplasm in the field genebanks offers a unique advantage of evolutionary continuum, at least to a large extent, as compared to the *ex situ* conservation in the seed banks where the evolutionary process and dynamics of the gene interaction in populations is halted. Therefore, live trees in the field gene banks are the only viable and economically cheaper option to conserve, multiply and expand these valuable perennial genetic resources. Realising the importance of germplasm conservation in field genebanks, ICAR-NBPGR is also conserving a large number of accessions of perennial plants in field genebanks in collaboration with its partner institutions in India. For example more than 700 accessions of mango (*Mangifera indica*) in ICAR-Indian Institute of Horticultural Research, Bengaluru, nearly 800 mango germplasm in ICAR-Central Institute of Subtropical Horticulture, Lucknow; about 170 Neem (*Azadirachta indica*) accessions in ICAR-Central Agroforestry Research Institute, Jhansi; 246 accessions of Jackfruit (*Artocarpus heterophyllus*), 162 accessions of Bael (*Aegle marmelos*) at the regional station, Ranchi of ICAR-NBPGR, more than 1400

accessions of *Morus* species at the Central Sericultural Germplasm Resources Centre, Hossur etc. are being conserved in field genebanks.

But, looking at the enormity of the diversity available in the woody perennials and the variation in the edapho-climatic conditions (hot arid to alpine and cold desert) in India, the number of accession conserved in the field genebanks is meagre. For example the number of accessions in some of the most important woody perennials such as Shisham (*Dalbergia sissoo*), *Prosopis cineraria, Tecomela undulata, Populus ciliata, Grewia optiva, Grewia tenax, Buchalania lazan* conserved in field genebanks is not more than 200 accessions per species. The major constraint is the lack of availability of enough area with the research institutions, and universities to accommodate a decent number of accessions to capture the genetic diversity present in a species across its distributional range. In such a scenario, avenue plantation or the roadside plantation offers a unique opportunity for conservation of woody perennial germplasm while fulfilling the national objective of greening the highways.

Roadside Plantation – An Opportunity for Woody Perennial Germplasm Conservation

***Patronage of public roads and roadside plantation in ancient India*:** India has a long history of patronizing plantations of flourishing trees with large canopies in the road sides. The visionary Indian Kings like Chandra Gupta Maurya, Ashoka the Great, and Sher Shah Suri had extensively planted fruit and shade trees along the roads for travel comfort and food availability to their subjects. The foundation of the present day Grand Trunk road was laid long back in the 3rd Century B.C. when Chandra Gupta Maurya constructed a road called *Uttar patha* (Northen road) extending from Pataliputra (Present day Patna) to Taxila in Pakistan. It was further extended to Khorasn in Afghanistan. Later, it was widened and extended to Bengal by the Mauryan King Ashoka. King Ashoka had also laid a large network of roads connecting many cities in the southern India and planted trees alongside the roads. During the 16th century A.D., Sher Sah Suri, developed a road called 'Sadak-e Azam' from Chitagong (in Bangladesh) to Kabul. The Moghul emperors gave patronage to this road which was then known as *Bad-Sahi-Sadak*. The Moghuls constructed *Kos Minars* at regular intervals to indicate the length of the roads and decentralize the road management (Roy, 2010; Jason, 2011; Jason, 2012). The British made it a motorable road which is now popularly known as the Grand Trunk Road. During the long history of highway development in India, plantation of useful trees on both the sides of the roads had been encouraged. Chandra Gupta Mauyra appointed officials to protect the roads and the plantations. Kautalya's Arthasastra even mentions different punishments for cutting or damaging roadside trees. Ashoka planted thousands of Banyan (*Ficus bengalensis*), Peepal (*F. religiosa*), Mango (*Mangifera indica*) etc. trees along the roads. In this way, he created special mango grooves by planting good quality plantations along the roads. The benefits of Jamun trees (*Syzhigum cumini*) along the Delhi roads, especially around the Lutyen's Delhi has been well recognized (Salbitano *et al*., 2016). These plantations are known as one of the most beautiful avenue plantation having fruit production potential of about 500 tonnes/ year. Besides, it is a very good protected source of high-quality perennial germplasm. Road side plantations and the plantations in the gardens nurtured by the royals in India are in fact some of the oldest assemblage of tree germplasm in the world, though these were not looked through the prism of the modern genetic principles to conserve genetic diversity. Their emphasis on tree plantation and concern for their protection had helped in assembling a great amount tree germplasm along the margins of the roads.

Current Tree Plantation Activities in India

Organized plantations was also undertaken throughout the 20th century during the British rule. Avenue Plantation as an activity of the Forest Department was undertaken in Uttar Pradesh, and a Land management circle was established in 1935 (Saha, 1996). After independence in 1947, major road side plantations were undertaken under Social Forestry Programmes in different states of India which were supported by international agencies like SIDA (Swedish International Development Cooperation Agency), CIDA (Canadian International Development Agency), DANIDA (Danish International Development Agency) etc. However, with the implementation of major road development projects (both National Highways and Rural Roads) during the last two decades, Government of India had developed major plantation schemes for the national highways. The major ones are the plantation activities under Green India Mission, MGNREGA (Mahatma Gandhi Rural Employment Guarantee Act) scheme, Green Highways Policy, 2015, Prime

Minister's Gramin Sadak Yojna (PMGSY, called PM's Rural Road Development Scheme), and Compensatory Afforestation Scheme under Compensatory Afforestation Fund Management and Planning Authority (CAMPA), National Afforestation Program (NAP), National Rural Livelihood Mission, Integrated Watershed Management Program, National Rainfed Area Authority etc. Under the MGNREGA, Roadside plantations on the National Highways, State Highways, PMGSY roads are being undertaken throughout the country to provide wage employment while developing productive assets and arrest roadside degradation, global warming etc. As per para 4(1), 1(v) of schedule 1of MGNREGA Act 2005 "Afforestation and tree plantation is to be carried out in common and forest lands, road margins, canal bunds, tank foreshores and coastal belts duly providing usufruct to the households covered in paragraph 5". Accordingly, advisory and guidelines had been issued by the MGNREGA Division, Ministry of Rural Development, Government of India vide circulation no 11017/17/2008/ NREGA (UN) (Part-II) dated 31st July 2014. Under this programme in the Financial Year 2020-21, nearly 18.69 million trees were planted on the roadsides covering a total road length of 54,130 km (including 544 km of National Highway) which benefited 2.93 million beneficiaries (MGNREGA Plantation Report:2020-21). Under the CAMPA, 4,48,914 ha had been stipulated for plantation under compensatory afforestation with a budgetary release of INR 50.32 billion (Appx. USD 750 million) from 2009-10 to 2013-14. This budget also included area under plantation other than the compensatory afforestation. Total area covered under plantation was 1467579 ha that included 389198 ha under compensatory plantation (http://egreenwatch.nic.in/Portal.aspx). With appropriate convergence, a sizeable work can be undertaken on plantation of woody perennial germplasm on the road margins. India has a huge network of national highways. The total length of National Highway in the country at present is 1,32,499 km. It includes the 5,846 kilometres 4 to 6 lane express ways popularly called as golden quadrilateral. Such massive expressways have given a tremendous boost to the national economic growth. Ministry of Road Transport & Highways and Shipping, Government of India had launched Green Highways (Plantation, Transplantation, Beautification & Maintenance) Policy, 2015 with the aim to promote greening of Highway corridors with participation of the community, farmers, private sector, NGOs, and government institutions. It was planned to keep aside 1% of the total project cost of all highways projects for the highway plantation and its maintenance. This could make available approximately INR 10 billion (Appx. USD 142 million) per year for plantation purpose and had the potential to generate employment opportunities for about 0.5 million people in rural areas. (https://morth.nic.in/green-highway). In the implementation plan, it had been emphasized to plant local species on the highway margins following the recommendations made by Indian Road Congress manual for roadside plantation 2009 (IRC:SP:21-2009). Although in the Indian Road Congress guidelines, use of locally available species has been emphasized, no consideration was given to collect and plant the genetic diversity of a species available in a specific locality. In a conservation plan, the most important aspect is the maintenance of Genetic diversity of a species which is defined as "*the variation or dissimilarity in the genetic makeup of the individuals of a species which is the source of their unique features*". The genetic diversity within a species is not only most essential for the survival of the species itself but also for the nutritional and livelihood security of mankind. This aspect of conservation of genetic diversity often takes a backstage in large scale plantation programmes where efforts are being made to accommodate more number of species in a unit area but not the genetic diversity within an individual species. While taking up such mass plantations, more often than not, the seeds/cuttings from a few selected plants are planted leading to loss of the genetic diversity of the area over a period of time due to developmental activities in the region. Under the Prime Ministers Gramin Sadak Yojna (PMGSY), it has been planned to construct 3,93,000 km new roads and upgrade 3,73,000 km existing roads in the rural areas. In a circulation from National Rural Road Development Agency, Ministry of Rural Development, Government of India in 2016, all the implementing agencies were instructed to undertake planation in the roadsides of these rural roads and develop convergence with the local MGNREGA programmes (https://pmgsy.nic.in/sites / default/files/ circular/ver_tree_plnt.pdf). Looking at the activities on such a huge network of road construction in India, opportunities to utilize the roadside planation for germplasm conservation is immense.

Roadmap for Highway Genebank

India has a designated National Highway of 1,32,499 km out of which the National Highway Authority of

India has taken up the task of developing 69432 km length. (https://nhai.gov.in/#/about-nhai; https://nhai.gov.in/#/). It can be safely assumed that appx 25m average width of land would be available on each side of the Highways. As per the guideline prepared by the NHAI, the 1st row of the plantation should be at least 14 m from the central line of the traffic lane to ensure road and traffic safety of the high speed vehicles (www.morth.nic.in). It means, nearly 10-11 m width would be available for plantation of the trees. The actual area available for germplasm plantation may be slightly less as some area may not be practically available because of road safety requirements like presence of steep curves, difficult terrain, overhanging walls in hill sides, presence of bare rocks etc. We may assume that at least 70% of the area should be available which implies that at least 50,000 ha will be available for tree plantation. In the 1st approximation, this land can accommodate nearly 20 million trees at an average spacing of 5 m × 5 m (spacing for individual tree types will vary). Only a fraction of such a big number will be sufficient to plant germplasm of fruit, fodder, timber, fuel, and fibre trees and conserve most of the genetic diversity present in almost all the important tree species available in the country. For rest of the space (area not covered under germplasm), the native population of the trees may be surveyed in the surrounding region of the track. All the seeds can be bulked, and subsets of the bulks can be used to raise nursery for plantation. In this way the diversity of the area can be conserved on the roadsides.

The National Highways in India passes through three types of lands: Forest land, Non-forest land, and community land in tribal areas covered under the 6th schedule of the constitution. Management of these highway plantations will be different for different types of the lands. In Forest Areas, the landownership is vested on the state forest departments. Joint Forest Management (JFM) approach may be adopted with appropriate convergence with Pradhan Mantri Van Dhan Vikash Yojna (PMVDVY) scheme launched by the government of India. The village forest development centre (Van Vikash Kendras) can be the focal point for devising maintenance and benefit sharing of the produce. In case of Tribal areas covered under the 6th schedule, the village institution can be utilized and the village *Darbars* (village councils) shall maintain and share the benefits as per the tribal laws and costumes. For the other Non-forest land, the guidelines of MGNREGA may be followed where each family near the highway should be allotted the *usufruct* of not more than 200 trees. Safety buffer between the road and the 1st line of tree, and the medians may be planted with grasses and medicinal herbs, shrubs having wild fruits etc. as per the NHAI guidelines. However, efforts should be made to accommodate diverse germplasm from the surrounding localities instead of planting from one or two sources.

A robust information management system is required to monitor issues related to the identity of these trees, their utility, management and protection against theft and loss as they will be the national treasure to safeguard: It is also required for replenishment of the seeds in seed genebank, supply of germplasm to the various end users like universities, students, breeders, state line departments etc. Rescue missions for germplasm recovery in case of road widening or other developmental works also require most precise identification of the accessions in the field. Therefore, all the trees can be geo tagged with very high degree of precision using a differential GPS (Global Positioning System) or any other high precision instrument. Those trees can be barcoded and RFID (Radio Frequency Identification) tags, either semi-passive or passive tags, can be embedded in the trees to store all the information such as passport data, date of plantation etc. about the tree. The passive RFIDs derive their energy from the readers by induction. Therefore, they will not require any power source or battery to become functional and can be theoretically utilized for a very longer duration of time. Such technologies can be modified to suit the needs of the germplasm conservation and management. These tags will help to revisit the trees precisely and record data on the trees. In some important locations or for valuable trees or rare plant materials, active tags having a Lithium ion battery can be used which will continuously transmit the information to a receiver and any disturbance to the trees can be immediately detected by the signal receiving station. ICAR-NBPGR is working on a collaborative programme with ICRAF (International Centre for Research in Agroforestry) to optimize this technology for germplasm conservation.

Unlike annual crops, trees have very long gestation period to enter into flowering and fruiting. Therefore, studying the traits through classical genetics methods like generating segregating materials, recombinant inbred lines, near isogenic lines, repeated selfing etc. are not feasible in the scale of money, time and space. But the modern genomic tools can circumvent many such

steps involved in classical genetics if a great variability of these underutilized but valuable tree species can be grown in a uniform plantation site like the margins of the national highways. This will provide a big field research infrastructure for the students, researchers, academicians to advance their research in woody perennials as most of the research organizations do not have such plantations in their institutions because of severe shortage of land resources.

The fruits and other products from these species will have the potential to serve towards nutritional security of the local population. The model can also be slightly modified to cater the needs of industries such as tourism, traditional food banquets etc. Another dimension can be added to the highway genebank for enhancing ecosystem services. Rainwater harvesting structures may be provided for irrigation to the plantation, and/or ground water recharge by using recharge filters and recharge pit. If implemented, the "Highway Genebank Model" will be a unique system of gene conservation of perennial species in the world where roadside plantation can be used for biodiversity conservation while providing a variety of other ecosystem services.

The plantations will serve as the source of valuable genes which the nation may require to fight against climate change, pest and diseases management, enhancing productivity etc. As an off shoot, it can improve the carbon footprint, reduce malnutrition, improve soil health, hydrology, reduce sound pollution, increase birds and other animals that are natural predators of many insect and pest and many other ecosystem services. It can also serve towards meeting the sustainable developments goals (SDGs indicator 2.5.1), and Nationally Determined Contributions (NDC) as per Paris Protocol (2015), the international commitments to which the Government of India is a signatory. It could be a win-win situation for all the stakeholders i.e. government, general public, plant and tree breeders, ecologist, nature lovers and the malnourished children who would be shouldering the future growth and development of the country.

With some of the trees, medicinal plants like *Tinospora codifolia* (Giloe), *Tylophora indica*, *Withania somnifera* (Aswagandha), *Aloe vera*, *Moringa oleifera* can be cultivated in the interspaces which can also support the local primary healthcare system and the surplus can go as a raw material to the Ayurveda industry.

Policy Convergence

Government of India has many policies, schemes and programmes for afforestation of road margins such as MGNREGA, CAMPA, NAP, Prime Minister Van Dhan Vikash Yojna (PMVDVY), IWMP (Integrated Watershed Management Programme), National Agroforestry Policy 2014, GIM (National Mission on Green India), Mission on Integrated Development of Horticulture (MIDH), National Bamboo Mission (NBM) etc. A convergence of such programmes will not only rationalize allocation and utilization of financial resources more efficiently but also make the output multi-objective. An outline of a possibility plan for policy synchronization and interdepartmental interaction for effective implementation of such a programme is given Fig 1.

Schema of Activities

A list of activities is given below that can be undertaken to implement a model plantation (Fig 2) for highway genebank:

1. The choice of species and planting design will depend on the local site conditions. The entire highway can be divided into segments of 100 km length or any other length suitable to the local conditions. The district flora or regional flora published by the Botanical Survey of India, the State Agricultural University, Central Universities, State Universities, KVKs, State Forest Departments, ICAR institutes dealing with fruit and forest trees etc. around the locality of plantation may be consulted for the choice of species. Local communities through the village councils (Gram Panchayat) must be involved in the process of species selection and diversity collection as they have very rich indigenous knowledge on the local flora and fauna. A PRA (Participatory Rural Appraisal) or RRA (Rapid Rural Appraisal) may be conducted which will be useful to prioritise the species and composition of the plantation. It will ensure higher success of the programme implementation.
2. The area needs to be surveyed with respect to soil type and land configuration. Most of the land on both sides of the highway may either be slopping on the sides, degraded having issues of water stagnation at the bottom of the slope due to excavation activities etc. In such cases, shallow ponds could be made at regular intervals to address the issue of water

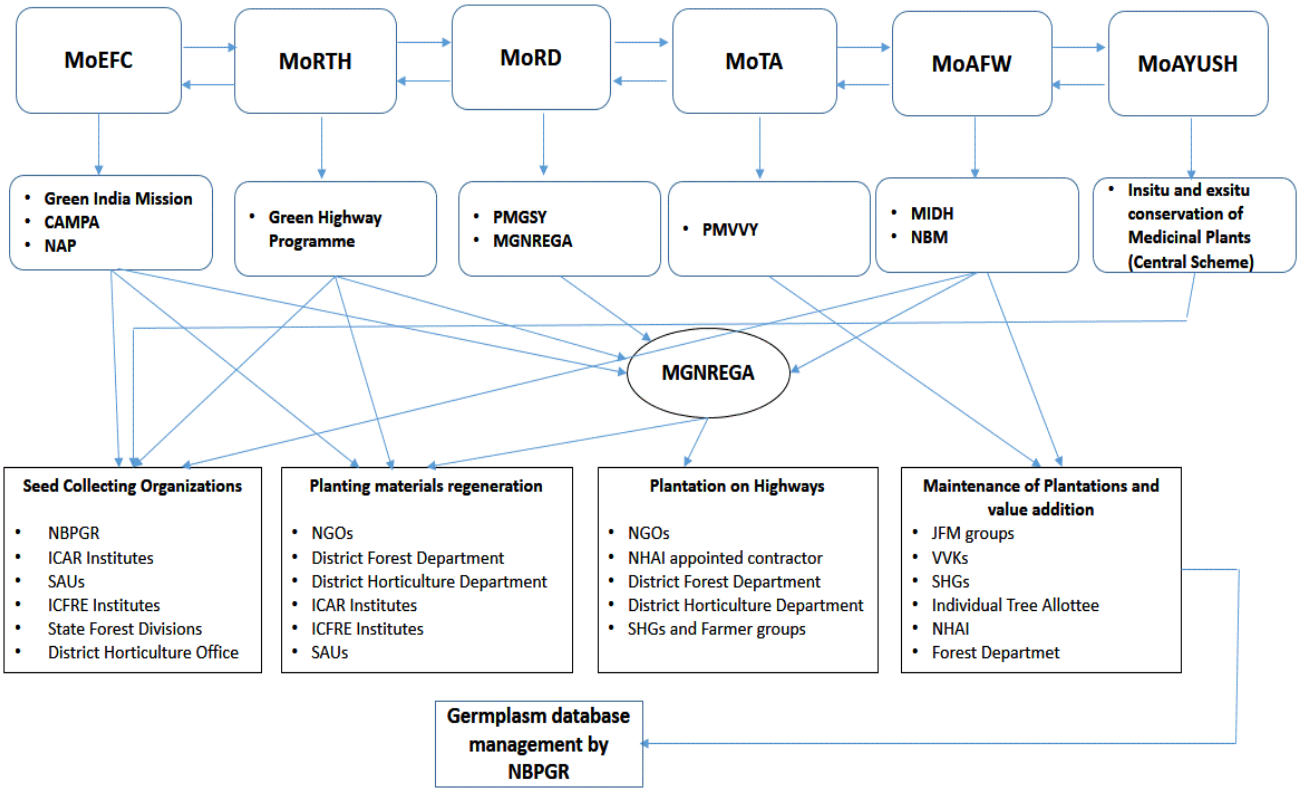
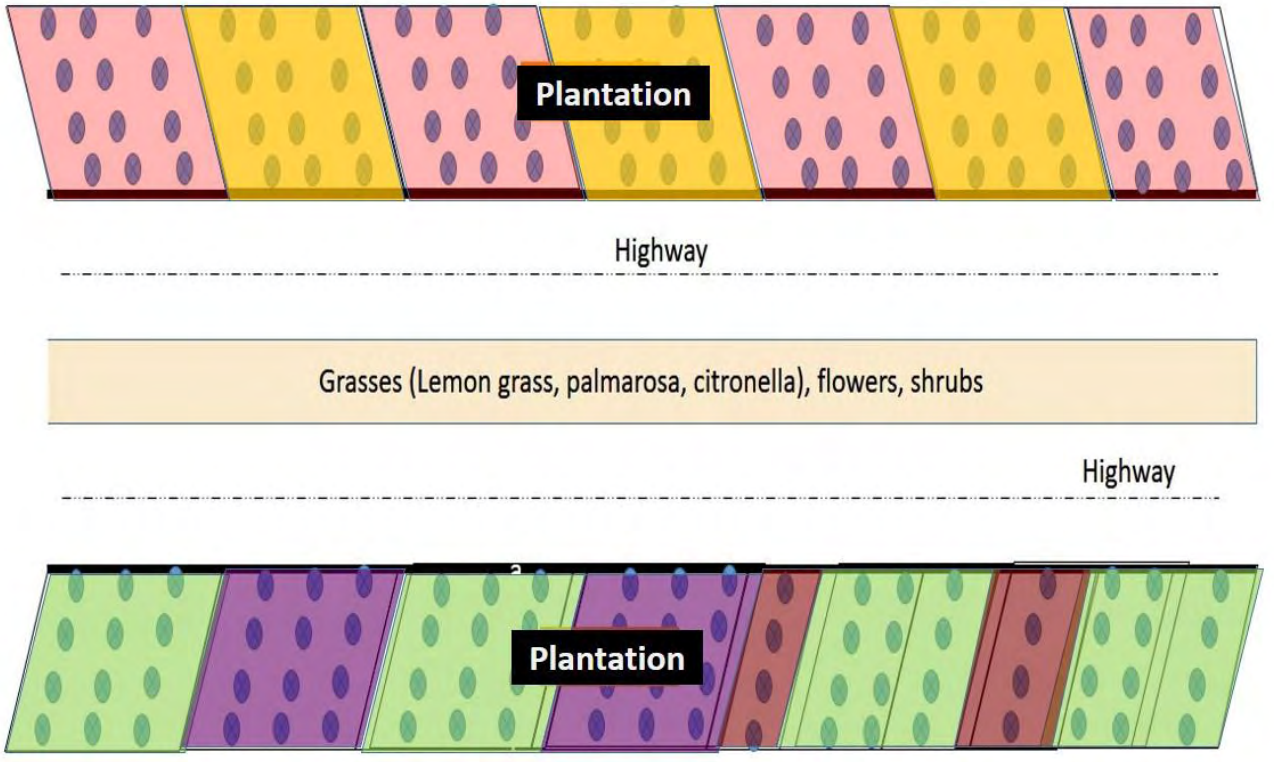


Fig. 1. A proposed plan for convergence of different Ministries and developmental schemes



(Similar colours represent same species but different accession)

Fig. 2. A plan outline of the plantation in the highway margin

ponding near the trees. These harvested water can be utilized for providing life-saving irrigation during rain deficit period.

3. In addition, use of modern tools of geoinformatics, a species suitability mapping of target roads would prove extremely useful. Such technologies will also provide an estimated value of carbon sequestration by such initiatives.
4. The source seeds/cuttings/propagules for plantation of a selected species has to be decided in such a way that it captures maximum genetic variability available in the locality. Expertize available with ICAR-NBPGR and local universities can be utilized for this purpose.
5. Nurseries are to be established near the plantation area. Village nurseries and nurseries established through Women SHGs may be involved to raise seedlings.
6. At least, 40 trees per accession should be planted in order to represent the total variability of the mother plant in the half-sib family/progenies.
7. Digitised records of each tree or population of a particular species will be maintained and seed samples with passport data will be conserved in the National Gene Bank established at NBPGR, New Delhi.
8. The NHAI, local forest department, NGOs, SHGs and individual tree allotees and village institutions may be brought to a common platform to devise the modalities for the management of the plantation.
9. Wherever possible, multitier plantation should be developed keeping view the light requirement of each species in every layer. While doing so the plantation guidelines prepared by the Indian Road Congress 2009 and approved by the National Highway Authority of India may be referred.
10. The highways are provided with channels to drain out the run off generated from the bitumen surface which goes to the small streams and finally to the big rivers; the water is not utilized for any gainful consumptive purpose. These run off, as high as 70-80 % of the rainfall (C value is 0.75-0.95 for road surface, roofs etc) can be harvested for irrigation to the plantation or the ground water may be recharged by using recharge filters and recharge pit.
11. Planting of trees on such lands will require use of advance technologies, so that after care of the trees is minimum and survival rate is higher. For example, use of hydrogels, will reduce the number of irrigations required for the young plantations, especially in the arid/drought prone areas. Similarly, instead of preparing a pit, the plantations can be done using bio-degradable bags, which will reduce the labour/input cost of planting and will enhance the survival percentage of the trees.
12. Incentives and reward schemes may be devised for successful maintenance and management of plantations.
13. Additional models used globally can be reviewed as part of the note as a learning lesson to implement such a valuable and need of the hour model of field preservation of perennial trees genetic resource.

In a nutshell we may exhort *"Save the trees, save the genes and secure the life of the future generations- May the Highways show the light"*.

List of Abbreviations with Translation from Hindi

CAMPA: Compensatory Aforestation Scheme under Compensatory Afforestation Fund Management and Planning Authority

ICAR: Indian Council of Agricultural Research

ICRAF-International Centre for Research on Agroforestry

INR: Indian Rupees

MGNREGA: Mahatma Gandhi National rural Employment Guarantee Act

MIDH: Mission for Integrated Development of Horticulture

MoAFW: Ministry of Agriculture and Farmers Welfare

MoAYUSH: Ministry of Ayurveda, Yoga and Naturopathy, Unani, Siddha and Homoeopathy

MoEFC: Ministry of Forest, Environment and Climate Change

MoRD: Ministry of Rural Development

MoRTH: Ministry of Road Transport and Highways

MoTA: Ministry of Tribal Affairs

NAP: National Aforestation Programme

NBPGR-National Bureau of Plant Genetic Resources

NHAI: National Highway Authority of India

PMGSY: Pradhan Mantri Gramin Sadak Yojna (Prime Minister's Rural Road Scheme)

PMVDVY: Pradhan Mantri Van Dhan Vikash Yojana (Prime Minister's Forest Resources Development Scheme)

VDK: Van Dhan Vikash Kendra (Forest Resources Development Centre)

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Indian J. Plant Genet. Resour. 34(1): 25–34 (2021)
DOI 10.5958/0976-1926.2021.00004.8

COMMENTARY

An Overview of Framework and Case Studies Related to ABS in Plant Genetic Resources

Pratibha Brahmi[1*], Vijaya Choudhary[2] and Vandana Tyagi[1]
[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*
[2]*Patent Associate, Lex Orbis, New Delhi-110001, India*

(Received: 05 February, 2020; Revised: 15 September, 2020; Accepted: 30 March, 2021)

The global framework to ensure benefit sharing arising out of the use of plant genetic resources is covered under different regimes such as the Convention on Biological Diversity (CBD), the International Treaty on Plant Genetic Resources and the Nagoya Protocol on Access to Genetic Resources. Complying with the CBD, the Government of India enacted the Biological Diversity Act, 2002 and set up the National Biodiversity Authority, State Biodiversity Boards, and Biodiversity Management Committees to regulate access and benefit sharing while utilizing biological resources and traditional knowledge. This article aims to highlight some cases of access and benefit sharing related to plant genetic resources to understand how the access and benefit sharing mechanism is applied in relation to plant genetic resources. Suggestions for improvements are listed in the conclusions including documentation of farmers and public institution bred varieties.

Key Words: Benefit sharing, Biological Diversity Act, Convention on Biological Diversity, ITPGRFA Nagoya Protocol, Plant Genetic Resources, Seed Sector

Introduction

Access to and utilisation of genetic resources is undergoing a paradigm shift with the advent of a new international benefit-sharing regime. It is crucial for PGR workers to be aware of various mechanisms for access and sharing of benefits for utilisation of plant genetic resources keeping in view the provisions of various international and national regulations, the realization of farmers' rights, breeders' rights, and the rights of patent holders. The issues are becoming more complex in view of the rapid advances in biotechnology where using virtual genetic resources is a possibility now. The relationship between IPRs and benefit sharing appears to be especially complex in the seed sector, where the material (variety) is either protected under the plant breeder's rights (PBRs) or plant patents, depending on the different domestic legal systems of countries.

A. Global Framework for Benefit Sharing of PGR

Convention of Biological Diversity (CBD)

The Convention on Biological Diversity (CBD) is the starting point for understanding the global regime on Access and Benefit sharing (ABS). The CBD, which entered into force in 1993, has three main objectives: 1) the conservation of biological diversity 2) the sustainable use of the components of biological diversity 3) the fair and equitable sharing of the benefits arising out of the utilization of genetic resources (UNCTAD, 2014). The major provisions in the CBD focusing on benefit sharing can be found in Article 8(j), 15, 16 and 19 of the Convention.

Though Article 8(j) of the CBD promotes the sharing of benefits arising out of the utilization of traditional knowledge of indigenous and local communities, it leaves the responsibility to achieve this objective on the domestic policies of the member countries. Article 15 of the Convention stipulates provisions regarding access to genetic resources. Article 16 focuses on access to and transfer of technology and Article 19 deals with handling of biotechnology and distribution of its benefits.

The two main concepts in the CBD that link the legal ABS to the national level and the provider country are Prior Informed Consent (PIC) and Mutually Agreed Terms (MAT). Prior informed consent (PIC) refers to permission given by the competent national authority of a provider country to a user prior to accessing genetic resources, in line with an appropriate national legal and institutional framework. Mutually agreed terms (MAT) refer to agreements reached between the providers of

[*]*Email: Pratibha.Brahmi@ icar.gov.in*

genetic resources and users on the conditions of access and use of the resources, and the benefits to be shared between both parties. (https://www.cbd.int/abs/about)

ABS serves as a compensation mechanism between the providers and the users of plant genetic resources. A brief account of international legal instruments that shape ABS involving plant genetic resources is provided in the following section to assess the emerging global approach.

1. Nagoya Protocol

Triggered by the limitations of the voluntary Bonn guidelines in operationalizing ABS, the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits arising from their Utilization to the Convention on Biological Diversity (The Nagoya Protocol, 2010) was adopted as a binding legal instrument to further facilitated access and sharing of benefits. The Nagoya Protocol sets out the rules and mechanisms for access to genetic resources and associated traditional knowledge (TK), and supports the fair and equitable sharing of benefits arising from their utilization. Along with the basic provisions of the CBD on ABS. The Protocol forms the central body of law that defines how the ABS system operates. The Nagoya Protocol rephrases and makes more concrete the objectives of the CBD pertaining to ABS (IEEP, Ecologic and GHK, 2012). Article 1 of the Protocol clarifies that benefit sharing includes appropriate access to genetic resources, appropriate transfer of relevant technologies, and appropriate funding. Accordingly, benefit sharing entails more than sharing a certain percentage of the profits when a product is developed on the basis of a genetic resource (Grieber *et al*., 2012). The Nagoya Protocol specifies that benefit sharing arrangements shall be established through MAT between the provider and user of genetic resources, thus on a contract basis. The Nagoya Protocol has also placed an ABS clearing house mechanism (ABSCHM) at its website https://www.cbd.int/abs/about/. All countries granting access to genetic resources upload the agreements on this site. In addition, procedures related to access from a country are uploaded at this ABSCHM for use by any researcher/entrepreneur https://absch.cbd.int/search/nationalRecords

2. ITPGRFA (The Plant Treaty)

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), 2004, popularly called "the Plant Treaty" establishes a multilateral system of access and benefit sharing for plant genetic resources, whereby contracting parties agree to virtually pool a subset of the genetic resources of 64 crops and forages to be used for "utilization and conservation for research, breeding and training for food and agriculture" (Article 12.3(a)). The benefits from use of plant genetic resources are to be shared fairly through methods such as exchange of information, access to technology, capacity building, sharing of monetary and other benefits of commercialization. The Treaty establishes a multilateral system (MLS) where parties who benefit monetarily from materials from the MLS are to make a payment to a joint fund which can be shared with all parties. Further, a Standard Material Transfer Agreement (SMTA) has been included in the Treaty, which should contain the benefit-sharing requirement (Moore and Tymowski, 2005) under certain conditions.

B. Access and Benefit Sharing in India

National Biodiversity Authority

Complying with the global framework, India has enacted the Biological Diversity Act (BD Act), 2002. The National Biodiversity Authority (NBA) is the apex authority dealing with all the matters relating to implementation of the Act and the Rules. The BDA established a three tier system for regulating the access to biological resources in India. At State level, the State Biodiversity Board (SBB) performs similar functions and at local level, the Biodiversity Management Committees (BMC) have been established for the implementation of specific provisions of the Act and Rules. NBA owes the central responsibility for ensuring fair and equitable sharing of benefit defined in the Act. The quantum of benefit shall be based on the purpose of access. The approvals are granted on case-by-case basis. Illustrative examples under different application forms are described (http://nbaindia.org/uploaded/pdf/ABS_ Factsheets_1.pdf)

Form-1: Access to biological resources and/or associated traditional knowledge

The application is approved after consultation with local bodies from whose jurisdiction the biological resources and associated traditional knowledge will be accessed and ascertaining that the material is not related to species that are rare, endangered and threatened. After the approval, an ABS agreement is signed between the NBA and the applicant. Section 40 exempts 190 species that are designated as normally traded commodities

(NTCs). The material used in conventional breeding and traditional practices is also exempted.

Form-2: Transfer of research results to foreign nationals, companies, non-resident Indians for commercial purpose or otherwise

Though section 5 exempts collaborative research from the requirement of prior approval of NBA, but when there is transfer of research results, the information presented in the application is reviewed by an expert committee to ascertain the purport, relevance and authenticity of the application. In the ABS agreement signed under this category of applications, clauses are included to ensure no third party transfers occur.

Example: The Indian Institute of Spices Research has – transferred bacterium *Pseudomonas aeruginosa* isolated from internal tissues of black pepper to Laboratory of Phytopathology, Wageningen University, the Netherlands for evaluation of antimicrobial compounds from bacterial endophytes against major pathogens of spice crops such as ginger, turmeric, black pepper and cardamom.

Form-3: Seeking Intellectual Property Rights (IPRs)

Section 6 of the Act requires mandatory approval of NBA in case invention is based on any research or information on a biological resource obtained from India. It further imposes royalty or benefit sharing fee arising out of the commercial utilization of such rights. Section 6 (3) provides for exemption if any person makes an application under the Protection of Plant Variety and Farmers Rights Act (PPVFRA).

Example: An ayurvedic doctor from Pune, India, has applied for obtaining a patent for preparation of an ayurvedic anti snake venom comprising four medicinal plants. In the treatment of victims of snake bite, this anti venom tablet 'pinak' acts as a temporary relief instantly before victim is taken to the hospital. In this case, NBA has fixed the benefit sharing as "2% of the Gross sales or Gross revenue of the product derived from the use of biological resources accessed." On commercialization of the patent product and as per the conditions of the agreement, the applicant has paid two instalments towards royalty as benefit sharing to the NBA. It is pertinent to mention that this is the first of its kind in India under the BD Act.

Form-4: Third party transfer of the accessed biological resources and associated traditional knowledge

Applicable in case of transfers of biological resources and associated knowledge amongst different users of value chain of research or commercialization.

Example: The Energy and Resources Institute (TERI) has sent dried root powder and extracts of Chlorophytum species for isolation and characterization of Biologically Active Saponins from Chlorophytum species to UFR des Sciences Pharmaceutiques et Biologiiques, Dijon, France. The MTA has also been developed between TERI, India and University of de Burgundy, France. The material transferred under the project will be utilized for identification of saponin molecules and study of cytotoxicity of saponins. The cytotoxic saponins identified in the project may further be worked on to develop anti-cancer drug while the insecticidal saponins may be developed into suitable formulation for utilization as environment friendly integrated pest management programmes.

Though the BD Act as well as the rules referred to monetary and non-monetary benefit sharing, it is the NBA guidelines on ABS, 2014 that clearly specifies the kinds and the method of calculating monetary and non-monetary benefits. In most of the cases, monetary benefit sharing was preferred over non-monetary benefit sharing.

Non-Monetary benefit sharing may be in the form of grant of joint ownership of intellectual property rights to the National Biodiversity Authority, or where benefit claimers are identified, to such benefit claimers; – transfer of technology; location of production and R&D units in areas which will facilitate better living standards to the benefit claimers; association of Indian scientists, benefit claimers and the local people with R&D in biological resources and bio-survey and bio-utilization; setting up of venture capital fund to aid the cause of benefit claimers; payment of monetary compensation and non-monetary benefits to the benefit claimers as the National Biodiversity Authority may deem fit.

However, as per the guidelines on Access and Benefit sharing issued by NBA, following forms of non-monetary benefit-sharing options may be included. Options are- providing institutional capacity building – including training on sustainable use practices; transfer of technology or sharing of R&D results within Indian institutions/individuals/entities; strengthening of capacities for developing technologies and transfer of technology to India and/or collaborative R&D programs with Indian institutions/individuals/entities;

– contribution/collaboration related to education and training in India on conservation and sustainable use of biological resources; location of production and R&D units, and measures for conservation and protection of species in the area from where biological resource has been accessed, contributions to the local economy and income generation for local communities; – sharing of scientific information relevant to the conservation and sustainable use of biological diversity, including biological inventories and taxonomic studies.

Monetary benefit sharing

As per the ABS Guidelines 2014, the biological material of high economic value is used for research purposes, an upfront – payment may be required to be paid. The amount of which is to be decided between the applicant and the NBA. In case the access of biological resources is for commercial utilization, the benefit sharing may include an upfront payment of not less than 5% on proceeds of auction or sale amount, as decided by the NBA or the SBB. For transfer of results of research, if the applicant has received any monetary benefit, (s)he shall transfer 3.0 to5.0% of the monetary consideration to the NBA as agreed in the ABS agreement. For cases involving commercialization of IPRs obtained on inventions related to genetic resources, the applicant shall pay to the NBA monetary and or non-monetary benefit as agreed upon between the applicant and the NBA. Where the applicant himself commercializes the process/product/ innovation, the benefit sharing should be in the range of 0.2 to 1.0% based on sectoral approach, calculated in term of annual gross ex-factory sale minus taxes. If the applicants license the process/product/innovation to a third party for commercialization, they shall pay to the NBA 3.0% to 5.0% of the fee received, and 2.0% to 5.0% of the royalty amount received annually from the assignee based on sectoral approach. For transfer of research results to another party, the applicant is required to pay 2.0%to 5.0% of any amount or royalty received from the transferee throughout the term of the agreement. In case the biological resource has high economic value, an upfront payment may also be mutually agreed upon.

The Protection of Plant Varieties & Farmers' Rights (PPV&FR) Act, 2001

The PPV&FR Act, 2001 in India is a sui-generis system established in compliance with Trade Related Aspects of Intellectual Property Rights (TRIPs) to protect IPR on plant varieties. The Act also contains provisions for determination of benefit sharing. Upon registration of a plant variety, the Authority shall publish contents of the certificate of registration inviting claims for benefit sharing under section 23 read with rule 41. Any person or group of persons or firm or government or non-governmental organization shall submit its claim of benefit sharing to such variety in the prescribed manner and within the prescribed period. The breeder of registered variety is intimated about the same and he may oppose such claim. Upon hearing both the parties, the Plant Variety Authority shall determine the quantum of benefit sharing taking into account the following criteria namely:

a. The contribution of the claimant in selecting, conserving and providing the genetic material,
b. The contribution of such genetic material in providing one or more traits which conferred high commercial value to the variety, and
c. The contribution of such genetic material to impart high combining ability to the parents of the hybrid variety relating to benefit sharing.

While disposing of the claim under section 23(4) of the Act, the Plant Variety Authority shall take into consideration the following aspects for determining the quantum of benefit sharing:

a. The extent and nature of the use of genetic material of the claimant in the development of the variety relating to which the benefit sharing has been claimed;
b. The commercial utility and demand in the market of the variety relating to which the benefit sharing has been claimed.

The amount of benefit sharing to a variety shall be deposited in the National Gene Fund established under section 45 of the Act. Hence, the benefit sharing under PPV&FR Act is only monetary benefits. This form of recognition is for communities or individuals contributions towards popularizing local varieties and indirectly a mechanism of benefit to conservers of local diversity of crop plants. Another mechanism to benefit to local farmers and communities is registration of farmers/ communities can register a variety of local importance with good economical or quality traits and they are provided all rights under PPVFR Act as provided to the breeders of a new variety. So far, the

benefit sharing under the Act is recognized in the form of Plant Genome Savior Award and Recognition. Under the Indian Patents Act, it is mandatory to disclose the source or geographical origin of biological material in the specification, when the invention is based on use of biological material (Section 10). In case of non-disclosure or wrong details are furnished, it can be a ground for revocation of granted patent (Section 64). Sections 25(1)(k) and 25(2)(k) of the Patents Act make provision for pre-grant and post-grant opposition against inventions involving traditional knowledge. Similarly, Sections 25(1)(j) and 25(2)(j) of the Patents Act makes provisions for pre-grant and post-grant opposition for not disclosing or wrongly disclosing the source or geographical origin of biological material used in the invention. Furthermore, Section 64 makes provision for revocation of patents where the complete specification was anticipated by the knowledge possessed by local or indigenous communities in India or elsewhere, or if the complete specification does not disclose or wrongly mentions the source or geographical origin of biological material used for the invention.

Nevertheless, there is no mutual cooperation between the Patents Act and the BD Act in dealing with benefit sharing. The Patents Act does not talk about benefit sharing at any stage in the Act. Section 6 of the BD Act makes it mandatory for the IPR applications to obtain prior approval from the NBA before obtaining patents from the Patent Office within or outside India. This requirement is being implemented at the Indian Patent Office with the help of the Guidelines for Processing of Patent Applications relating to Traditional Knowledge and Biological Material issued by the Controller of Patents on 8th November 2012. However, there are instances wherein this requirement is not being taken seriously by the Patent Office itself. It was noticed that patents were granted on many occasions where the applicant has not obtained prior approval from the BD Act.

Certain case studies from around the world may shed some light on how sharing of benefits is in practice in other countries when compared to India.

C. Global Case studies on benefit sharing related to plant genetic resources

1. The Genetic Resources Recognition Fund of the University of California, Davis, USA (2004)

A wild rice species *Oryza longistaminata* from Mali is resistant to rice blight. Blight resistance was attributable to a section of DNA, found on a single chromosome, termed *Xa21*. The University of California (UC), Davis team identified and cloned *Xa21*. UC Davis filed a patent on the *Xa21* gene sequence. UC Davis entered into agreements licensing the gene to two agricultural biotechnology companies and will use the Genetic Resources Recognition Fund as a mechanism to share any resulting financial benefits. The Fund money was planned to be utilized for funding Fellowships for scholars from source countries such as Mali. Depending on the magnitude of the monetary benefits that arise from the commercialisation of *Xa21*, scholarships may be offered to students from Mali (a country of origin that originally provided the genetic resources in question). GRRF has no money in the Fund as of now; this will only accrue if the licensee companies commence sales of product incorporating Xa21. There could also be voluntary contributions, however contribution to conservation of wild species (*Oryza longistaminata*) is an indirect benefit through raising awareness of the importance of genetic resources for crop breeding efforts. This case is a purely voluntary initiative. Many institutions/ universities are engaged in commercialization of genetic resources in the field of plant genetic resources, but few have taken initiative to develop mechanisms for benefit sharing and thus it's a rare example. An important lesson learnt is that where benefit sharing is a new concept, it is simple to develop a mechanism that fits into the existing procedures and institutional structures**.** (http://www.cropgeneticsinnovation.org/genetic-resources-recognition-fund-grrf/).

2. The Teff case, Ethiopia

Ethiopia is the centre of origin and diversity for Teff (*Eragrostis tef)*. The Teff grain is gluten free, and it is increasingly desired in Western markets. It also has various other attributes of interest to the food industry. In 2004 , a ten year access and benefit-sharing (ABS) agreement was concluded for the breeding and development of teff between the Institute for Biodiversity Conservation (IBC), the Competent National Authority for ABS in Ethiopia- the Ethiopian Agricultural Research Organization (EARO), and the small Netherlands-based company Health and Performance Food International (HPFI). The central focus of HFPI was to develop teff products for Western markets in forms such as bread, sports bars and beer. The agreement stipulates an array of long-term benefits to Ethiopia which includes:

(i) an agreement by HPFI to pay the IBC – a lump sum of profits arising from use of teff genetic resources;

(ii) royalties to the IBC of 30% of net profit from the sale of seeds of teff varieties;

(iii) a license fee, linked to the amount of teff grown by HPFI or anybody supplied seed by HPFI; and

(iv) contributions by HPFI of 5% net profit, no less than €20,000 per year, to a fund named the Financial Resource Support for Teff (FiRST), established to improve the living conditions of local farming communities and for developing teff business in Ethiopia. For this, HFPI agree to provide:

- support to local Ethiopian farming groups to grow high yielding Teff varieties;
- coaching and teaching farmers 'improved agricultural practices';
- introducing tools to improve the seeding and harvesting of Teff in Ethiopia;
- the introduction of high yielding Teff varieties;
- implementing new standards for storage and cleaning Teff.

The agreement also involves the transfer of Dutch scientific knowledge and experience with product innovation to Ethiopia. HPFI will also share its research results on teff and will involve Ethiopian scientists in its research. To this end a research breeding program has been set up between EARO in Debre Zeit. Unusually, the agreement sets out a commitment by HPFI to create joint ventures with Ethiopian counterparts to establish teff businesses in Ethiopia.

Though HFPI contributed to the fund as per the benefit sharing agreement until 2017 no benefits had been distributed to farmers. This has been due in part to a lack of clarity about its governance. Implementation of the ABS agreement also remains thwarted by a decision of the Ethiopian government to ban teff exports. The reasons for this are to support Ethiopians small scale agriculture and to ensure adequate local supply of teff. According to HFPI, there is no shortage of teff, but there is resistance within Ethiopia to changing farming methods and increasing volumes produced.

The complexity of these factors, and their unintended negative impact on the ABS agreement, yields important lessons for other ABS agreements where the contract deals not only with the provision of access to genetic material, but also with the trade of it as a commodity. Finally, the process has highlighted the critical need for provider countries to develop ABS negotiating and administrative skills and to have ready access to information about markets and market potential (Bayou, 2005). However, no benefit was accrued practically and Ethiopia lost the rights to utilize and gain benefits from its own resources in countries where the patent was valid. The case was well in advance of its time and considered as pilot case for the Implementation of the CBD in terms of access and benefit sharing. A very small amount of benefit in form of cash (about 4000Euros) and a research project were the only concrete benefits generated.

3. Ball Horticulture and the South African National Biodiversity Institute

The South African National Biodiversity Institute (SANBI) is a public institution engaged in conservation, sustainable use and promotion of economic use of exceptionally rich biodiversity of South Africa. In 1999, SANBI entered into a Research and Licensing Agreement with the Chicago-based company Ball Horticulture. In terms of the agreement, SANBI was to supply Ball with different categories of "live plant material", including all horticultural groups as well as research expertise and knowledge of the plants and their habitats. For providing this service, SANBI obtained an annual research service fee and royalty in case of commercialization. In the event of profits being derived from the deal, a Biodiversity Trust Fund was intended to be established by the SANBI, for the purpose of capacity building in the local horticultural industry and for conservation and community development projects. Part of the agreement is for Ball Horticulture to present one technical seminar on ornamental horticulture a year and to host interns each year for training in Chicago by Ball. A significant result of this training is that increased selection and breeding take place in-house at SANBI, enabling improved material to be sent to Ball, which commands a higher royalty for SANBI and reduces the time the product will take to reach market.

Several lessons emerge from this case that is instructive. The difficulties that SANBI has faced in switching hats between being a public interest body and a commercial player are especially useful to learn from.

More positively, there is now increasing recognition of the role that SANBI can play in initiatives to investigate the sustainable use of South Africa's indigenous plants. The expectations of technology transfer are also significant. The lack of experience in developing agreements of this nature by either SANBI or Ball also yields important lessons. Legal expertise was, and continues to be, limited in this field, and this significantly affects the effectiveness of negotiating and drawing up fair and equitable benefit-sharing agreements. Lastly, the partnership that has developed between SANBI and Ball is considered a useful model from which to develop other ABS arrangements in the horticultural sector and is believed by those involved to be a more ethical and sustainable approach than a once-off collection agreement (Sarah Laiid, 2008).

4. Natura, Brazil: The Use of Traditional Knowledge and Community-Based Sourcing of "Biological Materials" in the Personal Care and Cosmetics Sector

Natura is a Brazil based company involved in sale of cosmetics, personal hygiene, and perfume products. In 2000, Natura formed EKOS Line, which prepared natural based cosmetic products the raw material of which is sourced majorly from communities around Brazil. Natura's partnerships with communities for the sustainable supply of raw materials, and its use of traditional knowledge to develop new ingredients or products, pre-dated Brazilian ABS legislation. Prior to any legal framework, the company established a package of benefits and equitable practices that included:

1. providing training and capacity-building in agricultural techniques, and equipment and other materials to add value to raw materials, in order to promote greater benefits within the community;
2. supporting and assisting with the development and administration of community associations;
3. seeking prior informed consent and payment before using any images of people from communities in marketing; and
4. setting up funds in communities through allocation of a percentage of net sales; this is seen as an investment Natura makes in particular communities, and has been established in only one community to date, Iratapuru, and another is pending.

The company distinguishes between different types of relationships and benefits that result for local groups:

1. *Access Agreements* for genetic resources and traditional knowledge that include benefit sharing in nonmonetary forms, as well as a percentage of net revenue;
2. *Local Development* projects that include investments made by Natura in specific communities to build local institutions and capacity, not tied directly to accessing genetic resources or traditional knowledge;
3. *Supply partnerships*, which do not involve ABS agreements but include support for production and harvesting of raw materials, and facilitation of links between communities and third-party processors, from whom Natura buys processed products such as oils or extracts.

The agreement between Natura and the community was non-exclusive and involves payment of royalties and an upfront payment to the Association. The agreement has been signed by Natura and concerned association but has not yet been approved by CGEN (the administering body for both existing and any new sourcing partnerships, and those that involve accessing traditional knowledge) given the complexity of the issue and lack of clear legal guidance on access and benefit-sharing associated with traditional knowledge. (Sarah Laird, 2008)

5. Access and Benefit-Sharing Agreements in the Commercial Development of Hoodia

The present case is a well-documented example wherein the poor and uneducated indigenous community had to employ a lawyer and put up a fight to an unwilling government owned institution in order to share the benefits.

The product in focus is an appetite suppressant extracted from Hoodia (*Hoodia gordonii*), a leafless succulent plant native to the Kalahari Desert in South Africa. The fleshy stem of Hoodia was chewed by the members of the San community of southern Africa on their long hunting and gathering trips to quench thirst and suppress hunger. They shared this traditional knowledge with a Dutch anthropologist who published his finding in a book and following the clue, the South Africa's - CSIR began carrying out R&D into the properties of Hoodia and identified the active ingredient named 'P57' and got it patented. Later CSIR signed a license agreement with Phytopharm, a small British company dealing in phyto-medicine and later with Pfizer, a

US based pharma-giant, for further development and commercialization of the patented technology. Unilever was also contacted to market Hoodia-based products as anti-obesity drugs and also as functional foods. All this happened without the knowledge and permission of the San community. This act of CSIR was severally criticized by media and when the San people came to know about this, they formed the Working Group of Indigenous Minorities in Southern Africa (WIMSA) with an aim to represent San communities across different regions of Africa and to negotiate for benefit sharing with CSIR, the government organization guilty of biopiracy. After a long discussion, CSIR agreed to acknowledge the role of the San community, their TK and signed a MoU, the key provisions of which are mentioned below:

1. The San communities are to receive 8 percent of all the milestone payments that are received by CSIR from the license firm, Phytopharm, so long as the drug is in clinical development over the forthcoming years.
2. Of all royalties received by the CSIR from Phytopharm as a result of the successful exploitation of products, 6 per cent go to the San people for the duration of the royalty period, or as long as the CSIR received financial benefits from commercial sales of the products.
3. Any IP arising from the use of the TK related to Hoodia and from the patents for P57 will remain vested exclusively with the CSIR, and the San Council to have no right to claim any co-ownership of the patents or products derived from the patents.
4. Both the parties will conserve the biodiversity and undertake best-practice procedures for plant collection.
5. The CSIR will lay the groundwork for further collaboration in bioprospecting.

The San Hoodia Benefit Sharing Trust was formed for proper channelling of fund flow and its management to improve the living condition of San community. There are several challenges to this agreement as San people don't receive any revenue from the sales of many Hoodia based products currently traded in the international market because such products are commercialized outside of the CSIR agreement (Srivastava, 2016).

6. Osyris project

Osyris quadripartite, commonly known as African sandalwood is the source of oil used in form of compounds in cosmetics, perfumery, food and flavouring industry. The derivatives are being used in the Osyris project. Aditi International, Mumbai collaborating with Docomo Oils PLC, is developing products with the involvement of South Omo- tribals of Ethiopia people. Ethiopian Biodiversity Institute (EBI) grants access based on PIC and MAT. The company invested over $ 3 million to start the industry and provided 125 Ethiopians permanent employment. In terms of benefits, the company paid US$ 50000 as upfront payment and agreed to pay 3.5% of net profit. A minimum of $ 2 million of foreign revenue will flow to the country and the Aditi International has pledged to pay 2% of the cost of all raw material purchased from the community to establish nurseries towards rehabilitation and sustainable use. Collection site association also receives 30% of the purchase price of the raw material as assistance to grow and support initiatives within their communities (UNDP-GEF 2018)

D. Indian examples of benefit sharing

India's engagement with Access and Benefit Sharing (ABS) issues emanated through the most discussed *'Kani case'* where the Kani tribe and their traditional knowledge relating to the use of a plant called Arogyapacha was discussed. The local communities were recognized and rewarded for providing the genetic resource and associated traditional knowledge that resulted in commercialization of a drug with anti-fatigue properties called 'Jeevani'. This experience of ABS pre-dates the entry into force of the CBD (NBA Factsheet). Some of the cases that are post-CBD are discussed below:

1. PepsiCo India

In 2007, the National Biodiversity Authority entered into two agreements with PepsiCo, one for commercial access and the other for third-party transfer of *Kappaphycus alvarezii*, a type of seaweed (a species of red algae) from the Gulf of Munnar area of Tamil Nadu; for exporting it to Indonesia, Malaysia and the Philippines for commercial utilization in the food and cosmetics industry. NBA received certain amount of money from Pepsico but failed to distribute it to the local community till 2010. The reason being the non-constitution of Biodiversity Management Committees by State Bio-diversity Board of Tamil Nadu in coastal villages to distribute the benefits accrued with 754 benefit claimers spread across 4 districts in Tamil Nadu. This case shows that even when revenue

is collected from companies, the distribution of benefits can be difficult. Further, there is also lack of clarity about how community development is to be assisted. The fact that the training given to women self-help groups constitutes an important benefit from this agreement is not justified as it is not clear whether the above said training was for skills for sustainability or was just to facilitate exports. This illustrates the inadvisability of relying on raw materials as a source of revenue and development for local communities.

2. Bio India Biologicals

In another case, the NBA collected certain amount of money from Bio India Biologicals for the export of 2000 kg of nee*m (Azadirachta indica)* to Japan. According to the NBA, members of the local community of Amarchinta village in Andhra Pradesh collected and dried the leaves "by undertaking a few special operations" before handing it over to the company for export. The NBA states that it has transferred a "part of the royalty amount" to the local biodiversity body in Amarchinta for "planting neem saplings and creation of awareness about biodiversity conservation (Dhar *et al*., 2014). The sale of neem abroad for a small amount of money seems counter to the very principles on which the issue of biopiracy has been raised. Simply transferring a small amount of money to the local community to plant neem saplings is not much benefit sharing. Criticism of this approach with regard to benefit sharing is being voiced in India, questioning the reasons why local communities have not been consulted and why benefits have not yet reached the communities (Bhutani and Kohli, 2010). In this case, as in the PepsiCo example, the focus has been on a commodity rather than on genetic resources. This gives rise to questions about the implications of dealing with commodities under ABS laws, rather than purely genetic resources as envisaged under the CBD. There are cases of spices varieties developed by ICAR using farmers' traditional knowledge but as the varieties were old and community possessing traditional knowledge is difficult to locate the strategy to be adopted to share the benefit. In another case, a private seed company utilized a farmer variety in wheat breeding program. One time monetary benefit was given to the farmer and submitted the legal acquisition certificate when application for plant variety protection is made for the variety developed. Farmer was neither entitled to any IP right nor was any royalty given for benefit arising out of commercialization.

Discussion and Conclusion

The mechanism of benefit sharing is complex in the agriculture sector, as the varieties are protected by plant breeder rights, which is different from the patents granted in other fields. The framework for sharing benefits exists under national and international convention/agreements. The spirit of such instruments has not been translated into domestic laws. There is a need to develop the technical and administrative skills to make of existing provisions by analysing available case studies. The case studies show that, although monetary benefits were gained by the use of biological resources, the non-monetary benefit sharing needs to be encouraged by the Authorities while determining specifics of benefit sharing. In fact, while dealing with access to community related genetic resources; non-monetary benefits would be a lasting benefit to the community and conservation of biodiversity in the locality or region. Osyris project of Ethiopia is the perfect combination of monetary and non- monetary benefits derived from the use of genetic resources simultaneously addressing the conservation concerns. However, very few such cases are available where benefit sharing mechanism is defined for the use of plant genetic resources. There are several cases where highly valuable public domain ICAR/SAU crop varieties (varieties notified under section 5 of the Seed Act which crossed 15 yrs protection granted under Seeds Act) were utilized in the breeding program by private seed companies. Being in the public domain, use of these varieties have no obligation for benefit sharing. Companies are known to make large profits, whereas the benefits are not flowing back to the breeding institutions or conservation effort either in monetary or non-monetary ways.

There is a need to develop a database of all existing plant varieties in India with data on original breeders and public sector organizations as well as farmers varieties which have bred these varieties. There is a provision in the PPV & FR Act for such a Plant Variety Register [Sub-section (1) of Section 13]. This database could not only serve as a 'prior art' for reference, it may also help in cases of disputes, in the future. The NBA shall include mandatory listing of farmers varieties in People's Biodiversity Registers envisaged for every local body or Biodiversity Management Committees. It is expected that ICAR take some measures to bring public domain varieties within the ABS framework. This will not only generate revenue for ICAR/SAU but will also pave way for an effective benefit sharing system.

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Indian J. Plant Genet. Resour. 34(1): 35–42 (2021)
DOI 10.5958/0976-1926.2021.00005.X

RESEARCH ARTICLE

Assessment of Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Germplasm Grown under Rainfed Conditions of Kashmir

Sheikh M Sultan* and Susheel Kumar Raina
ICAR-NBPGR Regional Station, Srinagar-191132, Jammu & Kashmir, India

(Received: 17 June, 2020; Revised: 19 November, 2020; Accepted: 01 January, 2021)

Assessment of genetic diversity and germplasm improvement is fundamental for sustainable production of different crops including wheat. 200 accessions of wheat germplasm were evaluated during two successive *rabi* seasons of 2016-17 and 2017-18 along with two national (GW-322 and PBW-343) and one local (HS-240) checks at ICAR-NBPGR RS Srinagar. Principal component and cluster analysis were carried out involving 7 quantitative traits of plant height (cms), flag leaf length (cms), flag leaf width (cms), days to 75% spike emergence, days to 80% maturity, grain yield/plant (g) and 100-seed weight (g). Moderate positive correlations were observed between flag leaf length and days to 80% maturity as well as between these traits and plant height. Days to 80% maturity showed stronger positive correlation with 75% spike emergence which in turn was also strongly correlated with flag leaf length. The results of PCA revealed that the first 4 principal components contributed 76.1% of the total variability with first two components accounting for more than half (51.1%). The divergence analysis based on Euclidian method indicated the presence of adequate genetic diversity with four clusters showing distinct characteristics. 25 promising genotypes identified for each trait, could be useful to plan crosses and study the extent of heterosis.

Key Words: Cluster analysis, Genetic diversity, Principal components, Promising genotypes, *Triticum aestivum*

Introduction

Triticum aestivum L. known as common or bread wheat represents 90% of the total world wheat production while other 10% is contributed by *Triticum turgidum* subsp. *durum* which is known as durum wheat (Ateş Sonmezoğlu *et al*., 2012). In fact, bread wheat is a very diverse and widely adaptable cereal crop (Levandi *et al*., 2014) and is one of the most important and staple food crops in the world standing next to rice, both in area and production occupying 17% of crop acreage world over, feeding about 40% of world population and providing 20% of the total food calories and protein in human nutrition (Gupta *et al*., 2005). India is second largest producer of wheat after China and with 99.70 million tonnes during 2017-18 contributed 12.91% of total global production (Ramdas *et al*., 2019). In India, the major wheat producing states are Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra and Gujarat. These states contribute about 87.5% of total wheat production in the country (Kumar *et al*., 2014). In the union territory of Jammu and Kashmir, wheat is cultivated as *rabi* crop, however in Gurez and Tulail areas and also in adjacent union territory of Ladakh it is cultivated as summer crop. In Jammu province along with maize, it is the staple food crop while in Kashmir rice is the staple food crop and wheat is cultivated in limited areas predominantly as rainfed crop especially in remote hilly areas and in the foothills of the valley. In Ladakh, wheat is cultivated less commonly than naked barley, the latter being staple food crop of that region. Few decades back wheat was more commonly cultivated in Kashmir, however owing to the popularization of horticultural as well as fodder crops especially oats, there has been a drastic decline in wheat cultivation in the region. Absence of cold tolerant and short duration varieties may be among other reasons for loss of interest in this crop among local farmers. Nevertheless there has always been a good scope for wheat cultivation especially under rainfed conditions in dry areas of the region. The demand for wheat is expected to grow faster than any other major agricultural crop. With a limited scope for increasing the crop acreage the only option is to increase existing average yield as the production target in the country has been fixed at 140 million tonnes by

*Email: sheikhmsultan@gmail.com

the year 2050 (ICAR-IIWBR Vision Document, 2015). Exploring genetic diversity among wheat genotypes besides evaluation and utilization of this genetic diversity is fundamental to the sustainable production of the crop. It is very well documented that morphological and agronomic characterization provides a simple and direct way of determining genetic variations among genotypes while at the same time assessing their performance under normal growing conditions. The present study was therefore undertaken to assess the magnitude of genetic diversity and characters contributing towards total genetic diversity in some bread wheat genotypes under rainfed conditions of Kashmir for effective selection in future breeding programmes. In the study, cluster and principal component analyses has been used for genetic diversity analysis.

Materials and Methods

The study was carried out under rainfed conditions at the Experimental Farm of ICAR-NBPGR Regional Station Srinagar, Jammu and Kashmir (33°59′ N latitude, 74°47′ E longitude, 1639 m above sea level) during two successive *rabi* seasons of 2016/2017 and 2017/2018. The experimental site is situated on dry *Karewa* land having soil pH of 6.23 and average normal monthly rainfall 52 mm. Two hundred accessions of *Triticum aestivum* L. germplasm along with two national (GW-322, PBW-343) and one local (HS-240) check varieties were used in the present study. These 200 accessions are given in supplementary list. The germplasm was supplied by Evaluation Division of ICAR-National Bureau of Plant Genetic Resources, New Delhi. Some of the genotypes used in the study were earlier collected by the station from far-flung, remote and hilly areas of Kashmir and Ladakh. The experiments were laid out in augmented block design with bed width of 2 m and row to row and plant to plant distance of 25 cm and 10 cm respectively. Recommended agronomic practices and protective measures were followed to grow a healthy crop. Fertilizers @120:60:40 kg NPK/ha were applied for better crop production. Weeding was done by hand whenever necessary. Data on plant height (cm), flag leaf length (cm), flag leaf width (cm), days to 75% spike emergence, days to 80% maturity and grain yield/plant (g) were recorded on five randomly selected plants of each germplasm line ignoring those on peripheries. 100 seed weight (g) was also recorded in every genotype. These quantitative traits were then analyzed by cluster and principal component analysis. Principal components analysis (PCA) was carried out on the correlation matrix calculating the mean data of the accessions. The genotypes in each resultant cluster were also analyzed for basic statistics. Correlations between different traits were determined by Pearson's correlation. Statistical tests were carried out by the Statistical Package for Social Sciences (version 21) and OpenStat softwares.

Results and Discussion

Basic statistics on pooled data for quantitative traits showed a considerable variability in 200 accessions of wheat under study (Table 1). Very high variance was observed for plant height. Medium to high variance was observed for flag leaf length, days to 75% spike emergence and grain yield/plant. Small genetic variance was observed for flag leaf width, days to 80% maturity and 100-seed weight. In Kashmir, wheat is sown as *rabi* crop and its growth is arrested during winter months remaining under snow cover thus crop duration is significantly increased. If the winter is prolonged over the months of February and March and temperature is significantly reduced, the crop duration is further increased. Even in our present study during the year 2016/17, the days to 75% spike emergence and days to 80% maturity ranged from 136-137 days and 195-200 days respectively, while during the year 2017/18 these parameters ranged from 116-150 days and 180-185 days respectively. The reason for early spike emergence and maturity during later year of 2017/18 was comparatively drier winter with almost negligible snowfall and rainfall during the months of February and March. After the winter is over and temperature increases fast, the spike emergence and ultimately maturity ensues. Most of the wheat accessions used in the present study are reported to be early maturing types in other parts of the country. However, we have not been able to identify some significant early maturity lines under local Kashmir conditions.

Simple correlation analysis: In order to assess relationship between different traits, simple correlation coefficients between grain yield and its components has been computed and is presented in Table 2. While positive correlations of different magnitude were observed between different traits studied, the seed yield/plant showed weak negative correlation with plant height and flag leaf length. Stronger positive correlations were observed between days to 80% maturity and days to 75% spike emergence and between days to 75% spike emergence and flag leaf length.

Table 1. Basic statistics for seven quantitative traits of 200 accessions of wheat evaluated during 2016/17 and 2017/18

Trait	Mean ± SD	Minimum value	Maximum value	Variance
Plant height (cms)	96.9 ± 11.4	68.0	134.3	130.1
Flag leaf length (cms)	22.9 ± 2.4	16.8	31.4	5.7
Flag leaf width (cms)	1.49 ± 0.19	1.10	2.15	0.04
Days to 75% spike emergence	141.9 ± 4.6	131.5	152.0	21.7
Days to 80% maturity	190.7 ± 1.0	188.0	192.5	1.0
Grain yield/plant (g)	20.499 ± 5.533	5.933	45.820	30.6
100-Seed weight (g)	3.695 ± 0.533	2.250	5.350	0.3

Table 2. The Pearson correlation coefficient matrix for agro-morphological traits in 200 accessions of wheat evaluated during 2016/17 and 2017/18

Trait	PH	FLL	FLW	DSE	DMT	SY	SW
PH	1.0000						
FLL	**0.3031	1.0000					
FLW	**0.1473	**0.2813	1.0000				
DSE	**0.2165	**0.4138	**0.1589	1.0000			
DMT	**0.3020	**0.3680	**0.1484	**0.6039	1.0000		
SY	-0.0368	-0.0937	**0.1375	0.0621	0.0542	1.0000	
SW	0.0519	0.0411	**0.1378	**0.1520	0.0672	**0.2567	1.0000

PH=Plant height, FLL=Flag leaf length. FLW=Flag leaf width, DSE=Days to 75% spike emergence, DMT=Days to 80% maturity, SY=Grain yield/plant and SW=100-Seed weight

** Significant at 1% level of probability

Principal component and Cluster analysis: The quantitative trait of yield is a stated goal for plant breeders which is under the control of many genes, thus selection based on yield *per se* may not be successful for its improvement. Selection of yield contributing traits having relatively high heritability thus becomes important in overall improvement in yield potential. However, selection based on simple correlation coefficients between different traits may not be too helpful. Thus, multivariate statistical analysis of the agro-morphological data obtained on 200 wheat germplasm accessions during the course of present investigation has been done for deeper understanding of relationship between the traits. The correlation coefficient analysis has been found to be useful in the identification of characters that are positively correlated with yield (Maqbool *et al*., 2010; Bode *et al*., 2012) while the evaluation of phenotypic variability by multivariate analysis gives the possibility to include a large number of accessions and to identify the most suitable resources for special traits (Goel *et al*., 2015). The identified accessions for special traits can then be effectively used in wheat breeding programmes**.** Therefore, extent of genetic diversity in wheat accessions in present study has been measured by cluster analysis and principal component analysis (PCA) for their effective evaluation and utilization. The cluster analysis is an appropriate method for assessing family relationships (Mellingers, 1972) and the merit of using PCA over cluster analysis is that each germplasm line can be assigned to one group only (Mohammadi, 2002).

Results from the principal component analysis for the two year combined data showed that four components of PC1, PC 2, PC 3 and PC 4 accounted for 76.1% of the total variation in agro-morphological traits studied contributing 32.4%, 18.6%, 13.5% and 11.5% of the total variation respectively (Table 3). Eigen values given in the table show that relative discriminating power of the principal components was high for PC 1 (2.271) followed by PC 2 (1.304), PC 3 (0.942) and PC 4(0.806). The first four components explaining 76.1% of total variation were taken under study. The number of components was also determined with the help of the highest slope in Scree plot (Fig. 1). The Scree plot explains the percentage of variance associated with each principal component. The most effective traits in the first component were flag leaf length, days to 75% spike emergence and days to 80% maturity (Table 4). Major effective traits in the second component were grain yield/plant and 100-seed weight. In the third component, flag leaf width was the main effective trait while plant height and 100-seed weight were the most effective traits governing fourth

Table 3. Eigen values and percentage of total variance for PCA in 200 accessions of wheat evaluated during 2016/17 and 2017/18

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Eigen value	2.271	1.304	0.942	0.806	0.748	0.554	0.374
Percent variance	32.4	18.6	13.5	11.5	10.7	7.9	5.3
Cumulative percent variance	32.4	51.1	64.5	76.1	86.7	94.7	100.0

Table 4. Vector loadings for yield contributing traits in 200 accessions of wheat evaluated during 2016/17 and 2017/18

Trait	Communalities	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6	Vector 7
PH	0.989	-0.361	-0.176	0.230	0.788	-0.370	-0.068	-0.153
FLL	0.672	-0.469	-0.213	0.252	-0.129	0.232	0.758	0.162
FLW	0.911	-0.295	0.251	0.746	-0.359	-0.043	-0.401	-0.036
DSE	0.805	-0.518	-0.021	-0.396	-0.225	0.102	-0.113	-0.708
DMT	0.778	-0.513	-0.091	-0.383	-0.119	-0.159	-0.328	0.659
SY	0.925	-0.067	0.693	-0.138	-0.085	-0.594	0.369	-0.011
SW	0.993	-0.164	0.609	-0.067	0.402	0.647	-0.062	0.116

PH=Plant height, FLL=Flag leaf length. FLW=Flag leaf width, DSE=Days to 75% spike emergence, DMT=Days to 80% maturity, SY=Grain yield/plant and SW=100-Seed weight

component. The first PC thus, was more related to vegetative growth, second PC solely to yield and yield contributing traits whereas third and fourth PC contrasts variables that again related to vegetative growth. All the studied traits thus seem to effectively govern the variation in these four components. Traits loading more on first two principal components with Eigen values greater than 1 and contributing more than half of the variance were used to cluster 200 wheat genotypes into closely related groups. It has been observed that the first principal component accounts for maximum variability in the data with respect to succeeding components (Leilah and Al-Khateeb, 2005). According to Chahal and Gosal (2002), characters with largest absolute values closer to unity within the first component influence the clustering more than those with lower absolute values closer to zero. Besides, the first two principal components were used to cluster genotypes into groups since they contributed more than half of the total variation as also suggested by different authors (Ajmal *et al*., 2013; Poudel *et al*., 2017). According to Badu-Apraku *et al*. (2006), the traits that loaded more on PC1 and PC2 showed the strong discriminatory power in separating genotypes. Clustering was done through Ward's method. The critical examination of the dendrogram generated after the cluster analysis and PCA, revealed four clusters (Fig. 2). The mean value ± SD of all the traits studied of these four clusters are presented in Table 5. Seventeen (17)

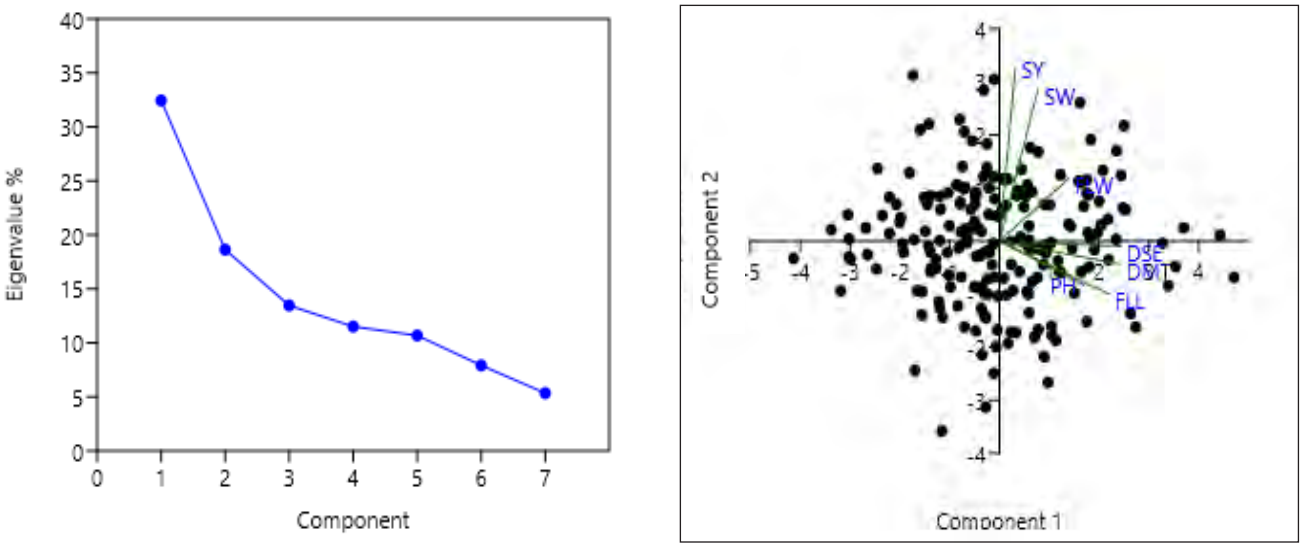

Fig. 1. Scree plot and Biplot of 200 wheat accessions based on first and second components

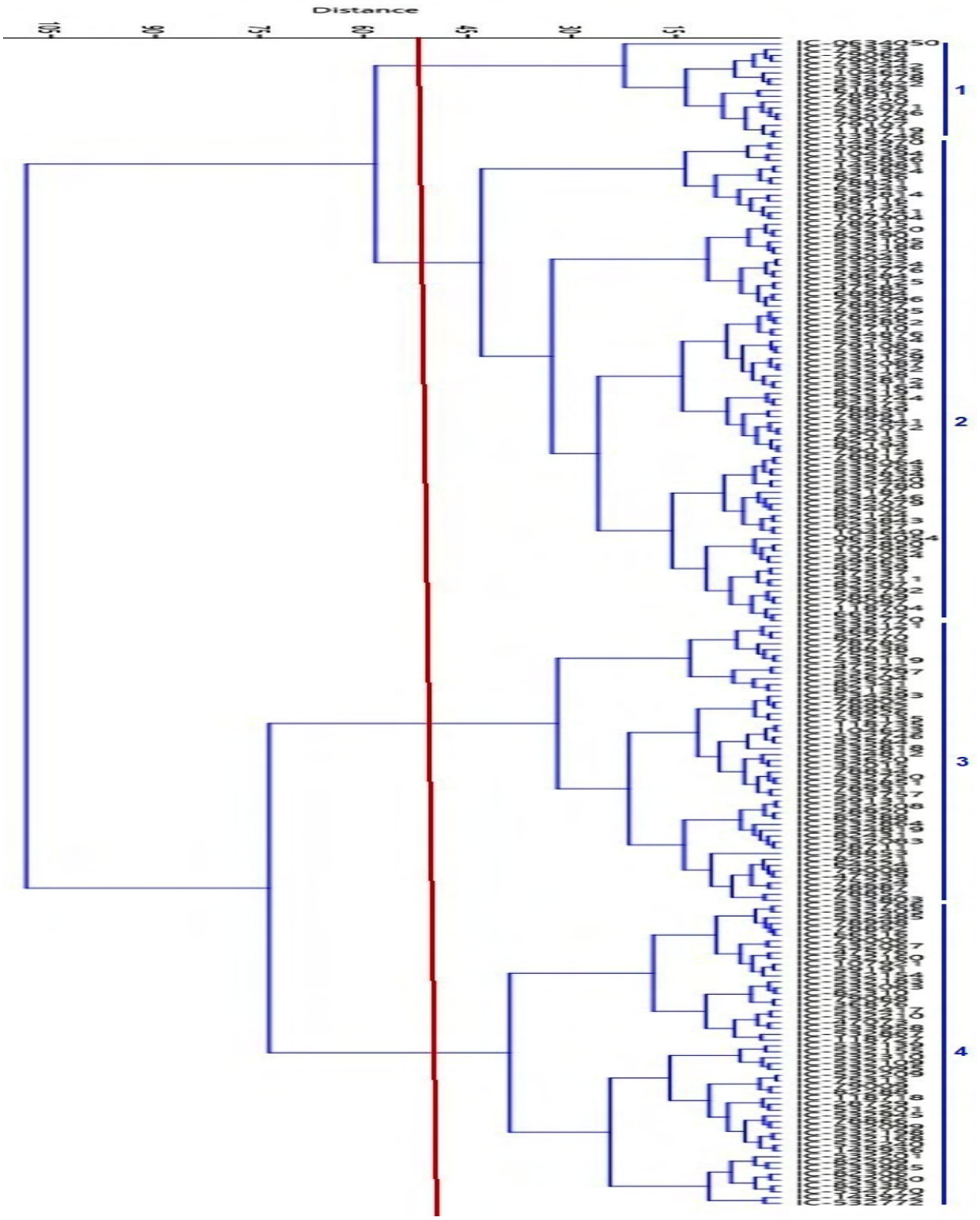

Fig. 2. Dendrogram of 200 wheat accessions based on agro-morphological traits using hierarchical cluster analysis (Ward's method)

Table 5. Mean and standard deviation for four clusters based on seven quantitative characters of 200 accessions of wheat evaluated during 2016/17 and 2017/18

Trait	Cluster 1 (17 accessions)	Cluster 2 (83 accessions)	Cluster 3 (48 accessions)	Cluster 4 (52 accessions)
PH	92.2 ± 9.6	96.2 ± 11.0	96.4 ± 9.5	100.8 ± 13.1
FLL	22.3 ± 1.4	22.2 ± 2.2	23.3 ± 2.3	23.9 ± 2.5
FLW	1.48 ± 0.16	1.49 ± 0.19	1.46 ± 0.19	1.54 ± 0.22
DSE	140.9 ± 2.5	139.1 ± 3.1	140.6 ± 2.8	148.2 ± 2.0
DMT	190.4 ± 0.9	190.4 ± 1.0	190.6 ± 0.9	191.5 ± 0.6
SY	30.180 ± 4.711	21.830 ± 2.686	13.900 ± 2.803	21.350 ± 4.280
SW	3.960 ± 0.450	3.690 ± 0.510	3.510 ± 0.510	3.800 ± 0.570

PH=Plant height, FLL=Flag leaf length. FLW=Flag leaf width, DSE=Days to 75% spike emergence, DMT=Days to 80% maturity, SY=Grain yield/plant and SW=100-Seed weight

Table 6. Promising accessions identified for each trait as a result of evaluation of 200 accessions of wheat (These accessions have performed equally well and were among top 25 accessions during both the years of 2016/17 and 2017/18)

Trait	Promising accessions identified	Best performing check mean value
Plant height (cms)	IC-79009, IC-532310, IC-533985, IC-532152, IC-36877, IC-59043, IC-532201, IC-532095, IC-532183	>PBW-343 (109.1 cms)
Flag leaf length (cm)	IC-532310, IC-78853, IC-532183, IC-79068, IC-36876, IC-532095, IC-78915, IC-82341, IC-532063, IC-78782	>GW-322 (25.25 cms)
Flag leaf width (cm)	IC-68984, IC-78915, IC-532063, IC-532183, IC-64224, IC-532083, IC-532864, IC-75224	>GW-322 (1.55 cms)
Days to 75% spike emergence	IC-62343, IC-145981, IC-82135, IC-532741, IC-532814, IC-28716, IC-532824, IC-78821, IC-107904, IC-532803, IC-82136, IC-532818, IC-82144	<PBW-343 (142.0)
Days to 80% maturity	IC-145970, IC-28716, IC-533757, IC-532071	<GW-322 (190.5)
Grain yield/plant (g)	IC-0634050, IC-78916, IC-61823, IC-78720	>GW-322 (26.604 g)
100-seed weight (g)	IC-532210, IC-533985, IC-118704, IC-82288, IC-532139, IC-118719, IC-75224, IC-532099, IC-78926, IC-61823, IC-53225, IC-532164, IC-79068, IC-534792, IC-532160	>GW-322 (3.562 g)

genotypes in cluster 1 represent only 8.5% of the total genotypes have highest grain yield/plant (g) and 100-seed weight (g). Cluster 2 constituted the biggest cluster with 83 genotypes representing 41.5% of the total genotypes characterized by comparatively lesser days taken for 75% spike emergence. Cluster 3 with 48 genotypes representing 24% of the total genotypes showed least values for grain yield/plant (g) and 100-seed weight (g). Finally cluster 4 with 52 genotypes representing 26% of the total genotypes have highest value of plant height (cms), flag leaf length (cms) and flag leaf width (g). Thus, four distinct clusters were observed in the present study as a result of the multivariate analysis. Although the cluster analysis groups genotypes on the basis of greater morphological similarity, the clusters did not necessarily include all genotypes from same origin (Zubair *et al*., 2007). Same is true of our study also, the accessions collected by our station from Jammu and Kashmir grouped in different clusters. The study has thus indicated the presence of appreciable variability in the agro-morphological traits within these 200 accessions of wheat. The accessions that ranked among the first 25 accessions for the studied traits during both the years of 2016/17 and 2017/18 and which were significantly superior to the check varieties have been identified as promising accessions (Table 7). For example, maximum grain yield/plant (g) has been recorded in accession IC-0634050 originally collected from a remote hilly area in Kashmir. This accession grouped as accession first in cluster 1. There is an ample scope and in fact need for exploitation of the accessions identified in the present study for utilization in wheat breeding programmes in the region.

Conclusion

The study has recorded tremendous amount of variability occurring in two hundred *Triticum aestivum* germplasm accessions studied here. PCA and cluster analysis has grouped these accessions in distinct groups. Selection of accessions from the first two principal components

Supplementary list of wheat germplasm accessions studied

S No.	IC No.	S No.	IC No.	S No.	IC No.	S No.	IC No.	S No.	IC No.
1	IC-532071	41	IC-28920	81	IC-75224	121	IC-532109	161	IC-532505
2	IC-82144	42	IC-82136	82	IC-104643	122	IC-532095	162	IC-118727
3	IC-534776	43	IC-532746	83	IC-532183	123	IC-532310	163	IC-104655
4	IC-532786	44	IC-32584	84	IC-82270	124	IC-78827	164	IC-82209
5	IC-61823	45	IC-532220	85	IC-532778	125	IC-532867	165	IC-533744
6	IC-532741	46	IC-47522	86	IC-78839	126	IC-534770	166	IC-533958
7	IC-53620	47	IC-532135	87	IC-532770	127	IC-533766	167	IC-82187
8	IC-532164	48	IC-78915	88	IC-59043	128	IC-82288	168	IC-78866
9	IC-532334	49	IC-532125	89	IC-118704	129	IC-79015	169	IC-145936
10	IC-79108	50	IC-534293	90	IC-533757	130	IC-532772	170	IC-82431
11	IC-78892	51	IC-532836	91	IC-532818	131	IC-79074	171	IC-59563
12	IC-78928	52	IC-55710	92	IC-532945	132	IC-47537	172	IC-28684
13	IC-532209	53	IC-532362	93	IC-78902	133	IC-532154	173	IC-532208
14	IC-79068	54	IC-532750	94	IC-82338	134	IC-534876	174	IC-107952
15	IC-532201	55	IC-78931	95	IC-47073	135	IC-532139	175	IC-78998
16	IC-62343	56	IC-532186	96	IC-145972	136	IC-107904	176	IC-78991
17	IC-532485	57	IC-532087	97	IC-533763	137	IC-532803	177	IC-79013
18	IC-68984	58	IC-532083	98	IC-47576	138	IC-32015	178	IC-47585
19	IC-78817	59	IC-78852	99	IC-78916	139	IC-79068	179	IC-532060
20	IC-78853	60	IC-532152	100	IC-82390	140	IC-532210	180	IC-79054
21	IC-533985	61	IC-532417	101	IC-82194	141	IC-532442	181	IC-82310
22	IC-145981	62	IC-53225	102	IC-82306	142	IC-82388	182	IC-532099
23	IC-532814	63	IC-28711	103	IC-534792	143	IC-532160	183	IC-532105
24	IC-28669	64	IC-82135	104	IC-522843	144	IC-532072	184	IC-82207
25	IC-66525	65	IC-78838	105	IC-82359	145	IC-107921	185	IC-82402
26	IC-64224	66	IC-532440	106	IC-532797	146	IC-59191	186	IC-78720
27	IC-79009	67	IC-66516	107	IC-73334	147	IC-79006	187	IC-79107
28	IC-145970	68	IC-532064	108	IC-522850	148	IC-532121	188	IC-82219
29	IC-28716	69	IC-532063	109	IC-82357	149	IC-532240	189	IC-118719
30	IC-104394	70	IC-82328	110	IC-78834	150	IC-78962	190	IC-532224
31	IC-534746	71	IC-78782	111	IC-532812	151	IC-532155	191	IC-532834
32	IC-55604	72	IC-82135	112	IC-532852	152	IC-532119	192	IC-79008
33	IC-532824	73	IC-532054	113	IC-534405	153	IC-36876	193	IC-82373
34	IC-79097	74	IC-75225	114	IC-532079	154	IC-104640	194	IC-533746
35	IC-59628	75	IC-28987	115	IC-59131	155	IC-82221	195	IC-532851
36	IC-532941	76	IC-47939	116	IC-28729	156	IC-532822	196	IC-118718
37	IC-82341	77	IC-534812	117	IC-532198	157	IC-532067	197	IC-78926
38	IC-534819	78	IC-118735	118	IC-532168	158	IC-82433	198	IC-532211
39	IC-532129	79	IC-36877	119	IC-75313	159	IC-78821	199	IC-0634050
40	IC-532864	80	IC-532780	120	IC-532096	160	IC-532207	200	IC-0634054

as well as from identified promising genotypes for each trait can be utilized for specific breeding purposes as possible parental lines. While we have not found any particular accession/s best for all the traits studied here, some accessions performed equally well for some of these traits as follows.

1. IC-532310, IC-532095 and IC-532183 are the genotypes with maximum plant height and flag leaf length, later accession i.e. IC-532183 is best for flag leaf width as well.
2. IC-533985 is the genotype with highest plant height as well as seed weight.
3. IC-78915, IC-532063, IC-532183 are best for both flag leaf length and flag leaf width.
4. IC-79068 is the genotype with greater flag leaf length and seed weight.
5. IC-75224 is the genotype with greater flag leaf width and seed weight.
6. IC-28716 has been found to be earliest genotypes

for both the traits of days to 75% spike emergence as well as days to 80% maturity.

7. IC-61823 is the genotype with maximum grain yield/plant as well as 100-seed weight.

Acknowledgements

The authors are highly thankful to the Division of Evaluation, ICAR–NBPGR, New Delhi for supplying wheat germplasm used in the present study.

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Indian J. Plant Genet. Resour. 34(1): 43–53 (2021)
DOI 10.5958/0976-1926.2021.00006.1

RESEARCH ARTICLE

Interception of Insect Pests using X-Ray Radiography during Quarantine of Plant Genetic Resources

Kavita Gupta*, SP Singh, Shashi Bhalla and DS Meena
Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

(Received: 20 May, 2020; Revised: 17 January, 2021; Accepted: 08 March, 2021)

X-ray radiography is a tool used in quarantine processing of 340 plant genera for detection of hidden infestation. X-ray of 22,146 samples belonging to 55 plant genera from a total of 9,48,751 imported samples of various crops during 2007- 2016 revealed presence of hidden infestation caused by bruchids and phytophagous chalcids in 1971 samples. Seven exotic bruchid species viz., *Acanthoscelides desmanthi* in *Desmanthus* spp. from Colombia, *A. obtectus* in *Phaseolus vulgaris* from South Africa and USA and in *Lathyrus sativus* from Lebanon; *Bruchus atomarius* in *Lens culinaris* from Lebanon; *B. dentipes* in *Vicia* spp. from ICARDA (Syria) and Lebanon; *B. ervi* in *Pisum sativum* and *L. sativus* from Lebanon and *Lens culinaris* from ICARDA (Syria), Lebanon, Morocco and Syria; *B. tristis* in *L. culinaris* and *Lathyrus sativus* from Lebanon and ICARDA (Syria), respectively; *Callosobruchus subinnotatus* in *V. subterranea* from Ghana and one seed chalcid *Bruchophagus roddi* in *Trifolium pratense* from USA were intercepted. Many of these were intercepted repeatedly from the same/ different source(s) year after year. All the infested samples were salvaged either through X-ray radiography or by using suitable disinfestation treatments. Many of the intercepted pests are not yet reported from India, and are therefore, of high quarantine significance.

Key Words: Bruchids, Exotic, Germplasm, Interception, Quarantine, X-ray radiography

Introduction

A large number of plant germplasm samples are being exchanged throughout the world for crop improvement programmes, more so, under the liberalized WTO regime. Such exchanges carry the risk of inadvertent introduction of exotic pests. If established, these pests could prove more devastating in the new geographical areas in the absence of their natural enemies and competitors. Quarantine testing of the planting material under exchange reduces this risk.

ICAR-National Bureau of Plant Genetic Resources (NBPGR) is the nodal agency in India to undertake the quarantine processing of germplasm including that of transgenics introduced into the country for research purposes. Over the years, effective quarantine processing at ICAR-NBPGR has resulted in the interception of a number of exotic pests. These include *Acanthoscelides obtectus* in *Cajanus cajan, Phaseolus vulgaris* and *Vicia faba* from Brazil, Bulgaria, Malawi; *Anthonomus grandis* in *Gossypium* sp. and *Hibicus* spp. from USA; *Bruchophagus gibbus* in *Medicago* spp. and *Trifolium* spp. from France, Germany, Italy and USA; *Leptinotarsa decemlineata* in potato from Europe and USA; *Popillia japonica* in root stocks of nursery crops from Japan and USA.

Certain groups of insects infesting seeds, *viz.,* seed wasps (Hymenoptera: Chalcidoidea), pulses beetles (Coleoptera: Bruchidae), and a few weevils/borers (Coleoptera: Curculionidae/Scolytidae) infest the developing seeds without showing any external signs or symptoms of their presence within. The quarantine risk becomes much higher with the exchange of seeds with such hidden infestation because these are not detectable through routine visual inspection.

These are several examples of transboundary movement of insects causing hidden infestation *viz.,* The douglas fir seed chalcid *(Megastigmus spermotrophus Wachtl.)* has spread from its original home in United States to Scotland (Mac Dougali, 1926), France (Vayssiere, 1931), Germany (Echerich, 1938) and New Zealand (Gourlay, 1930) alongwith the shipment of douglas fir *(Pseudotsuga taxifolia*) seeds. The rose

*Email: kavita.gupta@icar.gov.in, kavita6864@gmail.com

seed chalcid [*Megastigmus aculeatus* (Swedrus)] was introduced into New Jersey (USA) through the seeds of *Rosa multiflora* from Japan (Weiss, 1917). The crop losses reported to have been caused by various introduced chalcid pests include over 80% seed damage by *Bruchophagus roddi* in seeds of alfalfa (Stronge, 1962) and about 40% by *Systole albipennis* in various umbelliferous seeds (Gupta, 1962). Seed damage to the extent of about 40% has been reported in *Trifolium alexandrium* by bruchids, *viz.*, *Bruchidius alfieri* and *Bruchidius trifolii* (Abou-Roya, 1954). Recently, an Indian biotype of *Acanthoscelides obtectus* was detected in French beans from Himachal Pradesh (Thakur, 2010). These are detected through employment of special detection techniques such as X-ray radiography and transparency test.

Use of X-ray radiography was initiated in 1983 in the Division of Plant Quarantine, ICAR-NBPGR, New Delhi, India for detection of hidden infestation caused by bruchids and phytophagous chalcids when an initial list of host plant genera was prepared. Bhalla *et al.*, 2002 reported 340 plant genera belonging to 75 families are known to carry hidden infestation. The present paper highlights the detection of insect pests through X-ray radiography and how this technique has helped in detection of exotic pests in imported germplasm many of which are legumes thereby prevented their introduction into India. The quarantine significance of the pests intercepted is also discussed.

Materials and Methods

Over the past decade from 2007-16, a total of 9,48,751 samples were processed of which 8,79,934 were seeds (Table 1). All the seed samples were examined visually and under stereo-binocular microscope for any external symptom of insect infestation i.e. holes, rotting, swelling, deformity, etc. or presence of dead or alive insects/ mites, eggs/egg shells, immature stages, exuviae or excreta thereof. Seed samples belonging to the 340 plant genera known to carry hidden infestation of bruchids and phytophagous chalcidoids were compulsorily subjected to X-ray radiography (Bhalla *et al*., 2002). A total of 22,146 samples of seeds of 55 plant genera of various crops listed in Table-2 were exposed to X-ray radiography or seed transparency to detect presence of seed beetles.

Seeds were arranged on small 12 × 12 cm tray kept over the window in the X-ray cabinet and exposed to soft X-ray (Cabinet X-ray Systems, Faxitron Series MX 20, USA) kept at a distance of 60 cm from the source. It is a self-calibrated machine and depending on the seed structure, it automatically adjusts the exposure parameters to get a sharp image of the seed. The seed geometry on the plate was left undisturbed. This is a real-time computer controlled X-ray system; hence, the image as visualized on the monitor was saved for removal of seeds suspected to carry infestation from the seed geometry mechanically. Alternatively, another manual Faxitron X-ray system was also used where the seeds are spread on a sheet of paper that is placed on a black envelope containing the X-ray film and are exposed to soft X-rays generated at 22 Kv, 3 mA, at a distance of 30 cm from the source for 15 seconds. The envelope containing the exposed film was removed gently without disturbing the seed geometry and the film is developed/ fixer prepared for the purpose in a dark room. In both the cases, infested seeds were marked/ identified on the X-ray and corresponding (infested) seeds were hand-picked from the seed sample with original seed geometry. The dose, however, was varied with the size, shape or thickness of the seeds for the better resolution of image on the X-ray plate/ computer monitor. The dose was also standardized for different seeds as and when required, as was done in case of mango stones (exceptionally large seeds) for detection of mango stone weevil, *Sternochaetus mangiferae* as 60KV, 3 mA at a distance of 30 cm from source for 30 seconds (Kapur *et al*., 1997). Composition of the solutions used in developing and fixing the image on X ray film used were as per Bhalla *et al.*, 2009)

Internal infestation in samples of small seeds of *Casuarina, Eucalyptus, Medicago* and *Trifolium* spp. was difficult to detect through X-ray radiography, hence, these were subjected to transparency test by heating in lactophenol-acid fuchsin (Kaura 1959). Seeds were submerged in test tubes containing lactophenol-acid fuchsin and boiled for 10-20 minutes and left overnight. On next day, transparent seeds were observed for internal infestation with the help of stereo-binoculars.

The eggs and adult insects can be easily detected through naked eye observation or under stereo-binoculars. However, once the eggs hatch the first instar larva bores into the seed and the remaining development up to pupal stage is completed inside the seed, which can only be detected through X-ray radiography (Fig. 1). The adult insects were retrieved from the infested seeds either by

Table 1. Details of crop species X-rayed during 2007-16

Crop	Source	Year(s) of Import	Consignments (No. of Samples)	Samples Infested
Abelmoschus esculentus	Bangladesh, Germany, Taiwan, USA	2008, 2012, 2013, 2014	13(329)	3
Abelmoschus spp.	Niger, USA	2011, 2015	3(547)	20
Acacia sp.	Australia	2008	1(3)	02
Aeschynomene spp.	Ethiopia	2011	1(19)	
Arachis hypogaea	USA	2010, 2013	2(2)	
Arachis spp.	Ethiopia	2011	1(2)	
Brachypodium distachyon	USA	2010	1(1)	
Calopogonium spp.	Ethiopia	2011	1(5)	
Canavalia spp.	Ethiopia	2011	1(7)	
Caragana arborescens	USA	2013	1(10)	
Cassia angustifolia	USA	2011	1(5)	
Casuarina sp.	Australia	2008	1(1)	
Centrosema spp.	Ethiopia	2011	1(10)	
Cicer arietinum	Canada, ICARDA (Syria), Lebanon, Morocco, Spain, Syria, USA, Uzbekistan	2007, 2009, 2010, 2011, 2013, 2014, 2015, 2016	25(3782)	13
Cicer spp.	Syria	2011, 2009	2(7)	
Clitoria ternatea	Colombia	2012	1(102)	
Coriandrum sativum	Germany, Kyrgyzstan, UAE, Uzbekistan	2009, 2015, 2016	4(6)	3
Crotalaria juncea	USA	2016	1(1)	
Crotalaria spp.	USA	2013	1(33)	
Cuminum cyminum	UAE	2009	1(3)	
Desmanthus spp.	Columbia	2013	1(216)	16
Dolichos lablab	Taiwan	2013	1(35)	
Dolichos spp.	Ethiopia	2011	1(1)	
Elaeis guinensis	Malaysia	2015	1(20)	
Eucalyptus spp.	Australia	2008	1(1)	
Fagopyrum esculentum	Germany, Uzbekistan	2015, 2016	2(3)	
Foeniculum vulgare	UAE	2009	1(3)	
Gladiolus sp.	South Africa	2009	1(24)	03
Glycine max	USA	2013	1(3)	
Gossypium sp.	USA	2007, 2010	2(114)	
Gossypium anstral	Australia	2012	1(2)	
G. arboreum	Pakistan	2011	1(5)	
G. barbadense	USA	2008	1(80)	
G. hirsutum	Israel, Pakistan, USA	2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016	32(1817)	15
Helianthus annuus	Egypt, France, Switzerland, UK, USA	2007, 2008, 2009, 2011, 2013	14(836)	01
Hibiscus spp.	USA	2013	1(20)	
Jatropha curcas	Italy	2010	1(23)	
Lathyrus odoratus	Switzerland, Syria	2008, 2011	2(28)	7
L. sativus	ICARDA (Syria), Lebanon, Nepal, Syria, UK	2008, 2009, 2010, 2011, 2013, 2014, 2015, 2016	17(933)	41
Lathyrus sp.	Ethiopia, ICARDA (Syria)	2007, 2011	2(14)	
Lens culinaris	Australia, Canada ICARDA (Syria), Lebanon, Morocco, Nepal, Syria, Turkey, USA	2007, 2008, 2009, 2010, 2011, 2013, 2014, 2015, 2016	24(4919)	1435
Lens spp.	Syria	2008, 2009	3(495)	05
Lotus japonicas	Japan	2010	1(02)	
Lupinus spp.	Australia, USA	2012, 2014	2(26)	
Macadamia integrifolia	USA	2015	1(10)	

Crop	Source	Year(s) of Import	Consignments (No. of Samples)	Samples Infested
Macroptilium astropurpure	Ethiopia	2011	1(10)	01
Macrotyloma spp.	Ethiopia	2011	1(12)	
Mangifera indica *Mangifera* sp.	Israel	2012, 2016, 2009	5(2862)	02
Medicago lupulina	Switzerland	2010	1(05)	
M. sativa	Japan, USA	2008, 2013	2(09)	
Medicago spp.	New Zealand	2011	1(23)	01
Nenolonia spp.	Ethiopia	2011	1(05)	
Onobrychis vicifolia	Russia	2010	1(03)	03
Panicum maximum	USA	2008	1(01)	
Pennisetum glaucum	USA	2008	1(02)	01
P. purpureum	Ethiopia	2012	1(27)	
Phaseolus lunatus	Taiwan	2013	1(18)	
Phaseolus spp.	Ethiopia, Taiwan	2011, 2013	2(18)	
P. vulgaris	Canada, Colombia, Egypt, Kazakhstan, Nepal, Philippines, South Africa, USA, Uzbekistan	2007, 2009, 2010, 2012, 2013, 2014, 2015, 2016	16(438)	17
Phoenix dactylifera	Egypt	2007	1(04)	
Pisum sativum	Australia, Canada Spain, Switzerland, USA	2007, 2009, 2010, 2014, 2015, 2016	9(684)	28
P. fulvum	Spain	2009	1(08)	04
Pisum spp.	Germany	2016	1(03)	
Pueraria spp.	Ethiopia	2011	1(05)	
Rhynchosia spp.	Ethiopia	2011	1(16)	
Ricinus communis	USA, Uzbekistan	2015, 2016	2(95)	
Sesbania spp.	Ethiopia	2016	1(17)	06
Stylosanthes spp.	Ethiopia	2011	1(37)	
Theobroma cacao	Malaysia	2007	1(02)	02
Trifolium alexandrinum	Egypt, USA, Uzbekistan	2007, 2008, 2010, 2015	4(37)	04
T. pratense	USA	2007	1(76)	02
Trigonella foenum graecum	Syria	2010	2(54)	
	UAE	2009	1(03)	
Trigonella spp.	USA	2014	1(41)	
Vicia faba	Cyprus, Lebanon, Syria	2008, 2011, 2013, 2014, 2015, 2016	10(903)	115
V. narborensis	Lebanon	2014	1(01)	
V. sativa	Lebanon, USA	2013, 2014	2(07)	
Vicia spp.	Ethiopia, ICARDA (Syria), Syria	2007, 2009, 2011	3(48)	2
Vigna mungo	Nepal, USA	2009, 2014	2(34)	07
V. radiata	Australia, Nepal, Taiwan, Thailand	2007, 2008, 2009, 2015	4(321)	11
Vigna spp.	Ethiopia, Taiwan	2008, 2011	2(38)	
V. subterranea	Ghana	2008	1(02)	2
V. umbellata	Taiwan	2008	1(07)	
V. unguiculata	Belgium, Italy, IITA (Nigeria), Taiwan, Uzbekistan	2007, 2010, 2011, 2012, 2013, 2015	9(1698)	203
V. unguiculata subsp. *sesquipedalis*	Philippines, Taiwan	2010, 2015	2(24)	
Zornia spp.	Ethiopia	2011	1(19)	
			280 (22,146)	1971

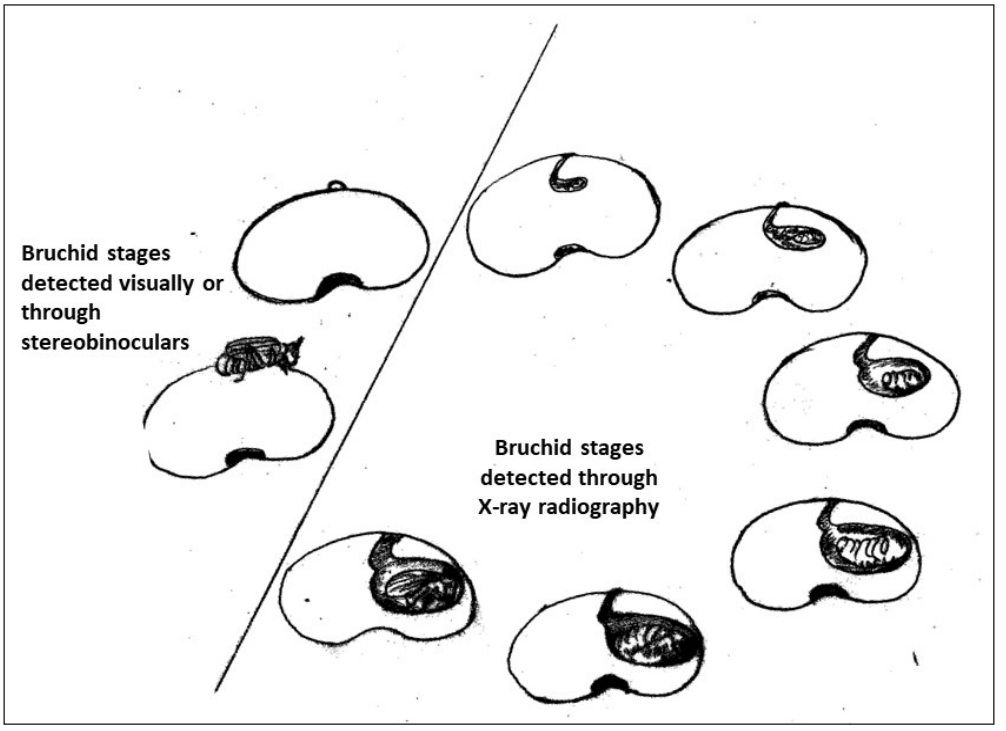

Fig. 1. Representative diagram of bruchid life stages detected through X-ray radiography

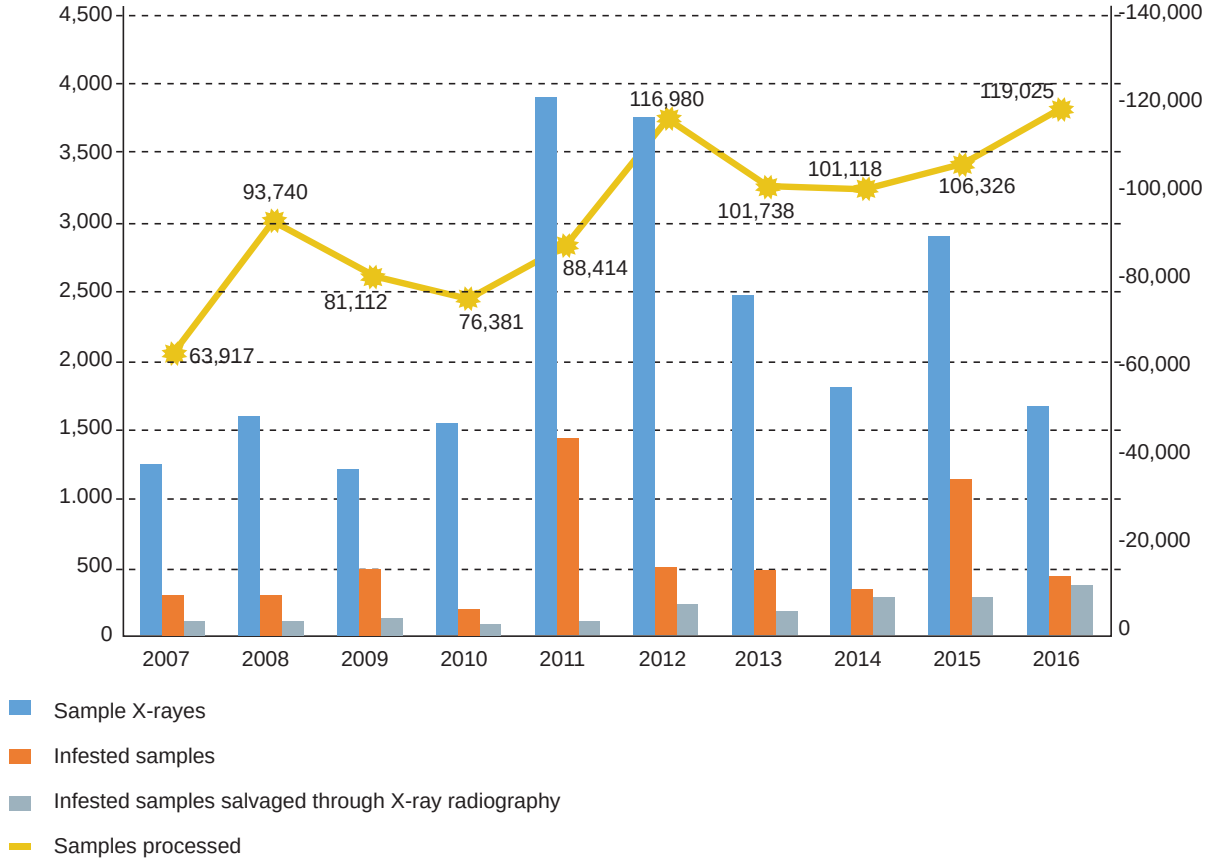

Fig. 2. Detection of insect infestation through X-ray radiography

keeping them at 28±1°C and 60±5% RH or soaking overnight in water. The insect pests thus retrieved were identified on the basis of published identification keys, digitized keys (Gupta *et al.,* 2011) and reference collection at ICAR-NBPGR. The infested samples were salvaged using either or in combination- mechanical cleaning, X-ray radiography (by removing infested seeds) and fumigation. Seeds found infested through X-ray radiography were salvaged by handpicking the infested seeds from the seed geometry as seen on the X-ray.

Results and Discussion

The year-wise details of imported seed samples X-rayed and found infested during 2007- 2016 are presented in Figure 2. A total of 9,48,751 seed samples were imported of which 22,146 were subjected to X-ray and 1,971 samples showed insect infestation through X-ray (Figure 2). More than 90% of the total samples imported were those of seeds. About 2.5% of the total seed samples belonged to one of the 340 plant genera earmarked for X-ray radiography of which approximately 35% were infested with bruchids.

Upon comparing the samples imported vis-à-vis the total infested seed samples by each intercepted seed beetle, it was clear that the maximum number of samples infested were of *Lens* spp. due to *B. ervi* followed by *Vigna unguiculata* and *Vicia faba.* However, despite few numbers of samples, 100% average infestation was observed in *Onobrychis vicifolia, Theobroma cacao* and *Vigna subterranea*. The average per cent infestation due to other exotic seed beetles varied from 8-60% (Table 1). Exotic insects were intercepted in the infested samples from 19 different source countries (Table 2).

It is clear that many of these crops were repeatedly imported year after year or several consignments in a year from the same or different source country which is indicative of its importance and demand among the indentors. The largest number of samples X-rayed (4,919) were of lentil divided in 24 consignments imported from nine source countries/ CG Centres, followed by five consignments of mango stones (2,862) from three countries; followed by 32 consignments of cotton (1,817) from three countries. The maximum consignments were for *Gossypium hirsutum* (32); followed by *Cicer arietinum* (25); followed by *Lens culinaris* (24). *G. hirsutum* was the only crop species that was imported every year from 2007-2016 while *Lens culinaris* was imported during nine of the ten years and *Lathyrus sativus* and *Phaseolus vulgaris* were imported during eight of the ten years under analysis.

The details of interception of exotic seed beetles, hosts on which intercepted and the source or country of import is presented in Table 2. A closer look at the Table 2 shows that as many as seven bruchid species were intercepted from the material received from ICARDA, CGIAR Centre, which supplies germplasm from different source countries. Four of these bruchids *viz., Bruchus dentipes, B. ervi, B. rufimanus* and *B. tristis* are not yet reported from India. In such a case, the infestation could be either from Syria or from the source country/ station of the material, which remained undetected due to its hidden nature. Six of the bruchid species have also been intercepted in material received from Lebanon of which five are exotic and not yet reported from India and hence, of great quarantine significance. Two exotic bruchid species were intercepted in material from USA. In addition, one species each of exotic bruchid was also intercepted from Colombia, Ghana, Morocco and South Africa (Table 2).

Seeds of *Lens* spp. including International Trial Nurseries imported several times over the years were found to be infested by five different species of bruchids, three of which are exotic *viz., B. atomarius, B. ervi* and *B. tristis*. *Lathyrus* spp also imported several times during 2007-16 showed infestation by five different species of bruchids, three of whom were exotic *viz., Acanthoscelides obtectus, B. ervi* and *B. tristis*. One exotic species each *viz., A. obtectus* on *Phaseolus vulgaris, B. ervi* on *Pisum* spp. and *Bruchophagus roddi* on *Trifolium pratense,* respectively were intercepted (Table 2).

Some details on the biology, losses caused, geographical distribution, host range and other information of phytosanitary significance during transboundary movement for each of the intercepted insect pest is presented below:

Acanthoscelides desmanthi was intercepted in *Desmanthus* spp. from Colombia is oligophagus pest feeding only on the species belonging to Genus *Desmanthus.* It has been reported from Colombia, Mexico and USA.

Acanthoscelides obtectus was repeatedly intercepted on *Phaseolus vulgaris* from several countries *viz.*, Lebanon, South Africa and USA is indicative of the severity of pest problem in the region (Table 2). It has

Table 2. Interceptions of pests in imported seeds examined through X-ray radiography

Insect pest	Host	Source
***Acanthoscelides desmanthi**	*Desmanthus* spp.	Colombia
***A. obtectus*	*Phaseolus vulgaris*	South Africa, USA
	Lathyrus sativus	Lebanon
Bruchidius trifoli.	*Trifolium alexandrium*	Egypt
**Bruchophagus roddi*	*T. pratense*	USA
Bruchophagus sp.	*Medicago* spp.	New Zealand
***Bruchus atomarius**	*Lens culinaris*	Lebanon
***B. dentipes**	*Vicia faba*	ICARDA (Syria), Lebanon
B. emarginatus	*Pisum sativum*	Spain
***B. ervi**	*P. sativum, Lathyrus sativus*	Lebanon
	Lens culinaris	ICARDA (Syria), Lebanon, Morocco, Syria
B. lentis	*L. culinaris*	ICARDA (Syria), Lebanon
***B. rufimanus**	*V. faba*	ICARDA (Morocco)
***B. tristis**	*L. culinaris*	Lebanon
	Lathyrus sativus	ICARDA (Syria)
Callosobruchus analis	*L. sativus*	ICARDA (Syria)
C. chinensis	*L. sativus*	Taiwan
	Lens culinaris	ICARDA (Syria)
	Macroptilium atropurpurius	Ethiopia
	Vigna unguiculata	Italy
C. maculatus	*V. mungo, V. radiata*	Nepal
	V. unguiculata	Italy
**C. subinnotatus*	*V. subterranea*	Ghana
Chalcids	*Daucus carota, Onobrychis vicifolia*	Russian Federation
Pectinophora gossypiella	*G. hirsutum*	Israel, USA
Systole coriandri	*Coriandrum sativum*	UAE
Immature stages of bruchids	*V. mungo*	USA
	L. culinaris	Morocco
	Crotolaria juncea	Ethiopia
	P. sativum	Australia
	P. vulgaris	USA
	Gossypium hirsutum	Israel

* Quarantine pest not yet reported from India
** Regulated pest under PQ Order 2003 and its amendments

a high potential for population growth due to its wide temperature tolerance i.e., it occurs in cool highland areas, warmer lowland tropics and some temperate regions. Eggs are lodged under cracks in the bean testa and on ripening pods (Howe and Currie, 1964, Meirleire, 1967). It is reported from several countries including a recent report of an Indian biotype and has a wide host range (Thakur, 2010).

Bruchidius trifolii is not yet reported to be a pest of *Trifolium* spp. in India although the genus *Bruchidius* has been reported on other host plants from India. Three species of *Bruchidius* are reported on *Trifolium* spp. from Egypt *viz*., *B. alfierii, B. poupillieri* and *B. trifolii* and none of them are reported from India (Gupta *et al*., 2011).

Bruchophagus roddi, a Eurytomid chalcidoid has been reported only on *Medicago sativa*. The larvae develop within a single alfalfa seed and they are easy to spread through the world in the seed trade. The seed wasp has continuing, overlapping generations, which means that all stages of the life cycle are present at any one time in any one area. *B. roddi* is closely related to its host plants and it can be found wherever alfalfa is grown. It is said to have a cosmopolitan distribution. In alfalfa seed-producing areas of North America, up to 80-90% of the harvested seed may be infested and this can cause great financial losses (CAB International, 2007).

Bruchus atomarius, which was detected on seeds of *Lens culinaris* from Lebanon is a pest reported on

Table 3. Exotic pests, their host range and geographical distribution

Insect Pest	Host Range	Geographical Distribution
Acanthoscelides desmanthi	*Desmanthus covillei, D. virgatus, D. virgatus* var. *depressus, Desmanthus* spp.	Colombia, Mexico, USA
A. obtectus	*Albizzia sp., Astragalus sp., Cajanus indica, C. sativus, Cicer arietinum, Cicer sp., Dolichos melanophthalmus, Erythrina sp., Fagopyrum esculentum, Glycine hispida, Lathyrus sativus, Lens esculenta, Lupinus albus, Mucuna pruriens, Phaseolus aconitifolius, P. aconitifolius latifolius, P. aureus, P. calcaratus, P. carcacalla, P. coccineus, P. latifolius, P. lunatus, P. lunatus macrocarpa, P. macrocarpus, P. multiflorus, P. mungo, P. vulgaris, Pisum arvense, P. sativum, Sesbania aegyptica, Tephrosia cuspidate, T. virginica, Vicia faba, V. sativa, Vigna catjang, V. ribra, V. sesquipedalis, V. sinensis, V. subterranea, Zea mays*	Widely distributed
Bruchidius trifolii	*Medicago sativa, Trifolium alexandrinum, T. incarnatum, T. maritimum, T. ochraceum, T. pretense, Trifolium* sp.	Algeria, Egypt, Israel, Libya
Bruchophagus roddi	Medicago arabica, *M. falcata, M. minima, M. polymorpha, M. sativa, M. sativa* subsp. *caerulea* and *M. sativa* subsp. *glomerata*	Argentina, Australia, Austria, Brazil, Bulgaria, Canada, Chile, Czechoslovakia (former), France, Germany, Hungary, India, Iran, Iraq, Israel, Kazakhstan, Kyrgyzstan, Moldova, Mongolia, New Zealand, Peru, Poland, Romania, Russian Federation, Serbia, Slovakia, South Africa, Spain, Sweden, Turkey, Turkmenistan, Ukraine, USA, Uzbekistan and Yugoslavia (Serbia and Montenegro)
Bruchus atomarius	*Lathyrus niger, L. pisiformis, L. pratensis, L. sphoericus, L. tuberosus, L. vernus, Lens esculenta, Lens* spp., *Phaseolus* sp., *Pisum sativum, Sarothamnus scoparius, Vicia angustifolia, Vicia cracca, V. dumetorum, V. faba, V. narbonensis, V. pisiformis, V. sativa, V. sapium, V. tenuifolia*	Algeria, France, Iran, Italy, Lebanon, Sweden, USSR (erstwhile)
B. dentipes	*Vicia faba, V. hyrcana, V. lutea, V. sativa, Vicia* sp.	Australia, Afghanistan, Greece, Iraq, Syria, Turkey, USSR (erstwhile)
B. emarginatus	*Cicer arietinum, Lathyrus angulatus, L. angustifolius, L. hirsutus, L. ochrous, Pisum arvense, P. sativum, Vicia peregrina, V. sativa*	Algeria, France, Germany, India, Israel, Italy, Lebanon, Syria, Turkey, USSR (erstwhile), Yugoslavia (former)
B. ervi	*Acacia brachystachya, Lathyrus latifolius, Lens esculenta, Ulex europaeus, Vicia ervilia, V. sativa*	Algeria, Australia (Verma *et al*., 1991), Cyprus, Egypt, France, Germany, Hungary, Iran, Israel, Italy, Lebanon, Martinique Island, Reunion Island, Syria, Turkey
B. rufimanus	*Vicia faba, V. hybrida, V. leucosperma, V. lutea, V. macrocarpa, V. minor, V. monanthos, V. narbonensis, V. pannonica, V. peregrina, V. sativa, V. tenuifolia, V. vestita, V. villosa, Vicia* sp., *Voandzeia subterranea*	Widely distributed
B. tristis	*Calycotome spinosa, Calycotome* sp., *Lens esculenta, Lens* sp., *Pisum sativum, Pisum* sp., *Ulex* spp., *Vicia ervilia, V. sativa*	Algeria, Canary Islands, Crete, Cyprus France, Greece, Italy, Malta, Spain, Syria, Turkey, USA, USSR (erstwhile)
C. subinnotatus	*Rhynchosia* sp., *V. subterranea*	South Africa, Zambia

Lathyrus sp. *Lens esculenta*, *Phaseolus* sp., *Pisum sativum* from Algeria, France, Iran, Italy, Lebanon, Sweden and the erstwhile USSR. It is reported to be univoltine and undergoes imaginal reproductive diapause for nine months in the southwest of France (CABI, 2007). A temporal synchronization has been reported between pod dehiscence and adult emergence from the seeds (Bashar *et al.*, 1994).

Bruchus dentipes detected in various species of *Vicia* is a pest specific to faba bean causing upto 76% damage (Hariri and Tahhan, 1983) and has been reported from very few countries in Australia, Greece, Syria

and Turkey is yet not reported from India (Table 3). Infestation ranges from 10- 90% with an average of about 42%, depending on location in the Mediterranean region and gamma irradiation is found effective as a quarantine disinfestation treatment for faba bean seeds infested with *B. dentipes* in Syria where it is a serious pest (Mansour and Al-Bacheer 1995).

Bruchus emarginatus although reported from India has a wide host range including species of *Cicer, Lathyrus, Pisum* and *Vicia.* It is reported from Algeria, France, Germany, Israel, Italy, Lebanon, Syria, Tunisia, Turkey, USSR (erstwhile) and Yugoslavia (erstwhile) (Gupta *et al.,* 2011).

Bruchus ervi intercepted in various *Lens* species from several countries including Syria has unconfirmed records of being present in Central Asia and Australia (CABI, 2007). It has been reported on *Acacia brachystachya, Lathyrus latifolius, Lens esculenta, Ulex europaeus, Vicia ervilia* and *V. sativa,* and has been recorded as a serious pest of *Lens* spp. in Algeria, Iran, Lebanon and Turkey with infestation level reaching upto 80% and loss of germination upto 100% (Hariri, 1981). It is a univoltine species which overwinters in seeds with higher survival, spread and establishment potential i.e., poses a higher quarantine risk. The pest was intercepted at NBPGR on *Acacia brachystachya* imported from Australia (Verma *et al.,* 1991) on which it was never reported earlier.

Bruchus lentis a specific pest of *L. culinaris* has been recorded to be serious pest in Algeria, Iran, Lebanon and Turkey. It is reported from 14 countries including India (Bhalla *et al*., 2004). Infestation level of up to 80% and loss of germination of up to 100% has been reported. It is univoltine and overwinters in seeds with high survival, spread and establishment potential. The pest has its distribution limited to a few countries from Europe, Central and South Asia and Africa, although reported from India, has been intercepted several times from different countries (Gupta *et al*., 2004, 2010, 2013)

Bruchus rufimanus intercepted from *Vicia faba* is reported to infest several species of grain legumes viz., *Cicer arietinum, Lathyrus* spp., *Lens* spp., *Lupinus angustifolius, Phaseolus* spp., *Pisum* spp., *Vicia* spp. and *Vigna subterranea* and has yet not been reported from India but is widely distributed in Europe, some parts of Asia and Africa, and hence, poses a higher quarantine risk. It is a univoltine species and *Vicia faba* seeds, sampled from 29 different areas of Morocco revealed an average infestation level of 33% (Boughdad and Lauge, 1997).

Although *Callosobruchus analis C. chinensis and C. maculatus* are reported from India, they pose a quarantine risk during import due to their high economic significance and possibility of presence of new strains (Applebaum *et al*., 1968). New strains or biotypes are also included in the category of pests according to the definition of 'pest' by IPPC (http://www.ippc.int/IPP/En/standards.htm).

Callosobruchus subinnotatus intercepted on Bambara groundnut *(V. subterranea)* from Ghana has been reported on *Rhynchosia* sp. and *V. subterranea* from parts of Africa. High mortality of different developmental stages of *C. subinnotatus* has been reported due to simulated solar heat in Bambara groundnut seeds (Lale and Vidal, 2000). While studies on modified atmosphere revealed that pupae of *C. subinnotatus* are most tolerant to hypercarbic and hypoxic atmospheres than adults (Mbata *et al*., 2000).

Pectinophora gossypiella larvae intercepted in seeds of *Gossypium* were kept under controlled conditions for adult emergence. *P. gossypiella* is an oligophagous pest and has been reported on cotton, okra, Deccan hemp (*Hibiscus cannabinus* [kenaf]) and roselle (*H. sabdariffa*) and few other members of family Malvaeceae. It is distributed throughout tropical America, Africa, Asia, Australasia, including subtropical regions, Pakistan, Egypt, USA (Arizona) and Mexico. *P. gossypiella* is a worldwide pest of cotton and in some regions of the world is a major economically important cotton pest. It is a quarantine pest in the USA and Russia (CAB International, 2007).

Systole coriandri, a chalcidoid reported on *Angelica archangelica* (Angelica) and *Coriandrum sativum* (coriander) from Hungary, Chile and Russia has been reported from India only from endemic pockets. *S. coriandri* is a specific seed and has been repeatedly intercepted in quarantine (Gupta *et al.,* 2005).

Salvaging and Quarantine Significance of In tercepted Pests

All the seed samples infested with pulse beetles were salvaged using various methods viz., mechanical cleaning done by removing infested/ deformed seeds, X-ray radiography and fumigation treatment. One thousand,

nine hundred and seventy one samples found infested through X-ray were salvaged by handpicking the infested seeds from the seed geometry as seen on the developed image of X-ray on the screen and/ or were fumigated with ethylene dichloride-carbon tetrachloride (EDCT) mixture @ 320 mg/l for 48 h or 640 mg/ for 24 h at 30°C or Aluminium phosphide @ 2g/ cu m for 72 h in an airtight container at normal atmospheric pressure.

Several of the above intercepted bruchids viz., *Acanthoscelides desmanthi, A. obtectus, Bruchophagus roddi, Bruchus atomarius, B. dentipes, B. ervi, B. rufimanus, B. tristis* and *Callosobruchus subinnotatus* are not yet reported from India, and hence, are of very high quarantine significance. Had they not been detected through X-ray radiography and intercepted in quarantine they could have gained entry into the country. It is important to note the distribution and host range of each of the intercepted species which indicates the potential pathways for the entry of these seed beetles into the country (Table 3). Several pulse beetles infesting various crops have moved across the world which include *A. obtectus* indigenous to North and South America but which got introduced into Asia, Africa, Europe and Australia; *C. analis* indigenous to Asia got introduced in Africa; *C. chinensis, C. maculatus* and *Caryedon serratus* indigenous to Asia and Africa got introduced in Europe, North and South America, Europe, North and South America and Australia; and South America and Australia, respectively; *Zabrotes subfasciatus* indigenous to North and South America got introduced in Asia, Africa and Europe (Southgate, 1978; Bhalla *et al*., 2006). The Plant Quarantine (Regulation of Import into India) Order 2003 also requires freedom of seeds of certain tree species like elm, oak, pine and grain legume seeds (both for planting and consumption) from certain crop or species specific pulse beetles or bruchids in the Phytosanitary Certificate and the special conditions of freedom from soil, quarantine weed seeds, prior approval from Department of Agriculture Cooperation and Farmers Welfare and fumigation are fulfilled during their import (Plant Quarantine (Regulation of Import into India) Order, 2003 and its subsequent amendments). In view of the interception of several exotic seed beetles of quarantine significance from more than 19 countries in the past ten years, it is essential to pay due attention to the regulations and the requirements thereunder. Several interceptions of exotic bruchids and chalcids of quarantine significance have been made as a result of X-ray screening of the listed plant genera. The advantages of X-ray radiography technique are that it is non-destructive (seeds remain viable), economically feasible, sufficiently rapid and reliable over a wide range of environmental conditions.

Conclusion

A total 1673 bruchid species belonging to 71 genera are reported from the world of which only 11 genera having 72 species are reported from India (Gupta *et al*., 2011). Thus, India has a risk of introducing >60 bruchid genera with >1500 species along with transboundary movement of plant species known to carry hidden infestation. Therefore, it is suggested to expose the listed plant genera to X-ray radiography at all the ports of entry (Bhalla *et al.*, 2002). This is especially important to prevent the entry of such hidden infestation which could become serious economic threats in India. Therefore, effective quarantine processing is of paramount importance for the safe exchange of seeds.

Acknowledgements

The authors gratefully acknowledge Directors, ICAR-NBPGR for providing the necessary facilities and the Heads, Division of Plant Quarantine, ICAR-NBPGR for their critical comments and to the retired senior colleagues of the Entomology Section for their suggestions.

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Indian J. Plant Genet. Resour. 34(1): 54–58 (2021)
DOI 10.5958/0976-1926.2021.00007.3

RESEARCH ARTICLE

Varietal Evaluation of the Strawberry (*Fragaria* × *ananassa* Duch) based on the Yield and Physico-chemical Parameters

Sachin Kumar*, Satya Prakash, Vipin Kumar and Arvind Kumar
Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut-250110, Uttar Pradesh, India

(Received: 06 December, 2019; Revised: 18 February, 2021; Accepted: 22 February, 2021)

The present experiment was carried out to study the physico-chemical characters of eleven strawberry genotypes to identify genotypes with higher yield and better quality fruits for Western Uttar Pradesh condition. Among all genotypes, maximum fruit length (37.9 mm), fruit breadth (33.4 mm) and fruit weight (13.3 g) were recorded in genotype Chandler. The early fruit setting was recorded in genotypes Gorella, Belrubi and Brighton whereas early fruit maturity was observed in genotypes Selva (98 days after transplanting) and Seascape (100 days after transplanting). The maximum fruit set (81.4 %), number of fruits per plant (22.3) and fruit yield per plant (311.1 g) were observed in genotype Chandler followed by Seascape and Confutura. The genotype, Chandler registered maximum values for total soluble solids (12°B), TSS/acid ratio (21.8), reducing sugar (7.9 %) and total sugar (9.4 %) alongwith minimum acidity (0.6 %). Chandler was comparatively superior for most of the yield and quality characters Therefore, it could be recommended for commercial cultivation in the north Indian plains.

Key Words: Biochemical parameters, Strawberry, *Fragaria*×*ananassa*, Fruit quality, Fruit setting

Introduction

Strawberry (*Fragaria* × *ananassa* Duch) is a natural hybrid being grown in cooler regions worldwide for delicious fruits with rich source of vitamins, minerals and various bioactive compounds (Oszmianski and Wojdylo, 2009). Strawberry is a non-climacteric fruit and a fruit reaches full maturity stage within 28-30 days after anthesis, with maximum fruit weight and size. The fruit is widely accepted for its characteristic aroma and sweetness. Strawberry has vast scope in areas which are located in vicinity of canning units and kitchen gardens. Strawberry is successfully grown in a broad range of climates including temperate, grassland, Mediterranean and subtropical areas (Hancock, 2000). Strawberry is mainly propagated through runners, which produce roots when they come into contact with soil. Runner development is stimulated by long day lengths (11-14 hours) and warm temperature (16-27 °C); therefore, runners emerge mostly during the summer months. In temperate climate condition, its plants behave like a small perennial herb (Finn and Strike, 2008) with shallow root system whereas in sub-tropical climate it behaves as annuals. These genetic characteristics results in the production of the fruits of different size, shape, taste and color (Mishra *et al*., 2015). Therefore, the sub-tropical areas of the country depends upon temperate region for runners every year, however, the produce comes earlier as compare to hilly areas and fetch good price. Yield and yield contributing characters are the ultimate goal of any crop production and the fruit quality and nutrient components is the basic requirement of a crop improvement. Therefore, the choice of a locally adaptable genotype is of paramount importance for successful strawberry cultivation (Asrey and Singh, 2004). Hence, studies about these important traits are necessary for successful cultivation of this crop in a new area. There are very little studies have been conducted on the performance of strawberry genotypes for yield and fruit quality parameters. Considering all above points, the current study was undertaken with the objective to evaluate the most adaptable strawberry genotypes for yield and physico-chemical characters under local of North Indian agro-climatic zone.

Materials and Methods

The present study was carried out at the Horticulture Research Centre of Department of Horticulture (29.04

*Email: sachinchoudhary2096@gmail.com

°N latitude and 77.42 °E longitude & 237 MSL), Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram, Meerut during 2014-15. The uniform and healthy runners of eleven strawberry varieties (Chandler, Douglas, Selva, Confutura, Etna, Gorella, Belrubi, Brighton, Seascape, Pajaro and Dana) were procured from IARI, Regional station, Shimla, Himachal Pradesh (Table 1). The characteristics features of 11 genotypes and physical variability for fruit size and shape is given in Table 1. The runners were transplanted in well prepared 1.5×1.5 meter raised beds with the spacing of 30×30 cm in the second fortnight of November, 2014-15. The experiment was laid out in a randomized block design with three replications. All the strawberry genotypes selected for the experiment were grown with recommended plant protection measures. Date of first fruit set and days to maturity in each genotype was recorded. Five plants of each genotype were selected randomly for observations. Fruit of different strawberry genotypes were classified into four shapes. Fruit length and fruit diameter of five randomly selected fruits were measured with Generic 150mm/6 Inch Lcd digital electronic carbon fiber Vernier Caliper and fruit weight was taken using electronic balance. Number of fruits/plant was recorded by calculating the per cent fruit set per plant with the formula given by Westwood (1993).

$$\text{Per cent fruit set} = \frac{\text{Number of fruit set}}{\text{Total number of flowers}} \times 100$$

Yield per plant (g) was recorded at the time of harvesting. Total soluble solids of fruits were determined using a portable hand refractometer (DH, SHR95 model). Fruit titrable acidity was determined as per the methods described by AOAC (1990). TSS/acid ratio was calculated by dividing total soluble solids by acidity, whereas reducing sugars and total sugars were determined as per the method suggested by Ranganna (1997). Data recorded on different parameters was analyzed by standard procedure using OPSTAT home page of CCSHAU, Hisar (Sheoran *et al.*, 1998) described by Panse and Sukhatme, 1995.

Results and Discussion

The results of the present investigation clearly indicate that all the strawberry genotypes exhibited significant variation with respect to all the studied parameters. The genotype Gorella, Belrubi and Brighton set the fruits early (96 days after transplanting) followed by Douglas, Selva, Confutura, Etna, Pajaro and Dana (98 days after transplanting) (Table 2). The genotype, Seascape set first fruit on 100 days after transplanting, whereas

Table 1. Characteristic features of strawberry genotypes selected for the study

S. No.	Name of genotype	Features	Source of genotype
1.	Chandler	The plants are vigorous, high-yielding, produce desirable fruits. Fruits are very large and firm. Fruits are long and wedge-shaped to large and conical, brilliant red color, glossy, and have an exceptional flavor Fruits are good for eating fresh or shipping and also very good for freezing.	IARI, Regional Station, Shimla (HP)
2.	Douglas	Vigorous plant, clear foliage and semi-erect habit. Great fruits, of elongate conical shape and orange red colour. Firm flesh, red-coloured with pink centre, good taste and resistance to transport damages. High yielder.	IARI, Regional Station, Shimla (HP)
3.	Selva	One of the most remonting varieties in Northern Europe in the past. Fruits are very firm and Suitable for export. Taste is neutral. Plants are easy to cultivate.	IARI, Regional Station, Shimla (HP)
4.	Confutura	Produces small-sized fruits, conical to flat shaped fruits. Fruits have 0.7 % acidity and sugar content is 8%.	IARI, Regional Station, Shimla (HP)
5.	Gorella	Fruits have firm fleshy skin, 0.85% acid and 7.0% sugar content. Globose conic fruit shape.	IARI, Regional Station, Shimla (HP)
6.	Etna	Produces medium-sized fruits, conical to flat shaped fruits. Fruits have 0.94% acidity and sugar content is 7%.	IARI, Regional Station, Shimla (HP)
7.	Belrubi	Produces large-sized, conical to wedge-shaped fruits. Fruits have a mild tart-sweet flavor due to acidity 0.98%, sugars 6% content	IARI, Regional Station, Shimla (HP)
8.	Brighton	Fruits are very firm and Suitable for export. Taste is neutral. Plants are easy to cultivate. Fruit shape is Globose conic.	IARI, Regional Station, Shimla (HP)
9.	Seascape	Fruits are large and productive with excellent flavor. Suited for northeastern growers. Also suitable for hanging baskets and containers	IARI, Regional Station, Shimla (HP)
10.	Pajaro	Fruits have firm fleshy skin featuring, 0.97% acid and 5.5% sugar content. Suitable for processing and dessert preparations.	IARI, Regional Station, Shimla (HP)
11.	Dana	Produces small-sized fruits, conical to flat shaped fruits. Fruits have 1.0 % acidity and sugar content is 7%.	IARI, Regional Station, Shimla (HP)

Table 2. Physical characters of strawberry fruits

Varieties	First fruit set (DAT)*	Fruit length (mm)	Fruit breadth (mm)	Fruit weight (g)	Fruit shape
Chandler	101	37.9	33.4	13.3	Conical & long wedge
Douglas	98	29.9	26.3	11.4	Globose conic
Selva	98	31.4	20.1	11.0	Globose conic
CONFUTURA	98	34.9	31.5	12.6	Flat conic
Gorella	96	33.3	27.9	11.3	Globose conic
Etna	98	25.3	19.5	9.2	Flat conic
Belrubi	96	32.6	24.4	11.2	Necked
Brighton	96	32.2	28.7	11.9	Globose conic
Seascape	100	36.5	31.6	13.0	Flat conic
Pajaro	98	28.0	22.4	10.7	Globose conic
Dana	98	29.8	22.2	8.8	Flat conic
Mean		32.1	25.2	11.4	
$CD_{0.05}$		1.75	1.82	0.87	

*DAT = Days after transplanting

Characterization for fruit traits

Varieties	Fruit set (%)	Number of fruit/plant	Days to maturity	Yield/plant (g)
Chandler	81.4	22.3	33.8	311.1
Douglas	77.3	19.3	31.6	220.0
Selva	71.5	14.8	29.5	179.1
CONFUTURA	79.1	21.6	32.0	296.6
Gorella	76.8	19.1	31.6	195.6
Etna	69.6	15.3	32.2	127.3
Belrubi	74.0	17.6	36.1	215.2
Brighton	72.5	16.3	34.5	210.8
Seascape	80.2	21.1	30.5	291.9
Pajaro	75.1	18.3	30.5	206.9
Dana	76.3	16.6	32.9	111.9
Mean	75.8	18.4	32.3	215.1
$CD_{0.05}$	1.53	1.47	1.58	9.91

genotype, Chandler observed quite late in first fruit set (101 days after transplanting). Fruit shape of different strawberry genotypes were classified into four shapes (Ishikawa *et al*., 2018). Genotype Chandler exhibited both conical and long wedge shaped fruits whereas Belrubi produced necked shaped fruits. The fruit shape of genotypes Douglas, Selva, Gorella, Brighton and Pajaro produced globose conic shaped fruits, while genotypes of Confutura, Etna, Seascape and Dana were flat conic in shape. These findings are in conformity with the earlier findings of Rahman and Ahmad (2009) and Rahman *et al*. (2015).

Genotype Chandler produced largest berries (37.9 mm) which was statistically at par with genotype Seascape (36.5) followed by Confutura (34.9 mm), Gorella (33.3 mm) while, smallest fruits were measured in Etna (25.3 mm) (Table 2). Maximum fruit breadth was measured in Chandler (33.4 mm) which was statistically at par with genotypes Seascape (31.6 mm) and Confutura (31.5 mm), whereas minimum fruit breadth was observed in Etna (19.5 mm). The maximum fruit weight was recorded in genotype, Chandler (13.3 g) which was statistically at par with Seascape (13 g) and Confutura (12.6 g) whereas minimum fruit weight was recorded in Dana (8.8 g). The results obtained by Pathak *et al.* (2006) and Kumar *et al.* (2011) was in conformity with the present findings. However, Kumar and Kumar (2011) and Moshiur *et al.* (2013) reported different results with respect to fruit length, fruit breadth and fruit weight which might be due to the prevailing environmental conditions of the areas and cultural practices followed during the experiment.

Significant results have been observed for yield, fruit set, number of fruit per plant and days to maturity

and are presented in Table 2. Maximum fruit set was recorded in genotype Chandler (81.4 %) which was statistically at par with Seascape (80.2 %) and closely followed Confutura (79.1 %) whereas Etna (69.6 %) observed minimum fruit setting. Earlier, Kumar and Kumar (2011) also showed similar result with respect to fruit set. Genotype Chandler produced maximum number of fruit per plant (22.3) which was statistically at par with Confutura (21.6) and Seascape (21.1). However, minimum number of fruit was produced by Selva (14.8). Similar reports for number of fruit per plant was also reported by Belakhud *et al.* (2015) and Neetu and Sharma (2018). Genotype Selva was earliest to mature (29.5 days) which was statistically at par with Seascape (30.5 days) and Pajaro (30.5 days) whereas late maturity was noticed in Belrubi (36.1 days) closely followed by Brighton (34.5 days). Similar variation was earlier reported by Kumar *et al.* (2011).

The genotype Chandler recorded maximum fruit yield per plant (311.1 g) which was significantly higher among other genotypes whereas closely followed by Confutura (296.6 g) and Seascape (291.9 g) (Table 2). The minimum fruit yield per plant was produced by Dana (111.9 g). The variation in yield per plant was due to the inherent character of the germplasm. Rahman and Ahmad (2009) found that yield per plant of strawberry varied significantly and ranged from 442.5 to 129.8 g. Present findings were consonant with the results of Rahman and Ahmad (2009), Rahman *et al.* (2015) and Neetu and Sharma (2018). The yield per plant recorded in the present study was quite different from the earlier studies conducted by Kumar and Kumar (2011) and this may be due to the different agro-climatic conditions of a particular area.

The biochemical characteristics also exhibited a significant variation in different genotypes of strawberry (Table 3). Maximum total soluble solids was recorded in the fruit of genotype Chandler (12^{o}B) which was statistically at par with Seascape (11.8^{o}B) and Confutura (11.6^{o}B) while, minimum total soluble solids was registered in the fruit of Pajaro (8.4^{o}B). The maximum acidity was recorded in genotypes Pajaro (1.1%) and Dana (1.1%) whereas the minimum acidity was recorded in genotypes, Chandler (0.55%) which was statistically at par with Confutura (0.62%) and Seascape (0.64%). Genotype Chandler recorded maximum TSS/acid ratio (21.8) which was statistically higher among all the other genotypes whereas minimum TSS/acid ratio was recorded in Pajaro (8.4%). Earlier Pathak *et al.* (2006), Kumar and Kumar (2011) and Kumar *et al.* (2011) also reported similar results for these parameters.

Maximum reducing sugar (7.9%) and total sugar (9.4%) was recorded in genotype Chandler which was statistically at par with Seascape (7.7% and 9.2%) and Confutura (7.4 % and 8.9%) whereas minimum reducing sugar was observed in Brighton (4.7%) and minimum total sugar was observed in Brighton (6.6%). The variation in biochemical parameters among the genotypes might be due to the variation of genotypes and mostly affected by environmental factors. Similar results with respect to the reducing and total sugar were also reported in few of the genotypes which we study in our conditions (Pathak *et al.* (2006), Kumar and Kumar (2011) and Rahman *et al.* (2015), Belakhud et al. (2015) and Bhatia *et al.* (2017).

Table 3. Fruit biochemical characters of different strawberry genotypes

Varieties	TSSoB	Acidity (%)	TSS/acid ratio	Reducing sugar (%)	Total sugar (%)
Chandler	12.0	0.6	21.8	7.9	9.4
Douglas	9.1	0.8	12.0	5.2	6.8
Selva	10.8	0.7	15.2	6.4	8.1
CONFUTURA	11.6	0.6	18.7	7.4	8.9
Gorella	9.7	0.8	11.7	5.5	7.2
Etna	9.7	0.9	10.3	5.7	7.4
Belrubi	9.6	0.8	11.9	6.3	8.0
Brighton	8.9	0.9	9.8	4.7	6.6
Seascape	11.8	0.6	18.5	7.7	9.2
Pajaro	8.4	1.1	7.5	5.2	6.8
Dana	9.6	1.1	9.0	6.1	7.7
Mean	10.1	0.8	13.3	6.2	7.8
CD0.05	0.64	0.11	1.74	0.52	0.49

Conclusion

On the basis of results obtained from the present experiment on varietal evaluation for yield and quality characters, it can be concluded that the genotype, Chandler performed excellent for most of the yield and quality characters studied which can be recommended for commercial cultivation in local of North Indian agro-climatic zone for fetching higher yield with better fruit quality. These strawberry genotypes need to test under multi-location trials in different agro-ecological regions to identify the best genotypes adaptable to different areas.

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Indian J. Plant Genet. Resour. 34(1): 59–63 (2021)
DOI 10.5958/0976-1926.2021.00008.5

RESEARCH ARTICLE

Characterization of Little Millet *(Panicum sumatrense)* Genetic Diversity in Yelagiri Hills of Tamil Nadu

A Gopikrishnan[1*], M Pandiyan[2], P Thilagam[1], P Veeramani[1] and S Nanthakumar[1]
[1]*Agricultural Research Station, Virinjipuram, Vellore District-632104, Tamil Nadu, India*
[2]*Regional Research Station, Virudhachalam, Cuddallore District-606001, Tamil Nadu, India*

(Received: 05 December, 2020; Revised: 22 January, 2021; Accepted: 29 January, 2021)

A local collection of 400 little millet accessions of traditional cultivars from villages of Yelagiri hills of Tamil Nadu were characterized for ten morphological characters by principal component analysis for determining pattern of genetic diversity and relationship among individuals. The largest variation was observed for the number of productive tillers per plant with coefficient of variation of 37.33% .The least variation was observed in days to maturity with coefficient of variation of 4.5%. A cumulative variation of 69.10% among ten characters was explained by first three axes. Correlation analysis revealed that straw yield, plant height, number of productive tillers, flag leaf sheath length, flag leaf length and panicle length, had highly significant and positive association with seed yield per plant and also exhibited significant positive inter correlation among themselves.

Key Words: Characterization, Diversity, Little millet, Traditional cultivars, Yelagiri hills

Introduction

Panicum sumatrense Roth. ex Roem. and Schultz (Samai, Indian millet, Little millet) is a small millet domesticated in India (Wet *et al.,* 1983). It is grown in rainfed land of various soil types with less input and in regions broadly differing in thermo and photoperiods. In Eastern Ghats of India, little millet cultivation occupies significant part of tribal agriculture providing staple food and income for the people of the region (Bhat *et al.*, 2018). Little millet is quick growing, short duration crop having the potential to withstand both drought and water logging conditions (Goron and Raizada 2015, Upadhyaya, *et al.*, 2014). Small millets are devoid of stored grain pests having long storage life and keeping quality. Little millet is considered as a good source of carbohydrate protein, fat, minerals and vitamins (Saleh *et al*. 2012). Little millet is highly self-fertilized crop (Arun *et al.*, 2012) grown for food and fodder. The average yield of little millet is low, even though it has a potential to yield up to 3t/ha (Manimozhi *et al*., 2014). The lower productivity of little millets is largely due to poor fertility of soils and non-adoption of better agronomic practices.

Information on landrace diversity and genetic relationships among breeding materials is basis for selection as well as for planning crop breeding program. Studies on descriptive statistics are helpful in the estimation of simple measures of variability like mean, range, standard deviation, and coefficient of variability which can be used for preliminary evaluation. To characterize and assess landrace diversity principal component analysis (PCA) is commonly used. Principal component analysis is based on data reduction technique from larger sets of data. It reforms many inter correlated variables in to smaller number of uncorrelated variables known as principal components. Each component is uncorrelated with other components but variables within the components are related (Amy and Pritts, 1991, Vishnu Varthini, *et al.*, 2014). The number of components taken out is equal to the number of variables taken for analysis and each component explained per cent (%) variation to the total variability. The first component gives large amount of the total variance than subsequent components. Thus, it is useful to proceed for genetic improvement of important traits rather than going for all the characters under study. Correlation is a measure of the degree and direction of association between two or more variables. Plant characters are having interrelationship with each other, while selecting a character there may be simultaneous effect on other characters also and it depends on the intensity of association between the two traits under consideration. Knowledge on correlation

[*]*Email: vagopikrishnan@gmail.com*

between yield and its component characters may be helpful in selection of suitable plant type. Cluster analysis is a method for evaluation of genetic similarity used to place the landraces into groups or clusters such that the landraces in a given cluster have a tendency to be similar to each other and landraces in different clusters tend to be dissimilar. Hence, the present investigation was carried out to assess the diversity and extent of variability of little millet cultivated in Yelagiri hills which are extension of Eastern Ghats located in north eastern Tamil Nadu. Little millet is cultivated extensively by the native people of Yelagiri hills. It is grown predominantly in this *area* under rainfed during *kharif* season as first crop in the month of June. We collected 400 accessions from 14 locations of Yelagiri hills. Here we report the extent of morphological variation recorded among the little millet accessions.

Material and Methods

Seeds of 400 entries of little millet were collected from 14 villages of Yelagiri hills during *kharif* 2014 and named as Sa1 to Sa400 (Table 1). The crop was grown during the r*abi* season 2014 at Agricultural Research Station, Virinjipuram which is situated at latitude of 12°5′ N and longitude of 78°E with sandy loam soil of pH 7.8. Each accession was raised in one row of 4 m length with 30 cm and 10 cm inter and intra row spacing respectively. Observations were recorded on five representative plants per row. Recommended cultural practices were followed. The accessions were characterized for 10 traits (Table 2) according to the little millet descriptors (IBPGR, 1985). The data were subjected to basic statistics, correlation analysis and Principal Component Analysis (PCA) using Statistical Tool for Agricultural Research (STAR) software package. The cluster analysis was done using Darwin's software.

Result and Discussion

The plant height was recorded the highest deviation from the population mean (Table 2) while panicle length (4.53), days to maturity (4.24), flag leaf length (4.12) and days to 50% flowering (3.57) also deviated considerably from the mean. When the frequency distribution is asymmetrical, the distribution is known as skewed and it indicates the trait is controlled by non additive gene action and may be influenced by environmental variables. The traits showing skewed distribution indicates mostly dominant gene action and positively skewed specify complementary gene interaction and negatively skewed denote duplicate gene interaction. Frequency distribution for different traits in 400 little millet accessions revealed different patterns of distribution (Fig. 1) The traits such as number of productive tillers, flag leaf length, flag leaf width, flag leaf sheath length, days to maturity, straw

Table 1. Little millet germplasm collected around Yelagiri hills

Traditional cultivars/land race	Number of entries collected	Names as	Place of collection
Chittan samai	20	Sa1-Sa20	Muthanoor
Vellai samai	30	Sa21-Sa50	Kottaiyur
Siruvellai samai	20	Sa51-Sa70	Atthanavoor
Kalman samai	20	Sa71-Sa90	Manjakollaputhur
Karunchittan samai	20	Sa91-Sa110	Mangalam
Chittan samai	30	Sa111-Sa140	Thayanur
Chittan samai	20	Sa141-Sa160	Putthur
Chittan samai	20	Sa161-Sa180	Paadaanoor
Koththu samai	20	Sa181-Sa200	Rayaneri
Chittan samai	20	Sa201-Sa220	Nilavur
Chittan samai	30	Sa221-Sa250	Mettukaniyur
Chittan samai	20	Sa251-Sa270	Pallakaniyur
Vellai samai	20	Sa171-Sa290	Kottur
Chittan samai	20	Sa291-Sa310	Jamunamarathur
Perunkolai samai	10	Sa311-Sa320	Jamunamarathur
Kolap samai	20	Sa321-Sa340	Jamunamarathur
Koluthana	10	Sa341-Sa350	Jamunamarathur
IR20 (Locally named as IR 20)	20	Sa351-Sa370	Jamunamarathur
Karunsamai	15	Sa371-Sa385	Jamunamarathur
IR50 (Locally named as IR 50)	15	Sa386-Sa400	Jamunamarathur
Total	400		

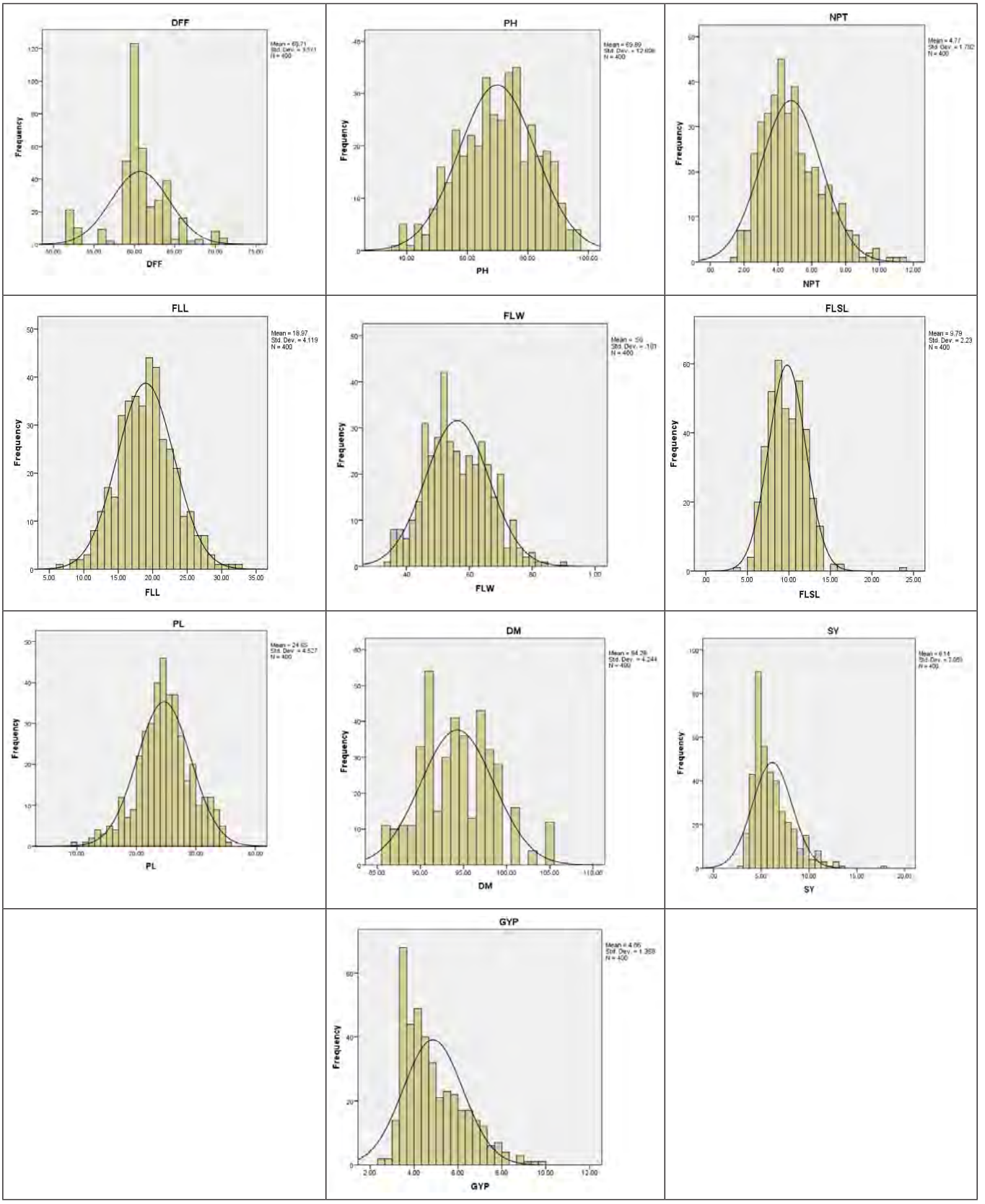

Fig.1. Frequency distribution of different quantitative traits. For trait description please see Table 1.

Table 2. Descriptive statistics based on 400 accessions of little millet

Traits	Minimum	Maximum	Mean	Std. Deviation	CV (%)	Skewness	Kurtosis
DFF	52.00	71.00	60.71	3.57	5.88	-0.17	1.61
PH (cm)	37.00	97.20	69.89	12.61	18.04	-0.19	-0.51
NPT	1.40	11.20	4.77	1.78	37.33	0.73	0.39
FLL (cm)	6.80	32.20	18.97	4.12	21.71	0.16	0.17
FLW (cm)	0.34	0.90	0.56	0.10	17.97	0.25	-0.31
FLSL (cm)	3.60	23.92	9.79	2.23	22.77	0.78	3.27
PL (cm)	9.52	35.40	24.65	4.53	18.36	-0.22	0.32
MAT	86.00	105.00	94.27	4.24	4.50	0.30	-0.20
SY (g)	2.88	17.54	6.14	2.06	33.53	1.44	2.83
GY (g)	2.38	9.7	4.86	1.36	27.95	0.94	0.40

DFF –Days to 50% Flowering, PH-Plant Height(cm), NPT-Number of Productive Tillers, FLL – Flag Leaf Length (cm), FLW – Flag Leaf Width (cm), FLSL-Flag Leaf Sheath Length (cm), PL-Panicle Length (cm), MAT-Days to Maturity, SY-Straw Yield, GY-Grain Yield per plant (g).

yield and grain yield were positively skewed indicating possible complementary gene interaction. Negative skewness was observed for days to 50% flowering, plant height, panicle length showing possible duplicate gene interaction. Negative kurtosis denotes absence of gene interaction while positive kurtosis indicates presence of gene interaction. The traits with leptokurtic distribution are controlled by few numbers of genes while platykurtic distribution are controlled by many number of genes. The traits such as days to 50% flowering, number of productive tillers, flag leaf length, flag leaf sheath length, panicle length, straw yield and grain yield per plant were leptokurtic while, plant height, flag leaf width and days to maturity were platykurtic.

Principal Component and Correlation Analysis

In the current study, first three principal components expressed cumulative variance of 69.10%. Principal Component 1 accounted for 39.66% of the total variability contributed by plant height (0.41), number of productive tillers (0.34), flag leaf length (0.25), flag leaf width (0.17), flag leaf sheath length (0.37), panicle length (0.29), straw yield (0.31) and grain yield per plant (0.32). Principal Component 2 was related to days to 50% flowering (0.53), plant height (0.15), flag leaf length (0.43), flag leaf width (0.27), panicle length (0.33), days to maturity (0.52), straw yield (0.16) and grain yield (0.07) that explained 15.94 % of total variability. Plant height (0.11), flag leaf length (0.25), flag leaf width (0.16), flag leaf sheath length (0.14), panicle length (0.38) contributed for the total variance of 13.50% from Principal Component 3. The biplot ordination indicated positive associations of straw yield, plant height, number of productive tillers, flag leaf sheath length, flag leaf length, panicle length, and seed yield per plant. Days to 50% flowering and days to maturity having obtuse angle with other traits indicated negative association with other traits.

Correlation Analysis returned positive association of Straw yield, plant height, number of productive tillers, flag leaf sheath length, flag leaf length and panicle length with seed yield per plant in the decreasing order and also significant positive inter correlation among themselves. Seed yield had significant negative association with days to 50% flowering and days to maturity. Days to 50% flowering had a positive association with days to maturity revealing the considerable commonness in the expression of genes responsible for these traits (Shinde *et al*., 2018; Anuradha *et al.,* 2017)

Conclusion

Four hundred little millet accessions representing 14 location of Yelagiri hills of Tamil Nadu were collected and characterized for 10 traits. Our results on preliminary characterization showed that detailed trait specific evaluation after purifying each accession would provide excellent parental lines and genetic stocks for crop improvement in little millet.

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Indian J. Plant Genet. Resour. 34(1): 64–69 (2021)
DOI 10.5958/0976-1926.2021.00009.7

RESEARCH ARTICLE

Evaluation of Water Stress Tolerance Indices for the Selection of Maize Genotypes

GK Mittal[1] and Bhuri Singh[2*]

[1]*Assistant Professor, Department of Biochemistry, SKN College of Agriculture, Jobner, Jaipur-303329, Rajasthan, India*
[2]*Assistant Professor, Department of Basic Science, College of Horticulture and Forestry, Jhalawar-326023, Rajasthan, India*

(Received: 15 August, 2020; Revised: 11 January, 2021; Accepted: 28 February, 2021)

Thirty genotypes of maize were evaluated in RBD with two replications under two regimes (i) no water stress and (ii) water stress during 2009-10 in *Rabi*. Eight water stress tolerance indices viz., stress tolerance (TOL), stress susceptibility index (SSI), stress tolerance index (STI), mean production (MP), geometric mean production (GMP), yield index (YI), stress susceptibility percentage index (SSPI) and modified stress tolerance index(MSTI) were calculated based on grain yield per plant (g) under water stress (Ys) and no water stress (Yp). Yield under Ys had significant positive association with STI, MP, GMP, YI and MSTI. Based upon the mean yield and stress tolerance indices, five genotypes GM-2, PM-3, EH-1731, EC-3160 and EH-1820 were found potentially drought tolerant.

Key Words: Correlation, Grain yield, Maize, Tolerance indices, Water stress

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crop in the world agricultural economy, as food for man and feed for animals and its serves as a source for high fructose, malt dextrin, germ oil, germ meal fibre and gluten products which have application in industries such as alcohol, textile, paper, pharmaceuticals, organic chemicals, cosmetics and edible oil (CRA, 2009). Maize can be grown under a wide range of climatic conditions and is particularly sensitive to water stress from one week before to two weeks after flowering (Grant *et al.,* 1989)**.** Therefore, high yielding maize could be achieved through full irrigation at the flowering stage, even if the soil water content is sub-optimal during the vegetative growth and grain filling stages (Igbadun *et al.,* 2007). Drought tolerance is a complex quantitative trait with low heritability. Breeding for tolerant to drought is complicated by the lack of rapid, reproducible screening techniques and the inability to routinely create defined and repeatable water stress conditions where large populations can be evaluated efficiently (Ramirez and Kelly, 1998). The most effective selection criterion, among various morphological, physiological, yield and yield related traits, for identifying drought tolerant genotypes is based on mean grain yield (the arithmetic and geometric) under drought stress and non-stress environments (Araus *et al*., 2002; White *et al*., 1994). Loss of yield is the main concern of plant breeders hence they emphasize on yield performance under stress conditions. The relative yield performance of genotypes in drought stressed and favourable environments seems to be a common starting point in the identification of desirable genotypes for drought conditions (Nouri *et al*., 2011). Thus, drought indices which provide a measure of drought based on loss of yield under drought-conditions in comparison to normal conditions have been used for screening drought-tolerant genotypes (Mitra, 2000). The objective of the present research was to identify drought tolerant maize genotypes on the basis of various quantitative criteria on their yield performance in water stress and no water stress at pre and post flowering stages such as stress tolerance (TOL), stress susceptibility index (SSI), stress tolerance index (STI), mean production (MP), geometric mean production (GMP), yield index (YI), stress susceptibility percentage index (SSPI) and modified stress tolerance index (MSTI).

Materials and Methods

The experiment was laid out with thirty genotypes of maize at Agronomy Farm, B.A. College of Agriculture, Anand 2009-10 in *Rabi*. Seeds of thirty diverse

[*]*Email: bhurisingh.gpb@gmail.com*

genotypes were obtained from Main Maize Research Station, Godhra, Agricultural University, Anand, Gujarat and All India Coordinate Research Project on Maize, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan) (Table1). These genotypes were sown in two replications with two different environments namely no water stress (S_0) and water stress (S_1) conditions at pre and post flowering stage. In each environment/replication, each genotype was sown in a single row plot of 4m length. The row to row and plant to plant distance was maintained 60cm and 20cm respectively. Irrigations were given at the time of seed sowing for establishing the crop in both environments. Till pre flowering stage, which coincides with 50-60 days after sowing, all genotypes were similar. At this stage water stress was created by withholding irrigation S_1while S_0 was given normal irrigation. At post flowering stage (80-90 days after sowing), water stress was created by withholding irrigation in S_1 while remaining so was given normal irrigation. All standard recommended agronomic practices were carried out during entire cropping season except irrigation. The cobs of the sampled plants were harvested seeds were weighed in (g) and recorded as grain yield per plant under both water stress and no water stress conditions at pre and post flowering stages and denoted as Ys and Yp, respectively.

Calculation of Water Stress Indices

Eight water stress tolerance indices were calculated using the following relationships:

- Stress tolerance (TOL) = Yp - Ys (Rosielle and Hamblin, 1981). The genotypes with low values of this index considered more stable in two different conditions.
- Stress susceptibility index (SSI) = [1 - (Ys/Yp)]/

Table 1. Details of genotypes with sources and pedigree used in study

S. No.	Genotypes	Maturity	Source/Pedigree
1	PM-3		AICRP on Maize, MPUA &T, Udaipur
2	EC-3135 (Forage)		AICRP on Maize, MPUA &T, Udaipur
3	EC- 3160 (Y)		AICRP on Maize, MPUA &T, Udaipur
4	EC-3157(NP-2)		AICRP on Maize, MPUA &T, Udaipur
5	GWC-9611	EE	Local collection in 96 (Panchmahals)
6	GYC-9646	M	Suwan-3 x Composite-74
7	GWC-9103	EE	A Cross-8223 x FMS
8	GWC-9701	M	Local collection in 97 (Panchmahals)
9	GYC-0402	M	IC-9414 (GDRM-188)
10	EH-1491		AICRP on Maize, MPUA &T, Udaipur
11	GWC-9101	EE	GM-1 x Pool-31
12	EH-1389		AICRP on Maize, MPUA &T, Udaipur
13	GYC-9325	EE	DTS-19
14	GYC-9837	M	Local collection in 98 (Sabarkantha)
15	GWC-9604	EE	Local collection in 96 (Panchmahals)
16	GWC-9626	EE	Local collection in 96 (Panchmahals)
17	GYC-9005	EE	MMH-42 x GM-2
18	GYC-9327	M	DTS-26
19	GWC-9631	M	LGC-40 x EH-2922
20	GWC-9413	EE	GDRM-187
21	GYC-9535	M	A Cross-8731 x DRM-6
22	GYC-0401	M	IC-9414 (GDRM-188)
23	GM-6 (White)		Released cultivar
24	GM-2 (Yellow)		Released cultivar
25	EC-3154		AICRP on Maize, MPUA &T, Udaipur
26	Texpeno Sequia		AICRP on Maize, MPUA &T, Udaipur
27	EH-1820		AICRP on Maize, MPUA &T, Udaipur
28	GYC-9315	EE	Harsh-10
29	EH-1731		AICRP on Maize, MPUA &T, Udaipur
30	GWC-0204	EE	Mandvi Gwritoli, Mwrigrol

E = Early, M = Medium, EE = Extra Early,\

[1 - ($\bar{Y}$s/$\bar{Y}$p)] (Fischer and Maurer, 1978). The genotypes with SSI< 1 considered more resistant to water stress conditions.

- Stress tolerance index (STI) = [Yp x Ys / $\bar{Y}^2$p] (Fernandez, 1992). The genotypes with high STI values considered tolerant to water stress.
- Mean productivity (MP) = (Ys + Yp) / 2 (Rosielle and Hamblin, 1981). The genotypes with high value considered more desirable.
- Geometric mean productivity (GMP) = √ Ys × Yp (Fernandez, 1992). The genotypes with high value considered more desirable.
- Yield index (YI) = (Ys)/($\bar{Y}$s) (Gavuzzi *et al.,* 1997). The genotypes with high value considered suitable for water stress condition.
- Stress susceptibility percentage index (SSPI) = [Yp – Ys/2($\bar{Y}$p)] × 100 (Moosavi *et al.,* 2008). The genotypes with low values considered stable in two different conditions.
- Modified stress tolerance index (MSTI) = KiSTI, K1 = Yp^2/ $\bar{Y}$p^2 and K2= Ys^2/ $\bar{Y}$s^2 (Farshadfar and Sutka, 2002). The genotypes with high value considered more desirable.

Ys and Yp represented yield for each genotype in water stress and no water stress conditions, respectively. Also, Ys and Yp were mean yield in water stress and no water stress conditions at pre and post flowering stages, respectively (for all genotypes). Statistically, efficiency of the water stress tolerance indices were evaluated based on their ability to discriminate between genotypes, correlation with grain yields of both the environments and their efficiency to identify the best high yielding and stable genotypes.

Statistical Analysis

Pooled analysis of variance was used to compute genotypes x environment interactions. Ranks were assigned to genotypes for each index. A genotype with least rank total was considered to be the best genotype. Based on indices, the genotype with the highest value for Ys, Yp, MP, GMP, STI, MSTI (K1), MSTI (K2) and YI and the lowest value for SSI, TOL and SSPI received the first rank. Besides, the most desirable water stress tolerance measures, the correlation coefficient between Yp, Ys and other quantitative indices of water stress tolerance were estimated using SPSS 20.0 statistical software (SPSS 2011).

Table 2. Pooled analysis of variance for grain yield per plant (g)

Source of variance	d. f.	Grain yield per plant (g)
Environment	1	3049.49
Genotype	29	220.80
G x E	29	117.35
Pooled Error	58	42.05

Results and Discussion

Pooled analysis of variance revealed significant differences among the environment, genotypes and environment × genotype interactions for grain yield per plant (g). This indicated differential/non-linear response of genotypes to the stress. The environment effect was the most important source of yield variation (Table 2). Mean grain yield per plant under S_0 was 49.14 g and ranged from 29.97 g (Texpeno Sequia) to 74.52 g (GWC-0204). While mean grain yield per plant under S_1 was 39.05 g and ranged from 17.07 g (Texpeno) to 56.64 g (EH-1731). Thus the result indicated that mean grain yield per plant (g) decreased under water stress and the range was wider in S_0 as compared to S_1. The genotypes GWC-0204, EH-1389, EH-1731, EC-3160, GWC-9101 and EC-3157 showed higher grain yield per plant (g) in S_0. Whereas, genotypes EH-1731, GM-2, EH-1820, PM-3, EC-3160 and GYC-9325 recorded higher grain yield per plant (g) in S_1 (Table3). To identify water tolerant genotypes using TOL index, higher value of TOL demonstrates more changes of genotype yield in water stress and no water stress conditions (Fernandez, 1992). Rosielli and Hamblin (1981) stated that selection based on TOL index leads to selection of genotypes with low yields in no water stress condition and have lower mean productivity (MP). The results of this experiment showed that GWC-9631, GYC-9325, GM-2, PM-3 and GWC-9611 were tolerant whereas GWC-0204, GWC-9101, GYC-9837and EH-1389 were sensitive to the water stress based on TOL index. For SSI, the higher value refers to more susceptibility to stress, indicating that GWC-9631, GYC-9325,GM-2, PM-3 and GWC-9611 were more tolerant genotypes. The SSPI resulted in the same genotype ranking as TOL. MP, GMP and STI showed similar ranking of genotypes relative to water stress tolerance. Based on STI, the greater the difference between the yields found in no water stress and water stress conditions at pre and post flowering stages, the smaller amount of water stress tolerance index and vice versa. Thus, genotypes EH-1731, GM-2, EC-3160, EH-1820, EC-3135 and PM-3 were found water stress tolerant with high STI and high grain yield per plant (g) under no

water stress and water stress conditions at pre and post flowering stages, whereas genotypes Texpeno Sequia, GWC-9103, GWC-9101 and GWC-9701 displayed the lowest amount of STI and grain yield per plant (g) under water stress condition at pre and post flowering stage. GMP showed the same genotype ranking as STI. For MP, the higher value refers to more tolerant to water stress condition. Therefore EH-1731, GM-2, GWC-0204, EC-3160 and EH-1820 were listed as tolerant whereas, the genotypes Texpeno Sequia, GWC-9103, GWC-9701 and GWC-9611 were susceptible to drought stress. YI can be used as a selection criterion, although it only ranks cultivars on the basis of Ys. Based on YI, genotypes EH-1731, GM-2, EH-1820, PM-3 and EC-3160 had the highest YI and Ys, hence were more tolerant whereas, Texpeno Sequia, GWC-9101, GYC-9837 and GWC-9103 had the lower YI and Ys. According to K1STI, the genotypes GWC-0204, EH-1389, EH-1731, EC-3160 and GWC-9101were the most tolerant whereas, the genotypes Texpeno Sequia, GWC-9611, GWC-9631 and GWC-9701 were the most sensitive. According to K2STI, the genotypes EH-1731, GM-2, EH-1820, PM-3, EC-3160 and GYC-9325 were the most tolerant whereas, the genotypes Texpeno Sequia, GWC-9101, GYC-9837, GWC-9103 and GWC-9701were the most sensitive (Table 3). It was concluded that MP, GMP and STI values are convenient parameters to select high yielding genotypes in both the water stress and no water stress conditions at pre and post flowering stages whereas relative decrease in yield under water stress, TOL, SSI and SSPI values are better indices to determine drought tolerance levels.

Correlation Coefficient

To determine the most desirable water stress tolerance index, the correlation coefficient between Yp, Ys and water stress indices were calculated The best indices are those which have positive correlation with grain yield per plant (g) in both S_0 and S_1 conditions at pre and post flowering stages and would be able to identify high yielding and drought tolerant genotypes (Talebi *et al*., 2007). Grain yield per plant (g) under water stress condition (Ys) had a weak positive association (r = 0.311) with grain yield per plant (g) under no water stress condition (Yp), indicating that high potential yield under optimal conditions does not necessarily result in improved yield in a water stress condition (and the opposite is true) because the genes controlling yield and drought tolerance are different (Rosielle and Hamblin, 1981). Similar findings were reported by Fernandez, 1992; Mohammadi *et al*., 2010; Farshadfar *et al*., 2014; Sahar *et al*., 2016. The grain yield per plant (g) under no water stress (Yp) had significant positive association with TOL (0.559), STI (0.701), MP (0.799), GMP (0.709), SSPI (0.558) and K1STI (0.990), whereas non-significant and positive association with SSI (0.358), YI (0.308) and K2STI (0.313). The grain yield per plant (g) under water stress (Ys) had significant positive association with STI (0.884), MP (0.820), GMP (0.889), YI (1.000) and K2STI (0.987), while K1STI (0.254) exhibited non-significant and positive character association. In addition, TOL (-0.615), SSI (-0.755) and SSPI (-0.615) showed significantly negative association with grain yield per plant (g) under water stress (Ys). The indices STI, MP and GMP exhibited good correlation with grain yield per plant (g) under both the S_0 and S_1 conditions, therefore, selection based on MP, GMP and STI will result in the selection of genotypes with higher drought stress tolerance and yield potential in both S_0 and S_1 conditions, while TOL, SSI, YI and SSPI exhibited good correlation with grain yield per plant under water stress conditions at pre flowering and post flowering stages. Similar findings were also reported by Siahsar *et al*., 2010 in lentil, Zare, 2012 and Saeidi *et al*., 2013 in barley, Singh *et al*., 2015 and Mohammed and Kadhem, 2017 in wheat. Thus, these indices may be used as selection criteria in breeding programme for water stress tolerance at pre and post flowering stages.

Ranking Method

The estimated values of various stress tolerance indices indicated that the identification of water stress tolerant genotypes based on a single criterion was contradictory. Different indices introduced different or same genotypes as water stress tolerant. To determine the most desirable drought stress tolerant genotype according to the all indices, mean rank of all indices were calculated and based on this criterion the most desirable and water stress tolerant genotypes were identified (Table 3). The genotypes GM-2, PM-3, EH-1731and EC-3160 were identified as the most tolerant genotypes for drought stress and genotypes EH-1820, GYC-9325 and EC-3135 were found moderately tolerant for drought stress, while genotypes Texpeno Sequia, GWC-9101, GWC-9103, GWC-9701 and GYC-9837 as the most sensitive for drought stress. Such strategies of using different tolerance indices and ranking pattern for identifying tolerant genotypes were used by several other workers

Table 3. Grain yield per plant (g) and water tolerance indices of maize genotypes in response to no water stress (S_0) and water stress (S_1) conditions at pre and post flowering stages

Genotypes	Grain yield per plant (g)				TOL	Rank	SSI	Rank	STI	Rank	MP	Rank	GMP	Rank	YI	Rank	SSPI	Rank	MSTI (K1)	Rank	MSTI (K2)	Rank	Sum	Overall Rank
	Yp	Rank	Ys	Rank																				
PM-3	50.4	15	49.55	27	0.85	4	0.08	4	1.03	25	49.98	24	49.97	25	1.27	27	0.86	4	1.05	15	1.61	27	197	18
EC-3135	53.1	18	47.96	24	5.14	12	0.46	11	1.05	26	50.53	25	50.46	26	1.23	24	5.23	12	1.17	18	1.51	24	220	22
EC-3160	58.07	27	49.42	26	8.65	16	0.71	13	1.19	28	53.75	27	53.57	28	1.27	26	8.80	16	1.40	27	1.60	26	260	29
EC-3157	54.97	25	41.98	19	12.99	21	1.13	20	0.95	21	48.48	22	48.04	21	1.08	19	13.21	21	1.25	25	1.16	19	233	26
GWC-9611	37.13	2	36.04	13	1.09	5	0.14	5	0.55	5	36.59	4	36.58	5	0.92	13	1.11	5	0.57	2	0.85	13	72	1
GYC-9646	54.57	23	44.93	23	9.64	19	0.84	18	1.01	23	49.75	23	49.52	23	1.15	23	9.80	19	1.23	23	1.33	23	240	27
GWC-9103	43.05	9	26.36	4	16.69	26	1.85	25	0.47	2	34.71	2	33.69	2	0.68	4	16.97	26	0.77	9	0.46	4	113	7
GWC-9701	38.28	4	32.02	5	6.26	13	0.78	15	0.51	4	35.15	3	35.01	4	0.82	5	6.37	13	0.61	4	0.67	5	75	3
GYC-0402	50.72	16	34.89	10	15.83	25	1.49	24	0.73	15	42.81	15	42.07	15	0.89	10	16.10	25	1.06	16	0.80	10	181	17
EH-1491	42.81	8	41.2	18	1.61	6	0.18	6	0.73	14	42.01	14	42.00	14	1.06	18	1.64	6	0.76	8	1.11	18	130	10
GWC-9101	55.42	26	21.52	2	33.90	29	2.91	30	0.49	3	0	6	34.53	3	0.55	2	34.48	29	1.27	26	0.30	2	158	14
EH-1389	60.82	29	34.5	8	26.32	27	2.06	27	0.87	17	47.66	19	45.81	17	0.88	8	26.77	27	1.53	29	0.78	8	216	21
GYC-9325	47.12	14	49.35	25	-2.23	2	-0.23	2	0.96	22	48.24	21	48.22	22	1.26	25	-2.27	2	0.92	14	1.60	25	174	16
GYC-9837	54.16	21	25.18	3	28.98	28	2.55	28	0.56	6	39.67	9	36.93	6	0.65	3	29.47	28	1.21	21	0.42	3	156	13
GWC-9604	47.11	13	32.56	6	14.55	24	1.47	23	0.63	10	39.84	11	39.17	10	0.83	6	14.80	24	0.92	13	0.70	6	146	11
GWC-9626	44.97	11	37.08	14	7.89	15	0.84	17	0.69	13	41.03	13	40.83	13	0.95	14	8.02	15	0.84	11	0.90	14	150	12
GYC-9005	51.27	17	42.32	21	8.95	17	0.83	16	0.90	19	46.80	17	46.58	19	1.08	21	9.10	17	1.09	17	1.18	21	202	19
GYC-9327	54.8	24	40.92	17	13.88	22	1.21	21	0.93	20	47.86	20	47.35	20	1.05	17	14.12	22	1.24	24	1.10	17	224	24
GWC-9631	37.98	3	43.23	22	-5.25	1	-0.66	1	0.68	12	40.61	12	40.52	12	1.11	22	-5.34	1	0.60	3	1.23	22	111	6
GWC-9413	39.53	5	35.59	11	3.94	11	0.47	12	0.58	7	37.56	5	37.51	7	0.91	11	4.01	11	0.65	5	0.83	11	96	4
GYC-9535	45.84	12	42.01	20	3.83	10	0.40	10	0.80	16	43.93	16	43.88	16	1.08	20	3.90	10	0.87	12	1.16	20	162	15
GYC-0401	54.23	22	39.92	16	14.31	23	1.26	22	0.90	18	47.08	18	46.53	18	1.02	16	14.55	23	1.22	22	1.05	16	214	20
GM-6	43.95	10	34.54	9	9.41	18	1.02	19	0.63	9	39.25	8	38.96	9	0.89	9	9.57	18	0.80	10	0.78	9	128	9
GM-2	53.8	19	54.83	29	-1.03	3	-0.09	3	1.22	29	54.32	29	54.31	29	1.41	29	-1.05	3	1.20	19	1.97	29	221	23
EC-3154	42.54	7	35.62	12	6.92	14	0.77	14	0.63	8	39.08	7	38.93	8	0.91	12	7.04	14	0.75	7	0.83	12	115	8
Texpeno	29.97	1	17.07	1	12.90	20	2.05	26	0.21	1	23.52	1	22.62	1	0.44	1	13.12	20	0.37	1	0.19	1	74	2
EH-1820	53.86	20	51.36	28	2.50	8	0.22	9	1.14	27	52.61	26	52.60	27	1.32	28	2.54	8	1.20	20	1.73	28	229	25
GYC-9315	40.65	6	38.86	15	1.79	7	0.21	7	0.65	11	39.76	10	39.74	11	1.00	15	1.82	7	0.68	6	0.99	15	110	5
EH-1731	59.27	28	56.64	30	2.63	9	0.21	8	1.39	30	57.96	30	57.94	30	1.45	30	2.67	9	1.45	28	2.11	30	262	30
GWC-0204	74.52	30	33.28	7	41.24	30	2.64	29	1.03	24	53.90	28	49.80	24	0.85	7	41.94	30	2.30	30	0.73	7	246	28

Ys = Grain yield per plant under water stress condition at pre and post flowering stages, Yp = Grain yield per plant under no water stress conditions at pre and post flowering stages, TOL=Stress tolerance, SSI=Stress susceptibility index, STI=Stress tolerance index, MP= Mean production, GMP=Geometric mean production, YI=Yield index, SSPI=Stress susceptibility percentage index and MSTI=Modified stress tolerance index.

such as Farshadfar *et al*., 2013 and Mohammed and Kadhem, 2017 in wheat.

Conclusion

Based upon the mean grain yield per plant (g) and various stress tolerance indices, the genotypes GM-2, PM-3, EH-1731 and EC-3160 were found most tolerant to water stress and genotypes EH-1820, GYC-9325 and EC-3135 were found moderately tolerant to water stress and genotypes Texpeno Sequia, GWC-9101, GYC-9837, GWC-9103 and GWC-9701 were found susceptible to water. The indices STI, MP and GMP exhibited good correlation with grain yield per plant (g) under both the water stress conditions while TOL, SSI, YI and SSPI exhibited good correlation with grain yield per plant (g) under water stress condition. Hence, these genotypes may be used in breeding maize for water stress at pre and post flowering stage. However, genotypes identified as tolerant to water stress in the present study should be further tested in multi-location trials for the development of superior synthetic and composite varieties/hybrids in maize.

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Indian J. Plant Genet. Resour. 34(1): 70–74 (2021)
DOI 10.5958/0976-1926.2021.00010.3

RESEARCH ARTICLE

Evaluation of Chilli Genotypes against Pepper Mottle Virus under Artificial Conditions

Shikha Sharma*, Abhishek Sharma and Salesh Jindal
Punjab Agricultural University Ludhiana-141027, Punjab, India

(Received: 13 August, 2020; Revised: 04 January, 2021; Accepted: 08 March, 2021)

One hundred and twenty four genotypes of *Capsicum annuum* were screened for resistance against *Pepper mottle virus* (PepMoV). Artificial screening was done via mechanical inoculation. Phenotypically resistant lines were further subjected against PepMoV antibodies in double antibody sandwich ELISA (DAS-ELISA). The results deciphered that seven genotypes viz., SM-478, IS-263, COO-226, VR-523, PL-412, IS-269, KC-312 exhibited resistant reaction (R), whereas twenty showed moderately resistant reaction. Virus distribution in hot pepper was seen via exposing different plant parts to DAS-ELISA. Maximum absorbance was recorded in leaf tissues. Further the effect of virus on seed yield was also observed in seven genotypes, which included two popular varieties viz., Punjab Tej and Suraj Mukhi and one hybrid CH-1. The results concluded that virus can cause up to 72 per cent seed yield loss in susceptible genotype *i.e* KRS-303.

Key Words: Chilli, Pepper mottle virus, Resistant sources, Seed yield

Introduction

Capsicum annuum (chilli) is an important vegetable and spice crop grown throughout the world. Chilli is a member of family Solanaceae and is native to the tropics and subtropics of America. The crop is attacked by a large number of diseases viz., viral, fungal, bacterial, nematode and phytoplasmal, which leads to great economic loss (Muthukumar and Bhaskaran, 2007). Natural occurrence of many viruses *e.g Pepper leaf curl virus, Pepper veinal mottle virus, Pepper vein banding virus* and *Pepper mottle virus* have been reported by different workers infecting chilli pepper worldwide (Green and Kim, 1991; Kaur *et al.,* 2014). *Pepper mottle virus* (PepMoV) is a potyvirus and belongs to the largest family of plant viruses (Shukla *et al.,* 1994). The virus was first recorded in USA during 1969 (Nelson and Wheeler, 1972) as a new strain of Potyvirus that infected peppers. By 1975 it became evident that PepMoV was contributing to crop losses in pepper growing areas of the United States. The virus infects many species of *Solanaceae* family, including several species of *Capsicum* (*C. annuum*, *C. frutescens*), *Datura* spp., *Lycopersicon esculentum, Physalis floriana*, tobacco (*Nicotiana* spp.) and nightshade (*Solanum* sp.) (Kaur *et al.,* 2014; Sharma *et al.*, 2019). The virus was reported to be of seed borne nature in India in 2018 (Sharma *et al.,* 2018). The management of viral diseases is majorly dependent upon resistant varieties cultivation. At present, there is clear evidence for four independent loci in *Capsicum,* each with alleles that confer resistance to viral isolates that belong to one or more of the viruses, PVY, PepMoV and *Tobacco etch virus* (TEV). Systemic movement of viruses inside the infected plant is well known. In resistant varieties, general location or types of tissues associated with the blockage have been identified, though most appeared to involve an inability of the virus to enter the phloem or exit the phloem or combinations thereof. Resistant varieties are available in both hot and sweet peppers. However, available commercial resistant varieties may not be effective against all isolates of PepMoV found. Given the seed borne nature of virus (Sharma *et al.,* 2018), the effect of virus on the seed yield in most popular varieties or hybrids was taken up. Furthermore, as the blockage of virus inside the plant is reported by previous workers, so tracing PepMoV in different parts of chilli plant was also investigated. Available germplasm was screened via artificial inoculation to hunt for resistant sources which can be further used in resistance breeding programme.

Material and Methods

Localization of PepMoV in different plant parts

Pepper seedlings of *cv.* SL-466 showing symptoms

*Email: shikhasharma-coapp@pau.edu

of PepMoV were tagged in the nursery. Seedlings exhibited symptoms such as mottling, vein banding and mosaic. To localize the virus in the whole plant parts the twigs and leaves of the plant were collected from the nursery stage. Later on the red ripe fruits were also collected from the tagged plant. The sap was extracted from above mentioned plant parts and was subjected to ELISA against PVY and PepMoV. Healthy plant parts were used for comparison.

Evaluation of Ppepper Germplasm against PepMoV

To find the sources of resistance against PepMoV, a total of 125 genotypes of *Capsicum annuum* were screened artificially using mechanical inoculation method. A genotype, SL-475 was used as susceptible check.

Maintenance of Inoculum

The pepper plants showing virus infection under field conditions were subjected to ELISA and the plants positive for *Pepper mottle virus* were used as inoculum source. The inoculum was multiplied by sap inoculating young healthy seedlings of susceptible genotype SL-475and was further maintained under insect proof conditions.

Artificial Screening by Mechanical Inoculation

The seedlings of 125 genotypes were raised in pro-trays using cocopeat, vermiculite and perlite in the ratio of 3:1:1. Nursery of genotypes was sown under insect proof conditions following proper cultural practices. Ten plants of each genotype were sap inoculated at 2-3 true leaf stage. The inoculum was prepared by grinding infected young leaves in a grinder with Phosphate buffer (0.01M). Sap inoculations were done in the evening hours. Before inoculating plants at 2-3 true leaf stage, celite-545 powder was dusted on to the upper side of leaves to cause injury for easy entry of virus inside the host. With the help of a cotton swab the sap was rubbed on the upper surface of leaves in same direction. After inoculation leaves were washed with double distilled water to avoid any injury by carborandum powder and to remove excess inoculum. The inoculated plants were kept in insect proof cage and observed regularly for symptom appearance from inoculation up to six weeks. Inoculation was repeated at an interval of three days twice. The disease incidence and severity was recorded on visual basis. The severity of plants was categorized as highly resistant, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible as scale suggested by Mughal and Khan (2011).

Confirmation of Resistance

After six weeks of visual observations, all the inoculated lines (both symptomatic and asymptomatic) were subjected to DAS-ELISA against antisera of PepMoV (Agdia).

Modified 0-5 severity scale for *Pepper mottle virus* screening (Mughal and Khan, 2001).

Symptoms	Severity grade	Disease reaction
No visible symptoms	0	HR
Mild mottling on the upper leaves	1	R
Banding of vein on few leaves, Mosaic initiation on all leaves	2	MR
Distinct mosaic and vein-banding symptoms on all leaves	3	MS
Severe mosaic and vein-banding along with narrowing of leaves, and misshapen leaf lamina	4	S
Severe mosaic and vein-banding, misshapen leaves and fruits, defoliation, small number of fruits	5	HS

Estimation of seed yield loss by PepMoV

Ten red ripe fruits from seropositive (Mild to High) plants of eight genotypes *viz.* CH-1, SL-475, IS-269, Punjab Tej, Suraj mukhi, FLP-483 and KRS-304were collected. The genotypes which were highly susceptible as well as which showed resistant response in DAS-ELISA were included to conclude the Experiment. Two widely adapted varieties viz., Punjab Tej and Suraj Mukhi and one popular hybrid (CH-1) were also included to see the effect of virus on seed yield. The seeds were extracted and counted. To calculate the per cent seed yield loss, seeds of ten healthy fruits were also taken into account. Per cent seed yield loss was calculated using formula:

$$\text{Per cent seed yield loss} = \frac{\text{HSY} - \text{ISY}}{\text{HSY}} \times 100$$

Results and Discussion

Localization of PepMoV in Different Plant Parts

The leaves and stems samples of pepper seedlings of *cv.* SL-475 and a healthy plant of same cultivar were exposed to DAS-ELISA against antisera of PepMoV. The absorbance value of leaves and stem of infected plants was 3.58 and 4 times higher than the healthy leaves respectively. Whereas the absorbance value of fruit and seeds in ELISA was 3.63 and 2.6 times greater

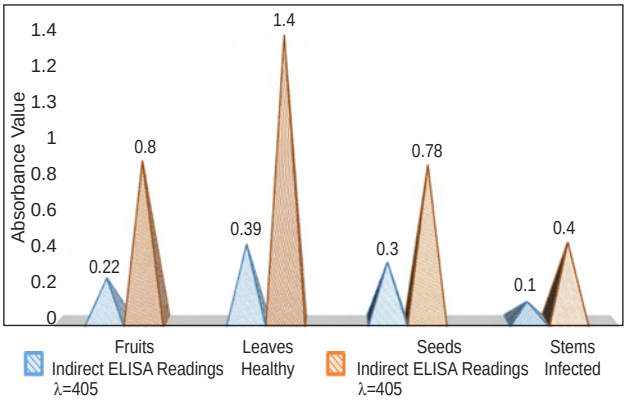

Fig. 1. Prevalence of PepMoV in different organs of pepper plants using indirect ELISA

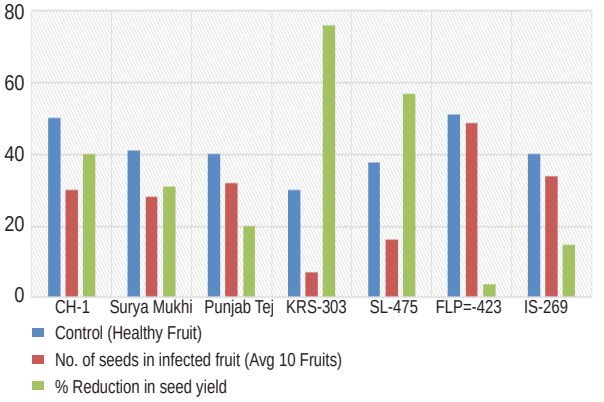

Fig. 2. Per cent reduction in seed yield due to PepMoV in Chilli

than the comparative corresponding parts of healthy plant of same genotype. It is evident from the results that virus was present systemically in the infected plant. However maximum viral load was in leaves, followed by fruits and seeds. Kogovsek *et al.* (2011) also found that the PVY inoculum was highest in infected leaves and stem.

Evaluation of Chilli Genotypes against *Pepper Mottle Virus* under Artificial Conditions

To find the resistance sources among the available genotypes, artificial or natural screening methods are adopted. In present study, artificial screening was performed to evaluate 125 genotypes of pepper against Pepper mottle virus disease at PAU, Ludhiana (Fig. 3). The plants were regularly observed for symptom appearance up to five weeks after inoculations and the genotypes were evaluated based on modified 0-5 scale (Mughal and Khan, 2001).Out of total 124 genotypes evaluated, seven genotypes viz., SM-478, IS-263, COO-226, VR-523, PL-412, IS-269, KC-312 were found to be resistant. Among rest of genotypes twenty showed moderately resistant reaction. Whereas twelve were moderately susceptible, fifty eight were susceptible and twenty eight were highly susceptible against PepMoV under artificial screening conditions (Table 1). The morphological responses showed by these genotypes after sap inoculation with the crude sap from *Pepper mottle virus* infected plant was also correlated and cross verified with the serological assay (DAS ELISA) as per Moury *et al.* (2005).

Capsicum annuum L. cv. Avelar was shown to have a monogenic, recessively inherited factor for resistance to Pepper mottle potyvirus (PepMoV) (Zitter and Cook, 1973; Guerini and Murphy, 1999). Resistance against

Scale for interpreting DAS-ELISA results*

OD at 405 nm	Response	Symbol
Same as Negative control	Negative	-
2-5 times higher than negative	Mild positive	+
5-10 times higher than negative	Positive	++
10-15 times higher than negative	Strong positive	+++

Chilli veinal mottle virus and *Pepper veinal mottle virus* was identified at AVRDC in two accessions of *C. annuum*, Perennial HDV and PSP-11, which were of Indian origin (Anonymous, 1990, 1991). However in India, information on resistant sources against PepMoV is very limited. Kaur *et al* (2018) screened 140 genotypes of hot pepper and found eight resistant sources against PepMoV. Unlike other insect pests and disease, for viral disease use of chemicals as control measure is not found to be very effective. Hence, for management of virus disease the best approach is use of resistant sources. These sources could serve as donors for promising resistance genes in breeding programmes to transfer the resistance into popular varieties or they may be used directly. So finding resistance sources will be the most economical, adaptable and sustainable approach for viral disease management.

Reduction in Seed Yield due to Pepper Mottle Virus Infection

As the virus was confirmed to be seed transmitted, the effect of the virus infection on seed yield with an emphasis on the seed formation was studied. Seed is the basic unit for the production of the crop. This virus exhibits symptom onto the fruits such as formation of green stripes with reduction in fruit size as published earlier (Sharma *et al.*, 2018). Popular varieties and hybrid of chilli along with genotypes were selected for

Fig. 3. Artificial screening of genotypes via mechanical inoculation against PepMoV

Table 1. Reaction of genotypes evaluated against PepMoV under artificial screening condition

Disease Reaction	Genotype
HS (28)	PLS-412, PPLS12-1, PP-416, SL-468, SL-475, SL-466, IS-262, VR-523, IS-264, KRS-311, KRS-310, KRS-309, KRS-308, KRS-307, KRS-306, KRS-305, KRS-304, KRS-303, KRS-302, PAU-513, FLS-31, Punjab Tej, Punjab Guchedar, Punjab Sindhuri, AC-105, AC-104, IHR-616, TC-7246
S (58)	PI-419, PL-121, PC-1-1, PPLS-12-1, PL-413, PL-420, PP-421, SL-462, SL-473, SP-479, C-142, FL-201, DL-161, PAU-114, PAU-115, JP-283, MSFL-1-2, MSC-31-4, PAU-212, PAU-215, PAU-216, SR-467, PP-418, PP-421, PAU-217, PP-416, PC-410, FLP-441, PAU-512, FLP-444, JH-271, UP-3, AN-21, PP-158, FLP-301, FLP-445, FLP-482, FLP-485, S-343, PU-423, PC-1, TC-7246, PBC-362, SR-481, SN-921, SN-923, UP-4-1, AC-103, VS-9, PP-414, UJ-503, PL-406, IS-261, AC-102, PC-408, YL-582, PP-402, CH-1,
MS (12)	SHHP-404, IS-266, IS-265, PAU-114, PAU-211, PAU-212, PAU-213, PAU-214, PAU-115, PAU-116, PAU-511, VR-521,
MR (20)	IS-267, IS-268, PAU-211, G-4, GC-222, YB-583, SN-480, PE-422, PE-415, IHR-583, Co-4390, PJ-424, KLC-111, KLC-112, FLP-483, FLP-431, 1-6-4, JL-282, US-501, ML-342,
R (7)	SM-478, IS-263, COO-226, VR-523, PL-412, IS-269, KC-312
HR	NIL

S-Susceptible, HS-Highly Susceptible, MS-Moderately Susceptible, MR-Moderately Resistant, R-Resistant

the experiment. From the naturally infected PepMoV plants, confirmed by DAS-ELISA, fruits were collected and numbers of seeds were counted from these infected fruits of Suraj Mukhi, Punjab Tej, SL-475, CH-1, FLP-483, KRS-303 and IS-269.

It has been found that the *Pepper mottle virus*, lead to the reduction in the number of seed formation, as compared to the healthy plants of the respective genotype (Fig 2). Maximum seed formation was observed to be negatively hampered in case of KRS-303 and

SL-475. It was noticed that in KRS genotype, per cent reduction in seed yield was maximum *i.e* 76 per cent, followed by SL-475 (57%). These two genotypes are found to be highly susceptible to PepMoV infection in artificial screening. Whereas, in the resistant genotypes effect on per cent reduction was minimum in FLP-423 (3.0%) followed by IS-269 (15%) genotype. Where as in popular chilli hybrid, the seed yield was reduced due to PepMoV upto 40 per cent. In other two popular varieties viz., Suraj Mukhi and Punjab Tej, adopted by farmers at large scale the per cent yield reduction was 31 and 20 per cent respectively. Earlier Kumari and Makkouk (1995) also reported the yield loss due to Pea seed borne mosaic potyvirus in different genotypes. They reported that yield losses can be upto 61 per cent due to virus infection. It has also been reported that in case of *Soybean mosaic virus* (SMV) infections that occur after flowering has less than 25% impact on yields or seed quality (Bowers and Goodman, 1979; Ren *et al.,* 1997a; Song *et al.,* 2016). It is evident from these findings that PepMoV can lead to sustainable damage in chilli production if further spread is not contained timely. The study has also found promising resistant sources against the virus infection which can further be utilised in resistance breeding programme against PepMoV. Hot pepper is one of the most important vegetable and spice crop of India. Due to the lack of effective management strategies against plant viruses the most economical approach left is growing of resistant sources. Moreover, if seed yield is affected, it necessities to investigate the underneath factors. The present study was conducted via keeping in view the same objectives. Thus, the promising genotypes identified in the present study can be exploited as source of resistance in breeding programme against this emerging pathogen and it also would became apparent to study the effect of PepMoV infection on seed yield in further developed varieties.

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Indian J. Plant Genet. Resour. 34(1): 75–78 (2021)
DOI 10.5958/0976-1926.2021.00011.5

SHORT COMMUNICATION

Biochemical Characterization of Wheat Polyphenol Oxidase Activity in Genebank Accessions

Kalyani Srinivasan, Reshma Shaheen, Aradhana Mishra, Arun Kumar MB, Eldho Varghese and Sherry Rachel Jacob*

Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

(Received: 02 July, 2020; Revised: 19 February, 2021; Accepted: 23 February, 2021)

A selected set of wheat accessions received at the National Genebank, were analyzed for the extent of variation in seed *Polyphenol oxidase* activity. Analysis of seed vigour data confirmed the non-destructiveness of the protocol. The method is proposed to be used for germplasm screening prior to sowing.

Key Words: Genebank, Germplasm, *Polyphenol oxidase*, Seed vigour, Wheat

Polyphenol oxidases are a group of enzymes having ubiquitous presence in the plant kingdom. Functionally, it catalyzes the hydroxylation and dehydrogenation of phenolic compounds to form *o*-quinones, which rapidly polymerize through non-enzymatic reactions, to form brownish melanin compounds (Taranto *et al.,* 2017). Wheat seeds are known to possess significant PPO content which is primarily localized in the outer caryopsis, in an insoluble form (Fuerst *et al.,* 2006). During grain processing for flour, the cells lose the compartmentalization due to which PPOs come in contact with the phenolic substrates which are otherwise localized within vacuoles, leading to the browning reaction in the processed products. Such browning caused by the seed PPO is an undesirable trait for the food processing industry since it has negative impact on the colour and flavor of the final product (Kruger *et al.,* 1992; Hatcher *et al.,* 1993 and Mc Caig *et al.,* 1999). Hence, there is a specific demand for varieties having lower PPO content in mature grains. However, it has also been established that PPO is a major defense enzyme, which contributes to the protective mechanism of the plant, against a broad spectrum of pathogens. The enzyme gets induced in response to plant-pathogen interaction and its extrinsic presence enables effective protection (Fuerst *et al.,* 2014). At least four to five distinct PPOs are reported to be expressed in seeds of hexaploid wheat (Massa *et al.,* 2007 and Beecher *et al.,* 2012) and there is significant diversity in the level of PPO content within wheat genotypes (Demeke and Morris, 2002). Precise information on the level of PPO activity will help in categorizing the genotypes for specific end-use and it will also facilitate their utilization in various breeding programmes. A high PPO genotype may not be desirable in the pedigree of a variety which is being developed for superior biscuit/pasta/noodle quality, due to the browning factor. But an optimum level of seed PPO would be essential to maintain the required defensive role against pathogens. In this context one should also consider the recent change in consumer preference and the surge in demand for whole wheat products that are considered to be the healthier choice. In such instances where retention of the bran is essential, a balanced PPO content will enable development of more diverse products without compromising on the flavor and shelf life. Hence, an attempt has been made to assess the range of PPO content in the wheat germplasm collection held in National Genebank, India.

A random group of 339 accessions that were received in the genebank as a single lot, after multiplication at a single location, were identified and subjected to whole kernel enzyme assay. Out of these 339 accessions, 50 accessions were of exotic origin and 289 accessions were indigenous. A non-destructive five-seed assay was used for the PPO estimation (James and Morris, 2001). From each accession, 5 seeds, in triplicate sets, were randomly selected and placed in 2 ml microcentrifuge tubes containing 1.5 ml of phenolic

*Email: sherry.jacob@icar.gov.in

substrate 3,4 dihydroxyphenyalanine (L-DOPA) prepared in 50 mM 3-(*N*-morpholino) propane sulfonic acid (MOPS) buffer of pH 6.5. The tubes were incubated for 2 hours at room temperature, with intermittent shaking. After 2 hours, the substrate was decanted and the change in absorbance was recorded at 475 nm, using a UV-VIS spectrophotometer. The control consisted of the substrate alone. One unit of PPO activity was calculated as change in 0.001 absorbance unit/min/ml. 120 accessions were randomly selected from within the 339 accessions, for seed vigour test. The test was aimed at validating the non-destructiveness of the protocol. It was verified by comparing the seed vigour prior to and after the assay, for 120 accessions. Seed vigour was estimated through the calculation of Vigour index, according to the protocol proposed by Abdul Baki and Anderson, 1973. After the germination test (fourteen days), 10 normal seedlings from both treatments and each replication were selected at random and their average seedling length (plumule tip to root tip) was recorded. The Vigour index were calculated using the formula as mentioned below:

Vigour Index = Germination (%) × Average seedling length of 10 seedlings (cm)

For analyzing the diversity in PPO activity amongst the wheat genotypes, the experiments were laid out in a completely randomized design. The data were subjected to analysis of variance using SAS9.3 software and significant effects ($p< 0.05$) were noted. Further, Tukey's HSD Test was done for pair-wise comparison of various effects. ANOVA tables along with critical differences at $P\leq 0.05$ for each set of analysis were generated. As the Tukey's subsets were extensive in number, only the extreme categories were represented in the manuscript.

The PPO activity showed significant variability amongst the analysed genotypes. Based on the enzyme activity, wheat genotypes were categorized into very high, high, medium and low activity groups. For this categorization, the Tukey's homogeneous subsets were analysed and the pattern of notations indicating the significant difference in mean values were used to demarcate the activity levels. Out of the 339 accessions that were analysed, 44 accessions were in low category (less than 1.0 abs/gm), 227 accessions were in medium category (having 1.1 – 5.0 abs/gm), 57 accessions were in high category (having 5.1 – 8.0 abs/gm) and 11 accessions were in very high category (more than 8.0 abs/gm; maximum absorbance value was 10.6). These categories were further corroborated with visual scoring, after seed staining.

In the very high category, six accessions were indigenous improved cultivars and five accessions were of exotic origin. Maximum absorbance value was recorded for IC111714 (elite line developed by IARI RS Pusa, Bihar), followed by IC290185 and IC111731(elite line developed by IARI RS Shimla). The exotic accessions with maximum PPO content were of Sudanese origin (EC174785 & EC174788). In the high category, eight accessions were exotic and 48 accessions were indigenous. In the medium category, 32 accessions were of exotic origin and 195 accessions were indigenous (99 accessions were elite lines that were part of varietal trials and 96 accessions were breeding lines). Under the low category, five accessions were of exotic origin and 39 accessions were indigenous (eight accessions were elite lines and 31 accessions were breeding lines). The lowest PPO activity was recorded in IC290204. Post hoc comparisons using the Tukey's test for least square means (LS Mean) is depicted in Table 1. The analysis categorized the accession with the maximum PPO absorbance value (IC111714) as a separate group, significantly different from all other accessions (Table 1A). Similarly, the accession IC290204, having lowest PPO activity categorized as a single entity subset (Table 1B).

Genotypes in the Low PPO activity group can be potential contributors for this trait in processed product industry. The Very High category genotypes need to be further analysed for the presence of any enhanced mechanism of biochemical defense, since PPO has a prominent role in protection of the seed against pathogens. The data reveals that a large proportion of accessions within this experimental material are in the medium PPO activity category. These PPO lines, as per passport information, are genotypes generated as a part of various varietal development programmes and were identified for conservation due to certain superior agronomic traits. The medium level of activity is ideal for varietal development in countries like India, where wheat consumption is basically in the form of whole grain products, rather than processed forms.

The seed vigour data was analysed in case of 120 accessions, to ascertain the non-destructiveness of the assay protocol. For confirming the non-destructiveness of a seed protocol, seed vigour is a more convincing parameter as compared to the routine germination test

Table 1. Post hoc table for accessions in the Very High and Low activity groups
(Standard error± 0.29819)

A. Very High activity group (descending order of enzyme activity)

S.No	National Identity	LS Mean	Tukey's subsets
1.	IC111714	10.38516582	A
2.	IC290185	10.05184798	AB
3.	IC111731	9.404829683	ABC
4.	EC174788	9.000309805	BCD
5.	EC174785	8.871267312	CDE
6.	IC111708	8.849107704	CDE
7.	EC174118	8.72549106	CDEF
8.	IC111722	8.547185198	CDEF
9.	EC174123	8.517820857	CDEFG
10.	EC177756	8.436340541	CDEFG
11.	IC290238	8.350422711	CDEFGH

B. Low activity group (10 accessions with lowest activity listed in ascending order)

S.No	National Identity	LS Mean	Tukey's subsets
	IC290204	0.28609544	(6) I
	IC28086	0.298078899	(6) HI
	IC290256	0.307416481	(6)GHI
	IC290178	0.328218535	(6)FGHI
	IC290188	0.346549349	(6)EFGHI
	IC290052	0.358376191	(6)EFGHI
	IC427824	0.395221434	(6)EFGHI
	IC290250	0.444000108	(6)DEFGHI
	IC290205	0.475852933	(6)CDEFGHI
	IC28501	0.485525754	(6)CDEFGHI

(6) in the Tukey's subsets stand for the sixth cycle of A-Z grouping, owing to large number of sub-set groups

because, loss of vigour during the experiment will have long-lasting implications while re-using the tested seeds. In order to verify whether the content of PPO plays any inhibitory role in radical emergence, correlation analysis was carried out. The analysis revealed that seed vigour is positively correlated with PPO activity in Very high (r = 0.480), high (r = 0.208) and medium(r = 0.289) PPO categories, whereas it was negatively correlated in the low PPO category (r = ¯0.447). This correlation trend indicates superior germination and rate of growth in genotypes with higher PPO content (except for Low PPO genotypes). Thereby, it can be stated that the presence of PPO in the seed coat and its phenol-oxidation capacity is not a hindrance to seed germination. ANOVA carried out on initial and final seed vigour data are represented in Tables 2 & 3. The coefficient of variation values in both the tables indicates highly significant relative vigour variability amongst the accessions.

Table 2. ANOVA for initial seedling vigour

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	39	1171.463	30.037	6.05	<.0001
Error	80	397.173	4.964		
Corrected Total	119	1568.636			

R-Square	Coeff Var	Root MSE	seedling_vigour Mean
0.746803	10.64443	2.228153	20.93258

Table 3. ANOVA for final seedling vigour

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	39	2513.73	64.45	5.34	<.0001
Error	80	965.55	12.069		
Corrected Total	119	3479.28			

R-Square	Coeff Var	Root MSE	seed_vigour_after_ppo Mean
0.722486	15.10430	3.474101	23.00075

The Tukey's HSD test was carried out within each category of PPO activity, for the seed vigour parameter, before and after the PPO estimation. There was a general increase in seed vigour values after the PPO analysis. This can be attributed to the effect of seed hydration that has occurred during the course of the experiment. But, there was no difference in the subset grouping pattern of the genotypes, thus indicating that the vigour parameter remained same, prior to and after the enzyme estimation (the representative table (Table 4) of Tukey's subsets in the high PPO category is depicted for reference). Thus, the non-destructability of the PPO assay could be conclusively proven. This test can hence, be conducted on a wide range of material since sample size will not be a limiting factor. Germplasm characterization experiments, where seed quantity is restricted, can include this parameter along with other

Table 4. *Post hoc* table of seed vigour parameter for representative accessions from the high PPO category

S.No	National Identity	LS Mean (Initial seed Vigour)	Tukey's subsets (common for initial and final vigour)	LS Mean (Final seed vigour)
1	IC228518	25.23	A	31.55
2	IC28542	25.0	A	30.79
3	IC26730	24.08	AB	29.35
4	IC26721	21.96	ABC	25.18
5	IC28526	21.78	ABC	24.87
6	IC26743	19.58	ABC	22.55
7	EC174786	19.58	ABC	22.13
8	EC177696	18.77	ABC	21.83
9	EC177687	17.89	BC	20.80
10	EC177682	15.9	C	19.03

descriptors, since the analyzed seeds can be subsequently sown without loss of viability. A positive correlation between PPO and seed vigour is also having significance in the context of conservation agriculture, wherein both the parameters will synergistically contribute to better field establishment.

Acknowledgement

Authors acknowledge Director, ICAR-NBPGR for guidance and support during this study.

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Indian J. Plant Genet. Resour. 34(1): 79–81 (2021)
DOI 10.5958/0976-1926.2021.00012.7

SHORT COMMUNICATION

Identification of Unique Type of Decorticated Grain Colour in Rice Designated as "Potato Green Colour"

AK Sarawgi[1*], AK Pachauri[1], S Vimala Devi[2] and Rakesh Singh[2]
[1]*Indira Gandhi Krishi Vishwavidyalaya, Raipur-492012, Chhattisgarh, India*
[2]*National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*

(Received: 07 February, 2019; Revised: 25 February, 2021; Accepted: 09 March, 2021)

The decorticated grain colour of rice has been classified into different categories as per the DUS testing guidelines as white, light brown, variegated brown, dark brown light red, red, variegated purple, purple and dark purple. We report here a completely new descriptor state based on characterization of 3806 rice germplasm lines. Accession IC464435 was identified with a unique decorticated grain of potato green colour.

Key Words: Characterization, Decorticated grain colour, Rice accession, Unique trait

Three thousand eight hundred and six genebank accessions received form NBPGR, New Delhi under ICAR Network project entitled "Consortium research platform on agrobiodiversity on germplasm characterization and evaluation" were characterized for different agro-morphological traits as per the DUS testing guidelines of rice. The experiment was conducted during *Kharif* 2019 at Research cum Instructional farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh.

Presently as per the DUS test guidelines decorticate grain colour is classified into nine different categories as white, light brown, variegated brown, dark brown, light red, red, variegated purple, purple and dark purple. The accession IC464435 was identified with black hull (Fig. 1A) unique decorticated grain colour similar to that of potato (tuber) when it comes above the earth surface and exposed to the sunlight. Hence identified seed coat colour in accession IC464435 is proposed to be considered with a new nomenclature "Potato green colour" (Fig. 1B). IC464435 may be used as the reference genotype for the proposed state, since the expression was stable across seasons. The detail of characters of IC464435 are given in Table 1.

The length of the panicle of IC464435 was categorized as long (29.73 cm.) if panicle length is found 26-30 cm. it is classified as long with the curvature of main axis as semi erect. Panicle angle is considered to be one of the most important agronomic traits in designing 'new plant type' of high-yielding rice varieties. Semi erect panicle also utilize solar energy effectively, accelerate CO_2 diffusion, and have improved ecological growing conditions in the middle and lower part of the rice canopy (Li *et al*., 2009). The plant produced number of effective tillers was categorized as few (mean 9.67) and well exerted panicles in the field. The colour of sterile lemma was Purple (Fig. 1C) and was noted at ripening stage.

The grain length of IC464435 was noted short (6.1-8.5 mm.) in size 7.6 mm (Fig. 1D) and grain width 2.3 mm. Decorticated grain length and breadth 5.7 & 2.0 mm respectively with the grain length breadth ratio was 3.30 mm and noted awnless. In general farmer prefers awnless grain (Pachauri *et al*., 2017) in rice germplasm. The weight of 1000 fully developed grains of IC464435 with (Fig. 1A) black hull colour was 16.70 g. Accession IC464435 classified for decorticated grain size and shape based on the rice length and length breadth ratio. Accessions IC464435 classified as short as well as medium shape.

Acknowledgement

The author express sincere thankful to the National Bureau of Plant Genetic Resources, New Delhi for providing the financial support to the ICAR Network project "Consortium research platform on

[*]*Email: sarawgi1@yahoo.co.in*

Table 1.1 DUS Characteristics of IC464435 rice accession

S. No.	Characters	Colour/Pattern	Score	Stage of recording
1	Coleoptile colour	Purple	3	Germination
2	Early plant vigour	Good	2	Seedling
3	Seedling height (cm.)	13.17		Seedling
4	Basal leaf sheath colour	Purple lines	3	Booting
5	leaf blade colour	Green	1	Booting
6	leaf pubescence	Medium	3	Vegetative
7	Auricle colour	Colourless	1	Booting
8	Ligule shape	Split	3	Booting
9	Days to 50% flowering (days)	97		Reproductive
10	Stigma colour	Light Purple	4	Reproductive
11	Panicle exertion	Well exerted	7	Ripening
12	Panicle attitude of branches	Erect to Semi erect	3	Ripening to maturity
13	Flag leaf angle	Semi erect	3	Heading
14	Awning	Absent	9	Ripening to maturity
15	Leaf senescence	Medium	5	Maturity
16	Days to maturity (days)	122	Medium	Maturity
17	Leaf length (cm.)	64.97	Long	Vegetative
18	Leaf width (cm.)	1.1cm.	Medium	Vegetative
19	Plant height (cm.)	161.67cm.	Very long	Reproductive
20	Panicle length (cm.)	29.73	Long	Reproductive
21	Numbers of effective tillers	9.67	Few	Reproductive
22	Lemma and Palea colour	Black	9	Maturity
23	Decorticated grain: colour	Potato green colour	Add to describe	Matured seed dehusked
24	Sterile lemma colour	Purple	4	Maturity
25	Spikelet : colour tip of lemma	Purple	5	Milk stage to ripening
26	Grain length (mm)	7.6	Short	Matured seed
27	Grain width (mm)	2.3	Narrow	Matured seed
28	Grain L/B Ratio	3.30		Matured seed
29	Decorticated grain: length (mm)	5.7	Short	Matured seed dehusked
30	Decorticated grain: width (mm)	2.0	Medium	Matured seed dehusked
31	1000 gr. wt	16.70 g.	Low	Matured seed
32	Grain yield per pl. (g.)	23g.		Single plant harvested, threshed and weight
33	Threshability	Easy	1	Maturity
34	Aroma	Absent	0	Matured seed dehusked and aroma

Fig. 1. (A) Hulk colour black, (B) Decorticated grain colour - Potato green colour, (C) Sterile lemma and Spikelet tip of lemma-Purple, and (D) Grain length IC: 464435

agro biodiversity on germplasm characterization and evaluation" project.

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Indian J. Plant Genet. Resour. 34(1): 82–85 (2021)
DOI 10.5958/0976-1926.2021.00013.9

SHORT COMMUNICATION

Profiling Pigmented Rice Germplasm for Iron and Zinc Concentration

S Velprabakaran[1*], S Rajeswari[1], P Jeyaprakash[2] and M Raveendran[3]
[*1]*Department of Genetics and Plant Breeding, AC&RI, Madurai-625104, Tamil Nadu, India*
[1]*Department of Plant Breeding and Head, Department of Cotton, TNAU, Cbe-3, Coimbatore-641003, Tamil Nadu, India*
[2]*Department of Genetics and Plant Breeding, AD AC & RI, Trichy-622001, India*
[3]*Department of Plant Biotechnology (CPMB), TNAU, Cbe-3, Coimbatore-641003, Tamil Nadu, India*

(Received: 04 April, 2020; Revised: 05 January, 2021; Accepted: 20 March, 2021)

The low level of micronutrients such as iron (Fe) and zinc (Zn) in cereals crops is a widespread nutrition and health problem in developing countries like Africa and South Asian countries. Nutrition enrichment is one of the important processes, for enhancing the micronutrient content like Fe and Zn content and their bioavailability in small grained crops like rice. Evaluation on wild genotypes for Fe and Zn content is the initial step of determining their nutritional availability. In this study, we examined 37 accessions of pigmented rice genotypes and performed their diversity analysis along with three ruling check varieties for Fe and Zn concentration. Iron concentration ranged from 4.4 to 19.6 mg/Kg and zinc concentration from 12.0 to 49.0 mg/Kg.

Key Words: Diversity, Iron, Pigmented rice, Variability, Zinc

Introduction

Black rice might have originated in Sri Lanka, Philippines, Bangladesh, Thailand, Myanmar and Indonesia. Black rice has diversity in terms of color due to anthocyanin content and other morphological characters (Chaudary and Tran, 2001). The content of iron (Fe) and zinc (Zn) in rice depends on the grain size (Zhang *et al*. (2012). Aromatic long grain basmati rices are known to be high in iron content. The high or low content of mineral elements in grain largely determines the nutrient value of rice. Single grain selection of narrow grains tend to increase the content of Zn, Mn and P; long grains tend to increase the content of Fe and Mn; short grains tend to increase content of Zn and P; while selection of single plants with bigger grain weight tends to increase the content of P. The iron content varied from 6.30 to 24.40 mg/kg and zinc content from 13.50 to 58.40 mg/kg

The highest Fe (Iron) content (ranged from 18 to 22 mg/kg) and Zn (Zinc) content (24 to 35 mg/kg) were found in aromatic rice varieties such as Jalmagna, Zuchem and Xua Bue Nuo Additional research using F2 derived populations demonstrated that the aromatic trait was not pleiotropic for iron or zinc concentrations (Gregorio *et al.,* 2000).

Objective

To profile pigmented rice for Fe and Zn concentration.

Materials and Methods

Genotypes: Investigation consisted of 37 genotypes with medium and long duration traditional paddy varieties from Tamil Nadu and Kerala states of India, and three improved varieties namely CR1009, IR20 and CO (R) 50 (Table 1.). These genotypes were selected based on the grain characters (Fig. 1), and collected from different sources, namely Paddy Breeding Station (Coimbatore), Hybrid Rice Evaluation Centre (Gudalore), Centre for Indian Knowledge System (CIKS) in Sirkali and Sharadashram, Ulunthurpet of Tamil Nadu.

Micronutrient analysis: For biochemical quality analysis well-grounded and fine flour samples were obtained using small volume (150 mg) powder mixer and used for biochemical analysis. One gram of powdered grain sample mixed with was 12 ml of triple acid mixture (9:2:1 Nitric acid: Sulphuric acid: Perchloric acid) and cold digested overnight. The digested samples were heated till the solution turned from brown color to colorless. The extract was diluted to 100 ml and used for the estimation of micronutrients. The extract was

[*]*Email: anbudanvel@gmail.com*

Table 1. Source of genotypes with mean performance of Iron and Zinc

S.No.	Genotype	Ac.No	Source	Iron (mg/kg)	Zinc (mg/kg)
1	Rajamudi	LC1301	Sharadashram, Ulunthurpet	14.80	37.00
2	Athur kitchali	LC1302	Sharadashram, Ulunthurpet	16.20	40.50
3	Thengai poo samba	LC1303	Sharadashram, Ulunthurpet	4.60	19.34
4	Valaan	LC1304	Sharadashram, Ulunthurpet	5.60	14.00
5	Kothandam	LC1305	HREC, Gudalore	4.88	15.88
6	Athira	LC1306	HREC, Gudalore	11.60	14.66
7	Karuvelli	LC1307	HREC, Gudalore	11.00	27.50
8	Karunguruvai	LC1308	CIKS, Sirkali	14.60	36.50
9	Arupatham samba	LC1309	Sharadashram, Ulunthurpet	19.60	49.00
10	Seeraga samba	LC1310	CIKS, Sirkali	14.40	36.00
11	Kullakar	LC1311	CIKS, Sirkali	9.20	23.00
12	Thondi	LC1312	HREC, Gudalore	7.60	19.00
13	Mappilai samba	LC1313	CIKS, Sirkali	10.00	25.00
14	Maranell	LC1314	HREC, Gudalore	8.40	21.00
15	Cheruli	LC1315	HREC, Gudalore	11.40	28.50
16	Kaliyan samba	LC1316	Sharadashram, Ulunthurpet	6.20	15.50
17	Kandasala	LC1317	Sharadashram, Ulunthurpet	11.00	27.50
18	Kappakar	LC1318	Sharadashram, Ulunthurpet	11.20	28.00
19	Kottara samba	LC1319	Sharadashram, Ulunthurpet	8.00	20.00
20	Karuppu kavuni	LC1320	CIKS, Sirkali	11.20	28.00
21	Nootripathu	LC1321	PBS, Coimbatore	**4.40**	18.66
22	Vellai chithiraikar	LC1322	PBS, Coimbatore	4.80	**12.00**
23	Sivappu chithiraikar	LC1323	PBS, Coimbatore	18.60	46.50
24	Mohini samba	LC1324	PBS, Coimbatore	15.40	38.50
25	Rasakadam	LC1325	PBS, Coimbatore	12.60	31.50
26	Kakarathan	LC1326	PBS, Coimbatore	14.00	35.00
27	Karthigai samba	LC1327	PBS, Coimbatore	11.80	29.50
28	Ottadayan	LC1328	PBS, Coimbatore	9.40	23.50
29	Sivappu sirumani	LC1329	PBS, Coimbatore	11.00	27.50
30	Kattikar	LC1330	PBS, Coimbatore	8.40	21.00
31	Purple puttu	LC1331	PBS, Coimbatore	18.40	46.00
32	Norungan	LC1332	PBS, Coimbatore	16.20	40.50
33	Kallurundai kar	LC1333	PBS, Coimbatore	8.40	21.00
34	Vel samba	LC1334	PBS, Coimbatore	6.20	15.50
35	Uppu molagai	LC1335	PBS, Coimbatore	12.00	30.00
36	Kallundai	LC1336	PBS, Coimbatore	8.60	21.50
37	Chinna puncha	LC1337	HREC, Gudalore	9.60	24.00
38	Swarna	LC1338	PBS, Coimbatore	12.20	30.50
39	CR1009	Variety	PBS, Coimbatore	8.00	20.00
40	IR 20	Variety	PBS, Coimbatore	10.40	26.00
41	CO (R) 50	Variety	PBS, Coimbatore	10.20	25.50

Fig. 1. Panicle diversity of different rice genotypes

also diluted to 50 ml and fed to the Atomic Absorption Spectrophotometer. The recorded optical density values were converted into micronutrient concentration (Fe and Zn) using standard curve at the wavelength of 213.86 nm and expressed in ppm unit.

Zinc content estimation: Similar procedure to that iron was followed and the available iron content in the sample was read. Data were recorded is replicated samples.

Result and Discussion

Fe content varied from 4.44 mg/kg (Nootripathu) to 19.60 mg/kg (Arupatham samba) with a grand mean of 10.78 mg/kg (Fig. 1) (Table 1). The extreme ranges of zinc (Zn) content were 12.00 mg/kg (Vellaichittiraikar) and 49.00 mg/kg (Arupatham samba) with a grand mean of 27.07 mg/kg The iron (Fe) content was observed to be high in the genotypes Arupatham samba, Karunkuruvai, seeraga samba, Mohini samba, Kakarathan and Karthigai samba; and low in Vel samba, Nootripathu, Vellai chithiraikar, CR 1009, Thengai poo samba, Valaan and Thondi. High Zinc (Zn) content was exhibited in Arupatham samba, athur kitchali, Rajamudi, seeraga samba, Sivappu chithirai kar, Mohini samba, purple puttu and Norungan; and low Zn for Vellai chithirai kar, Kattikar, Vel samba, CR 1009, Kottara samba, kaliyan samba, Kothandam, Athira and valaaan. The similar results were quoted in results from Gregario *et al.* (2000) who evaluated 1,138 brown rice genotypes for grain iron and zinc content at International Rice Research Institute (IRRI), Philippines. The iron content varied from 6.30 to 24.40 mg/kg and zinc content from 13.50 to 58.40 mg/kg. The highest iron content (ranged from 18 to 22 mg/kg) and zinc content (24 to 35 mg/kg) were found in aromatic rice varieties, such as Jalmagna, Zuchem and Xua Bue Nuo. Kennedy *et al.* (2002) reported that the range of iron content in rice was 0.70 to 6.35 mg/100 g.

In conclusion, the iron content was estimated higher in the genotypes Arupatham samba, Karunkuruvai, seeraga samba, Mohini samba, Kakarathan and Karthigai samba. High zinc content was exhibited in Arupatham samba, Athur kitchali, Rajamudi, seeraga samba, Sivappu chithirai kar and Mohini samba. In this analysis, we have identified both Iron and Zinc to be of higher value in Arupatham Samba and Mohini Samba genotypes. These genotypes may contribute to future Fe and Zn biofortified programmes.

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Indian J. Plant Genet. Resour. 34(1): 86–89 (2021)
DOI 10.5958/0976-1926.2021.00014.0

SHORT COMMUNICATION

Genetic Diversity Analysis of Bread Wheat Varieties and Pre-release Lines Evaluated Under Timely Sown Irrigated Conditions

Vijay Kamal Meena[1], RK Sharma[1*], Naresh Kumar[1] and Monu Kumar[2]
[1]*Division of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi-110012, India*
[2]*ICAR-Indian Agricultural Research Institute, Hazaribagh-825405, Jharkhand, India*

(Received: 28 May, 2020; Revised: 25 November, 2020; Accepted: 22 January, 2021)

The involvement of genetically diverse parental lines in crossing programme of spring wheat is of prime importance to create desirable variability. To assess the magnitude of genetic divergence for grain yield and its component characters, a set of 36 spring wheat genotypes were grown consecutively for two crop seasons i.e., 2016-17 and 2017-18 at ICAR-IARI, New Delhi in a randomized complete block design with three replications in timely sown irrigated conditions Significant genotypic differences were observed for all 13 morpho-physiological characters in both the crop seasons suggesting the presence of substantial genetic variability among the genotypes studied. Cluster formation through Euclidean analysis based on the morpho-physiological characters, grouped the 36 genotypes into four clusters and ten clusters during the crop season 2016-17 and 2017-18, respectively. Considerable differences in the cluster means for different traits led to identification of diverse genetic parental lines for different traits, which could be used in recombination breeding to generate desirable genetic variability.

Key Words: Bread Wheat, Cluster Analysis, Genetic diversity, Morpho-physiological

Introduction

Wheat (*Triticum aestivum* L. em. Thell.) is an important staple food which fulfills the major portion of total calories and protein requirement. In India, wheat was grown in 29.55 m ha under diverse environments with a record production of 101.20 mt and productivity of 3424 kg ha^{-1}during 2018-19. However, to sustain the food security for ever increasing population, there is a necessity to further improve the productivity level of wheat. Selection of genetically diverse parental lines for planned hybridization programme is essential to create broad spectrum of variability in segregating generation. Evaluation of genetic diversity among the newly developed and released genotypes or adapted germplasm lines can provide predictive estimates of genetic variation among the segregating progeny (Manjarrez- Sandoral *et al.,* 1997). The Mahalanobis D^2 statistic gives information about the genetic divergence and provides the basis for selection of parental lines form breeding programme. Here we report the magnitude of genetic diversity among a set of released and newly developed advanced lines evaluated under timely sown irrigated conditions.

Materials and Methods

The experimental material consisted of 36 genotypes (Table 1) that included released wheat varieties recommended for various production situations of different zones of the country and pre-release advance lines of bread wheat developed at Indian Agricultural Research Institute, New Delhi. The experiment was laid out in Randomized Block Design (RBD) replicated thrice under timely sown irrigated conditions and was conducted consecutively for two crop seasons *i.e.*, 2016-17 and 2017-18. Each genotype was sown in a six-row plot having a gross area of 5 m × 1.20 m with a row spacing of 20 cm using self-propelled Norwegian Seed Drill in a well prepared field. Recommended package of practices was followed to raise the healthy wheat crop. Observations in field were recorded from each experimental plot either on five randomly selected plants or on plot basis for 13 morpho-physiological characters *viz*., plant height (PH), days to 50 % heading (HDNG), number of spike per square meter (SPMS), number of grains per spike (GNPS), grain weight per spike in grams (GWPS), spike length in cm (SL), days

*Email: Sharma.rk.rk@gmail.com

Table 1. Details of experimental materials used in the study and developed at IARI, New Delhi

S.No.	Genotype	Pedigree/Parentage	Prod Cond.	Material
1	HD3171	PBW343/HD2879	Rainfed, Timley sown	Released Variety
2	DW1616	HW5028/HD2643//UP2565	Irrigated, Timely sown	Pre-released Line
3	HD2864	DL509-2/DL377-8	Irrigated, Late sown	Released Variety
4	HD3086	DBW14HD2733/HUW468	Irrigated, Timely Sown	Released Variety
5	HD3249	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVKAI	Irrigated, Timely Sown	Released Variety
6	DW1627	DW1422/WR1441//HRLSN-7	Irrigated, Timely Sown	Pre-released Line
7	DW1628	DW1411/HP1744//DW1440	Irrigated, Timely sown	Pre-released Line
8	DW1629	HD2967/LBE2003-1//LBRL-11	Irrigated, Late sown	Pre-released Line
9	HD3284	HD2844/F81513//MILAN-2/3/WH730	Irrigated, Timely sown	Pre-released Line
10	HD3252	BABX/LR43//BABAX/6/MOR/VEE#5DUCULA/3/DUCULA/4/MILAN/5/BAU/NILAN/7/SKAUZ/BAV92	Irrigated, Timely sown	Released Variety
11	DW1630	CL2762/HP1744//CHIRYA3	Irrigated, Late sown	Pre-released Line
12	HD2932	KAUZ/STAR//HD2643		Released Variety
13	DW1631	HD2967/ CHIRYA3//DW1451	Irrigated, Late sown	Pre-released Line
14	DW1632	HD2998/HD2733//DW1432	Irrigated, Late sown	Pre-released Line
15	WR544	NW 2078/CL1739//HD2960	Irrigated, V Late sown	Released Variety
16	HD3255	SOKOLL//PBW343*R/KUKUNA/3/ATTAILA/PASTOR	Irrigated, Timely sown	Released Variety
17	DW1633	VL796/HD2009//HD3003	Irrigated, Late sown	Pre-released Line
18	DW1634	HD2682/CL3156//WH542	Irrigated, Late sown	Pre-released Line
19	DW1635	UP2338/WR1909//NING8319//HD2967	Irrigated, Late sown	Pre-released Line
20	HD3090	SFW/VAISHALI//UP2405	Irrigated, Late sown	Released Variety
21	HD 3262	VL796/HD2009//HD3003	Irrigated, Timely sown	Released Variety
22	DW1636	HD2998/HD3160//PDW621-50	Irrigated, Late sown	Pre-released Line
23	DW1637	HD2967/HD3027	Irrigated, Late sown	Pre-released Line
24	DW1638	HD2967/HP1744//LBRL1	Irrigated, Late sown	Pre-released Line
25	DW1639	HD2998/HD2894//PS940	Irrigated, Late Sown	Pre-released Line
26	DW1640	HD2967/LBR1724//VHW4668	Irrigated, Late sown	Pre-released Line
27	HD3118		Irrigated, Late Sown	Released Variety
28	HD3265	DW1311/HD2894/HW5028	Irrigated, Timely sown	Pre-released Line
29	DW1642	HD2967/HD2844/F81-513//MAILAN2/3/WH730	Irrigated, V. Late sown	Pre-released Line
30	DW1643	HD 2967/E-4870	Irrigated, V. Late sown	Pre-released Line
31	DW1644	HD2998/DW1403	Irrigated, V. Late sown	Pre-released Line
32	DW1645	HD2921/HPW277//PBW 621-50	Irrigated, V. Late sown	Pre-released Line
33	HD3059	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	Irrigated, Late sown	Released Variety
34	HD3266	TRCH/5/REH/HARE//2*BCN/CROC-1AE.SQUARROSA(213)//PGO/4/HUITES	Irrigated, Late sown	Pre-released Line
35	DW1615	NW 2078/CL1739//HD2960	Irrigated, Timely sown	Pre-released Line
36	HDCSW18	PBW343/CL1538	CA Early sown	Released Variety

Table 2. Analysis of variance (ANOVA) for 13 traits recored for 36 wheat genotypes during Rabi 2016-17 and 2017-18

							2016-2017							
Sv	D.F.	HDNG	DTM	GFD	PH	SL	GWPS	GNPS	SPMS	YPMS	BYPMS	HI	TGW	CTD
Replication	2	0.8405	6.25	2.507	4.037	0.07	0.001	4.8425	100.75	0.1205	1144.732	8.6945	7.1545	0.261
Genotype	35	117.659**	68.233**	54.435**	140.835**	2.100**	0.316**	58.558**	17952.590**	96195.006**	153277.783**	1207.752**	167.702**	2.743**
Error	70	0.383	0.836	0.493	0.237	0.029	0.001	0.7	37.464	211.749	389.789	5.171	1.508	0.01
Se(D)		0.505	0.746	0.573	0.398	0.139	0.03	0.683	4.998	11.881	16.12	1.857	1.003	0.082
C.D. (1%)		1.01	1.492	1.145	0.795	0.279	0.06	1.365	9.989	23.748	32.22	3.711	2.004	0.163
C.V.(%)		0.891	0.963	2.76	0.71	1.944	3.285	2.269	1.749	3.637	2.123	5.078	4.108	3.379
							2017-2018							
Replication	2	3.528	3.028	2.287	2.4815	0.01	0.002	1.9535	40.2595	75.3425	1973.03	0.2055	5.003	0.0135
Genotype	35	336.312**	320.105**	56.047**	171.745**	2.910**	0.197**	202.662**	15829.666**	81075.507**	280902.598**	144.025**	262.160**	2.755**
Error	70	0.299	0.428	0.258	1.053	0.043	0.009	1.078	93.954	2,150.53	617.142	7.749	6.493	0.01
Se(D)		0.447	0.534	0.415	0.838	0.169	0.078	0.848	7.914	37.864	20.284	2.273	2.081	0.08
C.D. (1%)		0.893	1.067	0.83	1.675	0.338	0.155	1.694	15.819	75.68	40.542	4.543	4.158	0.161
C.V. (%)		1.058	0.82	1.806	1.43	2.077	5.518	2.292	1.998	5.555	1.383	5.957	6.476	2.752

Expansion of trait acronyms is given in material and method section

Table 3. Clustering of 36 genotypes based on D^2 Statistic during rabi 2016-17 and 2017-18

Crop season 2016-17		
Cluster #	Genotypes #	Genotypes in cluster
I	12	DW1639, DW1640, HD3318, HD3265, DW1642, DW1643, DW1644, DW1645, HD3059, HD3266, DW1615, HDCSW18
II	11	DW1631, DW1632, DW1630, DW1633, DW1634, DW1635, HD3090, HD3262, DW1636, DW1637, DW1638
III	12	HD3171, DW1616, HD2864, HD3086, HD3249, DW1627, DW1628, DW1629, HD3184, HD3252, HD3255, HD2932
IV	1	WR544
Crop season 2017-18		
I	22	HD3171, DW1616, HD3249, DW1628, DW1629, HD3184, HD3252, DW1630, DW1631, DW1632, HD3255, DW1634, DW1635, HD3090, HD3262, DW1636, DW1637, DW1639, HD3318, DW1642, DW1645, HD3266
II	1	HD2864
III	6	DW1633, DW1640, DW1643, DW1644, HD3059, HDCSW18
IV	1	DW1638
V	1	WR544
VI	1	HD3265
VII	1	DW1627
VIII	1	HD2932
IX	1	HD3086
X	1	DW1615

to maturity (DTM), grain filling period (GFD), grain yield per square meter in grams (GYPMS), biological yield per square meter in grams (BYPMS), harvest index (HI) and 1000-grain weight (TGW). The canopy temperature depression (CTD) was measured at anthesis stage using portable infra-red thermometer, Model AG-42, with a view of 2.5°. The data collected from field trials were subjected to statistical analyses. Analysis of variance was carried out following Panse and Sukhatame (1975). The genetic divergence among the genotypes was assessed by *inter se* genetic distances using D^2 statistic of Mahalanobis (generalized distance as recommended by Rao, 1952). The genotypes were grouped using Euclidean cluster analysis.

Result and Discussion

Significant genotypic differences were observed for all the traits under study in both the crop seasons suggesting the presence of substantial genetic variability among the genotypes chosen for the study (Table 2). Cluster formation based on Euclidean analysis of the morpho-physiological characters during the crop season 2016-17 grouped 36 genotypes into four clusters, but into 10 clusters based on 2017-18 data (Table 3). Out of 36 genotypes, some genotypes were grouped together in both the years. For example, a group of six genotypes *viz*., DW1639, HD3262, HD3318, DW1632, DW1645 and HD3266 occupied cluster I during both the crop seasons. Similarly, a group of nine genotypes *viz*., DW1630, DW1631, DW1632, DW1634, DW1635 DW1636, DW1637, HD 3262 and HD 3090 came together in cluster II and cluster I during 2016-17 and 2017-18, respectively. Likewise, eight genotypes *viz*., HD3171, DW1616, HD3255, HD 3249, DW 1628, DW 1629, HD 3184 and HD 3252 appeared together in cluster III in 2016-17 and cluster I in 2017-18. Interestingly, one genotype WR 544 appeared in different clusters in two cropping seasons. Seven genotypes DW1633, DW1638, HD3265 DW1615 DW1627 and HD2932 appeared in cluster I, II and III during 2016-17 but formed different clusters in 2017-18. This might be due to the differential expression of these genotypes to the varied environmental conditions of these two seasons.

Comparative evaluation of cluster means indicated that, for improving a specific character, choose the genotypes from the cluster exhibiting desirable mean values for that character. This indicated that cluster I and II during 2016-17 and cluster II and III during 2017-18 had desirable cluster means for more number of characters, therefore these clusters might be considered for selecting genotypes for breeding programmes. The diversity analysis in conjunction with the mean performance during both the crop seasons, genotypes DW1631 (grain and biological yield), HD 3318 and HD 3252 (higher grain weight/spike), HD 3318 and DW 1631 (more grain number /spike) HD 2932 (longer grain filling duration) and WR 544 (earliness), DW1630 and HD 3255 (longer spike) were apparently the best suited

genotypes for improving the respective traits and can be included in crossing programme to create genetic variability and to select for transgressive segregants.

Acknowledgement

The first author is grateful to Indian Council of Agricultural Research (ICAR), New Delhi, for providing Junior Research Fellowship for Master's Degree programme.

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Indian J. Plant Genet. Resour. 34(1): 90–92 (2021)
DOI 10.5958/0976-1926.2021.00015.2

SHORT COMMUNICATION

Profiling Total Phenolic Content of Different Seed Coloured Germplasm of Ratti (*Abrus precatorius*)

S Prabakaran[1*], Rakesh Bhardwaj[2] and Veena Gupta[3]

[*1]*Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi-110012, India*

[2]*Division of Germplasm Evaluation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*

[3]*Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*

(Received: 18 May, 2020; Revised: 9 April, 2021; Accepted: 9 April, 2021)

Abrus precatorius is a medicinal plant belonging to the family Fabaceae. The main biochemical constituent responsible for its medicinal value is abrin, a protein. The plant is native to India and has been used in the traditional medicinal system for the treatment of wide range of diseases. *Inter alia*, anti-oxidant activity is important since phenolic compounds play a crucial role in free radical scavenging. Ninety-nine accessions of *Abrus precatorius* from National Genebank at NBPGR were profiled for total phenolic content by folin ciocalteu reagent. IC0311747 (a completely white seeded accession) contained the lowest total phenolic content of 16.115 mg/g whereas IC0605143 (a completely black seeded accession) contained the highest total phenolic content of 44.637 mg/g.

Key Words: *Abrus precatorius,* Indian liquorice, Medicinal plant, Ratti, Total phenols

Introduction

Abrus precatorius is a popular medicinal herb also known as Indian licorice/Crabs eye/Coral bead/Ratti/Gunja belonging to family Fabaceae. The plant originated in South-East Asia (Okhale and Nwanosike, 2016) but is profusely found in Subtropical areas of the world. In India, the plant was widely distributed up to 1200m in the outer Himalayas and downwards to Southern India (Das *et al*., 2016). Its uses are well documented for siddha medicines in Tamil Nadu (Ghosh *et al.,* 2007). It is a perennial herb with variation in seed colour from black and red to white and grey combination. The biochemical constituents of *Abrus precatorius* seeds include abrin, abrol, abrasine, pre-casine and precol. Even a very small quantity of abrin (0.00015% of the compound) can be lethal (Lalithakumari *et al.,* 1971). Recently, Glycyrrhizin, a main component of *Abrus precatorius,* was shown to inhibit 6LU7 protein (COVID-19 enzyme responsible for replication of coronavirus in human body) and protease inhibitor responsible to affect coronavirus replication (Oladimeji, 2020).

National Genebank located at ICAR-NBPGR conserves 152 accessions (as on April, 2021) of *Abrus precatorius* collected from various wild habitats across the country particularly from Kerala and Odisha (18%). Phenolic compounds are secondary metabolites which are known to have wide range of functions in plants. Their functions includes antioxidant activity, free radical scavenging, singlet oxygen quenching, metal chelation, reducing activity etc. Here we report profiling of 99 *ratti* germplasm accessions for total phenolic content.

Materials and Methods

Seeds were collected from the germplasm accessions grown at NBPGR Experimental Farm, Issapur (Fig. 1). Total phenolic content was estimated by folin ciocalteu reagent. About 0.1g of ground *ratti* seed sample was taken in a 15ml centrifuge tube. Then 5 ml of 80% ethanol was added into the tube. After mixing it by vortexing, the tube was incubated in boiling water for 30 min. Cooled down contents were centrifuged at 10K rpm for 10 min. Transfer the supernatant to a new labelled centrifuge tube. From the residue, re-extraction was done by adding 5ml of 80% ethanol. Finally, the volume of pooled supernatants was made up to 10 ml using 80% ethanol. Dried 0.1ml extract was dissolved in 3ml of water and 0.5 ml of folin ciocalteu reagent was added followed by

[*]*Email: Surendar.karan1@gmail.com*

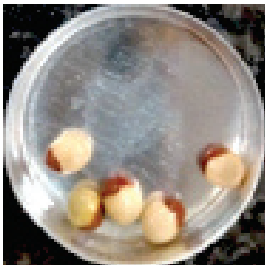
Fig. 1. Inflorescence of *Abrus precatorius* (IC400492) and seeds of IC 0310647 (Location: NBPGR Experimental Farm, Issapur)

2ml of 20% Na_2CO_3 and mixed by using vortex. After an hour, using the spectrophotometer, the absorbance was recorded at 650nm against the blank. The standard curve was drawn using the different concentrations i.e. 10, 20, 30, 40 and 50 µg/ml of gallic acid.

Results and Discussion

Seed colour as well as phenolic content exhibited variation among 99 accessions (Table 1). Total phenolics ranged from 18.568 mg/g complete white coloured accessions to 42.472 mg/g in complete black coloured accessions. IC311747, a complete white coloured accession, had the lowest total phenolic content of 16.115 mg/g whereas IC605143, a complete black coloured

Table 1. Phenolic range and mean of different seed coloured *ratti* accessions

Seed colour class	Image	Phenolic range (mg/g)	Mean (mg/g)
Complete white		16.115 to 21.337	18.568
Pink + brown		22.929 to 23.218	23.073
Cream + brown		23.266 to 23.958	23.689
Red + black		23.921 to 30.553	27.704
Complete black		39.213 to 44.637	42.472

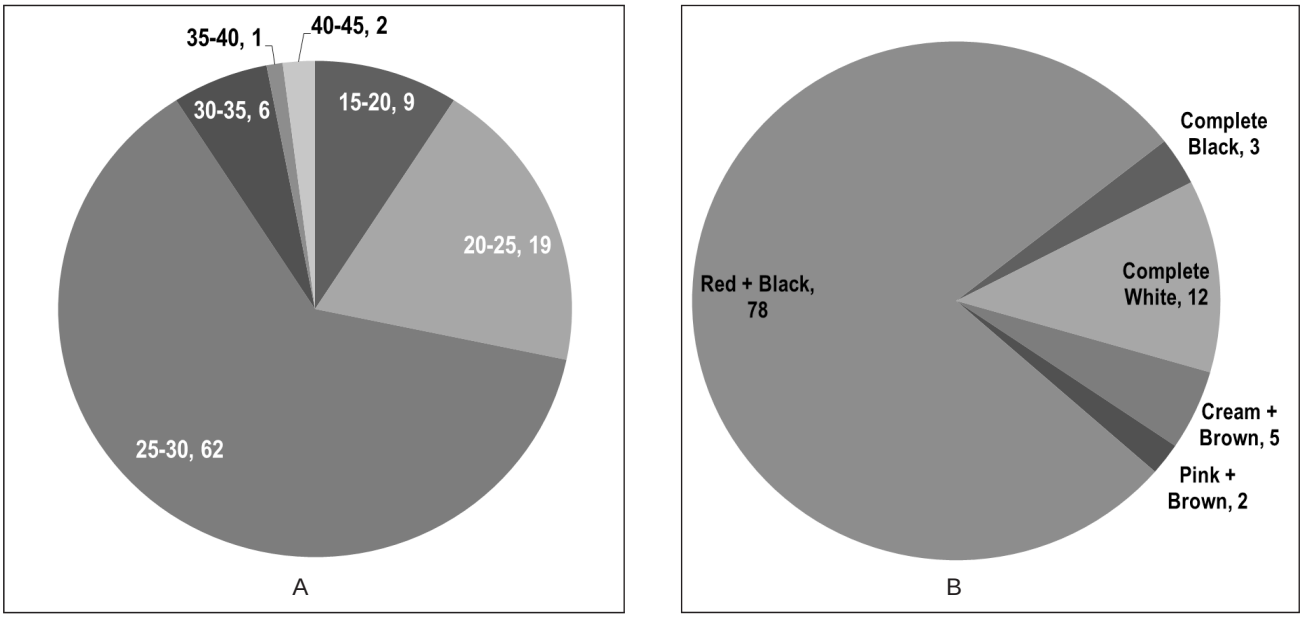


Fig. 2. (A) Variation in total phenolics (expressed in mg/g) and corresponding number of accessions; (B) Variation in seed colour and corresponding number of accessions among 99 ratti accessions profiled.

accession, had the highest total phenolic content of 44.637 mg/g. Maximum number of accessions bore red + black seeds (78) and most accessions (62) contained phenolics in the range of range of 25-30 mg/g (Fig. 2).

Variation in the phenolic content and seed colour indicate excellent variation that can be expected in *Abrus precatorius* accessions conserved in the genebank. However, detailed biochemical profiling for protein, saponins, antioxidants, oil extract, flavonoids and tannins can provide a better insight. Genetic diversity at DNA level can answer if the accessions collected from various locations are diverse within and across seed colour.

Acknowledgements

This work was carried out as part of Ph.D. (Plant Genetic Resources) thesis work of S. Prabakaran. Authors acknowledge the ICAR-IARI and ICAR-NBPGR for providing the facilities.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXXth meeting held on October 21st, 2019 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 71 germplasm lines out of 79 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. Kamini (IC599610) (IC0599610; INGR19033), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress

K Chattopadhyay*, BC Marndi, K Chakraborty and RK Sarkar
ICAR-National Rice Research Institute, Cuttack, Odisha, India
**(Email: krishnenducrri@gmail.com)*

Till date the most studied rice germplasm for salinity stress is 'Pokkali' accessions from coastal saline areas of Kerala. A *Saltol*-QTL for salinity tolerance at seedling stage was identified from Pokkali and introgressed in high yielding background. But many other salt-tolerant cultivars besides Pokkali are grown along India's eastern coast, especially in Odisha and West Bengal which may serve as sources of new QTLs for salinity tolerance. In West Bengal, Sundarbans (22° N, 89° E; 0–10 m above the mean sea level), covering parts of India and Bangladesh, is the largest single block of tidal halophytic mangrove forests in the world, where people mostly depend on rain-fed paddy cultivation. Even today they continue to grow traditional rice varieties because of their stable yield potential in coastal saline areas. However, these areas are increasingly vulnerable to frequent cyclones, high tidal waves, and erratic rainfall, which prompted rice growers and researchers to cultivate and conserve indigenous salt-tolerant lines. Kamini is one of such landraces which was collected from salt affected field at Gosaba block of South 24 Parganas (Sundarbans). In repeated control evaluation it was found tolerant to moderately tolerant (SES score-3-5) to salinity at vegetative stage under salinity stress (12 dSm-1).

Morpho-agronomic characteristics: This germplasm has intermediate early seedling vigour. In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is pale green. Leaf is glabrous. It is highly photosensitive (days to 50% flowering is 133.5). It is tall (125 cm) and having low tillering ability (7.5). It has long (26 cm), horizontal and well exserted panicle. It has small bold grain with grain length-breadth ration of 2.52 and 13.4 g test weight (Table 1). Grain yield is around 2.5 t/ha under moderate (6 dSm^{-1}) salinity stress condition.

Associated characters and cultivation practices: 'Kamini' (AC 44118) was found tolerant to salinity stress (EC 12 d Sm^{-1}) at seedling stage. Its tolerance was associated with low ratio of Na/K (0.25) in shoot (Singh and Sarkar 2014; CRRI 2012; Chattopadhyay *et al*. 2014). Performance index (PI), which gives quantitative information on current state of plant's ability to photosynthesis under stress was used to evaluate some salinity tolerant germplasm of rice including Kamini. The 'salinity factor index' (SFI) based on the salinity-induced changes in the PI during the stress and relative PI ($PI_{salinity}/PI_{control}$) were calculated. The genotypes were rated based on the SFI. The value of SFI was found positive only in Kamini. This was 0-0.5 in some Pokkali accessions and FL 478. This indicated that Kamini (AC 44118) might have better salinity tolerance ability than the genotype we are currently using a salt-tolerant donors (CRRI 2013; Singh and Sarkar 2014). *Saltol*-QTL derived from a Pokkali accession is a major QTL responsible for

*Compiled and edited by: Anjali Kak and Veena Gupta, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012

salinity tolerance at seedling stage. In our study, Kamini (AC44118) showed substantial allelic dissimilarity with FL 478 (a derivative line from Pokkali) in the *Saltol*-QTL region, indicating its allelic mismatch with Pokkali in the *Saltol* QTL region (NICRA 2012; Chattopadhyay *et al.* 2018). All these observations indicate the scope for identification of additional QTLs other than the *Saltol* from Kamini (AC 44118) for salinity tolerance in rice.

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2. Talmugur (AC 43228) (IC0596460; INGR19034), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress at Vegetative Stage

K Chattopadhyay[1], BC Marndi[1], AK Nayak[1], NJ Maitra[2], K Chakraborty[1], RK Sarkar[1] and BC Patra[1*]

[1]*ICAR-National Rice Research Institute, Cuttack, Odisha, India*

[2]*Ramakrishna Ashram, KVK, Nimpith Ashram, South 24, Parganas, West Bengal*

[*]*(Email:bcpatracrri@yahoo.com)*

'Pokkali' rice from coastal saline areas of Kerala is the most studied germplasm for salinity tolerance in rice. A *Saltol*-QTL for salinity tolerance at seedling stage was identified from one of the accessions of Pokkali and introgressed in high yielding rice background. But many other salt-tolerant cultivars, besides Pokkali, are grown along India's eastern coast, especially in Odisha and West Bengal which is found to serve as sources of new QTLs for salinity tolerance. In West Bengal, Sunderbans (22° N, 89° E; 0–10 m above the average mean sea level), covering parts of India and Bangladesh, is the largest single block of tidal halophytic mangrove forests in the world, where people mostly depend on rain-fed paddy cultivation. Even today people of this region continue to grow traditional low-yielding rice varieties because of stable grain yield. However, these areas are increasingly vulnerable to frequent cyclones, erratic rainfall and high tidal waves which compel rice growers to cultivate and conserve indigenous salt-tolerant lines. Talmugur is one of such landraces which was collected from salt affected rice fields at Mathurapur block of South 24 Parganas (Sunderbans). In repeated evaluation under control condition with salinity stress of EC= 12 dSm^{-1}, it was found to possess complete to moderately salinity stress tolerance (SES score- 3-5) at vegetative stage.

Morpho-agronomic characteristics: This landrace has early seedling vigour . In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is pale green. Leaf is pubescent. It is photosensitive (days to 50% flowering is 122), tall (135.5 cm) and having low tillering ability (5). It has horizontal and well exserted panicle (23.48 cm). It has small bold grain with grain length-breadth ratio of 2.26 and test weight of 24.3 g (Table 1). Grain yield is around 2.5 t/ha under moderate (6 dSm-1) salinity stress condition.

Associated characters and cultivation practices: 'Talmugur' (AC 43228) was found tolerant (SES score – 3-5) to salinity stress (EC 12 d Sm^{-1}) at seedling stage under control condition. Its tolerance was associated with low ratio of Na/K (0.25) in shoot (Research Highlights,

Table1. Minimal Descriptors for characterization and evaluation of rice germplasm, Talmugur (AC 43228; IC0596460)

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Early plant vigour	Tall	Tall	Tall
Coleoptile: Anthocyanin colouration	Absent	Absent	Absent
Basal leaf sheath colour	Green	Green	Green
Leaf blade colour	Pale green	Pale green	Pale green
Leaf pubescence	Pubescent	Pubescent	Pubescent
Leaf length (cm)	50.3	46.0	48.15
Leaf width (cm)	1.36	1.4	1.38
Days to 50 % flowering	121 (photosensitive)	123 (photosensitive)	122 (photosensitive)
Panicle exsertion	Well exserted	Well exserted	Well exserted
Stigma colour	Yellow	Yellow	Yellow
Apiculus colour	Purple	Purple	Purple
Number of effective tillers	5	5	5
Plant height (cm)	132	139	135.5
Panicle height (cm)	22.96	24.0	23.48
Panicle type	Horizontal	Horizontal	Horizontal
Awning	Absent	Absent	Absent
Days to maturity	151	153	152
Seed coat colour (kernel colour)	Brown	Brown	Brown
Grain length breadth ratio	2.16	2.36	2.26rtgh
100 grain weight (g)	2.55	2.3	2.43
Hull colour (husk colour)	Black	Black	Black
Threshability	Easy	Easy	Easy
Aroma	Absent	Absent	Absent
Grain yield per plant (g)	30.0	28.5	29.3
Abiotic Stress Note	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage

NICRA 2010-12; CRRI 2012; Chattopadhyay *et al.*, 2013; Chattopadhyay *et al.*, 2018). The experiment was repeated for four years (2011, 2012, 2017, 2018) taking susceptible check IR 29. *Saltol*-QTL derived from a Pokkali accession is a major QTL responsible for salinity tolerance at seedling stage. The UPGMA dendrogram and principal component analysis depicted that most of the salinity tolerant germplasm including 'Talmugur' from the 'Sunderbans' area were genetically closer to each other. Among the tested genotypes, Talmugur showed the highest allelic dissimilarity with FL 478 (a derivative line from Pokkali with *Saltol* introgression), indicating its highest allelic mismatch with Pokkali in the *Saltol* – QTL region (Chattopadhyay *et al.*, 2013). These observations indicate the scope for identification of additional QTLs other than the *Saltol* from Talmugur for salt tolerance at early vegetative stage in rice. In addition to that this germplasm was found to have anaerobic germination ability along with salinity tolerance (NICRA2010-12).

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3. Chettivirippu (AC 39394) (IC0413613; INGR19035), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress both at Seedling and Reproductive Stage

K Chattopadhyay, BC Marndi, K Chakraborty, BC Patra* and RK Sarkar
ICAR-National Rice Research Institute, Cuttack, Odisha, India
**(Email:bcpatracrri@yahoo.com)*

Rice is grown in the coastal saline areas of Kerala, sometimes at below sea level under Pokkali and Kaipad systems of cultivation. Pokkali refers to a system of rice cultivation which is characterized by prolonged partial flooding, and farmers practicing rice cultivation with shrimp farming. Virippu refers to rice crop growing under 'Pokkali' system in the autumn season. The rice germplasm and pure line selection from the traditional cultivars and landraces in this region are found to have single or multiple abiotic stress tolerance genes. Earlier *Saltol*-QTL for salinity stress tolerance at seedling stage was identified from one of the accessions of Pokkali and was introgressed into high yielding rice background. But researchers are still searching for donors for the reproductive stage salinity tolerance which can introduce QTLs for substantial reduction in yield penalty under salinity stress. This accession of Chettivirippu (IC 413613, AC39394) was collected from the village-Thirumalabhagom, Dist. Alappuzha in Kerala. In repeated evaluation under control condition with salinity stress, EC= 12 dSm-1, it was found tolerant (SES score- 3) to salinity at early vegetative stage. Most importantly it was also found moderately tolerant (<50% yield reduction) to salinity stress at reproductive stage.

Morpho-agronomic characteristics: This germplasm has intermediate seedling vigour. In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is medium green. Leaf is pubescent. It is medium duration (days to 50% flowering is 101), tall (140 cm) and having medium tillering ability (8.5). It has medium, semi-erect and well exserted panicle (23.5cm).It has medium bold grain with grain length-breadth ratio of 2.96 and test weight of 27.5 g (Table 1). The grain yield is around 2.5 t/ha under moderate (6 dSm-1) salinity stress condition.

Table 1. Minimal Descriptors for characterization and evaluation of rice germplasm, Chettivirippu (AC 39394; IC 413613)

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Early plant vigour	Intermediate	Intermediate	Intermediate
Coleoptile: Anthocyanin colouration	Absent	Absent	Absent
Basal leaf sheath colour	Green	Green	Green
Leaf blade colour	Medium green	Medium green	Medium green
Leaf Pubescence	Pubescent	Pubescent	Pubescent
Leaf length (cm)	63.2	60.5	61.85
Leaf width (cm)	1.02	1.03	1.03
Days to 50 % flowering	100	102	101
Panicle exsertion	Well exserted	Well exserted	Well exserted
Stigma colour	White	White	White
Apiculus colour	Straw	Straw	Straw
Number of effective tillers	8	9	8.5
Plant height (cm)	139.0	140.0	139.5
Panicle length (cm)	23.0	24.0	23.5
Panicle type	Semi-erect	Semi-erect	Semi-erect
Awning	Short partially awned	Short partially awned	Short partially awned
Days to maturity	132.0	134.0	133.0
Seed coat colour (kernel colour)	Light brown	Light brown	Light brown
Grain length breadth ratio	2.92	3.0	2.96
100 grain weight (g)	2.6	2.9	2.75
Hull colour (husk colour)	Brown	Brown	Brown

Table 1 Contd.

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Threshability	Easy	Easy	Easy
Aroma	Absent	Absent	Absent
Grain yield per plant (g)	30.7	31.9	31.3
Abiotic Note	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage

Associated characters and cultivation practices: Chettivirippu (AC39394) was found tolerant (SES score = 3) to salinity stress (EC 12 dSm^{-1}) at seedling stage. Its tolerance was associated with low ratio of Na-K (0.20) in shoot (CRRI Annual report 2011-12; NICRA, 2012; Nath *et al.,* 2013). The findings related to AC 39394 have been validated by repeating the experiment in *kharif* 2017 and *kharif* 2018. Chettivirippu (AC39394) was found moderately tolerant to salinity stress at flowering stage (NICRA, 2012; Chattopadhyay *et al*, 2013) with yield reduction much below 50%. This germplasm is detected as a unique germplasm which posses tolerance to salinity stress at both seedling stage and at reproductive stage. This germplasm is being utilized in breeding for tolerance to both seedling and reproductive stage.

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4. RP5972-13-1-6-67-129-266 (IC0632071; INGR19036), a Rice (*Oryza sativa*) Germplasm Tolerant to Low Soil Phosphorous Condition in the Background of MTU1010 with about 95.2% Background Recovery of the Recurrent Parent Genome and Yields More than MTU1010

RM Sundaram[1*], MS Anantha[1], VP Bhadana[1,2], SM Balachandran[1], B Parmar[1], LV Subba Rao[1], C Gireesh[1], M Sheshu Madhav[1], P Senguttuvel[1], M Anila[1], HK Mahadeva Swamy[3] and RR Kale[1]

[1]*ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad, India*

[2]*ICAR-Indian Institute of Agricultural Biotechnology, Namkum, Ranchi, Jharkhand, India*

[3]*ICAR- Sugarcane Breeding Institute (SBI), Coimbatore, Tamil Nadu, India*

[*](*Email:*r.sundaram@icar.gov.in, rms_28@rediffmail.com)

MTU1010 (also popularly called as Cotton Dora Sannalu), is a high yielding, short duration, elite mega-variety of rice cultivated across the country but does not perform well in soils which are low in available Phosphorus (for e.g. upland rice). In order to improve MTU1010 for its tolerance to low soil phosphorus (P), marker assisted back cross breeding (MABB) approach was deployed to transfer *Pup1,* a major QTL/gene associated with tolerance to low soil P from Swarna, a high yielding, long duration variety. In screening studies carried out earlier in a low soil P plot of ICAR-Indian Institute of Rice Research (ICAR-IIRR), Hyderabad, MTU1010 was observed to be highly sensitive to low soil P levels, while Swarna showed high level of tolerance. A cross was made between Swarna and MTU1010 during Kharif 2012 and the heterozygous F_1s (identified using parental polymorphic SSR marker, RM206) were backcrossed with MTU1010 to generate a total of 253 BC_1F_1s. They were then screened using the gene-specific markers for *Pup1*, viz., K46-1 (a dominant functional PCR-based marker) and K20-2 (a co-dominant PCR-based marker, which is closely

Table-1. Agro morphological traits of RP5972-13-1-6-67-129-266 MTU1010 NIL both in Normal and Low soil P.

Traits	MTU1010 parental line growing in Normal soil P (32ppm)	MTU1010- NIL (RP5972-13-1-6-67-129-266) growing in Normal soil P (32ppm)	MTU1010 parental line growing in Low soil P (3-5 ppm)	MTU1010- NIL (RP5972-13-1-6-67-129-266) growing in Low soil P (3-5 ppm)
Plant height (Including panicles) (cm)	91.77±0.43	101.37±0.09	69.33±0.59	81.10±0.29
Number of productive tillers (No.s)	15±0.33	20±0.33	4±0.33	8±0.67
Panicle length (cm)	21.40±0.06	24.13±0.54	15.57±0.41	23.17±0.20
Root length (cm)	29.12±0.69	31.70±0.64	18.10±0.15	32.97±0.23
Root volume (cc)	68.57±1.13	71.53±0.55	14.53±0.61	30.60±1.04
Grain yield per plant (gm)	30.60±0.53	36.73±0.27	4.16±0.07	18.03±0.18

linked to *Pup1* locus) to identify the BC_1F_1 plants (n = 129), which are heterozygous for *Pup1*. Such plants were then screened with a set of parental polymorphic SSR markers to identify a single positive BC_1F_1 plant possessing maximum introgression of the recurrent parent genome (~ 82 % recovery). This plant was then crossed with MTU1010 to generate BC_2F_1s. The process of marker-assisted backcrossing as explained above was repeated in BC_2F_1 generation, wherein a single *Pup1* positive plant possessing maximum recovery of the recurrent parent genome (i.e. MTU1010 genome) was identified (possessing 95.2% recovery) and selfed to generate BC_2F_2s. Plants homozygous for *Pup1* were identified at BC_2F_2 generation (n = 32) with the help of the gene-specific co-dominant marker, K20-2 and reconfirmed with the dominant functional marker K46-1 and they were further advanced through selfing till BC_2F_7 generation by adopting pedigree method of breeding. Phenotypic screening of ten selected BC_2F_7 lines of MTU1010 possessing *Pup1* was carried in the Low soil-P plot and normal plot of ICAR-IIRR, Hyderabad during *Kharif* 2015. One of the near-isogenic lines, RP5972-13-1-6-67-129-266 showed similar or significantly better performance in the both low-P and normal soil-P in comparison with MTU1010 in terms of several growth and yield related parameters (Table-1; Figure-1). This line can be cultivated by MTU1010 farmers in areas where there is low soil P and also where the soil P levels are normal, thus reducing the application of P fertilizers by 25-30 %. Further, the breeding line can also be used as a promising donor for quick transfer for *Pup1* into other rice varieties.

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5. IC121865 (IC0121865; INGR19037), Rice (*Oryza sativa*) Germplasm Resistant to Blast Disease

R Bansal[1], NK Gautam[1], LV Subbarao[2], M Srinivasa Prasad[2], H Rajashekara[3], BC Patra[4], M Variar[5], A Ramanathan[6], K Srinivasan[1], V Devi[1], JC Rana[7] and Ashok Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, India*
[2]*ICAR-Indian Institute of Rice Research, Hyderabad, Telangana, India*
[3]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand, India*
[4]*ICAR-National Rice Research Institute, Cuttack, Odisha, India*
[5]*Central Rainfed Upland Rice Research Station, ICAR NRRI, Hazaribagh, Jharkhand, India*
[6]*Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*
[7]*Bioversity International G-1, B-Block, NASC Complex, Pusa Campus, New Delhi, India*
[*]*(Email:ruchibansal06@gmail.com)*

Rice blast is the most devastating fungal disease of rice caused by *Magnaporthe oryzae* that occurs all over world. It routinely causes 10–30% yield losses, and in severe cases can result in complete losses in major rice-production areas (Zhao *et al*., 2018). *M. oryzae* can infect most parts of the plant, but infections of the panicle neck node or the panicle are the most damaging phases of the disease with reports of the disease occurring in more than 85 countries. When *M. oryzae* infects rice and produces symptoms of neck rot or panicle blast, normal panicle and seed development is inhibited (Devi *et al*., 2015). Due to the severity of disease, genetics of plant pathogen interaction has been studied thoroughly and several blast resistance genes have been identified, characterized and deployed in breeding. But due to high pathogen plasticity in the field, identification of new sources of blast resistance may be of immense importance to pathologists and breeders for further exploration of pathogen resistance mechanism in the crop and as a trait donor in the breeding program.

htrhUnder CRP-agrobiodiversity, 1,214 accessions of rice germplasm were screened for resistance to blast disease during *Kharif* 2016 at four AICRIP Centres i.e., VPKAS, Almora, TNAU, Coimbatore, CRURRS, Hazaribagh and IIRR Hyderabad. Germplasm was evaluated under field conditions at Almora and Hazaribagh and under controlled conditions at other locations. Location Severity Index ranged from 5.6 to 7.0 in different locations. Thirteen accessions (IC245865, IC246277, IC246403, IC246274, IC454167, IC121865, IC199562, IC218270, IC245927, IC246012, IC246228, IC246273 and IC246659) were found resistant across the locations. All the resistant accessions are indigenous and were collected from Punjab, Rajasthan and Andhra Pradesh.

The accession IC121865 collected from Rajasthan was found resistant to rice blast. Identified material can be used as donor for blast resistance in breeding program.

Screening of Rice germplasm under CRP- Agrobiodiversity project during *Kharif* 2016*

Accession Id	Location	Field/Controlled	Location Severity Index	Susceptibility Index	Promising Index
IC121865	VPKAS, Almora	Field	6.4	3.5	100
	TNAU, Coimbatore	Controlled	5.6		
	CRURRS, Hazaribagh	Field/Controlled	5.7		
	IIRR, Hyderabad	Controlled	7.0		

*Based on ICAR-IIRR AICRIP Annual Progress Report 2016, Vol 2, Plant Pathology

6. IC0199562 (IC0199562; INGR19038), Rice (*Oryza sativa*) Germplasm Resistant to Blast Disease

R Bansal[1*], NK Gautam[1], LV Subbarao[2], H Rajashekara[3], BC Patra[4], M Variar[5], A Ramanathan[6], K Srinivasan[1], V Devi[1], JC Rana[7] and Ashok Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, India*
[2]*ICAR-Indian Institute of Rice Research, Hyderabad, Telangana, India*
[3]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand, India*
[4]*ICAR-National Rice Research Institute, Cuttack, Odisha, India*
[5]*Central Rainfed Upland Rice Research Station, ICAR NRRI, Hazaribagh, Jharkhand, India*
[6]*Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*
[7] *Bioversity International G-1, B-Block, NASC Complex, Pusa Campus, New Delhi, India*
[*]*(Email:ruchibansal06@gmail.com)*

Rice blast is the most devastating fungal disease of rice caused by *Magnaporthe oryzae* that occurs all over world. It routinely causes 10–30% yield losses, and in severe cases can result in complete losses in major rice-production areas (Zhao *et al*., 2018). *M. oryzae* can infect most parts of the plant, but infections of the panicle neck node or the panicle are the most damaging phases of the disease with reports of the disease occurring in more than 85 countries. When *M. oryzae* infects rice and produces symptoms of neck rot or panicle blast, normal panicle and seed development is inhibited (Devi *et al*., 2015). Due to the severity of disease, genetics of plant pathogen interaction has been studied thoroughly and several blast resistance genes have been identified, characterized and deployed in breeding. But due to high pathogen plasticity in the field, identification of new sources of blast resistance may be of immense importance to pathologists and breeders for further exploration of pathogen resistance mechanism in the crop and as a trait donor in the breeding program.

Under CRP-agrobiodiversity, 1,214 accessions of rice germplasm were screened for resistance to blast disease during *Kharif* 2016 at four AICRIP Centres i.e., VPKAS, Almora, TNAU, Coimbatore, CRURRS, Hazaribagh and IIRR Hyderabad. Germplasm was evaluated under field conditions at Almora and Hazaribagh and under controlled conditions at other locations. Location Severity Index ranged from 5.6 to 7.0 in different locations. Thirteen accessions (IC245865, IC246277, IC246403, IC246274, IC454167, IC121865, IC199562, IC218270, IC245927, IC246012, IC246228, IC246273 and IC246659) were found resistant across the locations. All the resistant accessions are indigenous and were collected from Punjab, Rajasthan and Andhra Pradesh.

The accession IC199562 collected from Rajasthan was found resistant to rice blast. Identified material can be used as donor for blast resistance in breeding program.

Screening of Rice germplasm IC199562 under CRP- Agrobiodiversity project during *Kharif* 2016*

Location	Field/Controlled	Location Severity Index	Susceptibility Index	Promising Index
VPKAS, Almora	Field	6.4	3.5	100
TNAU, Coimbatore	Controlled	5.6		
CRURRS, Hazaribagh	Field/Controlled	5.7		
IIRR, Hyderabad	Controlled	7.0		

*Based on ICAR-IIRR AICRIP Annual Progress Report 2016, Vol2, Plant Pathology

7. NH219 (RP Bio 5477-NH219) (IC0632074; INGR19039), a Rice (*Oryza sativa*) Mutant with Higher Yield than Nagina22 in Normal and High Temperature Conditions. Dark Green Leaves, Drought Tolerant

N Sarla*, SR Voleti, D Subrahmanyam, SK Mangrauthia and P Yugandhar
ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad, India
**(Email:sarla_neelamraju@yahoo.com)*

Mutants are valuable resources for genetic variations in crop improvement. Nagina 22 (N22) is an early maturing drought and heat tolerant *aus* variety. NH219 is Ethyl Methane Sulphonate (EMS) induced mutant of variety Nagina 22 The mutant was developed as part of a DBT funded project "Characterization and use of EMS induced mutants of rice variety N22 for yield, drought and phosphorus use efficiency" at IIRR. The mutant was identified in M3 generation as one of the four dark green leaf (*dgl*) mutants which survived under prolonged drought and high temperature stress in *rabi* season upto tillering stage in DRR (now IIRR) field conditions tested for two years 2011, 2012. Histochemical staining showed that there was negligible ROS accumulation in cut leaves of NH219 heat treated at 40C for 72h compared to N22 (Panigrahy *et al.*, 2011). Later, heat tolerance was evaluated in lab conditions at seed germination and seedling growth stage at 30C and 40C and NH219 was better than N22 in heat tolerance parameters such as %germination, chlorophyll stability, leaf senescence index and the ability to keep dry weight same at 30C and 40C. (Prasanth *et al* 2012). When field evaluated in DRR, the yield decrease under heat stress was 33% in N22 but only 23% in NH219. Under severe heat conditions in heat tunnel in summer (*Rabi* 2014) N22 and NH219 were the only lines which set seed. N22 gave 2.30g/plant and NH219 gave 2.92g/plant out of several lines tested. NH219 was also tested in multi-location trials conducted by AICRIP Physiology in 2016 at 7 locations with uniform facility for field testing for heat tolerance (Hyderabad, Pantnagar, Pattambi, Rewa, Maruteru, Titabar and Chinsurah) keeping Gontra Bidhan3as National Check. NH219 gave mean yield of 385g/m2 in heat conditions with only 13.09% decrease over normal. Gontra Bidhan3 gave 460g/m2 in heat conditions with 25.2% decrease over yield in normal conditions. In multilocation trials too NH219 showed 13% decrease in yield under heat conditions at par with National Check Gontra Bidhan3 in 2016. NH219 is also tolerant to low Phosphorus in soil, has high Photothermic Index and radiation use efficiency based on AICRIP report 2013. It has dark green leaves and a high SPAD value of 39-40 compared to 30 of N22.

Process of development of NH219: M1 seeds of Nagina22 (N22) were provided to IIRR as part of the DBT Network Project on Characterization of EMS induced N22 mutants of rice to screen and characterize for several agronomic traits. M1 seeds were grown in normal conditions and M2 seed collected from each M1 plant. M2 and M3 were tested in normal and stress (drought and heat) conditions. Seeds harvested from normal conditions were used each year for screening under stress. These mutants are now in M13 and were advanced from panicle to seed mutant wise each season. Mutant line NH219 is a stable elite genetic stock for tolerance to high temperature as it shows less yield decrease in heat. It gives higher yield than N22 under normal or heat conditions.NH219 has darker seed and apiculus than N22. It has dark green leaves and panicle is well exserted with long peduncle.

8. NH162 (RP Bio 5477-NH162) (IC0632599; INGR19040), a Rice (*Oryza sativa*) Germplasm Tolerant to Drought, with Higher Yield than Nagina22 in Normal, Drought and Aerobic Conditions. Functionally Stay Green with Dark Green Leaves, Drought Tolerant, Higher Yielder in Aerobic Condition. Seed Hull Dark and Seed Type Slender

N Sarla*, SR Voleti, D Subrahmanyam, SK Mangrauthia and P Yugandhar and M Panigrahy
ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad, India
*(*Email: sarla_neelamraju@yahoo.com*)

Mutants are valuable resources for genetic variations in crop improvement. Nagina 22 (N22) is an early maturing drought and heat tolerant *aus* variety. NH162 is Ethyl Methane Sulphonate (EMS) induced mutant of variety N22. The mutant was developed as part of a DBT funded project "Characterization and use of EMS induced mutants of rice variety N22 for yield, drought and phosphorus use efficiency" at IIRR from 2007-2012. The mutant was identified in M3 generation as one of the four dark green leaf (*dgl*) mutants which survived under prolonged drought and high temperature stress in *rabi* season upto tillering stage in DRR (now IIRR) field conditions tested for two years 2011, 2012 . Later drought tolerance was evaluated in field condition during 2010 and 2011. Grain yield was 2-fold higher than N22 under normal, water limited conditions in field. NH162 is the stable mutants and high yielding mutant under both normal and water limited conditions. Histochemical staining showed that there was negligible ROS accumulation in cut leaves of NH162 heat treated. The mutant was stay green, dwarf, with higher tiller number, stem thickness, late duration with higher grain yield when compared with N22 under normal condition. The grains of NH162 has darker than N22. When field evaluated in DRR, the yield decrease under water limited condition was 42% in N22 but only 25% in NH162. During the dark induced senescence with cytokinin 6-benzyl adenine (BA), N22 showed rapid reduction in the Chl a/b ratio, chlorophyll content than NH162 where with and without 6BA treatment the chlorophyll content of NH 162 is not significantly different. Chl analysis revealed that Chl a/b ratios and Fv/Fm values were maintained during dark induced senescence (DIS) in N22-H-*dgl*162 [RPBio5477-NH162] and BA-treated N22 leaves. The non-denaturing green gel analysis was performed to study the effect of senescence and BA on stability of chlorophyll complexes. In the untreated leaves at 0 h, three distinct major bands representing the RC–LHC complex, the LHCs, and free pigments were observed. In the untreated N22 leaves, the complexes were drastically reduced by 72 h of DIS and degraded by 96 h of DIS, whereas all the bands remained intact in NH162 and BA-treated N22 leaves after 96 h of dark induced senescence. The mutant NH162 along with N22 were tested for drought tolerance at seeding stage. In N22 plants, leaf rolling appeared on the fifth day after withholding water, and the leaves became wilted on the eighth day, whereas in NH162, leaf rolling appeared on tenth day and wilted on the 14 day. On the 8th day for N22 and 14th day for NH162 recovery of plants was attempted by rewatering, and the recovery time was recorded on 24 hours after rewatering. NH162 plants recovered in 16-20 hours of rewatering, N22 plants recovered after 2 days of rewatering . Apart from these traits, NH162 is a loss of function mutant under very low P condition. Nine SSR markers RM260, RM206, RM215, RM224, RM242, RM252, RM205, RM1920, RM1 had polymorphism between N22 and NH162.

NH162 was also tested in multi-location trails conducted by AICRIP aerobic condition in 2016 and 2017 at 16 locations and 57 entries along with three checks. The grain yield was ranged from 1506 to 6330 kg/ha. NH162 performed better than hybrid (IIRRH 111-2 and best check CRR Dhan 21 in most of the locations. The mean panicle no/m^2 is 314. This mutant was performed well over checks in zone III (CTK, BBN, BKG, SBR, PTN, BI, JH, UP). In the year 2017 the variety was tested again in AVT-1 in Zone 3 it was ranked 3 among the 20 entries and 3 checks with grain yield of 5200 kg/ha NH162 is resistant to sheath rot and bacterial leaf blight. NH162 scored 1 in GDL location for brown spot, 1 for sheath rot location MTU, 1 for bacterial leaf blight in PNT and NWG. It has dark green leaves and a high SPAD value of 39-42 when compared to 28 of N22 in

dry bed condition.

Process of development of NH162: M1 seeds of Nagina22 (N22) were provided to IIRR as part of the DBT Network Project on Characterization of EMS induced N22 mutants of rice to screen and characterize for several agronomic traits. M1 seeds were grown in normal conditions and M2 seed collected from each M1 plant. M2 and M3 were tested in normal and stress (drought and heat) conditions. Seeds harvested from normal conditions were used each year for screening under stress. These mutants are now in M13 and were advanced from panicle to seed each season. Mutant line NH162 is a stable elite genetic stock for tolerance to water limited condition and also for high temperature (unpublished data for high temperature) as it shows 16% and 36% less yield decrease in both drought and heat. It gives higher yield than N22 under normal or drought conditions. NH162 has dark green leaves, higher tiller number, more stem thickness. The panicle length (range 16-20) and number of grains are almost double (range140-160) in the mutant.

9. RP Bio 4918-230S (IC0632075; INGR19041), a Rice (*Oryza sativa*) Germplasm with Resistance to Brown Planthopper (BPH) *Nilaparvata lugens*. Possesses High Resistance at Vegetative and Reproductive Stages

N Sarla[1*], V Jhansi Lakshmi[1], Mallikarjuna Swamy[2] and GR Katti[1]
[1]*ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-500030, India*
[2]*International Rice Research Institute, Los Banos, Philippines, India*
[*]*(Email:jhansidrr@yahoo.co.in)*

Rice is the principal food crop in India and is grown in an area of ~ 44 Million hectares and with a production of ~100 Million metric tonnes. Rice production is limited by various biotic and abiotic stresses of which insects are estimated to cause 21-30% yield loss. Among the insect pests, rice brown planthopper (BPH) *Nilaparvata lugens* (Stal) (Delphacidae: Hemiptera) is very serious pest which causes severe yield losses upto 100% under severe hopper burn situations.

The large scale cultivation of dwarf, early maturing, photoperiod insensitive, high tillering and high yielding rice cultivars coupled with the increased use of nitrogenous fertilizers had become congenial for brown planthopper infestation in farmers' fields. All growth stages of rice plant right from seedling to maturity stage are affected. Nymphs and adults stay at the base of the plant and damage the crop by sucking phloem sap which results in yellowing of leaves, reduced tillers and plant height, unfilled grains and death of the plant. Damage is more severe in reproductive stage of crop wherein round yellow patches appear in the field which later turns brownish due to drying of plants called as hopper burn. The patches of infestation may spread in the entire field, coalesce together and in severe cases complete destruction of crop occurs.

Since1970's several devastating BPH epidemics have been reported and now outbreaks of brown planthopper have become common and severe. Many insecticides are suggested for the control of this pest, but application of these chemicals interrupts the natural balance of rice ecosystem. Cultivation of resistant varieties is the better and environmentally safe substitute. Hence, breeding programme for development of BPH resistant varieties with different modes of host plant resistance (such as antixenosis, antibiosis and tolerance) is extremely important.

More than 30 genes and QTLs have been identified from cultivated and wild species introgression lines. Most of the genes for BPH resistance identified so far are against biotypes 1,2 and 3 and only few are resistant against biotype 4, which could be one of the reason for their ineffectiveness against BPH biotype which is most destructive and is distributed over the Indian sub-continent. Many of the donors which showed stable resistance across the biotypes have one or two major genes along with QTLs associated with resistance. Hence, it is important to identify new donors, novel genes/major QTLs effective against BPH biotype4 to pyramid them for stable resistance. The genes from wild rices are reported to be robust and stable.

The wild species of *Oryza* representing AA, BB, CC, BBCC, CCDD, EE, FF, GG and HHJJ genomes are a

rich reservoir of useful genes resistant to major biotic and abiotic stresses, more adapted to adverse and changing environmental conditions. The genetic variability for some of these stresses is restricted in the cultivated rice germplasm. Moreover, changes in insect biotypes are an enduring threat to increased rice production. There is thus a critical need to broaden the rice gene pool by introgressing genes for such traits from diverse sources. Therefore, it is important to discover these valuable genes hidden in wild rice species and use them in breeding programmes to develop resistant varieties. However, low crossability and limited recombination between chromosomes of cultivated and wild species limit the transfer of such genes. In addition, genes from wild rices are often linked with genes governing undesirable traits. So, development of advance back cross introgression lines is very essential, for selective transfer of only preferable genes and to avoid linkage drag. Creation of introgression lines using cultivated rice as recipient and wild rice as the donor is the most durable approach to explore primitive and broad genetic resources in rice breeding.

Most of the genes identified are based on the reaction at seedling stage but the maximum crop damage occurs at tillering and reproductive stage in farmer's field. Hence, it is necessary to know the effectiveness of donors/genes against BPH at later plant growth stages. Therefore, the present attempt was made to identifydonors for BPH resistance from introgression lines derived from *O.nivara* at seedling stage and also at maximum tillering and reproductive stage.

Process of development of RP Bio 4918-230S. With this background a set of backcross intogression lines were developed from one cross viz., Swarna/*O. nivara* (*accession no.* IRGC 81848 S) following single seed descent method. Swarna is a popular commercial variety susceptible to brown planthopper; *O. nivara* (*accession no.* IRGC 81848S) is a wild rice accession with AA genome. A backcross strategy was followed to develop the line RP Bio 4918-230S. A single plant of *O. nivara* (*accession no.* IRGC 81848 S) was used as a male parent and crossed to Swarna to generate F1 plants. These F1 plants derived from the cross between Swarna and *O. nivara* (IRGC 81848) were backcrossed to Swarna to produce BC1F1 plants. These BC1F1 plants were again backcrossed to Swarna to develop the BC2F1 generation. These BC2F1 were selfed till five generations to produce BC_2F_6 backcross introgression lines (BILs). 250 number of BILs were selected which were more like Swarna phenotypically and were screened for BPH resistance in the greenhouse and field conditions, out of which RP Bio 4918-230S and five more BILs were found resistant to BPH.

Phenotyping for Brown Planthopper Resistance: 250 number of BC_2F_6 backcross introgression lines (BILs) were screened for brown planthopper resistance by adopting mass screening test under controlled greenhouse conditions at Indian Institute of Rice Research. The method involved infestation of 12 day old young seedlings of the BILs grown in screening trays with BPH nymphs along with resistant (Ptb 33) and susceptible checks (TN1). When more than 90 per cent of TN1 plants were killed, the BILs were scored for the damage reaction, based on a 0-9 scale of Standard Evaluation System (SES). Out of the 250 number of BILs from Swarna/*O. nivara* screened, six BILs were found to be resistant and RP Bio 4918-230S was one of the BILs with brown planthopper resistance with a damage score of 1.8. Swarna and the susceptible check (TN1) recorded a damage score of 9, the resistant check PTB 33 recorded a damage score of 1.2 (Jhansi lakshmi *et al*., 2010) Fig 2 (a,b,c). The RP Bio 4918-230S was screened along with germplasm accessions in 2012 in DRR greenhouse and was found to be resistant with a damage score of 1.0 (Akanksha *et al*., 2017).

This BIL RP Bio 4918-230S was screened for brown planthopper resistance in the multilocation testing in 2010 in planthopper screening nursery (PHS) and performed better and promising in 6 out of 13 tests/ locations and recorded damage score of <5 in two locations (total 8 viz., DRR, Coimbatore, Mandya, Raipur, Ludhiana, Madurai and Gangavathi out of 13 locations) (Table 1).The susceptible check TN1 recorded a damage score of 9 and the resistant check PTB 33 recorded a DS of 1-5 (Ref: Screening nurseries 2010 AICRIP DRR and Progress report 2010 AICRIP DRR, DRR Annual report 2010-11). In 2011, RP Bio 4918-230S was retested in planthopper screening nursery (PHS) and was found promising in four locations viz., DRR, Coimbatore, Madurai and Raipur (Ref: Screening nurseries 2011 AICRIP DRR and Progress report 2011 AICRIP DRR, DRR Annual report 2011-12). In 2012, RP Bio 4918-230S was retested in Multiple Resistance Screening Trial (MRST) and was found promising in four locations viz., Cuttack, Ludhiana and Raipur (Ref: Screening nurseries 2012 AICRIP DRR and Progress

report 2012 AICRIP DRR, DRR Annual report 2012-13). In DRR, RP Bio 4918-230S was evaluated in 2012 in the field for planthopper reaction under hopperburn conditions and was found to be resistant in the tillering and reproductive stage (DRR Annual report 2012-13). The resistant check PTB 33 was resistant and susceptible check TN1 was completely susceptible with a damage score of 9. In APRRI-RARS Maruteru, the introgression line RP Bio 4918-230S was evaluated in 2014 in the field under natural infestation and it was found to be resistant.

Simultaneously RP Bio 4918-230S was evaluated for agronomic traits and quality traits and physiological parameters. It is a semi dwarf, mid duration culture (140 days) possessing medium grains. Quality wise it recorded medium head rice recovery (HRR) of 45% and intermediate amylose content (Table 2).

It has high photosynthetic efficiency (P_N)23.1 µmol CO_2 m^{-1} s^{-1}, Chlorophyll a 3.48 (mg/g), Chlorophyll b 1.26 (mg/g), total Chlorophyll 4.86 (mg/g) and Carotinoids 0.96 (mg/g) compared to the parents Swarna and *O. nivara* (Table 3) (Haritha *et al*., 2019).

It has given an yield advantage of 5.8% in zone 7 and an yield advantage of 9% over hybrid check PA 6444 in AICRIP IVT late trials (unpublished report).

This line could be used as elite genetic stock for resistance to brown planthopper (BPH), Nilaparvata lugens. It has resistance in seedling, vegetative and reproductive stages. It could be involved as donor parent in hybridization program for developing resistant varieties for brown planthopper**.**

Table 1. Reaction of RP Bio 4918-230S to BPH under natural and artificial infestation during 2009- 2014

Year/ location		2009	2010 PHS	2011 PHS	2012 MRST	2012	2014											
		DRR	DRR	CBT	MND	RPR	LDN	MDR	GGV	DRR	CBT	MDR	RPR	CTC	LDN	RPR	DRR	MTU
Greenhouse	RP Bio 4918-230S	1.8	4.5	5	1	1	1.6			5.2	3	3	0.3	1.0	1.2	0.6		
	PTB 33	1.4	1.7	5	1	1.3	1.5			1.7	5	4	0					
	TN1	9	9	9	9	9	9			9	7	8	9	9	7.7	9		
	Swarna	9																
Field	RP Bio 4918-230S				10%hb			0 DS	0/HILL								1	1
	PTB 33				5%hb			3 DS	25/ HILL								1.6	
	TN1				80%hb			9	34/ HILL								9	

DRR: Directorate of Rice Research, CBT: Coimbatore, MND: Mandya, RPR: Raipur, LDN: Ludhiana, MDR: Madurai, CTC Cuttack, MTU: Maruteru and GGV: Gangavathi

Table 2. Morphological characters of RP Bio 4918-230S and Swarna

Name of the variety	:	RP bio 4918-230S	Swarna
Plant height	:	81.42	101.27
Plant type	:	short	semidwarf
No. of tillers /plant	:	15.83	11.6
Days to 50% flowering	:	109.2	119.2
Seed to seed duration	:	139.15	148.15
Panicle type	:	Compact	Compact
No. of panicles /plant		13.17	10.64
Panicle exsertion	:	Well exserted	Well exserted
Panicle weight		2.03	2.65
Awning	:	present	absent
Yield/plant (g)		16.53	18.57
1000 grain weight	:	18.6g	15.1g
Kernel length	:	7.43	6.3mm
Kernel breadth	:	2.58	2.1mm
L/B ratio	:	2.88	3
Grain type	:	Medium	Medium
Kernel appearance	:	Grain chalkiness absent	Very occasionally chalky

Name of the variety	:	RP bio 4918-230S	Swarna
Hulling recovery		75.6%	73.9%
Milling recovery	:	65.3%	68.6%
Head rice recovery (HRR)	:	44.9%	56.3%
Alkali spreading value (ASV)	:	4	5
Amylose content (AC)	:	25.5%	26.54%
Gel consistency	:	31 mm	43 mm
Yield potential		5.45t/ha	5.5-6.0 t/ha

Table 3. Physiological characters of RP Bio 4918-230S and Swarna

Name of the variety	:	**RP bio 4918-230S**	**Swarna**
Photosynthetic efficiency (P_N) µmol CO_2 m^{-1} s^{-1}	:	23.1	14.58
Chlorophyll a (mg/g)	:	3.48	3.24
Chlorophyll b (mg/g)	:	1.26	1.06
Total Chlorophyll (mg/g)	:	4.86	4.3
Carotinoids (mg/g)	:	0.96	0.91

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10. BH 1146 (IC0415843; INGR19042), a Wheat (*Triticum aestivum*) Germplasm Tolerant to Waterlogging and Resistant to Spot Blotch

G Singh*, BS Tyagi, V Gupta, C Singh, A Gupta and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

**(Email:gysingh@gmail.com)*

Bread wheat (*Triticum aestivum L.*) genotype BH 1146 (Fronteira/Mentana//Ponta Grossa1) was selected and identified following method of breeding as selection from introduction. In a series of field experiments conducted under normal and waterlogged soils during four years (2012-2016), the proposed genotype (BH 1146) was rated as highly tolerant for waterlogged soil conditions. The genotype was identified based on stress tolerance index and lowest percent reduction under water logged conditions as compared to normal conditions (Table 1

& 2). Therefore, BH 1146 will be a potential source to be used as a donor to incorporate genes which will be suitable for higher production and productivity even under heavy rainfall and prolonged water stagnant situations. It is important to mention that the incidence of spot blotch disease of wheat is very high under such wet conditions which also affects the yield as well as grain quality.

Table 1. Selection indices (WL tolerance) and salient agro-morphological features of BH 1146.

Parameters	BH 1146	DBW 88 (best check among top 15 entries)
Stress tolerance index (STI)	0.778	0.746
Harmonic mean (HM)	893	850
Geometric mean productivity (GMP)	896	878
Mean relative performance (MRP)	2.58	2.45
Yield stability index (YSI)	0.837	0.602
Reduction percent	16.3	39.8

Table 2. Performance of BH 1146 and other wheat genotypes under non-waterlogged (NWL) and waterlogged (WL) conditions (unpublished data).

Genotype	Plant height		Days to maturity		Tillers/meter		100 grain weight		Grain yield/plot	
	NWL	WL	NWL	WL	NWL	WL	NWL	WL	NWL	WL
BH 1146	130	120	146	152	121	54	36	31	321	191
DBW 39	98	82	143	149	97	22	36	16	391	104
HD 2967	86	73	141	149	118	22	34	12	360	106
DBW 14	69	61	144	149	35	23	36	23	305	107
DBW 17	83	82	141	147	123	22	33	20	298	145
HD 2009	85	79	142	148	95	22	32	20	309	137
KRL 3-4 (C)	121	108	142	149	196	23	39	31	224	117

Table 3. Reaction of BH 1146 and Sonalika against spot blotch disease across different locations/environments and years

Location/ Environment	Crop season	BH 1146 (Proposed genotype)	Sonalika (Susceptible check)
Coochbehar	2012-13	24	89
	2013-14	13	89
Kalyani	2012-13	24	89
	2013-14	24	89
Karnal	2012-13	13	79
	2013-14	13	79
Poly house (artificial epiphytotics)	2012-13	35	99
	2013-14	24	99

Coincidently, the proposed genotype has also been found as highly resistant to spot blotch disease across locations and years. The recombinant inbred lines (RILs) were developed cross Sonalika (susceptible) /BH 1146 (resistant) and were evaluated along with parents for spot blotch resistance at natural hot spot locations viz; Cooch behar and Kalyani (West Bengal) as well as under field and artificial epiphytotics conditions in poly house for two years. The phenotyping results revealed that BH 1146 possesses high degree of tolerance against spot blotch (Table 3).

The data presented in above two tables clearly established superiority of BH 1146 over susceptible checks and test entries for both the highlighted traits (Waterlogging and spot blotch) and thus proposed for registration as genetic stock. In view of the above merits, BH 1146 could be prospective genotype to be utilized as a donor parent for improving tolerance to waterlogging along with spot blotch resistance for the area spread over 11 million ha of area across northern India.

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11. RWP 2014-18 (IC0630581; INGR19043), a Short Duration Wheat (*Triticum aestivum*) Germplasm with High 1000-grain weight

R Chatrath*, GP Singh, H Khan, S Kumar, CN Mishra, R Kumar, V Gupta, P Jasrotia, PL Kashyap, HM Mamrutha, Om Parkash, M Lal and SS Yadav

ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

**(Email: Ravish.Chatrath@icar.gov.in)*

Delay in wheat sowing in NHZ and NWPZ results in poor tillering and crop growth is generally slow due to low temperature. High temperature during grain filling stage also affects grain yield. For ameliorating these problems, the short duration varieties having plasticity for sowing period, resistance to yellow rust and tolerance to terminal heat stress are required.

RWP 2014-18 was from a cross DBW22/DBW30 through modified pedigree method of breeding. It was evaluated for three years (2015-16, 2016-17 and 2017-18) in Short Duration Screening Nursery (SDSN) of AICW&BIP. Under late sown conditions of NHZ, RWP2014-18 showed consistently superior yield performance over all the checks varieties.

RWP 2014-18 had significantly higher yield compared to all the checks with three year average mean yield of 330 g/plot compared all the checks viz. WR 544 (238 g/plot), HD2932 (227 g/plot), Sonalika, (227 g/plot), and NIAW34 (260g/plot).RWP 2014-18 is early flowering and early maturing genotype with days to heading of 110 which is at par with checks and matures in 152 days after sowing on an average n NHZ. It also has high grains per spike (av. 46) very high 1000 grain weight of 50g under late sown condition.

Table 1. Mean performance of RWP2014-18 in SDSN identified for earliness and high yield in NHZ during three years of evaluation (2015-16, 2016-17 and 2017-18)

Trait	Genotype	Checks			
	RWP 2014-18	Sonalika	WR544	HD2932	NIAW34
Mean Yield (g/plot)	330	227	238	227	260
Heading days	110	107	106	111	109
Maturity days	152	154	152	155	154
Grains/spike	46	37	44		
1000 gr. wt.	50	46	43	46	44

12. IC0529962 (IC0529962; INGR19044), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch (*Bipolaris sorokinina*). Stability for Grain Yield Performance

J Kumari[1], S Kumar[1], N Singh[1], SS Vaish[2], S Das[3], A Gupta[4], MS Saharan[5], JC Rana[6], R Bansal[1], SR Jacob[1], AK Singh[1], Lakshmi Kant[7] and Ashok Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India*
[2]*Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India*
[3]*Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, India*
[4]*ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India*
[5]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India*
[6]*Bioversity International G-1, B-Block, NASC Complex, Pusa Campus, New Delhi, India*
[7]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand, India*
**(Email: jyoti.kumari@icar.gov.in)*

Spot blotch disease leads to significant yield losses ranging from 18 to 50% in warm and humid regions of the world comprising Eastern India, Bangladesh, Terai region of Nepal, Latin America, China and Africa (Saari 1998; Singh *et al*., 2007; Gurung *et al*., 2014). Besides, losses in grain yield, leaf blight causes seed discoloration, shriveled seeds and loss in seed viability. In order to reduce the yield loss, development of wheat varieties with spot blotch resistance is priority of wheat breeders and therefore search of novel donor for spot blotch resistance is urgently required.

Under CRP-agrobiodiversity, one thousand four hundred and eighty-three spring wheat germplasm (*Triticum aestivum* L.) lines comprising Indian as well as exotic lines were screened for resistance to spot blotch disease during winter 2014-15 at hot spot locations *i.e*., Banaras Hindu University, Varanasi and Uttar Banga Krishi Vishwavidyalaya, Cooch Behar. Severity of the disease at different stages beginning from tillering to dough stage was recorded. Twenty-eight accessions were resistant or highly resistant at both locations. These 28 accessions were validated during the winter season (2015-2016). These germplasms were also evaluated at four environments for agronomic traits. Out of 28 accessions, seven (IC564121, IC529684, IC443669, IC443652, IC529962, IC548325 and EC178071-331) were highly resistant across the locations and over the years of study (Kumari *et al*., 2018) and also confirmed under controlled condition during year 2017-18 at Division of Plant Pathology, IARI, New Delhi. These accessions comprised one exotic and six indigenous accessions belonging to Uttarakhand and Haryana. These lines can be deployed for identification of resistance gene and genomics study and also may be used in the breeding germplasm. Out of these, the accession IC529962 had at par mean yield as best check and had wider adaptability across the locations hence can be expedited for direct cultivation or for the development of high yielding and disease resistant cultivars.

Table 1. Spot blotch resistant germplasm with their disease reaction, maturity and yield

Accessions	Name/Source	Grain Yield (g/m row length)	Thousand Grain Weight (g)	Days to Maturity	Mean AUDPC value	DS (High)	DS (Av.)	Category
IC564121	Lal mundiya/ Pauri, Uttarakhand	91.90±7.18	25.78±1.75	122	362±13	23	13	HR
IC529684	VWFW-2299/Almora, Uttarakhand	117.90±11.44	28.30±1.62	127	79±17	23	12	HR
IC443669	PHR-1025/Karnal, Haryana	177.51±12.65	39.81±0.66	119	88±19	23	12	HR
IC443652	HUW-549/Karnal, Haryana	121.23±4.18	39.75±0.71	117	77±16	24	13	HR
IC529962	Almora, Uttarakhand	105.13±6.05	25.78±1.71	121	92±20	12	12	HR
IC548325	Shimla, Himachal Pradesh	161.97±19.06	37.62±0.60	109	174±42	23	12	HR
EC178071-331	Mexico	104.06±8.29	32.73±1.23	114	325±19	24	13	HR
Sonalika	Susceptible check	70±5.46	36.87±1.49	123	2630±22	69	59	S
DBW39	Resistant check	114±6.69	37±1.34	125	583±12	35	24	R

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13. IC0529684 (IC0529684; INGR19045), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch (*Bipolaris sorokinina*)

J Kumari[1], S Kumar[1], N Singh[1], SS Vaish[2], S Das[3], A Gupta[4], MS Saharan[5], JC Rana[6], R Bansal[1], SR Jacob[1], AK Singh[1], Lakshmi Kant[7] and Ashok Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India*
[2]*Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India*
[3]*Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, India*
[4]*ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India*
[5]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India*
[6]*Bioversity International G-1, B-Block, NASC Complex, Pusa Campus, New Delhi, India*
[7]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand, India*
**(Email: jyoti.kumari@icar.gov.in)*

Spot blotch disease leads to significant yield losses ranging from 18 to 50% in warm and humid regions of the world such as Eastern India, Bangladesh, the Terai of Nepal, Latin America, China and Africa (Saari 1998; Singh *et al*., 2007; Gurung *et al*., 2014). Besides, losses in grain yield, leaf blight causes seed discoloration, shrivelled seeds and loss in seed viability. In order to minimize the yield loss and attain yield stability, development of spot blotch resistant wheat variety is priority of wheat breeders and therefore search of novel donor for spot blotch resistance is urgently required.

Under CRP-agrobiodiversity, one thousand four hundred and eighty-three spring wheat germplasm (*Triticum aestivum* L.) lines comprising Indian as well as exotic lines were screened for resistance to spot blotch disease during *Rabi* season 2014-15 at hot spot locations *i.e.*, Banaras Hindu University, Varanasi and Uttar Banga Krishi Vishwavidyalaya, Cooch Behar. Severity of the disease at different stages beginning from tillering to dough stage was recorded. Twenty-eight accessions were resistant or highly resistant at both locations. These 28 accessions were validated during the next *Rabi* season (2015-16). These germplasm were also evaluated at four environments for agronomic traits. Out of 28 accessions, seven (IC564121, IC529684, IC443669, IC443652, IC529962, IC548325 and EC178071-331) were highly resistant across the locations and over the years of study(Kumari *et al*., 2018) and also confirmed under controlled condition during year 2017-18 at Division of Plant Pathology, IARI, New Delhi. These accessions comprised one exotic and six indigenous accessions belonging to Uttarakhand and Haryana. These lines can be deployed for identification of resistance gene and genomics study and also in the breeding germplasm. Out of these, the accession IC529684had at par mean yield as best check and can be used for direct cultivation or for the development of high yielding and disease resistant cultivars.

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Table 1. Spot blotch resistant germplasm with their disease reaction, maturity and yield

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IC564121	Lal mundiya/ Pauri, Uttarakhand	91.90±7.18	25.78±1.75	122	362±13	23	13	HR
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IC443652	HUW-549/Karnal, Haryana	121.23±4.18	39.75±0.71	117	77±16	24	13	HR
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EC178071-331	Mexico	104.06±8.29	32.73±1.23	114	325±19	24	13	HR
Sonalika	Susceptible check	70±5.46	36.87±1.49	123	2630±22	69	59	S
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Singh G, DP Singh, R Chatrath, BS Tyagi, GP Singh, SK Singh, J Shoran (2007a) Combating *Helminthosporium* leaf blight in wheat through resistance breeding. *Indian Journal of Genetics and Breeding*.**67**(3): 293-296.

14. IC290150 (IC0290150; INGR19046), a Wheat (*Triticum aestivum*) Germplasm Resistant to Stem Rust, Leaf Rust and Stripe Rust Pathotypes Prevalent in Indian Condition. Based on Linked Marker Analysis Germplasm has Combination of Different Leaf Rust, Stem Rust, Stripe Rust and Spot Blotch Resistance Genes *Lr*46+, *Lr*67+, *Yr*5, *Yr*15, *Yr*36, *Yr*48, *Sr*13, *Sr*24/*Lr*24, QSb.bhu-2B

S Kumar[1], S Archak[1], RK Tyagi[1], J Kumar[2], VK Vikas[3], AK Sharma[4], J Kumari[1], S\R Jacob[1], R Parimalan[1], AK Singh[1], KC Bansal[1], Ashok Kumar[1], M Sivasamy[3], P Jayaprakash[3], SC Bhardwaj[5], MS Saharan[6], R Gogoi[6], K Singh[1] and GP Singh[4]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India*
[2]*ICAR-National Institute of Biotic Stress Management, Raipur, Chhattisgarh*
[3]*ICAR-IARI Regional Station, Wellington, Tamil Nadu, India*
[4]*ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India*
[5]*ICAR-IIWBR Regional Station, Flowerdale, Shimla, Himachal Pradesh, India*
[6]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India*
[*]*(Email: Sundeep.Kumar@icar.gov.in)*

A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of rust and spot blotch resistance.Genebank accessions comprising three species of wheat–*Triticum aestivum*, *T. durum* and *T. dicoccum* were screened sequentially at multiple disease hotspots, during the 2011-14 crop seasons, carrying only resistant accessions to the next step of evaluation. Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance and profiled using molecular markers. In the primary evaluation, 19,460 accessions were screened at Wellington (TamilNadu), a hotspot for stem and leaf rusts. We identified 4925 accessions to be resistant and these were further evaluated at Gurdaspur (Punjab) a hotspot for stripe rust and Cooch Behar (West Bengal), a hot

spot for spot blotch. A second round evaluation identified 498 accessions potentially resistant to multiple rusts and 868accessions resistant to spot blotch. Evaluation of rust resistant accessions for seedling resistance against seven virulent pathotypes of three rusts under artificial epiphytotic conditions identified 137 accessions with multiple disease resistance. Molecular analysis to identify different combinations of genetic loci imparting resistance to leaf rust, stem rust, stripe rust and spot blotch using linked molecular markers, identified 45 wheat accessions containing resistance genes against all three rusts as well as a QTL for spot blotch resistance. Among identified 45 germplasm lines, germplasm line IC290150 which showed the presence of resistance genes for stem rust, leaf rust and stripe rust and spot blotch *Lr46+, Lr67+, Yr5, Yr15, Yr36, Yr48, Sr13, Sr24/Lr24, QSb.bhu-2B* may be considered promising multiple disease resistant germplasm and could be included in breeding program as parents for developing new durable multiple rust resistant cultivars.

The evaluation detail for the genebank accessions during years 2011-14 is being presented in the diagram mentioned below. In addition, this germplasm line was also found resistant to all three rusts under NBPGR multi-location evaluation programme conducted during 2004-2009 as per Sharma *et al*., 2012.

15. DCMS 1A & 1B (IC0630582 & IC0630583; INGR19047), a New CMS (A) line of Wheat(*Triticum aestivum*) in PBW 343 Background with Diversified CMS Source (CMS1A) along with Maintainer (B) Line

SK Singh*, S Kumar, RP Gangwar and GP Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India
(Email: Sanjay.singh4@icar.gov.in)

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re-oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The proposed genetic stock DCMS1A was developed using MTSA 2A based CMS line CMS1A (MTSA 2A/BCN) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set (Virmani *et al*., 1997).

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during 4 consecutive crop seasons of 2014-15, 2015-16, 2016-17 and 2017-18. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage (Virmani *et al*., 1997; Aruna *et al*., 2013). The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new

CMS line DCMS 1A (Table1).

In hybrid development programme based on three line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 1A was ranged from 95-100 days with mean of 98 days whereas average plant height was 95 cm with range of 91-100 cm. Compared to this, the maintainer line DCMS 1B (PBW343) showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line. The results indicated improvement in spike length and spikelet number per spike in DCMS 1A as compared to the maintainer line. The maturity days was more in the DCMS 1A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 1. Performance of DCMS 1A and its maintainer for quantitative traits

Year	DCMS1A (CMS-A line)						DCMS 1B (PBW 343: Maintainer-B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2014-15	100	100	93	12	23	148	100	96	10	19	148
2015-16	100	99	94	11	23	144	100	96	10	23	138
2016-17	100	95	100	11	21	143	95	101	11	19	139
2017-18	100	96	91	12	23	136	95	92	10	19	136
Mean	100	98	95	11	23	143	98	96	10	20	140

Table 2. Performance of DCMS 1A and its maintainer DCMS 1B for morphological traits

Traits	DCMS 1A	DCMS 1B (PBW 343)
Coleoptile colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber

In addition, few morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 343 (Table.2).

It may be concluded that the proposed genetic stock DCMS 1A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity

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16. DCMS 2A & 2B (IC0630584 & IC0630585; INGR19048), a New CMS (A) line of Wheat (*Triticum aestivum*) in PBW 343 Background with Diversified CMS Source (CMS 10A) along with Maintainer (B) Line

SK Singh*, S Kumar, RP Gangwar and GP Singh

ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India

**(Email: Sanjay.singh4@icar.gov.in)*

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re-oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum*

timopheevii based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The proposed genetic stock DCMS 2A was developed using CHUAN 18A based CMS line CMS10A (CHUAN 18A/CHUAN 18B//7*KAUZ/HEVO) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated.

:HTable 1. Performance of DCMS 2A and its maintainer for quantitative traits

Year	DCMS2A (CMS- A line)						DCMS 2B (PBW 343: Maintainer- B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2014-15	100	100	90	12	21	148	100	96	12	19	147
2015-16	100	101	91	9	21	143	100	97	10	23	138
2016-17	100	95	101	13	23	143	95	102	11	19	139
2017-18	100	97	88	10	21	136	95	87	9	19	137
Mean	100	98	93	11	22	143	98	96	11	20	140

In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during 4 consecutive crop seasons of 2014-15, 2015-16, 2016-17and 2017-18. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 2A (Table 1).

In hybrid development programme based on three line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 2A was ranged from 95-101 days with mean of 98 days whereas average plant height was 93 cm with range of 88-101 cm. Compared to this, the maintainer line DCMS 2B showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line. The results indicated improvement in spikelet number per spike in DCMS 2A as compared to the maintainer line. The maturity days was more in the DCMS 2A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

In addition, few morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 343(Table 2).

Table 2. Performance of DCMS 2A and its maintainer DCMS 2B for morphological traits

Traits	DCMS 2A&2B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	white
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

It may be concluded that the proposed genetic stock DCMS 2A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

17. DCMS 4A & 4B (IC0630586 & IC0630587; INGR19049), a New CMS (A) Line of Wheat (*Triticum aestivum*) along with Maintainer (B) Line

SK Singh*, S Kumar, RP Gangwar and GP Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India
(Email: Sanjay.singh4@icar.gov.in)

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re-oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The proposed genetic stock DCMS 4A was developed using CHUAN 18A based CMS line CMS12A (CHUAN18A/CHUAN18B/3/7*SERI/NKT//2*KAUZ) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during crop seasons 2013-14, 2014-15, 2015-16, 2016-17 and 2017-18. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 4A (Table 1).

Table.1. Performance of DCMS 4A and its maintainer for quantitative traits

Year	DCMS 4A (CMS- A line)						DCMS 4B (PBW 343: Maintainer- B line)				
	Male sterility (%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	101	91	-	-	-	99	95	-	-	-
2014-15	100	100	100	12	21	148	100	98	11	19	147
2015-16	100	101	101	12	25	142	100	99	10	23	138
2016-17	100	95	92	12	21	142	95	96	11	19	139
2017-18	100	97	96	12	21	138	96	93	11	23	136
Mean	100	99	96	12	22	143	98	96	11	21	140

In hybrid development programme based on three line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 4A was ranged from 95-

101 days with mean of 99 days whereas average plant height was 96 cm with range of 91-101 cm. Compared to this, the maintainer line DCMS 4B showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line DCMS 4A. The maturity days was more in the DCMS 4A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

In addition, few morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 343 (Table 2).

Table 2. Performance of DCMS 4A and its maintainer DCMS 4B for morphological traits

Traits	DCMS 4A &4B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	White
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

It may be concluded that the proposed genetic stock DCMS 4A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

18. DCMS 5A & 5B (IC0630588 & IC0630589; INGR19050), a New CMS (A) line of Wheat (*Triticum aestivum*) along with maintainer (B) line

SK Singh*, S Kumar, RP Gangwar and GP Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India
(Email: Sanjay.singh4@icar.gov.in)

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re-oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The proposed genetic stock DCMS 5A was developed using CHUAN 18A based CMS line CMS13A (CHUAN 18A/CHUAN 18B//7*CMH80A542/CNO79) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during crop seasons 2013-14, 2014-15, 2015-16, 2016-17 and 2017-18. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 5A (Table 1).

In hybrid development programme based on three line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 5A was ranged from 95-104 days with mean of 99 days whereas average plant height was 98 cm with range of 96-102 cm. Compared to this, the maintainer line DCMS 5B showed average days to heading of 100 days and plant height of 99 cm which is in tune to CMS line DCMS 5A. The results indicated improvement in spike length and spikelet number per spike in DCMS 5A as compared to the maintainer line. The maturity days was more in the DCMS 5A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 1. Performance of DCMS 5A and its maintainer for quantitative traits

Year	DCMS 5A (CMS- A line)						DCMS 5B (PBW 343: Maintainer- B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	104	96	-	-	-	106	101	-	-	-
2014-15	100	102	97	12	21	151	100	100	11	19	148
2015-16	100	101	98	11	23	143	104	101	8	19	138
2016-17	100	95	97	11	21	144	95	98	11	23	139
2017-18	100	95	102	14	25	138	95	97	9	19	139
Mean	100	99	98	12	23	144	100	99	10	20	141

Table 2. Performance of DCMS 5A and its maintainer DCMS 5B for morphological traits

Traits	DCMS 5A	DCMS 5B (PBW 343)
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber

In addition, few morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 343(Table.2).

It may be concluded that the proposed genetic stock DCMS 5A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

19. DCMS 6A & 6B (IC0630590 & IC0630591; INGR19051), a New CMS Line of Wheat (*Triticum aestivum*) in PBW 343 Background along with maintainer Line

SK Singh*, S Kumar, RP Gangwar and GP Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India
(Email:Sanjay.singh4@icar.gov.in)

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re-oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The proposed genetic stock DCMS 6A was developed using CHUAN 18A based CMS line CMS17A (CHUAN18A/3/7*KAUZ*2/MNV//KAUZ) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during 4 consecutive crop seasons of 2013-14, 2014-15, 2015-16 and 2016-17. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 6A (Table 1).

In hybrid development programme based on three line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 6A was ranged from 95-104 days with mean of 99 days whereas average plant height was 96 cm with range of 94-98 cm. Compared to this, the maintainer line DCMS 6B showed average days to heading of 100 days and plant height of 99 cm which is in tune to CMS line DCMS 6A. The results indicated improvement in spikelet number per spike in DCMS 6A as compared to the maintainer line. The maturity days was more in the DCMS 6A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 1. Performance of DCMS 6A and its maintainer for quantitative traits

	DCMS 6A (CMS- A line)						DCMS 6B (PBW 343: Maintainer- B line)				
Year	Male sterility (%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	104	96	-	-	-	106	101	-	-	-
2014-15	100	102	97	12	21	151	100	100	11	19	148
2015-16	100	101	98	11	23	143	104	101	8	19	138
2016-17	100	95	97	11	21	144	95	98	11	23	139
2017-18	100	95	94	11	21	137	95	95	10	19	137
Mean	100	99	96	11	22	144	100	99	10	20	141

Table 2. Performance of DCMS 6A and its maintainer DCMS 6B for morphological trait

Traits	DCMS 6A& DCMS 6B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	White
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

In addition, few morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 343(Table.2).

It may be concluded that the proposed genetic stock DCMS 6A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

20. QLD112 (IC0632081; INGR19052), a Wheat(*Triticum aestivum*) Germplasm with Soft Grain

K Gopalareddy*, BS Tyagi, Venkatesh K, SK Singh, Satish Kumar, CN Mishra, Arun Gupta, Vanita Pandey, Gyanendra Singh and GP Singh

ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India

**(Email:gopalareddy.k@icar.gov.in)*

Grain hardness is an important trait in wheat quality with a profound effect on milling, baking and end-use qualities of wheat. It is common to differentiate soft and hard wheat in the world trade for product specific utility. Soft wheat is more friable, requires less energy to mill, and produces flours and meals with finer particles and lower starch damage, which are suitable for cake and biscuit production. Soft grain textured wheat produces tender and largerbiscuits.

QLD112 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 36th IBWSN364/36th IBWSN172//VL908 (Pedigree: BABAX/LR42//BABAX/5/ BOW//BUC/ BUL/3/WEAVER/4/STAR/6/ VL908). The genotype was evaluated at 4 centers in Quality Component and Wheat Biofortification Nursery (QCWBN) during 2018-19. QLD112 was found to be superior with 15 grain hardness index to all the testing genotypes and best soft grain check variety HS490 (30: grain hardness index) (Table 1). QLD112 recorded the lowest grain hardness index in all the tested centers compared to the best check variety (HS490) for low grain index. QLD112 recorded lowest grain hardness index of 16, 15, 15 and 15, respectively at Delhi, Kanpur, Vijapur, and Pune centres. Whereas, the check variety HS490 recorded 27, 24, 33, and 37, respectively at Delhi, Kanpur, Vijapur, and Pune centres. QLD112 was 100% superior over check variety HS490. Low grain hardness index is very important factor to obtain high spread factor of biscuit and better biscuit quality. Thus, QLD112 would be a potential source to be utilized in future breeding programs to develop bread wheat varieties suitable for better biscuit making.

Table1. Grain hardness index of QLD112 during 2018-19 as compared to the best available soft grain check variety HS490

Zone	Location	Proposed Genotype	Best Check Variety
		QLD84	HS490
NWPZ	Delhi	16	27
NEPZ	Kanpur	15	24
CZ	Vijapur	15	33
PZ	Pune	15	37
Mean (National)		15	30
% Superiority of QLD 112 over best Soft grain check variety		100%	

21. QLD102 (IC0632082; INGR19053), a Wheat (*Triticum aestivum*) Germplasm with High Sedimentation Value

K Gopalareddy, BS Tyagi, Venkatesh K, H Khan, AK Sharma, V Gupta, C Singh, G Singh and GP Singh

ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India

**(Email: gopalareddy.k@icar.gov.in)*

Sedimentation value measures the strength of gluten and determines the wheat for specific utility. Weak, medium and strong gluten as measured by low, medium and high sedimentation value are best suited for biscuit, chapatti and bread making, respectively.

QLD102 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 36thIBWSN172/PBW502/3/PBW533//H9811/WH542 (Pedigree: BOW//BUC/BUL/3/ WEAVER/4/STAR/5/ PBW502/6/PBW533//H9811/WH542). The genotype was evaluated at 15 centers in Quality Component Screening Nursery (QCSN) during 2017-18. QLD102 was found to be superior with67.2 sedimentation value to the best check variety UP2672 (63.2) and all other check varieties C306 (46.4), HS490 (44.5), and NIAW1415 (49.7) (Table 1). QLD102 recorded high sedimentation value compare to all the tested check varieties at all the centers. QLD102 was 6.4%, 44.8%, 51.0%, and 35.3%

Table1. Grain hardness index of QLD102 during 2017-18 as compared to the check varieties UP2672, C306, HS490, and NIAW1415

Zone	Location	Proposed Genotype	Best Check	Other check varieties		
		QLD102	UP2672	C306	HS490	NIAW1415
NWPZ	Ludhiana	68.8	67.2	46.0	40.7	50.0
	Durgapura	69.7	64.8	43.3	51.1	51.7
	Delhi	69.7	63.1	44.7	43.9	54.8
	Pantnagar	67.2	62.7	42.7	41.3	46.8
	Karnal	70.1	70.1	46.2	45.8	53.5
	Hisar	54.1	57.4	42.5	39.7	44.9
NEPZ	Kanpur	71.3	64.0	46.4	47.8	51.5
	Sabour	56.6	57.4	45.1	40.5	47.8
CZ	Junagadh	69.7	64.2	57.0	47.2	49.0
	Vijapur	66.5	67.0	51.0	46.0	47.0
	Indore	66.8	65.6	46.4	42.7	50.7
	Powarkheda	70.5	58.8	45.4	44.2	47.4
PZ	Pune	71.3	60.1	45.4	38.0	48.0
	Dharwad	66.0	60.7	47.6	56.0	53.5
	Niphad	70.1	65	46.8	42.7	48.6
	Mean	67.2	63.2	46.4	44.5	49.7
% Superiority of QLD 102 over check varieties			6.4%	44.8%	51.0%	35.3%

superior over the check varieties UP2672, C306, HS490, and NIAW1415, respectively. Sedimentation value is being used as a screening tool in wheat quality breeding programs globally to develop product specific wheat cultivars.

Thus, QLD102 would be a potential source to be utilized in future breeding programs to develop product specific wheat varieties.

22. IIWBR Phy 1 (IC0632600; INGR19054), a Wheat (*Triticum aestivum*) Germplasm with High phytase Level in the Background of PBW 502. Low Phytic Acid

Sewa Ram*, S Narwal, B Singh, T Khandale, Om Prakash Gupta, V Pandey and GP Singh
ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana, India
**(Email:sewa.ram@icar.gov.in)*

Though, it contains significant amount of essential nutrients such as proteins, minerals and vitamins; bioavailability of minerals to human beings is reduced because of presence of anti-nutritional factors such as phytic acid in wheat grains. Degradation of phytic acid by phytase enzyme present in the food can lead to enhanced bioavailability of Fe and Zn. Though, our earlier study reported 3.4 fold differences in phytase level among wheat varieties developed in India (284 FTU/Kg to 962 FTU/Kg with the mean value of 516 FTU/Kg) (Ram *et al* 2011), there was further need to expend diversity in phytase and phytic acid levels. Therefore, in the present investigation, mutant lines were generated using EMS mutagenesis in the background of wheat variety PBW 502 grown in North Western plains Zone in India and evaluated for phytase levels using microlevel tests developed in our laboratory.

Mutant lines were developed by treating PBW 502 seeds (around 3000) with 0.75% Ethyl Methyl Sulphonate overnight and followed by sowing in the field during 2008-09. The M1 seeds were sown during 2009-10 and more than 1000 plants were generated. 800 lines were advanced into higher generations using single seed descent method and evaluated for phytase levels during 2014-15, 2015-16, 2016-2017 and 2017-18. Mutant lines exhibited phytase levels ranging from 261 to 2578 with the average value of 1273

Table 1. Characteristics of PBW 502 and Mutant line (IIWBR Phy1) for Phytase levels (Average of 4 years data).

	Phytase level (FTU/Kg)	Phytic acid (%)	Yield
PBW 502	720 FTU/Kg	1.32	56.3 Q/Hect
Mutant line (IIWBRPhy1)	2400 FTU/Kg	0.92	57.5 Q/Hect

FTU/kg while PBW 502 exhibited phytase activity 720 FTU/kg. Ten Mutant lines were identified for very high phytase levels (>2000 FTU/kg) and sound grain characteristics. One of the mutants had high phytase level (2400 FTU/kg) and also high yield and good grain characteristics suitable for use in breeding. In addition it has low phytic acid content (Table 1). Since phytase levels is a trait which is mainly governed by genetics and less influenced by the environment (Ram *et al*; 2011), the genotype developed can be used in crossing programme for enhancing phytase levels for improving bioavailability of micronutrients to human beings.

23. IC113045/ F-13/ (IC0113045; INGR19055), an Early maturing, Extra Dwarf Barley (*Hordeum vulgare*) Germplasm in Six-Rowed Hulled Genetic Background

V Kaur*, J Kumari, SR Jacob and Ashok Kumar

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

**(Email: vikender.kaur@icar.gov.in)*

Barley (*H. vulgare* L; 2n=14) is one of the oldest cultivated cereal and has been grown in India since ancient times. Barley is an important feed and fodder crop, besides it provides essential raw material for malting and brewing industries. Presently, it is the fourth most important cereal crop worldwide after maize, rice and wheat in terms of production. In India, it is cultivated on residual moisture by resource poor farmers under low input conditions and about 44% area under barley cultivation is rain-fed. Therefore, identification of trait specific accessions through evaluation of germplasm collections is a pre-requisite to diversify the parental material for sustained and continued increase in yield and quality of this crop. In this context, 4968 accessions of barley germplasm from National Gene Bank were characterised for agro-morphological traits at ICAR-NBPGR during the year 2016-17 and the trait specific accessions were validated in subsequent years (2017-19). Accession IC113045, exhibited dwarf plant habit in six-rowed and hulled genetic background with average plant height of 44.39 cm compared to recent check varieties of NWPZ namely BH959 (94.84 cm) and BH902 (110.04 cm) (Table 1). Dwarf plant height is highly desirable as barley is a lodging prone crop. In addition, it also showed early maturity in 117 days compared to checks BH902 (130 days) and BH959 (128 days). Early types are essential in most barley producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Average days to spike emergence and 100-grain weight for IC113045 were 56 and 3.34 g, respectively. The grains are hulled and white in colour.

Table 1. Year wise data of plant height in barley accession IC113045

Year	Field evaluation Location	Plant Height (cm)		
		IC113045	Check var.1 (BH959)	Check var. 2 (BH902)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	45.96	91.54	106.83
2017-18	ICAR-NBPGR, New Delhi	41.33	90.30	105.80
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	42.95	103.22	119.29
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	47.33	94.32	108.25
Mean		44.39**	94.84	110.04

**significantly superior at $P_{0.001.}$

24. IC0113052 (IC0113052; INGR19056), a Long spiked with more number of grains/spike Barley (*Hordeum vulgare*) Germplasm in Two-Rowed and Hulless Genetic Background

V Kaur*, J Kumari, SR Jacob and Ashok Kumar
ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India.
**(Email: vikender.kaur@icar.gov.in)*

Once regarded as poor man's food and fodder cereal, barley has gained importance again owing to its increased use in multigrain blends, health tonics, malting and brewing industries. The new challenges for production in the era of climate change envisage involvement of diverse germplasm for further exploitation in breeding. In this context, 4968 accessions of barley germplasm from National Gene Bank were characterised for agro-morphological traits at ICAR-NBPGR during the year 2016-17 and the trait specific accessions were validated in subsequent years (2017-19). Accession IC113052, a two-rowed barley germplasm exhibited long spikes with average spike length of 13.74 cm compared to recent two-rowed check variety DWRB101 (7.82 cm) (Table 1). In addition, grains/spike, an important yield contributing trait were higher in IC113052 (32.44) compared to check DWRB101 (26.93), while plant height was lower (87.57 cm) which is desirable as barley is a lodging prone crop. Average days to spike emergence and maturity for IC113052 were 88 and 122, respectively. The grains are hulless and white in colour. Being hulless, this germplasm accession can be explored for consumption as food grain.

Table 1. Year wise data of spike length in barley accession IC113052

Year	Field Evaluation Location	Spike length (cm)	
		IC113052	Check var. (DWRB101)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	13.23	8.00
2017-18	ICAR-NBPGR farm, IARI, New Delhi	13.50	7.46
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	13.80	7.97
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	14.44	7.83
Mean		13.74**	7.82

**significantly superior at $P_{0.001.}$

25. EC667420 (EC667420; INGR19057) an Early Maturing Hooded Barley (*Hordeum vulgare*) Germplasm in Six-Rowed Hulled Genetic Background

V Kaur*, J Kumari, SR Jacob and Ashok Kumar
ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India.
**(Email: vikender.kaur@icar.gov.in)*

Barley (*H. vulgare* L; 2n=14) is an important feed and fodder crop in India. In India, it is cultivated on residual moisture by resource poor farmers under rain-fed conditions. Hence, breeding for early maturity is a main breeding target. In this context, *a*ccession EC667420, a six-rowed barley germplasm was recorded showing early maturity with average 117.50 days to attain maturity compared to check variety BH902 (131.25 days) (Table 1). Early types are essential in most barley producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Furthermore, the awn type was recorded as sessile hoods in this accession. The hooded trait is desirable for fodder purpose barley as absence of awns allow more palatability and lip smacking in animals while the injurious awn reduces the feed value of straw for livestock (Takahashi, 1955; Yuo *et al.*, 2012). In addition, spike length was more in

Table 1. Year wise data of days to attain physiological maturity (DPM) in barley accession EC667420

Year	Field evaluation Location	DPM (days)	
		EC667420	Check var. (BH902)
2014-15	ICAR-NBPGR farm, Issapur, New Delhi	120	128
2015-16	ICAR-NBPGR farm, Issapur, New Delhi	115	132
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	114	136
2017-18	ICAR-NBPGR farm, IARI, New Delhi	121	129
Mean		117.50**	131.25

**significantly superior at $P_{0.001.}$

EC667420 (11.27 cm) compared to check BH902 (8.22 cm).Average days to spike emergence and 100-grain weight for EC667420 were 85.5 and 4.38 g, respectively. The grains are hulled and white in colour.

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26. EC492301 (EC492301; INGR19058) a Barley (*Hordeum vulgare*) Germplasm with Awnless Spikes

V Kaur*, J Kumari, SR Jacob and Ashok Kumar

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

**(Email: vikender.kaur@icar.gov.in)*

The accession EC492301 has been identified for awnless spikes, which is a rare trait in barley as inflorescences are usually characterized by stiff bristles/awns in this crop. Under agricultural conditions, the long and stiff awn has persisted as a nuisance to farmers because they hinder manual harvesting and storage. More importantly, the injurious awn reduces the feed value of straw for livestock (Takahashi, 1955; Yuo *et al*., 2012). Thus awnless trait is desirable for fodder purpose barley as absence of awns allow more palatability and lip smacking in animals. Awnless forms (*lks1) reported as natural mutants in Himalayas are largely unknown*, *however* several natural mutant alleles of *lks2* (The short awn 2) represented as short awned or awnleted are present in the East Asian barley gene pool, including India, Nepal, China, Korea, and Japan (Yuo *et al*., 2012). During domestication and subsequent varietal differentiation, selection efforts were done to reduce awn length however, despite such selection pressure; most barley has retained rather long awns. Hence, the awnless trait has breeding value to develop awnless varieties. The close linkage between the genes V (awned) and Lk (awnless) is the main reason behind the scarcity of awnless forms reported in barley and mainly awned varieties are grown for production purpose (Tsvetkov and Tsvetkov, 2007). The molecular basis of awn elongation in grasses is still unclear. Barley provides excellent materials for such studies because many major genes subject to simple Mendelian inheritance are known to affect awn length in this species (Lundqvist and Franckowiack, 2003). In this perspective, the awnless forms possess potential to study the underlying genetic base of this rare trait. Moreover, EC492301 is the only accession characterised with awnless spikes among the entire assembly of germplasm (~8000 acc.) conserved at National Gene Bank. Regarding other agro-botanic features of EC492310, it is a six-rowed barley exhibiting prostrate growth habit. The spike length was recorded to be 6.57 cm, plant height was 105.82 cm. Average days to spike emergence, and days to attain physiological maturity were 107 and 141, respectively. The grains are hulled and white in colour.

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27. IC542197 (IC542197; INGR19059), an Early Maturing Barley (*Hordeum vulgare*) Germplasm in Two-Rowed and Huskless Genetic Background

V Kaur*, J Kumari, SR Jacob and Ashok Kumar

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

**(Email: vikender.kaur@icar.gov.in)*

Early types are essential in most barley producing areas in India to escape drought and terminal heat. In this regard, barley germplasm accession IC542197 was identified showing early maturity in 109 days in two-rowed and hulless genetic background compared to two-rowed cultivar DWRB101 (129 days) and hulless variety BHS352 (125 days) used as checks (Table 1). The hulless grain trait in two-rowed barley is scarce as mostly hulless grain type is associated with six-rowed spike structure. In addition, hulless barley is an important food crop in the high altitude regions of J&K (cold desert of Leh-Ladakh), hilly Uttrakhand and Himachal Pradesh, where it is consumed by local people in the form of *sattu* as well as for the preparation of local beverage. Mainly hulless barley is grown and consumed for food purpose as absence of hulls require little or no processing after harvesting and can be rolled or ground into flour directly. In addition to early maturity, the hundred grain weight, an important yield contributing trait was higher (4.99 g) for IC542197 in comparison to checks, BHS352 (3.01 g) and DWRB101 (4.82 g).Average spike length and plant height for IC542197 was 9.48 cm and 104.60 cm, respectively. The grains are white in colour.

Table 1. Year wise data of days to attain physiological maturity (DPM) in barley accession IC542197

Year	Field Evaluation Location	DPM (days)		
		IC542197	Check var.1 (BHS352)	Check var. 2 (DWRB101)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	104	125	129
2017-18	ICAR-NBPGR farm, IARI, New Delhi	110	120	123
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	108	127	130
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	113	124	128
Mean		109**	124	128

**significantly superior at $P_{0.001.}$

28. S 614-13/SPV2263 (IC0632083; INGR19060), a Sorghum (*Sorghum bicolor*) Germplasm Resistant to Anthracanose and IVDMD 56%

P Kumari[1*], SK Pahuja[1], S Arya[1], UN Joshi[1], DS Phogat[1], C Aruna[2] and Vilas A Tonapi[2]
[1]*CCS Haryana Agricultural University, Hisar-125004, Haryana, India*
[2]*Indian Institute of Millets Research, Hyderabad-500030, Telangana, India*
[*]*(Email: pummy.hau@gmail.com)*

Forage quality is an important selection criterion in fodder crops especially in case of forage sorghum and IVDMD% is one of the most important quality components in forage sorghum. The genotype S 614-13 was developed by pedigree selection method from HJ 513 (Non sweet forage sorghum variety) x IS 2389-1 p29-1-3-4 and was selfed up to F6 generation. This germplasm is tall having 260 cm plant height, sweet, 9.5% TSS with good foliage and 56 % IVDMD (Table: 1).This genotype has high IVDMD and shows resistance against anthracnose (Table: 2) and other foliar diseases. This has also shown promise for shoot fly resistance and has moderate multiple leaf disease resistance. The genotype S 614-13 with a combination of improved quality traits and multiple foliar disease resistance may be of interest to forage sorghum breeder aiming at improving IVDMD of forage sorghum along with foliar disease resistance especially anthracnose.

Table 1. Performance of S 614-13 for IVDMD % in AICRP Trials

	IVDMD%				
Year of Testing	Proposed Genotype	Check I	Check II	CD@ 5%	% increase over best check
	SPV 2263 (S 614-13)	CSV21F	HC 308		
2013-14	56.0	52.0	52.0	4.0	7.69 %

Table 2. Performance of S 614-13 for anthracnose in AICRP Trials

	Anthracnose resistance				
Year of Testing	Proposed Genotype	Resistant Check I	Resistant Check (Local) II	CD@ 5%	% increase over check
	SPV 2263 (S 614-13)	Pant Chari-5	Local Check		
2013-14	3.0	4.7	4.1	1.3	36% less disease attack as compared to resistant check over the locations

29. IG 96-401 (EC397366; INGR19061), a Buffel grass (*Cenchrus ciliaris*) Germplasm Rich in sugar (more than 7%). Suitable for Ensiling (Silage Preparation) and Prostrate Growth Habit.

S Singh[*], T Singh, KK Singh, MM Das, MK Srivastava, SK Mahanta, AK Misra, R Katiyar and PK Ghosh
ICAR-Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh, India
[*]*(Email: singh.sultan@rediffmail.com)*

Buffel grass *(Cenchrus ciliaris)* is a potential grass for pasture plantation due to ease of establishment and forage production in harsh environments (Cox *et al*., 1988) and occupies the major component of *Dichanthium–Cenchrus–Lasiurus* grass cover of India (Dabadghao and Shankarnarayan, 1973).Active growth of *C. ciliaris* occurs mainly during monsoon months which results in surplus availability of green fodder. These surplus green fodder need to be conserved for feeding livestock during lean periods. But low sugar content (2-4%) is the main limitation for ensiling tropical grasses as a minimum of 7-8% of sugar is required for bacteria to initiate the ensiling process (McDonald *et al*., 1991).

A total 108 accessions of *Cenchrus* were evaluated for water soluble carbohydrates (WSC) content and biomass production potential for two consecutive

years at ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. After two years evaluation 14 accessions (IG99-124, IG97-379, IG-97-377, IG97-403, IG96-358, IG96-87, IG97-75, IG97-378, IG96-401, IG96-414, IG96-3108, IG96-96, IG96-89 and IG96-50) having WSC>7%were selected and further tested for ensiling. Selected accessions were further multiplied and the silage was prepared from IG96-96, IG96-358, IG96-50, IG96-401, IG96-403 and natural *Cenchrus*. The silage prepared from IG 96-401was of good quality (Table 1)as evident from their pH (4.06) and lactic acid values (0.95% fresh basis). Growth habit of IG96-401 is prostrate with medium plant height (82.3cm) and days to 50% flowering (68 days), tillers number per plant were about 79.2 and leaf colour were normal green.

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-401 having adequate sugar to initiate ensiling. The IG96-401 may be further propagated in grazing lands and common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

Table 1. Sugar contents and silage quality of *C. ciliaris* genotype IG96-401*

Parameters	IG96-401
Sugar %	1st cut 7.7 2nd cut 7.2
DM%	33.88
pH	4.06
Lactic acid % (Fresh basis)	0.95
Lactic acid % (Dry matter basis)	2.81
NH3- N g/Kg (Fresh basis)	0.39
NH3- N/Kg (Dry matter basis)	1.16
Total -N g/Kg (Fresh basis)	1.68
TN g/kg (Dry matter basis)	4.95
NH3- N % Total nitrogen	23.65

*Values are mean of 4-5 observations

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30. IG 96-50 (IC0630758; INGR19062), a Buffel grass (*Cenchrus ciliaris*) Germplasm with High Water Soluble Carbohydrate. Good for Silage Preparation. Leaf Colour Pale-Low Chlorophyll Content

S Singh*, T Singh, KK Singh, MM Das, MK Srivastava, SK Mahanta, AK Misra, R Katiyar and PK Ghosh
ICAR-Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh, India
(Email: singh.sultan@rediffmail.com)

Cenchrus ciliar ensiling. For large scale silage production selected lines were multiplied and the silage was prepared from IG96-96, IG96-358, IG96-50, IG96-401, IG96-403 and natural *Cenchrus*. The silage prepared from IG 96-50 was of good quality (Table 1) as evident from their pH (4.61) and lactic acid values (0.47 % fresh basis). Growth habit of IG96-50 is semiprostrate with tall plant height (116 cm) and late days to 50% flowering (90 days), tillers numbers per plant were low (about 27) and unique pale leaf colour.

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-50 having adequate sugar to initiate ensiling. The IG96-50may be further propagated in grazing lands and common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

Table 1. Sugar contents, fodder yield and ensiling properties of *C ciliaris* genotype IG96-50*

Parameters	IG 96-50
Sugar %	1st cut 8.4 2nd cut 7.3
GFY (t/ha)	96.8
DMY (t/ha)	23.3
DM%	27.37
pH	4.61
Lactic acid % (Fresh basis)	0.47
Lactic acid % (Dry matter basis)	1.71
NH3- N g/Kg (Fresh basis)	0.50
NH3- N/Kg (Dry matter basis)	1.83
Total -N g/Kg (Fresh basis)	1.76
TN g/kg (Dry matter basis)	6.43
NH3- N % Total nitrogen	28.77

* Values are mean of 4-5 observations

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31. IG 96-96 (IC0630759; INGR19063), a Buffel grass (*Cenchrus ciliaris*) Germplasm with High Water Soluble Carbohydrate. Good for Silage Preparation.

S Singh, T Singh, KK Singh, MM Das, MK Srivastava, SK Mahanta, AK Misra, R Katiyar and PK Ghosh
ICAR-Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh, India
**(Email: singh.sultan@rediffmail.com)*

Cenchrus ciliaris is a potential grass for pasture plantation due to ease of establishment and forage production in harsh environments (Cox *et al*., 1988) and occupies the major component of *Dichanthium–Cenchrus–Lasiurus* grass cover of India (Dabadghao and Shankarnarayan, 1973). Active growth of *C. ciliaris* occurs mainly during monsoon months which results in surplus availability of fodder. These surplus monsoon grasses need to be conserved for feeding livestock during lean periods. Woolford (1984) mentioned that good quality grass silage can be obtained by ensiling grass that contains WSC ranged from 60 to 80 g kg-1 DM.

Total 108 lines of *Cenchrus* were evaluated for water soluble carbohydrate (WSC) content and fodder yield production for two consecutive years at ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. After two years evaluation 14 accessions (IG99-124, IG97-379, IG-97-377, IG97-403, IG96-358, IG96-87, IG97-75, IG97-378, IG96-401, IG96-414, IG96-3108, IG96-96, IG96-89 and IG96-50) having more than 7% WSC were selected. Selected accessions were further multiplied for ensiling with natural *Cenchrus*. The silage prepared from IG96-96 was of good quality (Table 1) as evident from their pH (4.97) and lactic acid value (0.35 % fresh basis). Growth habit of IG96-96 is erect with short plant height (42.8cm) and early days to 50% flowering (55 days), tillers number per plant were about 65 and leaf colour was dark green.

Table 1. Sugar contents, fodder yield and ensiling properties of *C. ciliaris* genotype IG96-96*

Parameters	IG 96-96
Sugar %	1st cut 9.79 2nd cut 8.08
GFY (t/ha)	91.3
DMY (t/ha)	18.2
DM%	25.80
pH	4.97
Lactic acid % (Fresh basis)	0.35
Lactic acid % (Dry matter basis)	1.37
NH_3-N g/Kg (Fresh basis)	0.71
NH_3-N/Kg (Dry matter basis)	2.74
Total-N g/Kg (Fresh basis)	2.00
TN g/kg (Dry matter basis)	7.75
NH_3-N % Total nitrogen	35.42

*Values are mean of 4-5 observations

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-96 having adequate sugar to initiate ensiling. The IG96-96 may be further propagated in grazing lands and

common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

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32. SM2254-8 (IC0632070; INGR19064), an Intergeneric (Sorghum x Maize cross) Forage Sorghum (*Sorghum bicolor*) with Low HCN. High IVDMD

KBRS Visrada*, P Sanjana Reddy, R Venkateswarlu, Aruna C and VA Tonapi
ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad, Telangana, India
**(Email: visarada@millets.res.in)*

Crop improvement in sorghum has reached a plateau in realizing yield gains and further improvement requires introduction of variation through other methods like wide hybridization. Distant hybridization between incompatible species introduces *de novo* variation that can be used in crop improvement programs (Wang *et al.*, 2009). An attempt was made at the ICAR-Indian Institute of Millets Research, Hyderabad, to cross the superior genotypes from sorghum with maize parental lines through pollen treatment. There was wide phenotypic variation in F_2 generation derived from the two crosses (DSR, 2010, 2013). The variants were advanced through selection for specific traits and evaluated in the field trials. Forage segregates from the above were studied with an objective to determine their performance for forage traits *vis* a *vis* standard checks as well as to determine the association of the traits with forage yield. One of the promising forage lines is SM2254-8, having low HCN and high digestibility. This line is derived from the pollination of sorghum parental line, the 126A, pollinated with the maize line, the CM208.

Morpho-agronomic characteristics: The proposed genotype, SM2254-8, is a forage pre-breeding material. The plants are tall, have multiple tillers. Panicles are loose and long. It has low HCN content and high *in vitro* dry matter digestibility (Table 1). HCN content (54.1 ppm) is lower as compared to 71.3 ppm in SSG59-3 and 60.6 ppm in CSV21F and higher *in vitro* dry matter digestibility (IVDMD) 57.0% against checks SSG59-3 (53.0%) CSV21F (52.3%). It is on par with checks for rest of the traits such as green fodder yield of 527.0 q/ha compared to checks (SSG59-3 571.3q/ha, and CSV22F 576.0q/ha), total soluble sugars 4.5% compared to checks (5.0 and 4.5) (Visarada *et al.*, 2017).

Associated characters and cultivation practices: Low Low HCN content and high in vitro dry matter digestibility are the important traits for the improvement of forage sorghum hybrid parents and varieties. Forage traits were tested across two locations, Pantnagar and Hisar in India and the genotype, SM2254-8, is found promising for low HCN and high IVDMD. SM2254-8 is a novel source for genetic variability developed through wide hybridization of sorghum and maize. This genetic stock is a unique material as the cross between Sorghum and Maize has been accomplished for the first time in the inter-generic breeding.

Table 1. Forage yield, quality and phenological traits of sorghum-maize intergeneric derivative, 2254-8

Trait	Test genotype	Check 1	Check 2
	2254-8	SSG59-3	CSV21F
GFY 2 cuts (q/ha)	527.0	571.3	576.0
DFY 2 cuts (q/ha)	111.7	128.3	139.7
TSS (%)	4.5	5.0	4.5
HCN (ppm)	54.1	71.3	60.6
Protein (%)	8.3	8.7	8.3
IVDMD(%)	57.0	53.0	52.3
Early vigour (score 1-4)	4.00	3.75	3.25
Plant height (cm)	201	194	210
No. of leaves/plant	21.9	17.5	18.2
No of tillers	3.65	3.83	2.25
Leaf length (cm)	81.5	80.0	85.9
Leaf breadth (cm)	5.15	4.15	5.85
Leaf stem ratio	0.38	0.40	0.35
Stem girth (cm)	5.33	4.53	6.65
GFY= green fodder yield			
DFY= dry fodder yield			

TSS= total soluble sugars
Entries- 16; Checks- 2; Locations: 2

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33. EC724523 (EC724523; INGR19065), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita*)

NK Gautam*, Z Khan, BH Gawade, SC Dubey, N Singh, Babu Ram, A Kumar and K Tripathi

And

34. EC723686 (EC723686; INGR19066), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita*)

NK Gautam*, Z Khan, Bharat H Gawade, SC Dubey, N Singh, Babu Ram, A Kumar and K Tripathi

And

35. EC725122; TVu-9544 (EC725122; INGR19067), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root Knot Nematode (*Meloidogyne incognita)*

NK Gautam*, Z Khan, BH Gawade, SC Dubey, N Singh, Babu Ram, A Kumar, Gayacharan and K Tripathi

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

**(Email: nkgautam54@gmail.com)*

Root-knot nematodes, constitute a major group of plant-parasitic nematodes affecting crop production substantially. *Meloidogyne incognita* is an important constraint in the production of leguminous crops including cowpea in tropical and subtropical regions of the world (Sikora *et al*., 2005). Its infection leads to development of root galls, which impede normal uptake of water and nutrients. Root gall formation suppresses rhizobium nodulation and hampers nitrogen fixation in leguminous crops. Intensive root galling often results in permanent wilting, premature defoliation, and eventually plant death in cowpea. The nematode-resistant cultivars are an eco-friendly and economically feasible means for the management of root-knot nematodes. Therefore, 350 accessions of cowpea were screened at ICAR-NBPGR, New Delhi during the years 2013 to 2015 to identify the source of resistance to *M. incognita*. Preliminary screening was conducted in pots filled with nematode infected soil containing 3 second stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and a gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system (Taylor and Sasser, 1978). Host responses of cowpea germplasm were determined using gall index (GI) and designated as immune (GI= 0.0), resistant (GI $\leq$ 2.0) and susceptible (GI>2.0) (Sasser *et al.*, 1984). Selection was made for those accessions showing <10 root galls during preliminary screening and were rescreened by artificial inoculation under net house conditions to confirm their resistance consistency. Based on the number of root galls induced by *M. incognita*, three selected accessions (EC0723686, EC0724523, EC0725122) were found resistant with <10 root galls per root system. Nematodes penetration into roots were decreased in resistant accessions as compared to susceptible accessions. Similarly, egg-mass formation was also reduced in the resistant accessions and were observed smaller in size with fewer eggs (Khan *et al*., 2018). In conclusion, the drastic reduction in nematode penetration into the roots, reduction in gall formation, and lower number of egg masses suggest that resistance

may be both pre-infectional as well as post-infectional in resistant cowpea accessions. These resistant accessions may be useful in cowpea plant breeding programs for nematode management.

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36. IC559673 (IC0559673; INGR19068), a Lentil (*Lens culinaris*) Germplasm Resistant to Root-Knot Nematode

NK Gautam*, Z Khan, BH Gawade, SC Dubey, N Singh, Babu Ram, A Kumar, Gayacharan and K Tripathi
ICAR-National Bureau of Plant Genetic Resources, New Delhi, India
(Email: nkgautam54@gmail.com)

Root-knot nematodes (*Meloidogyne* spp.) are one of the most widespread and damaging agricultural pests in the world causing an estimated US $100 billion loss/ year worldwide (Oka *et al*., 2000). *Meloidogyne incognita* is one of the major limiting factors affecting plant growth and yield of lentil crop (Sharma *et al*., 2005; Khan *et al*., 2017). Management of root-knot nematodes, using resistant cultivars is considered as one of the best alternatives, which is eco-friendly as well as economically feasible. However, very little information is available on screening of lentil germplasm to root-knot nematodes. Therefore, present experiments were conducted to evaluate and identify resistant source in lentil germplasm. Evaluation of 300 accessions of lentil germplasm was done at ICAR-NBPGR, New Delhi during the years 2014 and 2015 for nematode resistance. Preliminary screening was conducted in pots filled with nematode infected soil containing two second stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system. Host responses of lentil germplasm accessions were determined using gall index (GI) and designated as immune (GI= 0.0), resistant (GI $\leq$ 2.0) and susceptible (GI>2.0) using standard procedure (Sasser *et al*., 1984). Those accessions showing <10 root galls in preliminary screening were selected for rescreening by artificial inoculation under net house conditions. Based on number of root galls, two accessions, IC559673 and IC559890 were found consistent in resistance reaction, as <10 galls per root system were observed (Khan *et al*., 2017; Fig. 1). Nematodes penetration occurred into roots of both resistant and susceptible accessions, but penetration rate was significantly lower in resistant accessions as compared to the susceptible accession (IC560206). Very few, smaller and distorted nematode egg masses were formed in the resistant lentil accessions, suggesting that the nematodes penetrating the resistant plant roots were further inhibited in their growth and development. Variations in nematode penetration into roots, root gall formation and egg mass formation in the resistant accessions could be due to their genetic differences for nematode resistance.

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37. IC208329 (IC0208329; INGR19069), a Lentil (*Lens culinaris*) Germplasm with High Protein Content (27.4 %-28.5%)

NK Gautam*[1], R Bhardwaj[1], S Yadav[2], N Singh[1], K Tripathi[1], P Suneja[1], B Ram[1] and A Kumar[1]

and

38. IC208326 (IC0208326; INGR19070), a Lentil (*Lens culinaris*) Germplasm with High Protein Content (27.4-28.06 %)

NK Gautam*[1], R Bhardwaj[1], S Yadav[2], N Singh[1], K Tripathi[1], P Suneja[1], B Ram[1] and A Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, India*

[2]*ICAR-Indian Agricultural Research Institute, New Delhi, India*

*(*Email: nkgautam54@gmail.com)*

Malnutrition problem is basically of protein deficiency among children of developing countries (Amjad *et al.*, 2006). Hence, there is a need to identify high protein and amino acids rich lines either for direct consumption or for breeding programme. Plant genetic resources possess genetic variability for different agronomical and nutritional traits (Kumar *et. al.*, 2016). Selection of superior germplasm and bio-fortification of crop varieties is an option to combat the problem of protein malnutrition. Lentil is an inexpensive, sustainable and affordable source of vegetable protein that is mostly consumed as dry seeds. Protein quality is determined on the basis of amino acids composition more importantly the essential amino acids (EAAs) which can not be synthesized by human beings and therefore, EAAs are key parameters in food quality assessment. In lentil sulphur containing methionine is a major limiting amino acid followed by aromatic amino acids (Longwah *et. al.*, 2017). The experimental material consisting of five hundred seventy germplasm was grown at NBPGR experimental farm for five years (2000-01, 2001-02, 2013-14, 2014-15, 2015-16) under standard agronomic package of practices to identify and select promising germplasm especially rich in protein and amino acids. Protein content was estimated by Kjeldahl nitrogen multiplied by factor 6.25 as per AOAC method number 2001.11. Amino acids profiling was done using waters Aceq-tag kit on waters HPLC system equipped with fluorescent detector. Two germplasm accessions, IC208326 and IC208329 were found superior for high protein content, 27.4-28.5% with 1.5-2.0 times higher content of total aromatic amino acids and methionine (Table 1). In conclusion identified lines having higher percentage of protein and rich in amino acids methionine, arginine and tyrosine etc. can be used directly for consumption as well as for improvement of lentil cultivars with value added products after purification of proteins or amino acids.

Table 1. Total protein content and amino acids profile of selected lentil accessions

Year	Accessions	IC201700	IC208329	IC208326	IC208351	Precoz
2015-16	Protein (%)	25.2 ± 0.56	28.5 ± 0.39	27.6 ± 0.54	23.7 ± 0.36	21.3 ±0.24
2014-15		26.3 ± 0.38	28.4 ± 0.62	27.7 ± 0.76	25.5 ± 0.18	23.3 ±0.18
2013-14		25.9 ± 0.34	28.6 ± 0.06	28.06 ± 0.14	25.6 ± 0.63	22.8 ±0.16
2001-02		26.2 ± 0.43	27.4 ± 0.53	27.7 ± 0.37	25.2 ± 0.56	21.4 ±0.21
2000-01		26.0 ± 0.64	27.5 ± 0.44	27.4 ±0.48	24.3 ± 0.18	22.6 ±0.17
Amino acids (g/100 g protein) 2015-16	Serine	4.99 ± 0.38	6.28 ± 0.33	6.34 ± 0.30	5.39 ± 0.02	5.56 ±0.12
	Histidine	6.67 ± 0.78	9.15 ± 0.35	7.08 ± 0.07	1.21 ± 0.94	2.20 ±0.09
	Proline	4.85 ± 0.25	4.64 ± 0.05	4.99 ± 0.33	4.48 ± 0.18	5.22 ±0.08
	Tyrosine	4.86 ± 0.82	7.15 ±0.41	6.97 ± 0.44	2.71 ± 0.09	2.93 ±0.23
	Methionine	1.16 ± 0.13	2.23 ± 0.17	1.5 ± 0.05	1.59 ± 0.01	1.01 ±0.18
	Lysine	7.21 ± 0.42	5.81 ± 0.45	7.11 ± 0.61	9.59 ± 0.38	6.47 ±0.32
	Leucine	6.98 ± 0.15	7.17 ± 0.03	7.23 ± 0.06	5.89 ± 0.29	7.72 ±0.13
	Phenylalanine	7.02 ± 0.49	7.28 ± 0.30	7.55 ± 0.29	3.84 ± 0.48	5.32 ±0.21

Each column contains mean and S.D. of mean

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39. IC0559890 (IC559890; INGR19071), a Lentil (*Lens culinaris*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita)*

NK Gautam*, Z Khan, BH Gawade, SC Dubey, N Singh, Babu Ram, A Kumar, Gayacharan and K Tripathi

ICAR-National Bureau of Plant Genetic Resources, Pusa, New Delhi-110012, India

**(Email: nkgautam54@gmail.com)*

The root-knot nematode, *Meloidogyne incognita* is one of the major limiting factors affecting plant growth and yield of lentil crop. For the management of root-knot nematodes, use of resistant cultivars is considered as one of the best alternatives, which are eco-friendly as well as economically feasible. Resistant cultivars can also be employed as a component of integrated nematode management along with other strategies. Through screening experimentation, two accessions of lentil, IC-559673 and IC-559890 are identified as a resistant to *M. incognita*. Evaluation of 300 accessions of lentil was done at ICAR-NBPGR, New Delhi during year 2014 and 2015. Preliminary screening was conducted in pots filled with nematode infected soil, containing two infective stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and a gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system. Host responses of lentil germplasm were determined using GI to be designated as Immune (I) when GI= 0.0, resistant (R) GI $\leq$ 2.0 and susceptible (S) >2.0 to each accession (Taylor and Sasser 1978). Those accessions showing <10 root galls were rescreened using artificial inoculation strategy under controlled conditions for confirmation of resistance consistency. Two accessions, IC559673 and IC559890 were consistent in resistance reaction (<10 galls per root) and hence selected for registration (Khan *et al*., 2017).

The reduced nematode penetration into roots and reproduction revealed negative effect of lentil resistant accessions on nematode. Nematode penetrations occurred in both the resistant accessions, but significantly lowered compared to the susceptible lentil accession (IC560206). Very few smaller and distorted nematode egg masses formed in the resistant lentil accessions, suggesting that the nematodes penetrating the resistant plant roots were further inhibited in their growth and development (Table 1). Variations in nematode penetration into roots, root gall formation and egg mass formation in the resistant accessions may reflect their genetic differences related to the nematode resistance, and their planting could provide a useful tool to manage root-knot nematodes in lentil crop.

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Table 1. Host status of lentil accessions for resistance to *Meloidogyne incognita* and response of resistant/susceptible accessions to nematode penetration and egg mass formation

Accession number	Number of galls per rootsystem (mean±SD)[a]	Percent reduction over control accession	Gall index	Host status	Nematode penetration rate (%) at DAI[b]				No. of egg masses per root after 45 DAI (mean±SD)[a]
					2 DAI	4 DAI	7 DAI	14 DAI	
IC559890	7.0±2.23	94.11	2	Resistant	2.86	5.3	5.78	5.22	2.8±1.92
IC559673	4.2±1.78	96.47	2	Resistant	1.86	5.86	6.56	6.2	1.6±0.54
IC560206 (Control)	119±14.66	0	5	Susceptible	5.76	14.38	17.38	19.62	194.2±15.22

[a]Means and standard deviations are of five replications, [b]DAI- days after inoculation.

40. IC0317520 (IC317520; INGR19072), a Lentil (*Lens culinaris*) Germplasm with Extended Funiculus for Fast Water Uptake

K Tripathi[1*], A Pandey[1], PG Gore[1], R Bhardwaj[1], N Singh[1], Gayacharan[1], JC Rana[2], V Gupta[1], M Arya[3], SB Choudhary [4], GP Mishra[5] and A Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India*
[2]*Bioversity International-India Office, G-1, B Block, NASC Complex DPS Marg, Pusa Campus, New Delhi, India*
[3]*ICAR-National Bureau of Plant Genetic Resources, RS, Bhowali, India*
[4]*ICAR-National Bureau of Plant Genetic Resources, RS, Ranchi, India*
[5]*ICAR-Indian Agricultural Research Institute, Pusa, New Delhi, India*
[*]*(Email: kuldeep.tripathi@icar.gov.in)*

A unique seed morphotype of lentil (*Lens culinaris* Medik.) with extended funiculus was identified during mega germplasm characterization programme at ICAR-NBPGR, New Delhi undertaken during *Rabi* 2017–2018. Based on comparative study with selected accessions for seed morphology, nutritional traits and physiology, this accession was identified with very distinct and prominent funiculus on the seed coat and higher rate of water uptake. It was a first report of seed morphotype in lentil with extended funiculus. All the accessions selected for imbibition behaviour study were of the same moisture content. Imbibition curves clearly indicated that water absorption and weight gain of the seeds were highest in atypical accession as compared to normal cultivars used in the study. When imbibed seeds were used for germination, it showed 100% germination. Funicle was remain intact with seed in 1-month old seedlings that indicate uniqueness of atypical accession in holding funicle as fixed character. IC145263 showed a range of water uptake from 0.1614 to 0.2609 in an interval of 12 h, IC145281 showed a gradual increase from 0.2107 to 0.3634 in 7 h and then became static with 0.37 values. Highest water uptake was observed in seeds with completely intact funicle as compared to seeds with completely covered funiculus and completely removed funiculus. In later even after 12 h imbibition there was no water uptake and after 36 h, only 30–40% seeds were imbibed which may be due to absorbtion through the seed testa surface or micropylar region. This indicated that funiculus may be facilitating trapping of water flow between embryo and testa and control water uptake in the atypical accession. For trait stability this unique accession was evaluated under multi-location trial at NBPGR, New Delhi, NBPGR, RS, Ranchi and Bhowali in *rabi* 2018-19 and this unique trait was expressed across the locations.

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41. IC0120963 (IC120963; INGR19073), Extra Early Maturing (53 days) Moth Bean (*Vigna aconitifolia*) Germplasm

O Singh[*], K Singh, N Shekhawat, AK Singh, V Gupta and K Singh

ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India
[*]*(Email: omvir2007@rediffmail.com)*

Moth bean also known as matki, math, dew bean {*Vigna aconitfolia* (Jack.) Marechal} has been known for high degree of adaptation in hot- arid climatic situation due to its inbuilt capacity for its tolerance to drought and high temperature. In view of generating the more productive and adaptive varieties for harsh and hostile climatic conditions the shortening of maturity period was remained desirable trait to be identified in germplasm of mothbean. The all released varieties of mothbean have been grouped in late maturity (>75 days), medium maturity (65-75days and early maturity (60-65 days) based on their maturity period. The released variety FMO-96 variety maturing in 58-59 days (Manga *et al.*, 2015) otherwise none of the accessions or released varieties matures earlier than

60 days. Mothbean germplasm characterization and evaluation has been a continued programme at NBPGR Regional Station, Jodhpur. During 2012 an accession IC 120963was identified to be matured uniformly in 53 days. It takes 30-32 days in flowering uniformly. The early maturity of this accession has been verified during subsequent years till 2016. This is the first accession of mothbean that has been reported from NBPGR Regional Station, Jodhpur that matures in 53 days.

Associated characters and cultivated practices: Being early in maturity (53days) mothbean accession IC 120963 escapes drought, generally recurring at later stage of the crop. Late maturing varieties (>75 days) as a rule generally suffer from the terminal drought and diseases. Consequently, these varieties have virtually wiped out from the cultivation map of this crop. This extra early maturing accession of mothbean is capable to yield better and withstood in the scorching heat and depleting soil moisture. Extra early maturing varieties due to short growing seasons, usually successfully escape drought and sometimes devastating diseases like (Yellow Mosaic Virus) and Cercospora leaf spot in mothbean. Such varieties are however, more suited to hot-arid climatic conditions like western Rajasthan. Where rainfall generally too low (200-250 mm) and temperature is high during growth period of the crop. Extra early maturing varieties of mothbean have high yield potential d (6-8 q/ha) and have increased harvest index up to 35% (Kumar, 2002). Thus this identified early maturing accession can be used in breeding programme of mothbean to shorten the crop duration.

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42. IC039289 (IC039289; INGR19074), an Early Maturing (50 days) Germplasm of Mung Bean (*Vigna radiata*)

O Singh, K Singh, N Shekhawat, AK Singh, V Gupta and K Singh
ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India
**(Email: omvir2007@rediffmail.com)*

Mung bean (green gram) or mung (*Vigna radiate L. Wilczek*) known for high degree of adaptation in rain fed arid situation due to tolerance to drought and high temperature is one of the major pulses grown in Rajasthan and other parts of the country. The short duration varieties are more suited in harsher climatic conditions as they mature before the onset of harsher climatic conditions. The germplasm of any crop species is the best source to identify early maturing (short duration) genotypes to be used in the breeding programme to shorten the length of crop duration. Regional Station of NBPGR, at Jodhpur has collected and conserved 2745 accessions of mung bean which are being characterized and evaluated and multiplied at its research farm. During characterization and evaluation study of mung bean germplasm in 2013 to 2016 at ICAR-NBPGR Regional station Jodhpur in an augmented block and randomized block designs during summer and *kharif* seasons the mung bean germplasm accession IC-39289 matured in just 50 days. It took 28 to 30 days in flowering uniformly and matured uniformly in another 20-22 days. This is the earliest maturing accession reported by NBPGR Regional Station, Jodhpur till date.

Associated characters and cultivated practices: Being early in maturity (50 days) mung bean accession IC-39289 escapes drought, generally recurring at later stage of the crop. Late maturing varieties as a rule generally suffer from the terminal drought and diseases. Consequently, these varieties are virtually wiped out from the cultivation map of this crop. This extra early maturing accession of mung bean is capable to yield better and withstand the scorching heat and depleting soil moisture. Extra early maturing varieties due to short growing seasons usually could evade drought problems and escaped devastating diseases like (Yellow Mosaic Virus) and Cercospora leaf spot successfully. An average yield of IC 39829 accession is recorded about 14.5 q/ha and it produces bold shiny seeds with seed weight of 6.34g per 100 seeds.

43. P-637 (IC0241565; INGR19075), a Post Emergence Herbicide (Metribuzin) Tolerant Pea (*Pisum sativum*) Germplasm

AK Parihar[1*], GP Dixit[1], N Kumar[1], CP Nath[1], SK Chaturvedi[2] and NP Singh[1]
[1]*ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh, India*
[2]*Rani Lakshmi Bai Central Agricultural University, Jhansi, Uttar Pradesh, India*
[*]*(Email:ashoka.parihar@gmail.com)*

Field pea (*Pisum sativum L.*) is an important cool season legume crop of the world and is a rich source of protein (21.1-32.9%), carbohydrate, minerals and vitamins which are good for human and livestock consumption and health (Parihar *et al*., 2016). The productivity of this crop is affected by several biotic and abiotic factors. Among these factors, weeds can cause > 75 percent reduction in crop yield (Tripathi *et al*., 2001; Singh *et al*. 2016). Weeds have competition to the crops for nutrient, water, sunlight, space and also harbour many insect-pest and diseases (Gaur *et al.* 2013), subsequently, the performance of crop in term of the yield is drastically reduced. Presently, pre-emergence herbicide (pendimethalin) and manual weeding at 30-35 days after sowing is recommended in pea. However, manual weeding is proving difficult because of labour scarcity at critical time of weeding and increasing cost. Therefore, to control the later flush of weeds, use of post-emergence herbicides becomes important. But, no post-emergence herbicide is available for controlling broad-leaved weeds like *Medicago denticulala, Vicia sativa, Convolvulus arvensis, Chenopodium album, Phalaris minor* and others. Therefore, an effective and efficient weed management is essential to achieve potential yield (Nath *et al*., 2017). Field pea is a poor competitor to weeds owing to its slow initial growth and wider plant spacing that provide congenial environment for weeds to grow. Besides, its succulent plant type also do not allow second manual weeding as it can cause damage to the crop. Therefore, herbicide tolerance cultivars may offer larger elasticity for use of post-emergence herbicides and are immediately required by the *P. sativum* growing farmers. An attempt has been made at ICAR-IIPR, Kanpur, Uttar Pradesh to identify the genotypes with resistance to the post-emergence herbicide metribuzin in Field pea. Metribuzin (4-Amino-6-tert-butyl-3-methylsufanyl-1, 2, 4-triazin-5-one) is a potential broad-spectrum herbicide used in soybean and wheat crops. It inhibits the photosystem-II pathway, which demonstrates adverse effect on the fully developed leaves and subsequently on plant growth. Thus far no report is available on herbicide tolerance in *P. sativum*. Also, till date no systematic study was conducted to see the efficacy of this post-emergence herbicide in fieldpea. In present investigation total 822 genotypes were examined for their sensitivity under preliminary screening against metribuzin at 0.5 kg ai/ha during the winter season of 2015-16 at ICAR-IIPR, Kanpur. Of the tested genotypes, a set of eighty five promising genotypes were re-evaluated with same dose during the winter season of 2016-17 with visual phyto-toxicity score. Based on two years screening (2015-16 & 2016-17), a set of fifteen genotypes was made comprising of tolerant, moderately tolerant, sensitive and highly sensitive genotypes. These genotypes were examined in larger plot for resistance against popular post-emergence herbicide metribuzin 500 g a.i./ha during winter season of 2017-18. The plants were observed for herbicide phyto-toxicity on three different stages i.e. 15 days after herbicide application (DAHA), 30 DAHA and 60 DAHA. Based on scoring for the visual appearance and phyto-toxicity on plants, a genotype 'P-637' was found tolerant. This genotype has constantly registered tolerance for metribuzin 500 g a.i./ha during three years of screening. Hence, this genotype can be utilized as a potential donor in future fieldpea breeding programme towards development of herbicide (metribuzin) tolerant varieties and in other basic studies.

Morpho-agronomic characteristics: The genotype (P-637) is medium tall type (70-75 cm) and leafy type.It has red colour flowers, pigmented pods and yellow green (tan colour) dimpled seeds. It flowered and matured in 64 days and 125 days respectively. The 100-seed weight is 16.0-17.0 gm and pod length is 4-5cm. The average yield of the genotype (P-637) is 14-15 qt/ha.

Associated characters and cultivation practices: This genotype has anthocyanin on stem and leaves of plants. Its leaves total chlorophyll and carotenoids content is 2.302 (mg/g fresh weight) and 0.143 (mg/g fresh

weight), respectively. The chlorophyll a content (1.909 mg/g fresh weight) and chlorophyll b content is (0.39 mg/g fresh weight). This genotype also has powdery mildew resistance. It can be grown on different type of soil; however, a well drained soil is essential to achieve good yield potential of this genotype. The field should be prepared well by two to three ploughings. The seeds treatment should be done with fungicide like Thirum/ Captan/Carbendazim @ 3.0 g/kg seed + rhizobium culture @ 1 packet/10 kg + Trichoderma @ 4.0 g/kg at 4-5 days before sowing. The optimum sowing time is second fortnight of October with 100 kg/ha seed rate. At the time of field preparation 40 kg N, 40-60 kg P_2O_5:20-30 kg K_2O: 20 kg S: 15 kg $ZnSO_4$ should be applied as basal application. First irrigation should be given at 45 days and second, if needed, at pod filling stage. This genotype has good worth as a donor in future fieldpea breeding programme towards development of herbicide (metribuzin) tolerant varieties and in other basic studies.

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44. AL 1747 (IC0632084; INGR19076), a Pigeon Pea (*Cajanus cajan*) Germplasm Moderately Resistant to Pod Borer. Indeterminate Growth Habit. Early Maturing (130-140 days)

I Singh[1], S Singh[1*], JS Sandhu[1], GK Taggar[1], R Singh[1] and IP Singh[2]
[1]*Punjab Agricultural University, Ludhiana, India*
[2]*ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh, India*
[*]*(Email: sarvjeet62@pau.edu)*

Development of pigeonpea cultivars with resistance to pod borer has a considerable potential in pest management. The genetic stock, AL 1747, is moderately resistant to pigeonpea pod borers, *Helicoverpa armigera* and *Maruca vitrata*. It has indeterminate growth habit and belongs to early maturity group (130-140 days). It has been developed at Punjab Agricultural University, Ludhiana (Punjab) from a cross *Cajanus scarabaeoides* ICPW 213 (wild species) × AL 201 (cultivated variety) using backcross method followed by pedigree selection.

Morpho-agronomic characteristics: AL 1747 was evaluated under field conditions against pod borer in advance stage screening (multilocation) research trials at National level (2010-2013) at five different locations of India. The per cent pod damage in AL 1747 was 11.88% as compared to 13.25, 14.37 and 30.51% in local checks PAU 881, AL 201 and infester, respectively. At Ludhiana, AL 1747 recorded significantly lowest cumulative pod damage (12.11%) due to both borers (*M. vitrata* and *H. armigera*), whereas, susceptible infester recorded significantly higher cumulative pod damage of 29.97 per cent (Taggar *et al.*, 2015). On the basis of its performance, AL 1747 was recommended as a donor in the early maturity group as per the Proceedings and Recommendations of AICRP Pigeonpea Entomology, at Annual Group Meet of AICRP Pigeonpea held at MPKV, Rahuri, 2014 (Anonymous 2014).

Associated characters and cultivated practices: Under field conditions, AL 1747 registered significantly lower number of *Maruca* webs per plant and a lower percentage of pod damage as compared to other test genotypes evaluated under field conditions (Wubneh and Taggar 2016a).

Mechanism of resistance: Under artificial infestation, larval weight gain, per cent pupation and mean pupal weights were significantly lower when the *M. vitrata* larvae were fed on flowers of AL 1747, thus confirming antibiosis as a mechanism of resistance against the pod borer. Nutritional indices such as efficiency of conversion of ingested food (ECI), efficiency of conversion of digested food into body matter (ECD) and relative growth rate (RGR) for pod borer, *M. vitrata* were significantly lower in AL 1747 (Wubneh and Taggar, 2018).

Bases of resistance: Biochemical analysis of AL 1747 revealed a higher activity of polyphenol oxidase, diamine oxidase, polyamine oxidase and tyrosine ammonia lyase in pod wall infested with *H. armigera* (3.2, 2.9, 5.7 and 3.7 fold, respectively). Besides, higher status of ascorbate oxidase in both uninfested and infested developing seeds of AL 1747 was also observed earlier (Kaur *et al*., 2015). The condensed tannins were higher in developing seeds and pod wall after *H. armigera* herbivory (2.5 and 5.6 fold, respectively) in AL 1747 (Kaur *et al*., 2014). Studies conducted on biophysical basis of resistance to pod borer revealed that AL 1747 possessed significantly higher non-glandular trichome density on leaves and pods (Wubneh and Taggar, 2016b).

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45. VRPM-901-5 (IC0630592; INGR19077), a Pea (*Pisum sativum*) Germplasm Capable of Producing 3-5 Pods/Peduncle at Multiple Flowering Nodes (Multi-Podded Genotype)

J Devi[1], SK Sanwal[1,2], RK Dubey[1], GP Mishra[1,3], S Chandra[1], PM Singh[1], B Singh[1]

[1]*ICAR-Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh, India*

[2]*ICAR-Central Soil Salinity Research Institute, Karnal, India*

[3]*ICAR-Indian Agricultural Research Institute Pusa, New Delhi, India*

[*]*(Email: jyoti17iivr@gmail.com)*

The inflorescence trait, number of flowers per peduncle/node is among one of the major yield attributes that has played a significant role in genetic improvement of legumes through various breeding programmes. Multi-flower is the condition when plant bears more than 2 flowers on a single flowering node/peduncle, alternatively referred to as many-flowered raceme or multi-podded phenotype. In garden peas, with very limited variation, single or double pod bearing habit is most common feature of present day cultivars. However as reported in pea and other legumes, development of three or more pods per node, while maintaining the pod size over one and two, appears an attractive option to increase the yield (Devi *et al*., 2018). The newly bred 'VRPM-901-5' is a mid-season pea genotype capable of producing 3-5 flowers/pods at multiple flowering nodes (Fig. 1). This genotype was developed by using single plant selection approach from a cross 'VL-8 × PC-531' made during 2011-12 at ICAR-Indian Institute of Vegetable Research, Varanasi located at 82°52′37″

E and 25°18′21″ N at an elevation of 83 m above the mean sea level.

Morpho-agronomic characteristics: 'VRPM-901-5' is a mid-season genotype that requires 50 days for days to first flowering and first picking can be done in 75-80 days after sowing. The first multi-flowering node appears on average 21st node. Pods are 7.5-9 cm in length and light green in colour. The yield of a cultivar is dependent on the number of flowers produced and percentage conversion of these flowers to pods. VRPM–901–5, appeared most promising for pod yield per plant (208g) and were significantly superior to the double-podded cultivars PC–531 (120g) and VL-8 (126g) as well to the single podded genotype NO-17 (60g) over study period of four years. (Table 1). The higher yield potential of VRPM–901–5 could be attributed to the formation of more number of flowers (48-52) and pods per plant (32-48) in the multi-podded line than in the double or single-podded lines. Further, this line was also having longer flowering duration and flowering starts from 7th week after sowing and continue up to 16th week after sowing (Devi *et al.,* 2018). Our study also showed that VRPM-901-5 produced a significantly higher number of flowers than the double podded cultivars because of higher number of reproductive nodes per plant (Devi *et al.,* 2018).

Associated characters and cultivation practices: VRPM-905-1 is susceptible to powdery mildew; however, disease can be escape if sowing is done between last week of October to first week of November. Further, this genotype is tolerant to leaf minor and aphids under field condition. The optimum temperature for seed germination is about 22±2^{o}C.Due to its prolific branching and longer plant height, a wider spacing of 40×10 cm is recommended than normal spacing of 30×10 cm. Standard cultivation practises can be adopted to raise a healthy crop.

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Table 1. Mean performance of 'VRPM-901-5' genotypes compared with triple, double and single podded cultivars through Tukey-Kramer's HSD test (pooled over years).

Years	Genotypes	MNFP/N	DTF	AFMFN	TFP	BPP	PDL	PD	PL	PW	PPP	APW	SPP	PH	YPP
Pooled over the years	VRPM-901-5	5	50.6b	21.1a	52.5a	2.3a	6.9b	0.23a	8.2b	1.06c	40.5a	5.7bc	5.1b	121.0b	208.0a
	VRP-500	3	49.3b	16.1b	33.9b	1.9bc	5.7c	0.23a	7.6b	1.38b	29.1b	6.0b	7.0a	80.3c	152.7b
	PC-531*	2	50.1b	0.0c	23.3c	1.6cd	8.3a	0.20b	9.3a	1.65a	19.6c	7.3a	7.0a	64.3d	120.5b
	VL-8*	2	69.3a	0.0c	35.9b	1.2d	5.6c	0.20b	6.2c	1.15c	29.0b	5.2c	6.7a	115.3b	126.9b
	NO-17*	1	50.0b	0.0c	25.5c	2.2ab	6.2c	0.20b	6.2c	1.12c	19.2c	3.3d	5.0b	163.8a	60.5c
	LSD (5%)		0.94	0.47	2.22	0.14	0.21	0.01	0.27	0.05	2.33	0.25	0.23	4.27	11.8
	R2		92.51	98.6	79.76	61.3	79.8	49.4	77.2	84.6	67.9	82.7	73.16	92.17	74.4

Values followed by the same letter in each column are not significantly different by Tukey-Kramer's HSD test

($p < 0.05$);MNFP/N=Maximum number of flower produced/node; DFF: Days to first flowering; AFMFN: Appearance of first multi-flowering node (No); TFP: Total number of flower produced; BPP: No. of primary branches per plant; PDL: Peduncle length (cm); PDD: Peduncle diameter (cm);PL: Pod length (cm); PW: Pod width (cm); PPP: No. of pods per plant; APW: Average pod weight (g); SPP: No of seeds per pod PH: Plant height (cm) and YPP: Yield per plant (g); *Multi-flowering nodes were not present in the double podded cultivar PC–531,VL–8 and single podded genotype No17.

46. BR-2 (IC0632605; INGR19078), a Medium Maturity Group Cauliflower (*Brassica oleracea*) Resistant to Downy Mildew with Resistance Governed by Single Dominant PPa3 Gene.

S Singh*[1], P Kalia[1], SR Sharma[2], BB Sharma[1], P Saha[1], BS Tomar[1] and P Sharma[1]
[1]*ICAR-Indian Agricultural Research Institute, New Delhi, India*
[2]*ICAR-IARI Regional Station, Katrain, Himachal Pradesh, India*
*(*Email: singhshrawan@rediffmail.com)*

Cauliflower is an important vegetable crop across the world. In India, it is being grown on 0.45 million ha area with annual production of 8.4 million tonnes (NHB Database, 2017). Downy mildew [*Hyaloperonospora parasitica* (Pers.: Fr) Fr. Constantinescu and Fatehi formerly *Peronospora parasitica*] is major disease of cauliflower which causes heavy toll to mid group of Indian cauliflower during November – December months. It also affects seed crop of early group cauliflower. Although, chemical control is effective but their use is of consumer health concerns. Hence, resistant varieties offers a more practical and long-term solution for effective control of downy mildew disease.

The 'BR-2' has strong resistance to downy mildew pathogen while this pathogen devastates the susceptible genotype 'PHJ'. Percent disease incidence (PDI) of the genotype was observed to be 6.5 % under artificial inoculation condition (Table 1) (Singh *et al*., 2013). Over the years, it maintained resistance level which indicates about durable resistance in BR-2. A single dominant gene *Ppa3* is responsible for downy mildew resistance in 'BR-2' and it has been mapped with three molecular markers $OPC14_{1186}$, $OPE14_{1881}$, and $ISSR23_{1103}$. Among them, $OPC14_{1186}$ was located 22.3 cM from *Ppa3* gene (on top-arm end) while $OPE14_{1881}$ and $ISSR23_{1103}$ flanked the geneat 10.6 cM and 26.4 cM, respectively on other side of the gene on linkage map (Singh *et al*., 2012).

Agro-morphological traits: The cauliflower genotype 'BR-2' is one of the BR-series progenies derived from a cross (S. No. 15×MGS-2-3) between two mid-late maturity group genotypes (Sharma *et al*., 1972). It has medium vigorous semi-erect plants with bluish green leaves. Plant stem is of medium length and plant spread is broad. Leaves are long and have prominent mid-rib, broad lobes and medium puckering on margins. Curds are very compact, cream white and medium in size and average curd weight is 710.5 g. It is mid-late group genotype (16-20 °C temperature for curd initiation) and attains curd maturity during December end to mid January. The crop becomes ready to harvest in 80-85 days after transplanting in its normal growing season. The flower colour of 'BR-2' is yellow, stalk length is medium and flowering occurs during February end to mid-March. The self-incompatibility is weak hence it produces seeds profusely. A single dominant gene *Ppa3* control of downy mildew resistance in 'BR-2' can be explored in hybrid breeding and to empower commercial susceptible varieties.

Table 1. Response of 'BR-2' and commercial cauliflower varieties to downy mildew

Genotype	Maturity group	Horticultural traits	Disease score (1-5 scale)*	PDI (%) through artificial inoculation	Disease reaction	Curd weight in well managed crop (g)
BR-2	Mid-late	Cream white, compact, solid curds	0.0-1.0	6.5	Resistant	710.5
Pusa Himjyoti 'PHJ'	Mid-late	White, compact curds	3.0-4.0	77.0-89.3	Highly susceptible	645.5
Pusa Sharad	Mid-early	White, compact granular curds	3.0-4.0	70.5-87.5	Highly susceptible	725.2

*On disease scale of 0 – 5; PDI = Percent disease incidence

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47. AHW/BR-5 (IC0627526) (IC0627526; INGR19079), a Watermelon (*Citrullus lanatus*) Germplasm with Stable Andromonoecious Sex Form

BR Choudhary*, SM Haldhar and PL Saroj
ICAR-Central Institute for Arid Horticulture, Bikaner, Rajasthan, India
(Email: choudharybr71@gmail.com)

Watermelon [*Citrullus lanatus* (Thunb.) Matsam. & Nakai] is an important crop belonging to Cucurbitaceae family with (2n=2x=22). Watermelon act as a coolant, thirst-quencher, detoxifier, diuretic, febrifuge, and, according to some natural healers, an aphrodisiac. The fruits of watermelon are fleshy, juicy and sweet. Mostly eaten fresh, provide a delicious and refreshing dessert in hot weather. The major nutritional components of the fruit are carbohydrates (6.4 g/ 100g), vitamin A (590 IU) and lycopene (4100 µg/ 100g), an anti-carcinogenic compound found in red flesh of watermelon which is beneficial in prevention of heart attacks and certain types of cancer. It is a rich in iron content among all members of cucurbitaceous crops. The rind is rich in citrulline, an amino acid that contributes to the removal of ammonia from the body and wound healing. Watermelon is native to Tropical Africa chiefly the Kalahari Desert (the current nations of Namibia and Botswana) where wild forms are still found (De Candolle, 1882). Whitaker and Davis (1962) also describe the existence of a secondary diversification centre in India. Watermelon is thought to have been domesticated in Africa at least 4000 years ago and now grown worldwide, particularly in regions with long, hot summers (Robertson, 2004).

Table 1. Salient characteristics of AHW/BR-5 (IC-0627526)

Trait	Description
Days taken to produce 50% pistillate flowers after sowing	45-50
Node number at which first female flower appeared	9-12
Days to first fruit harvest after sowing	80-85
Fruit weight (kg)	2.08-2.78
Fruit diameter (cm)	14.68-17.80
Rind thickness (cm)	1.38-1.92
TSS (%)	10.80-11.74
Sex form	Andromonoecious
Leaf shape	Pentalobate
Fruit shape	Round
Rind colour	Light green devoid of stripes
Flesh colour	Red

A wide range of genetic variability has been observed in quantitative and qualitative traits of watermelon (Choudhary *et al*., 2016). Watermelon is mainly monoecious (staminate and pistillate flowers borne on the same plant separately) in sex expression however, andromonoeciuos (staminate and perfect flowers borne on the same plant) sex form is also found rarely. Identified an andromonoecious plant from segeregating population and homogenized through repeated inbreeding. The developed material (AHW/BR-5; IC-0627526) possess unique trait *i.e.* stable andromonoecious sex form and able to set fruits under net house conditions without pollinators and produced viable seeds. AHW/BR-5produced round, red fleshed fruits having light green rind devoid of stripes in 80-85 days after sowing weighing 2.08-2.78 kg with 10.80-11.74% TSS and 1.38-1.92 cm thick rind.

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48. NRCGCS-602 (HOS-130 or HOP_IL_130) (IC0630593; INGR19080), a Groundnut (*Arachis hypogaea*) Germplasm with High Oleic Acid (80%) Content

SK Bera* and T Radhakrishnan
ICAR-Directorate of Groundnut Research, lvenagar Road, Junagadh, Gujarat, India
**(Email:berask67@yahoo.co.in)*

Edible oil with higher oleic acid content reduces riskin cardio-vascular disease (CVD), while higher linoleic acid increases tumerogenesis and CVD. High oleic to linoleic acid ratio enhance oxidative stability of the oil. In normal groundnut oleic acid content ranges from 35% to 50%, while oleic to linoleic acid ratio ranges from 0.5 to 3.0. The groundnut germplasm, NRCGCS 602 with 81% oleic acid content and oleic to linoleic acid ratio of 30 has been developed through marker assisted breeding in ICAR-Directorate of Groundnut Research, Junagadh for the first time in India. The NRCGCS 602 is an advance breeding line developed from a cross between ICGV 06100×Sunoleic 95R. The ICGV 06100 is a high oil content (55%) breeding line developed by ICRISAT, Hyderabad, while the Sunoleic 95R is a high oleic acid content (80%) breeding developed by Florida Agricultural Research station, USA. ICGV 06100 was crossed with Sunoleic 95Rto introgress ahFAD2A and ahFAD2B mutant alleles, which enhance the oleic acid content in groundnut, from Sunoleic 95R to ICGV 06100. Allele-specific polymorphic chain reaction (AS-PCR) markers were deployed to select plants with ahFAD2A and ahFAD2B mutant alleles in F_1 and F_2 generations. While cleave damplified polymorphic sequence (CAPS) markers were used to select homozygous plants forahFAD2A and ahFAD2B mutant alleles in F_2 generation. NRCGCS 602 was selected in early generation (F_2) using AS-PCR and CAPS markers. The selected line was further advanced to F_7 generation for seed enhancement and biochemical analysis. Kernels harvested in *kharif* 2015, *kharif* 2016, Summer 2017 and *kharif* 2017 seasons were used in biochemical analysis. Biochemical analysis of NRCGCS 602over four seasons confirmed as high oleic as well as high oil content line. NRCGCS 602 has semi spreading growth habit with 30-35 cm height; light green leaves; average 4-5 primary branches. It produces 50%flowering in 25 days after sowing (DAS) and matures in ll5-120 DAS during rainy season. The genotype produces an average pod yield of 296 g per square metre with 7l% shelling outturn. Pods are medium in length having moderate reticulation, beak and constriction. Pods are mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 33 g and contain 55% oil. The genotype has 81% oleic acid content and 2.6% linoleicacid content with an oleic to linoleic ratio of 30. This will be a potential donor for high oleicas well as high oil content in groundnut.

49. NRCGCS-605 (HOS-145 or HOS-IL_MAS_145) (IC0630594; INGR19081), a Groundnut (*Arachis hypogaea*) Germplasm with High Oleic Acid (80%) Content

SK Bera* and T Radhakrishnan
ICAR-Directorate of Groundnut Research, lvenagar Road, Junagadh, Gujarat, India
**(Email: berask67@yahoo.co.in)*

Edible oil with higher oleic acid content reduces risk in cardio-vascular disease (CVD) while higher linoleic acid increases tumerogenesis and CVD. High oleic to linoleic acid ratio enhance oxidative stability of the oil. In normal groundnut oleic acid content ranges from 35% to 50%, while oleic to linoleic acid ratio ranges from 0.5 to 3.0. The groundnut germplasm, NRCGCS 605 with 81% oleic acid content and oleic to linoleic acid ratio of 30 has been developed through marker assisted breeding in ICAR-Directorate of Groundnut Research, Junagadh for the first time in India. NRCGCS 605 is an advance breeding line developed from a cross between ICGV 06100×Sunoleic 95R. ICGV 06100 is a high oil content (55%) breeding line developed by ICRISAT while Sunoleic 95R is a high oleic acid content (80%) breeding line developed by Florida Agricultural Research

station, USA. ICGV 06100 was crossed with Sunoleic 95R to introgress *ahFAD2A* and *ahFAD2B* mutant alleles, which enhance the oleic acid content in groundnut, from Sunoleic 95R to ICGV 06100. Allele-specific polymorphic chain reaction (AS-PCR) markers were deployed to select plants with *ahFAD2A* and *ahFAD2B* mutant alleles in F_1 and F_2 generations. While cleaved amplified polymorphic sequence (CAPS) markers were used to select homogygous plants for *ahFAD2A* and *ahFAD2B* mutant alleles in F_2 generation. NRCGCS 605 was selected in early generation (F_2) using AS-PCR and CAPS markers. The selected line was further advanced to F_7 generation for seed enhancement and biochemical analysis. Kernels harvested in *kharif* 2015, *kharif* 2016, Summer 2017 and *kharif* 2017 seasons were used in biochemical analysis. Biochemical analysis of NRCGCS 605 over four seasons confirmed as high oleic as well as high oil content line. NRCGCS 605 has semi spreading growth habit with 25-30 cm height; light green leaves; average 4-5 primary branches. It produces 50% flowering in 25 days after sowing (DAS) and matures in 115-120 DAS during rainy season. The genotype produces an average pod yield of 286 g per square metre with 67% shelling outturn. Pods are medium in length having moderate reticulation, beak and constriction. Pods are mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 33 g and contain 55% oil. The genotype has 81% oleic acid content and 2 % linoleic acid content with an oleic to linoleic ratio of 30. This will be a potential donor for high oleic as well as high oil content in groundnut.

50. CS 52-SPS-1-2012 (IC0630607; INGR19082), an Indian mustard (*Brassica juncea*) Germplasm with High Tolerance to Salinity (ECe 14-15 dS/m) and Alkalinity (pH 9.4-9.5). High 1000- Seed Weight (8.0-9.0g). High Photosynthetic Efficiency under Salinity Stress

J Singh*, PC Sharma and V Singh
ICAR-Central Soil Salinity Research Institute, Karnal, Haryana
**(Email: jogendra.singh@icar.gov.in)*

Indian mustard [*Brassica juncea* (L.) Czern and Coss] is an important oil-seed crop in the world and is grown in more than 50 countries across the globe, which often experiences saline stress as it is grown extensively in the arid and semi-arid regions of the world. Globally, 932.2 million hectare area is affected with salinity and sodicity stresses (Metternicht and Zinck, 2003), out of which, an area of nearly 6.73 million hectare is affected by these stresses in India (Singh *et al.*, 2014). Salinity stresses contribute to yield losses and this low economic yield is related to the crop's susceptibility. There is a greater need to improve crop plants for salinity tolerance. Hence, it becomes necessary to develop salt tolerant genotypes in Indian mustard. One of the approaches is the characterization of the available germplasm for identification of tolerant accession that provides an initial germplasm base/donor for breeding salt-tolerant crops.

At ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal, we have identified a mutant from CS 54 (Salt tolerant variety released by CVRC in 2005) population and maintained its genetic purity by individual plant selection method in salt affected soils for high seed yield and tolerance to soil salinity conditions. This genotype also was characterized for its photosynthetic efficiency using portable infrared gas analyzer [LI-6400XT, Li-COR, USA).

Morpho-agronomic characteristics: On the basis of 2014 to 2016 evaluation trials conducted for saline (Soil Salinity ECe 15 dS/m; Irrigation water salinity EC_{iw} 9-18 dS/m) and alkalinity (pH 9.4-9.5) conditions under field and pot house at ICAR-CSSRI, Karnal, the CS 52-SPS-1-2012 seed yield of 2.2 t/ha which was 22% and 46% higher than yields of two checks i.e. CS 54 and Kranti, respectively. It also provided 5% higher oil yield than Kranti and CS 54. This strain matures, on an average, in 122 days and takes 52 days to flower. The strain attains the height of approximately 166 cm and produces high number of primary branches (6), secondary branches (11), main shoot length (78) and 1000 seed weight (8.0-9.0g) (Table 1).

Table 1. Performance (yield contributing traits, adaptation traits, quality traits), tolerance to salinity/ alkalinity stress and biochemical evaluation data of CS 52-SPS-1-2012 under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)

Name of Genotype	Year of reporting	Yield contributing traits under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)							
		Plant height (cm)	No. of primary branches	No. of secondary branches	Main shoot length (cm)	No. of pods on main shoot length	No. of Seed/ pod	1000 Seed weight (g)	Yield (t/ ha)
Kranti	2014	199	5	13	84	55	15	5.0	1.4
	2015	200	5	11	80	45	15	5.0	1.50
	2016	209	5	11	75	45	14	5.0	1.67
Mean		202.7	5.0	11.7	79.7	48.3	14.7	5.0	1.5
CS 54	2014	180	5	12	85	50	14	5.4	1.7
	2015	184	5	12	82	50	15	5.5	1.75
	2016	194	5	11	77	50	14	5.5	2.05
Mean		186.0	5.0	11.7	81.3	50.0	14.3	5.5	1.8
CS 52-SPS-1-2012	2014	164	5	10	76	48	14	9.0	2.1
	2015	165	6	12	80	50	15	9.1	2.15
	2016	170	6	12	80	55	15	8.9	2.38
Mean		166.3	5.7	11.3	78.7	51.0	14.7	9.0	2.2

Name of Genotype	Year of reporting	Quality traits under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)			
		Oil (%)	Protein (%)	Erucic acid (%)	Crude fiber (%)
Kranti	2014	39.0	19.8	45.6	10.5
	2015	37.2	18.8	46.3	11.0
	2016	38.2	18.2	46.0	11.2
Mean		38.1	18.9	46.0	10.9
CS 54	2014	37.6	19.9	48.3	10.1
	2015	38.6	19.8	49.6	11.5
	2016	39.0	19.0	49.0	11.0
Mean		38.4	19.6	49.0	10.9
CS 52-SPS-1-2012	2014	39.9	20.1	35.7	9.9
	2015	39.8	20.2	34.6	9.5
	2016	39.9	20.0	33.8	9.6
Mean		39.9	20.1	34.7	9.7

Associated characters: The net photosynthesis, stomatal conductance, water use efficiency and transpiration rate decreased substantially in the mustard at higher salinity (EC_{iw} 15 dS m^{-1}) as compared to control (Singh *et al*., 2019). The lowest reduction at 15 dS m^{-1} in photosynthesis rate (55.85%); stomatal conductance (33.33%); transpiration rate (48.19%) was recorded in CS 52-SPS-1-2012 while other genotypes surpasses more than 50% reduction in photosynthetic traits. Further, CS 52-SPS-1-2012 also showed least reduction in the instantaneous water use efficiency (14.80%) and CO_2 assimilation rate (26.74%) as compared to control. Looking to its high 1000 seed weight, better oil parameters and high photosynthetic efficiency under high salt stress condition CS 52-SPS-1-2012 is being proposed for registration as a national genetic stock/ donor for the development of salt tolerant mustard genotypes to affected soils and water conditions.

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51. DRMR10-40 (IC0632085; INGR19083), an Indian Mustard (*Brassica juncea*) Germplasm with Drought Tolerance

VV Singh*, ML Meena, HS Meena, Arun Kumar, Priyamedha, Ramswaroop Jat and PK Rai
ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan, India
**(Email: singhvijaveer71@gmail.com)*

DRMR 10-40 was derived from base population developed by intermating of DRMR 06-1942, DRMR 06-1946, NDYR 8, NDYR 10 and Rohini. The base population was grown for successive years for promising selections. During 2012-13 one genotype namely DRMR 10-40 was isolated and found promising under moisture stress conditions. The genotype was tested under AICRP-RM plant physiological trials during 2014-15 and 2015-16 at 5-7 locations (AICRP Rapeseed-Mustard, 2015 and 2016). Pooled summary over the years and locations indicate that proposed genotype has shown less reduction in RWC, SPAD, seeds/silique, 1000 seed weight and seed yield as compared to drought tolerant checks. The drought susceptibility index (DSI) value of the proposed genotype was lowest as compared to checks (Table 1). This indicates drought tolerant characteristics of the DRMR 10-40 and promising genotype can be utilized in breeding programme aimed at developing high yielding drought tolerant varieties.

Morpho-agronomic characteristics: Morphological traits of the DRMR 10-40 is as follows: Plant Height (cm),164; Days to maturity, 135; Primary branches/ plant (no.), 4.9; Secondary branches/plant (no.), 5.1; Main shoot length (cm), 75.5; Siliquae/plant (no.), 157; Siliqua length (cm), 3.7; Seeds/siliqua (no.), 14.1; 1000 seed weight (g), 5.4; Oil content (%), 41.9; Seed yield/ plant (g), 15.8.

Table 1. Pooled summary of physiological parameters (Drought tolerance) for proposed genetic stock DRMR 10-40 and checks in physiological trials during 2014-15 to 2015-16

Parameter (s)	No. of locations	DRMR 10-40	Check varieties		
			RB 50	Kranti	RH 406
Relative water content (Reduction %)	5	**8.1**	8.5	10.6	13.6
SPAD values (Reduction %)	5	**3.9**	5.5	3.6	10.5
Seeds/siliqua (Reduction %)	5	**5.5**	6.7	10.3	7.3
Seed yield (Reduction %)	7	**18.3**	18.1	18.7	18.5
Drought susceptibility Index (DSI)	7	**0.63**	0.69	0.70	0.74

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52. DRMR 2059 (IC0520764; INGR19084), an Indian Mustard (*Brassica juncea*) Germplasm with High temperature Tolerance at Seedling Stage. High Temperature Tolerance at Terminal Heat Stress

VV Singh*, A Kumar, HK Sharma, HS Meena, B Ram, Priyamedha, BL Meena, I Mawlong, P Sharma, RS Jat and PK Rai
ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan, India
**(Email: singhvijaveer71@gmail.com)*

DRMR 2059 (IC 520764; JBT-41/92) is an indigenous germplasm of Indian mustard (*Brassica juncea* L.) collected from Deoghar, Jharkhand. The DRMR 2059 was tested for physio-biochemical parameters and found superior over checks (BPR-543-2, BPR-543-4, Urvashi) in terms of percent increase in RWC (Bud stage,

0.97%; Pod stage, 5.94%) and CSI (pod stage, 2.53%) (DRMR Annual Report 2016-17). During screening for high temperature tolerance (seedling stage), DRMR 2059 recorded significantly superior seed yield/plant (19.5g/plant) over the best check BPR541-4 (16.9g/plant) (DRMR Annual Report, 2017-18). During 2018-19 DRMR 2059 was evaluated for high temperature tolerance at seedling stage both under laboratory and field conditions at 4 locations (Hisar, Kanpur, Ludhiana, Mumbai) along with checks under plant physiological traits (AICRP-RM, 2019). Seedling mortality ≤20% and DW/10 seedlings ≥ 40mg were used parameter for rating genotypes tolerant under controlled conditions and field conditions. Average seedling mortality (%) of DRMR 2059 under controlled conditions over four locations was 17.3% and DW/10 seedlings over four locations was 51.4 mg (Table 1). For field conditions genotype was tested at three locations (Dholi, Kanpur, Ludhiana). Based on mean of three locations for seedling mortality (17.5%) and DW/10 seedlings (6.0 g) DRMR 2059 rated tolerant to high temperature at seedling stress(Table 1). Field evaluation of DRMR 2059 over 4 locations (Dholi, Hisar, Kanpur and Ludhiana)showed yield reduction≤20% and HSI≥0.6 hence considered highly tolerant to terminal heat stress with relatively lesser depression in membrane stability, seed weight and seeds/siliqua (Table 1). Thus, DRMR 2059 possesses high temperature tolerance at seedling stage and terminal heat stress. This line can be used as a donor in mustard hybridization programme.

Morpho-agronomic characteristics: Morphological traits of the DRMR 2059 is as follows: Plant Height (cm),183; Days to maturity, 136;Primary branches/ plant (no.), 6.4; Secondary branches/ plant (no.), 11.7; Main shoot length (cm), 81.7; Siliquae/plant (no.), 322; Siliqua length (cm), 5.6; Seeds/ siliqua (no.), 16.7; 1000 seed weight (g), 5.7; Oil content (%), 40.97; Seed yield/ plant (g), 25.56.

Table 1. Pooled data of DRMR 2059 over locations (Four locations) during 2018-19 under AICRP-RM trials for different parameters

Genotypes	Controlled condition		Field condition		Genotypes	Membrane stability reduction (%)	Seed yield reduction (%)	HSI
	Seedling mortality (%)	DW/10 seedlings (mg)	Seedling mortality (%)	DW/10 seedlings (g)				
DRMR 2059	17.3	51.4	17.5	6.0	DRMR 2059	11.31	16	0.777
RGN 73 (ZC)	52.8	43.7	34.2	6.3	NRCHB 101 (ZC)	19.02	31.1	1.08
PM25 (NC)	23	49.3	19.8	5.5	PM-26 (ZC)	14.24	24.9	0.944
JD 6 (ZC)	30.2	41.1	33.1	3.8	JD 6 (ZC)	13.33	26.7	1.016
Kranti (NC)	44.3	42	27.4	5.1	Kranti (NC)	16.88	21.2	1.115
RH 749 (ZC)	30.7	45.2	23.2	5.7	RH 749 (ZC)	15.6	21.9	0.913

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DRMR Annual Report (2016-17) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur 321303 Rajasthan, page 28-29

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53. DRMR 4001 (IC0632086; INGR19085), an Indian Mustard (*Brassica juncea*) Germplasm for Drought Tolerance

HS Meena*, VV Singh, A Kumar, B Ram, PD Meena, BL Meena and PK Rai
ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan, India
**(Email: singh_hari2006@yahoo.co.in)*

Indian mustard (*Brassica juncea* L.) is an important oilseed crop of India. It is major source of income especially for marginal and small farmers in rainfed areas of 7 states. This is mostly grown on light textured soils with conserved moisture from monsoon rains. The crop inevitably suffers from moisture stress (drought)

during reproductive period when stored water becomes depleted. This leads to a heavy loss of seed yield during severe conditions. Therefore, it is highly needed to have some good sources of drought tolerance that will be utilized for development high-yielding drought-tolerant varieties. The genotype DRMR 4001 was derived from a cross between BEC 107 (*B. juncea*) × HC 2 (*B. carinata*) at DRMR, Bharatpur. This genotype was isolated as a pure line through pedigree selection and found promising under moisture stress conditions. The genotype was tested under AICRP-RM plant physiological trials during 2015-16 and 2016-17 at 4-7 locations. Pooled summary over the years and locations indicates that proposed genotype DRMR 4001 has less reduction RWC, SPAD, 1000-seed weight, seed yield and other important traits as compared to drought tolerant checks. The drought susceptibility index (DSI) value of proposed genotype was lowest as compared to checks (Table 1). This indicates drought tolerant characteristics of DRMR 4001 and the genotypes can be utilized in breeding programmes for development of high-yielding drought-tolerant varieties. Hence, this promising line needs protection through germplasm registration.

Table 1. Pooled summary of physiological parameters (Drought tolerance) for proposed genetic stock DRMR 4001 and checks in physiological trials during 2015-16 to 2016-17

Parameter	No. of locations	DRMR 4001	Check varieties		
			RH 406	RB 50	Kranti
Relative water content (Reduction %)	7	9.9	12.9	10.0	13.4
SPAD Values (Reduction %)	7	15.4	15.6	17.4	5.0
Seed yield (Reduction %)	7	23.3	23.1	25.6	25.0
1000 seed weight (Reduction %)	6	11.4	13.1	15.6	16.2
Drought Susceptibility Index (DSI)	7	0.77	0.81	0.94	0.81
Seeds/siliqua (Reduction %)	7	10.9	10.3	10.0	8.1
Harvest Index (Reduction %)	7	10.1	15.8	14.8	13.1
Oil content (Reduction %)	4	2.9	2.6	3.5	3.0
Biological yield (Reduction %)	7	17.7	14.2	19.0	19.5

54. DRMR 4005 (IC0632087; INGR19086), an Indian Mustard (*Brassica juncea*) Germplasm with Thermo Tolerance at Juvenile Stage Coupled with High Seed and Oil Yield

HS Meena*, VV Singh, A Kumar, B Ram, PD Meena, BL Meena, HK Sharma and PK Rai
ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan, India
**(Email: singh_hari2006@yahoo.co.in)*

Indian mustard (*Brassica juncea* L.) is an important oilseed crop of winter in India & plays a vital role in edible oil pool of the country. High temperature at juvenile stage (germination / seedling stages) is becoming a severe threat in major mustard growing states like Rajasthan and Haryana and badly affecting the production. An optimum temperature around 25°C is required for proper germination and seedling establishment in this crop. However, due to changing climatic conditions the temperatures during last many years crossed this limit in major mustard areas and soil temperature reaches up to 40-42°C affecting seed germination and plant stand in the field. This prevents early sowing, generally on conserved moistures recommended in many areas. Therefore, it is highly needed to have germplasm lines with heat tolerance at seedling stage and will be utilized in breeding programmes.

The genotype DRMR 4005 was derived from a cross between SEJ-2 × K 28 at DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising for thermo tolerance at seedling stage coupled with high seed & oil yield and suitable for early sown conditions. The genotype was tested under AICRP-RM plant physiological trials during 2017-18 and 2018-19 at 6 locations (environments) and plant breeding trials during 2016-17 and 2017-18 at 11locations. Pooled summary over the years and locations indicates that proposed genotype DRMR 4005 has less seedling mortality (<20%), high RWC

Table 1. Pooled summary of physiological parameters (thermo tolerance) and performance for oil yield & contributing traits of proposed genetic stock DRMR 4005 and checks under AICRP-RM trials during 2016-17 to 2018-19.

Parameters	No. of locations	DRMR 4005	Check varieties			
			PM 25	JD 6	Kranti	PM 28*
Seedling mortality (%)	6	16.6	23.4	33.2	30.8	--
Dry weight (g) of 10 seedlings	6	7.8	8.6	7.6	5.5	--
SPAD values (Chlorophyll content)	6	40.8	40.1	35.3	37.9	--
Relative water content (%)	6	79.1	74.5	68.2	72.4	--
Seed yield (kg/ha)	11	2330	1983	2131	--	2148
Oil yield (kg/ha)	11	955	808	868		881
1000 Seed weight (g)	11	4.7	4.9	4.4	--	4.3
Oil content (%)	11	41.0	40.8	40.7	--	41.0
Days to maturity	11	131	124	133	--	127

***Latest Release check for early mustard in Zone II.**

(%), SPAD values (chlorophyll), dry seedling weight along with high seed & oil yield as compared to heat tolerant (seedling stage) checks (Table 1). Proposed genotype DRMR 4005 has 8.39 to 18.19% higher oil yield and 8.47 to 17.49 % higher seed yield over the checks. This indicates thermo tolerant (at seedling stage) characteristics of DRMR 4005 and it can be utilized in breeding programmes for development of high-yielding thermo (heat) tolerant varieties with high seed and oil yield, as it has better yield traits. Hence, this promising line needs protection through germplasm registration.

55. IC0268345 (IC0268345; INGR19087), a Linseed (*Linum usitatissimum*) Germplasm with High Seed Oil Content (43.65%) and More Number of Primary Branches

V Kaur[1*], S Kumar[1], R Yadav[1], S Kumari[2], DP Wankhede[1], J Radhamani[1], J Aravind[1] and A Kumar[1]
[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India.*
[2]*Division of Biochemistry, ICAR-IARI, Pusa Campus, New Delhi, India.*
**(Email: vikender.kaur@icar.gov.in)*

Linseed is one of the oldest domesticated crops in the world and is considered to be originated and domesticated in Indian sub-continent. Two distinct morphotypes namely seed-type and fibre/flax type are recognized in linseed. In India, it is grown as *rabi* oilseed crop mainly utilized for industrial purpose and as edible oil. Breeding for high oil content is one of the main objectives of linseed breeding. Wide diversity in linseed germplasm indicates a considerable potential for improving this crop for both agronomic and quality traits (Kaur *et al.*, 2017). A wide range of variation in oil content with mean of 38.3% was observed in Canadian collections of 2934 accessions of linseed from 72 countries (Diederichsen and Fu, 2008).In this perspective, one landrace accession IC0268345 from Dindori district of Madhya Pradesh was identified for high oil content up to 43.65% (Table 1) along with other desirable agronomic traits such as number of primary branches per plant, moderately

Table 1. Year wise data of oil content in linseed accession IC0268345

Year	Field evaluation location	Laboratory- Biochemical analysis	Oil Content (%)		
			IC0268345	Check var.1 (Rashmi)	Check var. 2 (RLC-76)
2014-15	ICAR-NBPGR, New Delhi	ICAR-NBPGR	41.78*	37.50	39.10
2015-16	ICAR-NBPGR, New Delhi	ICAR-NBPGR	42.45*	38.20	38.90
2016-17	ICAR-NBPGR, Issapur farm, New Delhi	Division of Biochemistry, ICAR-IARI	43.50	38.15	38.45
2017-18	ICAR-NBPGR, New Delhi	Division of Biochemistry, ICAR-IARI	43.65	37.35	38.30
Mean			42.85**	37.80	38.68

*adjusted pooled mean value is 42.7% for year 2014-15 and 2015-16 as mentioned in Kaur *et al.*, 2018.
**significantly superior at $P_{0.001.}$

high seed yield per plant. The identified accession can have potential utility in linseed breeding program for central India particularly Madhya Pradesh – the major linseed producing state in terms of area, production and productivity. In addition, the landrace (IC0268345) *per se* holds greater promise as perfect germplasm accession for participatory breeding which has implications on social welfare of resource poor farmers as well as conservation of genetic diversity *in situ*.

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56. NRC 142 (IC630595; INGR19088), a Lipoxygenase 2 Free Soybean (*Glycine max*) Germplasm. Free from Kunitz Trypsin Inhibitor

Anita Rani* and Vineet Kumar
ICAR-Indian Institute of Soybean Research, Indore, Madhya Pradesh, India
**(Email: anitavks@yahoo.co.in)*

Soybean was introduced in India with the expectation that the crop being one of the most economical sources of protein would combat rampant protein malnutrition among masses. Apart from the proteins, presence of several nutraceutical molecules reduces the risk of the onset of lifestyle diseases (Kumar *et al.*, 2010). However, soybean did not gain popularity as a protein source despite the declining per capita availability of pulses, the staple source of protein in Indian diet. Presence of anti-nutritional factor, namely, Kunitz trypsin inhibitor (KTI) and off-flavour generating lipoxygenases in soybean grains constrain their utilization in food uses. Kunitz trypsin inhibitor present in soybean seeds affects the digestibility of proteins and if left active in the soy products may cause pancreatic hypertrophy. Lipoxygenase is the off-flavour generating enzyme which exists in 3 isozymic forms, namely, lipoxygenase 1, lipoxygenase 2 and lipoxygenase 3 in soybean seed. These isozymes act upon polyunsaturated fatty acids, when the seeds are crushed to process soy food products, thereby releasing aldehyde and ketone compounds. Of these 3 isozymes, lipoxygenase 2 (Lox 2) is the principal contributor to the off-flavour. Though both KTI and lipoxygenase 2 are heat labile but the heat treatment incurs extra cost and affects the solubility of proteins. Genetic elimination of these two formidable undesirable components from soybean seeds is the dire need of soy food industry. ICAR-IISR has already developed and commercialized KTI free soybean genotypes, namely, NRC 101 and NRC 102. The institute has developed NRC 127, which is the first KTI free soybean variety released for farmers in Central zone. The institute has also developed and commercialized lipoxygenase 2 free soybean, namely, NRC109 to soy food industries. However, soy food industries are seeking soybean genotypes free from KTI as well as lipoxygenase 2.

To develop soybean genotype free from both KTI and lioxyegnase-2 for soy food industries, NRC 142 was developed from a triple cross JS 97-52 x PI 596540 x PI 542044, through marker assisted forward breeding. PI 542044 and PI 596540 were the donors for null alleles of KTI and lipoxygenase 2, respectively. Presence of null alleles of lipoxygenase-2 and KTI in the plants during advancement of generations of JS 97-52 × PI 596540 × PI 542044 were tested using null allele-specific primers of Lox2 designed by Shin *et al.* (2012), and that of KTI designed by Moraes *et al.* (2006) and deployed in development of KTI free lines (Kumar *et al.*, 2013). For this purpose, genomic DNA was extracted from the young leaves using the CTAB method and used as template for amplification using the null allele specific primers for lipoxygenase-2 and KTI. Presence of null allele of lipoxygenase-2 plants in each generation was validated by rapid assay in the seeds, according to Suda *et al.* (1995) and presence of null allele of KTI was validated by native PAGE. Template DNA isolated from NRC142, JS 97-52, PI 596540 and PI 542044were amplified with null allele specific primers of lipoxygenase 2 and KTI. Null Lox2 specific marker generated amplicons of 550 bp size in NRC142, similar to the donor parent PI 596540 but

no amplicon in JS 97-52 and PI 542044, while null KTI specific marker generated amplicons of 420 bp in NRC142 similar to donor parent PI 542044, while no amplicon in JS 97-52 and PI 596540 The seed extracts of NRC142 along with its parents were subjected to native PAGE. A 21Kda band of KTI was observed in JS97-52, while it was absent in NRC142 and the donor of null allele PI 542044.The seed extracts of NRC142 along with its parents were also subjected SDS PAGE and rapid test for testing absence of lipoxygenase.

Morpho-agronomic characters: The plant of NRC142 bears white flowers in 40 days, attains height of 75 cm, and reaches harvest maturity in 98 days. The seeds are of light-yellow colour with black hilum, and weight of 100 mature seeds (10% moisture) is 14.4 g. The yield potential of this genotype is 3.2 tonnes/ha. The genotype would serve as excellent raw material for soy food industry, and more importantly, being high yielding with additional quality traits can fetch better prices to farmers. This is the first genotype developed in India, which is free from lipoxygenase 2 as well as Kunitz trypsin inhibitor.

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57. Dun-nun II-2-15/EC34101 (EC34101; INGR19089), a Photoinsensitive Soybean (*Glycine max*) Germplasm. Source of Recessive Photoperiodic Allele e3

VS Bhatia[1], S Gupta[1*], S Yadav[1], RK Singh[2], G Kumawat[1], GK Satpute[1] and K Jumrani[1]

[1]*ICAR-Indian Institute of Soybean Research, Indore, Madhya Pradesh, India*

[2]*Indian Council of Agricultural Research, Krishi Bhavan, Dr. Rajendra Prasad Road, New Delhi, India*

[*]*(Email: sanitaishu@gmail.com)*

Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length, which depends on latitudes, is less than their critical day length. Although soybean adapts to a very wide range of latitudes, its individual accessions adapt to a narrow latitudinal band. India lies in the latitudes between 6°-37° and latitude specific adaptation is observed in soybean accessions and varieties (Bhatia *et al*, 2003). At IISR, Indore, we have identified six photoinsensitive accessions. Soybean germplasm accession EC 34101 originally acquired from Hungary has been identified as photoperiod insensitive through screening of 2071 germplasm accessions under long day conditions created by extending day length with incandescent light (ILD) (Bhatia *et al*, 2008; Singh *et al*, 2008; Gupta *et al.*, 2017). EC 34101 flowered in same number of days to flower in ILD as in ambient day length showing no effect of photoperiod on flowering. EC 34101 has been characterized for genes underlying photoperiod insensitivity and maturity traits using allele specific markers, and its genotype has been determined as *E1E1E2E2e3e3E4E4*(Gupta *et al*, 2017). Polymorphic markers between six photoinsensitive accessions (MACS 330, EC 325097, EC 325118, EC 333897, EC 34101, EC 390977) and 25 varieties/accessions have been identified and diversity studies have placed MACS 330 in a separate cluster and EC 333897, EC 34101 and EC 325118 are grouped together (Gupta *et al*, 2014).

Characteristic botanical and morpho-agronomical features of EC 34101 are given in Table 1 and its consistent flowering response over latitudes, in comparison to photosensitive varieties Pb1, JS 335, JS 80-21 and Type 49, is shown in Figure 1.

Genotype EC 34101 is a useful germplasm source for breeding of photo-insensitivity, earliness and semi-

determinate growth habit in soybean. These traits are desirable for development of soybean cultivars for growing in new areas across latitudes for wider adaptation and increasing cropping intensity of the crop. Identified allele specific markers would be useful for gene pyramiding for earliness and photo-insensitivity using marker assisted breeding.

Table 1. Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype EC 34101

Trait	Value	Trait	Value
Hypocotyl pigment	Green	Early Plant Vigour	Good
Leaf color	Green	Leaf Shape	Intermediate
Number of leaflets	3	Stem determination	Semi-determinate
Flower Colour	White	Photoperiod sensitivity score	Photoinsensitive
Pubescence	Present	Pubescence color	Gray
Pubescence density	Normal	Pubescence type	Erect
Seed Colour	Yellow	Hilum colour	Brown
Number of primary branches	2.8	Days to flower	30 (30)*
Plant height	33.0 cm	Days to maturity	84 (82)*
Pod color at maturity	Tan	No. of seed/pod	2.0
100-seed weight	12.0	No. of nodes/plant	9.4
Number of pods/plant	36.4	Pod colour	Light Brown
Cotyledon colour	Yellow	Seed coat colour	Yellow
Seed Coat Pattern	Light hilum	Hilum Colour	Brown

*Value in parenthesis denotes flowering in extended day length conditions.

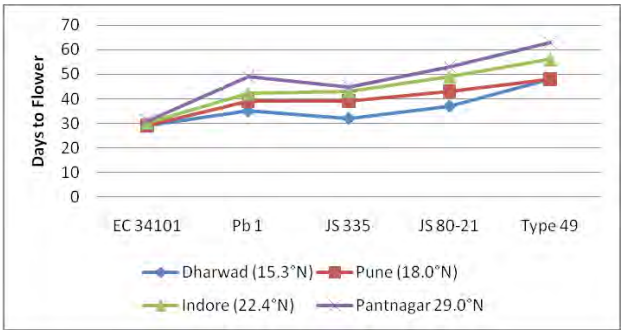

Fig. 1. Latitudinal consistency of photoinsensitive accession EC 34101 for days to flowering

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58. AGS 25 (EC150149; INGR19090), a Soybean (*Glycine max*) Germplasm with Source of Earliness

S Gupta[1*], G Kumawat[1], GK Satpute[1], R Tripathi[1], N Agrawal[1], Shivakumar M[1], M Ratnaparkh[1], VS Bhatia[1], Philips V[3],, SP Mehtre[4], K Singh[5], C Gireesh[6], M Arya[2], J Radhamani[2], AN Srivastava[7], SM Husain[1], SK Pandey[1] and Y Mohan[1]

[1]*ICAR-Indian Institute of Soybean Research, Indore, Madhya Pradesh, India*
[2]*ICAR-National Bureau of Plant Genetic Resources, New Delhi, India*
[3]*Agharkar Research Institute, Pune, Maharashtra, India*
[4]*Marathwada Agricultural University, Parbhani, Maharashtra, India*
[5]*GB Pant University of Agriculture and Technology, Pantnagar, India*
[6]*ICAR-Indian Institute of Rice Research, Hyderabad, Telangana, India*
[7]*JNKVV, Jabalpur, Madhya Pradesh, India*
[*]*(Email: sanitaishu@gmail.com)*

Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length (depends on latitudes) is less than their critical day length. Soybean

genotypes grown at higher latitudes have high critical day length and are photoinsensitive as they can flower under very high day length. However, when soybean is grown near equator or where days are short or under short day conditions like delayed sowing due to late monsoon arrival, it flowers precociously without sufficient vegetative biomass to support good grain yield. For such conditions long juvenile trait is useful as it allows plant to remain in vegetative conditions even under extreme short day conditions. Commercial soybean cultivation in countries near equator (lower latitudes) became possible only after the identification of long juvenile trait (Hartwig, 1970). Delayed flowering in long juvenile lines results in the gain of more height, nodes, grain yield and other agronomic characters (Lawn, 2011a&b).Introduction of this trait has helped extend soybean cultivation in lower latitudes and made Brazil the second largest soybean producing country in the world (Gavioli, 2013).India lies in lower latitudes between 6°-35°N latitudes. Soybean is a rainfed crop in India and its sowing starts with the onset of monsoon. Under delayed monsoon conditions soybean sowing is undertaken in shorter day length condition which results in yield penalty due to early flowering. Although sources of long juvenility are known but performance of these resources is poor in Indian conditions. We have identified a novel long juvenile germplasm resource AGS 25 by screening of germplasm under delayed sowing conditions (ICAR-IISR annual reports 2010-11, 2011-12). This germplasm has been tested for adaptation in AICRP multi-location germplasm evaluation trials and it has shown the potential to delay flowering and gain high biomass in these locations (AICRPS annual report 2014-15 and 2015-16). This germplasm was hybridized with popular soybean varieties JS 93-05 and JS 95-60 and long juvenility trait was found to be governed by single recessive gene (ICAR-IISR annual report 2013-14). AGS 25 has been used in breeding programmes and many high yielding long juvenile advanced breeding lines have been developed and are under AICRPS trial (ICAR-IISR Indore annual report 2016-17 and AICRPS technical programme 2019-20). Recombinant inbred lines of JS 93-05 x AGS 25 and JS 95-60 x AGS 25 have been developed and used for QTL identification and gene responsible for long juvenility was identified on chromosome 16 where earlier reported long juvenile gene *e9* resides. A novel recessive allele of *E9* developed due to single nucleotide polymorphism has been identified and attributed for long juvenile response of AGS 25. Sequencing of AGS 25 at known photoperiodic loci identified its genotype as E1E1E2E2E3E3E4E4Dt1Dt1.

Characteristic botanical and morpho-agronomical features of AGS 25 are given in Table 1.

Genotype AGS 25 is a useful germplasm source for breeding for long juvenility and wider adaptation. These traits are desirable for development of soybean cultivars suitable for sowing under wider array of sowing dates and latitudes. Identified new allele has been converted to CAPS marker and would be helpful in breeding for long juvenility using marker assisted breeding.

Table 1. Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype AGS 25

Trait	Value	Trait	Value
Hypocotyl pigment	Purple	Early Plant Vigour	Good
Leaf color	Light Green	Leaf Shape	Intermediate
Number of leaflets	3	Stem determination	Semi-determinate
Flower Colour	Purple	Photoperiod sensitivity score	Photosensitive
Pubescence	Present	Pubescence color	Tawny
Pubescence density	Normal	Pubescence type	Semi-appressed
Seed Colour	Yellow	Hilum colour	Brown
Plant height	91.4	Days to flower	64
100-seed weight	6.6	Days to maturity	106
Cotyledon colour	Yellow	Seed coat colour	Yellow
Seed Coat Pattern	Dark hilum	Strophile at hilum	Present
Surface lustre	Dull	Lodging score	Severe
Pod Colour	Light Brown	Primary branches/plant	6.2
Pods/plant	50.4	No. of nodes/ plant	18.4

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59. EC174527 (EC174527; INGR19091), a Basil (*Ocimum basilicum*) Germplasm with Essential Oil Rich in Linalool Content (~ 61.18 ± 4.41%) in Oil Isolated from Aerial Plant Parts

AP Raina*, A Kumar and V Gupta
ICAR-National Bureau of Plant Genetic Resources, New Delhi, India
(Email: Archana.raina@icar.gov.in; aprraina@yahoo.co.in)

The genus *Ocimum* L. (Lamiaceae) is an extremely versatile and largest group consisting of about 150 specieswhich are found in tropical and sub-tropical regions of Asia, Africa and South America. Most members of this genus are annual or perennial, highly aromatic, branched herbs or shrubs. *Ocimum basilicum* L. (Sweet basil) is one of the most important species which is planted as a popular culinary and medicinal herb. The basil essential oils are usually extracted from the leaves and flowering tops of basil plants. The plant shows great chemical and morphological variability because of the abundant cross pollination, inter-specific hybridization, polyploidy. The essential oils exhibited a wide and varying array of chemical compounds, depending on variations in chemotypes, leaf and flower colors, aroma and origin of the plants. There are significant differences in the chemical composition and amounts and kinds of aromatic components in the essential oils of basil depending on the species/variety and environmental conditions of the cultivation locations (Pushpangadan and Bradu, 1995). According to the chemical composition and geographical origin, *Ocimum* species were classified into three large groups: European type, Exotic or Reunion type and African type. Lawrence (1988) established four essential oil chemotypes (methyl chavicol, linalool, methyl eugenol and methyl cinnamate) and also numerous subtypes. The chemical composition of basil is highly variable depending largely on the source, and can vary by extraction method and with developmental stages (Verma *et al*., 2013). Variations in chemical composition of basil oil play an important role in evaluating their utilization and value for industrial applications (Raina *et al*., 2017 and 2018)

Ocimum species have been extensively used as spices, flavouring agents and as source of commercial essential oils. These are known for their diverse use in folk medicine for the treatment of various gastric and urinary diseases, insomnia, inflammation and constipation. The essential oil obtained from these species has found important application in perfumery, flavour and pharmaceutical and medicinal uses. *Ocimum* species are reported to have diverse biological activities like antibacterial, antimicrobial, antioxidant, antipyretic, insecticidal, antispasmodic. These volatile oils have been applied in perfumery, to inhibit growth of microorganisms, in food preservation and in aromatherapy.

The present exotic germplasm collection of *O. basilicum* EC174527 was imported from Germany in 1986. The germplasm was grown in Experimental Fields of ICAR-NBPGR, New Delhi for characterization and evaluation of agro-morphological and quality traits for four years. It was evaluated for the economically important quality trait of essential oil obtained from aerial parts of plant by hydrodistillation. Detailed chemical profiling of essential oil isolated from aerial plant parts of EC174527 by GC/MS exhibited linalool-rich chemotype was present in this collection. Validation of this value-rich superior accession of *Ocimum* germplasm was performed over consecutive four years for major aroma compound and identified trait-specific value-rich germplasm accessions EC174527 (linalool 61.18 ± 4.41%). Linalool is an important compound highly prized for its use in perfume and flavor industry. The essential oils of basil extracted from leaves and flowering tops are used in food flavours, dental and oral products, in fragrances and in traditional medicines. Essential oils derived from *O. basilicum* offers a bright future for perfumes and flavours industry.

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60. IC599290 (IC599290; INGR19092), a Velvet Bean (*Mucuna pruriens)* Germplasm with High L Dopa Content in Seeds (7.1% DWB)

AP Raina*, RC Misra and DR Pani

CAR-National Bureau of Plant Genetic Resources, New Delhi, India

*(*Email*: *Archana.raina@icar.gov.in, aprraina@yahoo.co.in*)

Mucuna pruriens (L.) DC *var. pruriens* Wilmot-Dear (family Fabaceae) is an important medicinal plant, which has long been used as a traditional medicine in India due to the presence of bioactive compound L-DOPA (L-3,4-dihydroxy phenylalanine) in seeds and serves as potential drug for the treatment of Parkinson's disease. The plant is commonly known as Kewanch or Kaunch in Hindi, Atmagupta in Sanskrit and Velvet bean in English. It is a twining annual legume, originally from Eastern India and Southern China and later widespread in other parts of the tropics including Central and South America. The genus *Mucuna* consists of about 120 – 130 species of annual and perennial legumes and about fifteen species are found in the lower hill slopes and plains of India. It is widely used in traditional Ayurvedic, Unani, and Homoeopathic system of Indian medicine for the management of male fertility, as neuro-protective, anti-snake venom/ scorpion stings and an aphrodisiac (Sathiyanarayanan & Arulmozhi 2007).

It is a constituent of more than 200 indigenous drug formulations. Active compound L-DOPA (L-3,4-dihydroxy phenylalanine), a non-protein amino acid is a precursor of the neurotransmitter dopamine and is being used in the treatment of Parkinson's disease a degenerative disease of the nervous system and is characterized by muscular rigidity difficulty with balance and walking, depressions and dementia. L-DOPA, a dopamine precursor, either alone or in combination with and aromatic amino acid decarboxylase inhibitor is the most effective drug for the treatment of this disease, since dopamine fails to pass through the blood brain barrier. Use of biological sources for production of L-DOPA, is always desirable and advantageous because the chemical synthesis results in racemic DL-mixture, which is inactive and further separation of enantiomerically pure L-dopa from this mixture, is very difficult and cumbersome. In addition, D-DOPA interferes with the activity of dopa decarboxylase, the enzyme involved in the production of dopamine in the brain. L-dopa isolated from *Mucuna* was found to be more effective than the synthetic product.

Keeping in view the increasing demand for herbal drugs, importance of this species and vast diversity of *Mucuna* germplasm available in Indian sub-continent, efforts were made to characterize diverse germplasm of *Mucuna pruriens* collected from wild habitats of Odisha located in Eastern coastal areas of India. A total of 34 accessions were collected, characterized and evaluated in respect of agro-morphological and economic traits at NBPGR Regional Station, Cuttack.

Agro-morphological characterization and chemical evaluation of *M. pruriens* germplasm resulted into identification of a value-rich genetic stock of *M. pruriens* IC599290(collector number RCM/GD/75)with high L-dopa content of 7.1 % on dry weight basis in seeds by HPTLC for four years 2013-2014 to 2016-2017 (Raina and Misra, 2018). This genotype was identified for high L-DOPA content in seeds against normal range of 2.2 to 5.3 reported in Indian conditions. This germplasm was collected from wild areas of Jajpur district in the coastal delta zone of Odisha. Pods contained 5 to 6

seeds, black, shining, glossy and 0.9 - 1.1 x 0.76 - 0.80 cm. This genetic stock can be used as a source for L-DOPA for commercial cultivation and exploitation for the pharmacological properties. It may be an affordable alternative for patients suffering from Parkinson's disease.

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61. CSIR-IHBT-CL-Y-1 (IC0623597; 19094), a Calla Lily (*Zantedeschia elliottiana*) with Trumpet Flower Shape. Bright Yellow Flower Colour and Stalk Length >40cm

A Kumar*, Sanatsujat Singh, B Bhargav and RK Sharma
CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh
**(Email: sanatsujat@ihbt.res.in)*

The parental genotypes of *Zantedeschia elliottiana* CSIR-IHBTCL-ZE-1 (light yellow coloured) and CSIR-IHBT-CL-ZE-2 (Red purple coloured) were crossed and variable colours of calla lilies were obtained in the progenies which were morphologically characterized for floral traits. The genotype CSIR-IHBT-CL-Y-1 has been selected for its unique cylindrical trumpet flower shape and attractive bright yellow colour. The genotype along with parents were evaluated for two years with respect to flower production potential and other agronomic attributes *viz*., flower stalk length, stalk diameter, leaf size and numbers, plant height, number of flowers per plant and number of shoots under field and protected conditions. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits and evaluated for agronomic performance over a period of two years and CSIR-IHBT-CL-Y-1was found superior to the parental lines. The genotype has been released as cultivar 'Him Sumukh' (CSIR-IHBT-CL-Y-1) by CSIR-Institute of Himalayan bioresource Technology, Palampur, having high vegetative propagation potential for commercial utilization.

62. HIM SHWETA (CSIR-IHBT-CL-W-1) (IC0623597; 19094), a Calla lily (*Zantedeschia elliottiana*) with White Flower Colour, Large Spathe and Stalk Length (>80cm)

A Kumar*, Sanatsujat Singh, B Bhargav and RK Sharma
CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh
**(Email: ashok@ihbt.res.in)*

In *Zantedeschia aethiopica*, hybridization programme was undertaken using two parental genotypes CSIR-IHBT-CL-ZA-1 and CSIR-IHBT-CL-ZA-2. Variable floral shapes of calla lilies were obtained in the progenies which were evaluated for agronomic traits under protected and field conditions. The genotype CSIR-IHBT-CLW- 1 has been selected for desirable flower shape and white colour. The evaluation of selection along with parents was done for two years with respect to flower production and agronomic parameters viz. flower stalk length, stalk diameter, leaf size and numbers, plant height, number of flowers per plant and number of shoots and the selection was found promising compared to parental lines. The genotype has been released as cultivar 'Him Shweta' (CSIR-IHBT-CL-W-1) by CSIR-Institute of Himalayan Bioresource Technology, Palampur, having high vegetative propagation potential for commercial utilization.

63. CSIR-IHBT-Gr-13-1 (IC0623707; 19095), a Gerbera (*Gerbera jasmeonii*) with Double Flower Shape. Standard Size (>10cm Flower Diameter)

Sanatsujat Singh*, A Kumar, B Bhargav and RK Sharma
CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh
**(Email: sanatsujat@ihbt.res.in)*

Hybrid F_1 genotypes of gerbera were developed through controlled crossing program and mature seeds obtained from different cross combinations were used for the establishment of *in vitro* gerbera cultures. Seeds were cultured on MS basal medium and the developing micro-shoots from seeds were further cultured on MS media supplemented with different doses of growth regulators to achieve shoot proliferation. Of the different media, highest number of micro-shoots, number of leaves and leaf length were observed in MS medium supplemented with 1 mg/L BAP + 0.03mg/L IBA + 0.025 mg/L NAA which gave best proliferation among the gerbera genotypes. Half strength MS medium supplemented with 0.4 mg/L IBA was found best for *in vitro* rooting. Rooted plantlets were successfully hardened in trays filled with moist sand and transferred to sleeves for cultivation in soil. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits and evaluated for agronomic performance over a period of two years. Based on mean performance of hybrid gerbera genotypes compared to respective parents, gerbera genotype CSIR-IHBT-Gr-13-1was found promising having double flower shape of standard size (flower diameter of 10.5 cm) and is red in color. The genotype has been released as cultivar 'Him Gaurav' by CSIR-Institute of Himalayan bioresource Technology, Palampur, with high micro-propagation potential for commercial utilization.

64. CSIR-IHBT-Gr-24-6 (IC0623708; 19096), a Gerbera (*Gerbera jasmeonii*) with Semi Double Flower Shape. Standard Size (>10cm flower diameter). Yellow Orange Flower Colour

Sanatsujat Singh*, A Kumar, B Bhargav and RK Sharma
CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh
**(Email: sanatsujat@ihbt.res.in)*

Parental lines of gerbera were used controlled crossing program and mature seeds obtained from different cross combinations were used for the establishment of *in vitro* gerbera cultures. Seeds were cultured on MS basal medium and the developing micro-shoots from seeds were further cultured on MS media supplemented with different doses of growth regulators to achieve shoot proliferation. Of the different media, highest number of micro-shoots, number of leaves and leaf length were observed in MS medium supplemented with 1 mg/L BAP + 0.03mg/L IBA + 0.025 mg/L NAA which gave best proliferation among the gerbera genotypes. Half strength MS medium supplemented with 0.4 mg/L IBA was found best for *in vitro* rooting. Rooted plantlets were successfully hardened in trays filled with moist sand and transferred to sleeves for cultivation in soil. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits (Figure 1) and evaluated for agronomic performance over a period of two years. Based on mean performance of hybrid gerbera genotypes compared to respective parents, gerbera genotype CSIR-IHBT-Gr-24-6 was found promising having semi-double flower shape of standard size (flower diameter of 11.7 cm) and is yellow orange in color. The genotype has been released as cultivar 'Him Aabha' by CSIR-Institute of Himalayan bioresource Technology, Palampur, which also has high micro-propagation potential for commercial utilization.

65. IIHRV1 (IC0624189; INGR19097), a China Aster (*Callistephus chinensis*) Germplasm for Flower colour: NN155D, White group, Fan 4

Rajiv Kumar[1*], T Manjunatha Rao[1], Sangama[1] and T Janakiram[2]
1*ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India*
2*(Horticultural Science-I), ICAR, KAB-I, New Delhi, India*
**(Email: Rajiv.Kumar11@icar.gov.in)*

China aster is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for loose flower, cut flower, landscape, floral decoration, making garlands and *venis* (Rao *et al.*, 2012). The China aster germplasm IIHRV1 is derived from cultivar Arka Poornima through individual plant selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13^{o} 58' N Latitude, 78^{o}E Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHRV1 is unique for white flower colour (NN155D), semi-double flower form with pseudo ray florets.

Morpho-Agronomic Characteristics: The China aster germplasm IIHRV1has average plant height (54.50cm), number of branches per plant (9.75) and number of flowers per plant (20.00).

Associated characters and cultivation practices: The flowers of China aster germplasm IIHRV1 is white (White group, NN155D, Fan 4), semi-double flower type with 4-5 rows of pseudo ray florets. It has average flower head diameter (3.09cm), length of outer sepals (2.19cm), length of pseudo ray florets (0.66cm), breadth of pseudo ray florets (0.25cm), length of disc florets (0.61cm) and vase life (10.33days).

It grows best in open and well drained loamy soil with soil pH 6 to 7. A temperature of 20^{o} to 30^{o}C during day and 15^{o} to 17^{o}C during night with relative humidity of 50-60% is most suitable for its growth and flowering. Thirty days seedlings are transplanted at a spacing of 30 cm x 30 cm. Plants are pinched 35 to 40 days after transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra. The germplasm IIHRV1 is suitable for cut flower and floral decoration.

Table 1. Morpho-agronomic description of China aster germplasm IIHRV

Traits Description	Average value
Plant height (cm)	54.50
Number of branches per plant	9.75
Number of flowers per plant	20.00
Flower head diameter (cm)	3.09
Length of outer sepals (cm)	2.19
Length of ray florets (cm)	0.66
Breadth of ray florets (cm)	0.25
Length of disc florets (cm)	0.61
Vase life (days)	10.33
Flower colour as per RHS Colour Chart	White group, NN155D, Fan 4
Flower form	Semi-double
Utility	Cut flower and decoration

References

Rao TM, Rajiv Kumar and PB Gaddagimath (2012) China aster. *Extension Bulletin*. The Director. ICAR-IIHR, Bengaluru, pp 1-16.

66. IIHRV2 (IC0624190; INGR19098), a China Aster (*Callistephus chinensis*) with New Flower Form: Semi-double with Pseudo Ray Florets

Rajiv Kumar[1*], T Manjunatha Rao[1], Sangama[1] and T Janakiram[2]
1*ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India*
2*(Horticultural Science-I), ICAR, KAB-I, New Delhi, India*
**(Email: Rajiv.Kumar11@icar.gov.in)*

China aster is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for loose flower, cut flower, landscape, floral decoration, making garlands and *venis* (Rao *et al.*, 2012). The China aster germplasm IIHRV2 is derived from cultivar Arka Violet Cushion through individual plant selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru,

Karnataka (13^{o} 58' N Latitude, 78^{o}E Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHRV2 is unique for violet flower colour (N81A), semi-double flower form with pseudo ray florets.

Morpho-agronomic characteristics: The China aster germplasm IIHRV2 has average plant height (64.50cm), number of branches per plant (12.00) and number of flowers per plant (32.00).

Associated characters and cultivation practices: The flowers of China aster germplasm IIHRV2 is violet colour (N81A, Purple Violet group, Fan 2), semi-double flower form with 4 to 5 rows of pseudo ray florets. It has average flower head diameter (2.79 cm), length of outer sepals (1.59cm), length of pseudo ray florets (0.55 cm), breadth of pseudo ray florets (0.21 cm), length of disc florets (0.48cm) and vase life (10.93 days).

It grows best in open and well drained loamy soil with soil pH 6 to 7. A temperature of 20^{o} to 30^{o}C during day and 15^{o} to 17^{o}C during night with relative humidity of 50-60% is most suitable for its growth and flowering. Thirty days seedlings are transplanted at a spacing of 30 cm × 30 cm. Plants are pinched 35 to 40 days after transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra. The germplasm IIHRV2 is suitable for cut flower and floral decoration.

Table 1. Morpho-agronomic description of China aster germplasm IIHRV2

Traits Description	Average value
Plant height (cm)	64.50
Number of branches per plant	12.00
Number of flowers per plant	32.00
Flower head diameter (cm)	2.79
Length of outer sepals (cm)	1.59
Length of ray florets (cm)	0.55
Breadth of ray florets (cm)	0.21
Length of disc florets (cm)	0.48
Vase life (days)	10.93
Flower colour as per RHS Colour Chart	N81A, Purple Violet group, Fan 2
Flower form	Semi-double
Utility	Cut flower and floral decoration

References

Rao T M, Rajiv Kumar and P B Gaddagimath (2012) China aster. *Extension Bulletin*. The Director. ICAR-IIHR, Bengaluru, pp 1-16.

67. IC0625848 (IC0625848; INGR19099), a Fruit Fly Resistant Ber (*Ziziphus mauritiana*) Germplasm

Om Vir Singh*, K Singh, S Roy, RK Tyagi, AK Singh, PR Meghwal, N patel and V Gupta
ICAR-National Bureau of Plant Genetic Resources, New Delhi, India
**(Email: omvir2007@rediffmail.com)*

Indian jujube (*Ziziphus mauritiana* L.) commonly known as ber, belongs to the family *Rhamnaceae*, is mainly distributed in the tropic zone of southern Asia, Australia, and Africa including Taiwan and China. The productivity and quality of ber fruits are adversely affected by a number of insect pests among them fruit fly (*Carpomiya vesuviana*) considered the most serious pest which can cause damage up to 80% of the crop under severe condition (Cherian and Sunderam, 1941). Although these insects can be controlled by applying insecticides on the crop (Gyi *et al.*, 2003), inbuilt genetic resistance offers better option to control the incidence of insects. In susceptible cultivars the infestation starts with the fruit setting. The adult female lays eggs singly by inserting its ovipositor in the young developing fruit. After 2 to 5 days the larvae hatch, start feeding on the pulp and make galleries in it. Generally, only one larva is found in one fruit. The excreta of the larva accumulate in the galleries, results in rotting of the fruit. Infested fruits become deformed and their growth becomes stunted. A large number of such fruits drop off. The larval stage lasts 9 to 12 days. Full grown (6 mm length) larva finds its way out by making a hole in the fruit skin and drops to the ground. The larva bores down to soil upto the depth of 2 to 12 cm where it pupates and occasionally pupation takes place within infested fruits (Bagdavadze *et al.*, 1977). The pupal period lasts about 2 weeks after which the adult fly (5 to 8 mm long and 3 mm broad) emerges. Pairing and oviposition occur during day light and at night, fly usually rests in the canopy and it completes two generations per year (Berdyeva, 1978).

At Jodhpur Regional Station of ICAR-NBPGR, the 80 live trees of wild, land races and cultivated varieties are being maintained in the field gene bank. Trait specific mean values of three replications over four years of some of the selected cultivars of ber have been recorded for fruit and seed characters. Data were recorded on infestation of fruit fly on the selected cultivars at the interval of 10 days in three trees during 2017-18 and 2018-19. In all cases, 10 randomly selected fruits were examined carefully for oviposition marks, occurrence of exit hole in the fruits and number of larva present inside fruit through peeling of fruits with knife to confirm the stone and fruit fly damage and percentage of infested fruits was calculated. TSS of these fruits was also calculated .It is evident that a large genetic variation is present among cultivars for fruit fly resistance. "*Tikdi*" the land race of ber that had been collected and planned by DP Chopra, Economic Botanist, at ICAR-NBPGR Regional Station, Jodhpur on 28-06-1968 had shown absolute resistance to fruit fly. It also appears from the concentration of TSS in the ber fruits is not having any impact on resistance or susceptibility for fruit fly.

The fruits of *Tikdi* rarely contain insect larva and their excreta. There was no visible oviposition marks or exit hole in its fruits over the growing period. In contrast all other accessions taken for study had fruit fly infestation. The grown plants of *Tikdi* are highly tolerant to drought and resistant to frost. Owing to these qualities it is used as a root stock for other commercial varieties of *ber*. Trees are vigorous with upright growth habit and have higher leaf fodder production potential.

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68. IC0625849 (IC0625849; INGR19100), a Stoneless Ber (*Ziziphus mauritiana*) Germplasm

Om Vir Singh*, K Singh, R Gowthami, N Shekhawat and V Gupta
ICAR-National Bureau of Plant Genetic Resources, New Delhi, India
(Email: omvir2007@rediffmail.com)

Indian jujube (*Ziziphus mauritiana* L.) commonly known as ber, belongs to the family *Rhamnaceae*, is mainly distributed in the tropic zone of southern Asia, Australia, and Africa including Taiwan and China (Pasternak *et al*., 2009). The ripen fruits of the plant are mostly consumed raw but sometimes they are stewed also (Morton, 1987). In ber fruits its pulp portion is soft and edible whereas stone portion is very hard and not edible. The 60-90% part of the fruit is made up of inedible stone in most of the popular ber varieties (Om Vir *et al.*, 2015). Pulp character is an important character of ber fruit if breeding is aimed for long storage life (Krishna *et al.* 2014). The pulp: stone ratio is an important character as it indicates towards the edible portion in the fruit (Saran *et al.*, 2006). Thus there is need for improvement of *Z. mauritiana* for its fruit quality. The choice of suitable cultivars is of paramount importance for its success. The twelve accessions of ber germplasm, maintained in the field gene bank of National Bureau of Plant Genetic Resources Regional Station Jodhpur were characterized and compared on the basis of fruits characters *viz.*, fruits, pulp and presence or absence of stone in the fruits. Accordingly, observations were recorded on ten fruits from each replication (with three replications) in each case for four years *i.e*. year 2014-15 to 2017-18. Observation on ripen fruits and stones were recorded when fruits had attained its full size and were ready for harvesting. The chief characteristic features of different ber accessions under study are presented in Table 1 to Table 4. A landrace IC0625849 was recorded with a unique trait *i.e.*, the stone part of the fruit of this landrace is merely absent and small, soft and shriveled edible seeds were present, thus this landrace is named as stoneless ber, whereas, in all other accessions the large sized stone is present. It is observed that 97-99 % part of the fruit of the IC0625849 is made up of edible fleshy pulp. While in other accessions only 10 to 40 % part of the fruit was made up of edible pulp and rest of the part (60-90 %) of the fruit is made up

of stone that is inedible. The highest pulp: stone ratio was noted in IC0625849 and it was recorded as high as 100 per cent, while the least pulp: stone ratio was recorded in IC-0625848 among the studied germplasm. Complete absence of stone in stoneless ber could be useful in breeding programme for development of ber fruit cultivars with stoneless fruits.

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69. MSH/14-113 (IC0630606; INGR19101), an Interspecific Potato Hybrid [Interspecific Potato Somatic Hybrid P8 (*Solanum tuberosum* + *S. pinnatisectum*) × cv. Kufri Jyoti (*S. tuberosum*)]. with Diverse Genetic Base Very High Resistance to Potato Late Blight Disease. High Tuber Dry Matter Content

JK Tiwari*, SK Luthra, V Kumar, R Zinta, Mehi Lal and SK Chakrabarti
ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India
**(Email:ageshtiwari@gmail.com)*

Interspecific potato hybrid (MSH/14-113) is a back-cross progeny of advanced stage clonal selection (BC_1-C_5). MSH/14-113 was developed by crossing somatic hybrid clone 'P8' and potato cv. Kufri Jyoti. The parent 'P8' is an interspecific somatic hybrid and was produced by protoplast fusion between *Solanum tuberosum* dihaploid 'C-13' and wild potato species *S. pinnatisectum*. MSH/14-113 possesses wider genetic base from cultivated (*S. tuberosum*) and wild species (*S. pinnatisectum*). MSH/14-113 possesses very high resistance to late blight disease- the most devastating disease of potato, and also has high dry matter content- an important for processing trait. This shows successful exploitation of interspecific potato somatic hybrid 'P8' in developing a promising advanced stage interspecific potato hybrid (MSH/14-113) with high resistance to late blight and high dry matter content. Besides, SSR alleles (103 and 144 bp) were linked to the interspecific potato hybrid MSH/14-113 were identified for genetic fidelity, of which SSR allele 103 bp was introgressed into MSH/14-113 from the parent P8, having very high resistance to late blight. A few DUS descriptors of MSH/14-113 are: purple sprout, semi-compact plant foliage, tall plant height, green stem colour, open leaf structure, small leaf length, narrow leaf width, anthocyanin colouration is present on flower bud, white-purple flower corolla, small flower size, yellow anther colour, irregular anther cone, normal pistil, longer stylar length, white cream tuber colour, smooth skin, ovoid shape, shallow eye depth and white tuber flesh colour.This interspecific potato hybrid with diverse genetic background, having very high resistance to late blight disease and high tuber dry matter content has potential to employ in potato breeding programmes to widen the cultivated gene pool.

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70. Allohexaploid (H1) (IC0628060; INGR19102), an Allohexaploid (*Brassica juncea* + *Sinapis alba*) Germplasm resistant to *Alternaria brassiceae* and *Sclerotinia sclerotiorum*. Tolerant to temperature

P Kumari and SR Bhat
ICAR-National Institute for Plant Biotechnology, Pusa Campus, New Delhi, India
**(Email: preetesh79@gmail.com*

The Brassicas serve as important sources for vegetables, oilseeds and cultivated throughout the word. The crop suffers from biotic factors such as *Alternaria* blight caused by the *Alternaria Brassicae* and *Sclerotinia* stem rot caused by the *Sclerotinia sclerotiurum* are the major limiting factors along with the abiotic factors high temperature and drought. The yield reduction due to *Alternaria* blight up to 47% and severe conditions raised upto 70 percent (Kolte *et al.,* 1987 and Shukla, 2005). The *Alternaria* blight does not only causes reduction in seed yield but also adversely affects oil and meal quality. The resistance sources for these diseases are not available within cultivated gene pools. However the wild relative of Brassica, namely, *Sinapis alba*, has been reported to possess resistance to *A. brassicae* (Brun *et al*., 1988; Conn *et al*., 1988; Sharma *et al*., 2002) and *Sclerotinia sclerotiorum* (Morrall and Dueck 1882, Li *et al*., 2009). Therefore, with the aim of introgression of these valuable genes into cultivated Brassicas. We have developed somatic hybrid (H1) through PEG mediated protoplast fusion. The hypocotyl protoplast of *Brassica juncea* RLM-198 and mesophyll protoplast of *Sinapis alba* were isolated and fused as per previous standardized protocols (Kirti *et al.,* 1990). We have standardized the regeneration media and found very good regeneration frequency. The regenerated shoots were attained roots into half MS medium and acclimatized very well in the net house conditions. The hybridity was confirmed through morphological, molecular and cytological basis. The hybrid carried complete nuclear genomic constitution of the parent (amphidiploid *B. juncea* =AABB and diploid *S. alba*=SS). The hybrid acquired organelles (chloroplast and mitochondria) from *B. juncea*. The chromosomal constitution of the Allohexaploid Brassica (H1) was confirmed through mitotic counts and Genomic In situ Hybridization (GISH) by using the FITC labeled *S. alba* genome as a probe. The hybrid possessed total sixty chromosomes in their somatic cells. The Allohexaploid (H1) obtained thirty six chromosomes from *B. juncea* and twenty four chromosomes from *S. alba.* All the twenty four chromosomes of *S. alba* were hybridized with FITC labeled *S. alba* probes. The present somatic hybrid maintained meiotic pairing between the homologous chromosomes. Therefore, bivalent formation was maintained and monovalent/ multivalent formation was not evident.

Morpho-agronomic characteristics: The somatic hybrid was grown vigorously in net house as well as in field conditions. The plant attained the height approx 320 cm when sown in the last week of October. The prominent trichomes were found on the stems and leaves of the somatic hybrid. The pollen viability of the Allohexaploid Brassica (H1) was found more than 90% and very good female fertility. This is a first instance when somatic hybrid possessed very good male and female fertility. Due to normal meiosis, the hybrid is stable over the generations.

Associated characters and cultivation practices: The Allohexaploid (H1) was found resistant to *Alternaria* blight and *Sclerotinia* stem rot during the screening up to six seasons at four different environments along with hot spot conditions to the disease in four successive years. The present allohexaploid showed temperature tolerance up to 40°C during the flowering and seed setting stages. The normal meiosis and stability of the somatic hybrid proved the feasibility of the cultivated Brassicas at the hexaploid level. However, the cultivated Brassicas exist at the tetraploid level now but beyond this ploidy level, the fertile Brassicas are not reported so far. Therefore, this is a novel genetic resource for carrying high degree of resistance for two major diseases of oilseed brassicas such as *Alternaria* blight and *Sclerotinia* stem rot. Allohexaploid Brassica (H1) will be unique because of their crossable nature to all oilseed and vegetable Brassica. Thus, it would be used as genetic resource for resistance breeding and development of climate resilient varieties. The population derived from this somatic hybrid (H1) can be exploited for searching resistance genes of *Alternaria* blight and *Sclerotinia* stem rot.

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71. J.93-58 (IC0625993; INGR19103), a Potato (*Solanum tuberosum*) Germplasm with Better Water Use Efficiency than Popular Cultivars. High Yielder

Raj Kumar[1,*], GS Kang[1], N Singh[2], SK Chakrabarti[3]

[1]*ICAR-Central Potato Research Station, Post Bag No.1, Model Town P.O., Jalandhar, Punjab, India*

[2]*ICAR-Central Potato Research Institute Campus, Modipuram, (Meerut), Uttar Pradesh*

[3]*ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh*

[*]*(Email: rajcprs@hotmail.com)*

Improving water use efficiency is required in response to growing water scarcity. In India Potato is grown under diverse agro-climatic conditions. Many areas in India have limited water resources for irrigation. Keeping this in view a line J.93-58 was bred at Central Potato Research Station Jalandhar that can give comparatively higher yield at relatively lower water availability.

Morpho-agronomic characteristics: Tubers of J.93-58 are oblong shape, white skin, with shallow eye depth and cream flesh colour. The flower corolla colour is white. Foliage is compact and plant is medium tall. Leaflets are ovate lanceolate. Sprout colour is white-green. It is a high yielding with very good water use efficiency as it produce yield better than popular varieties at lower doses of water. J.93-58 was selected from amongst 100 genotypes, mainly advance breeding lines tested under water deficient and sufficient conditions. Evaluation for water use efficiency was done for 4 consecutive years during 2012-2016. The trial was laid out with three soil moisture regimes i.e. 0.20-0.25, 0.40-0.45 and 0.60-0.65 bars/atm soil moisture tension at 15 cm soil depth. The germplasm, J.93-58 performed well under various soil moisture regimes. The yield performances of J.93-58 at various soil moisture regimes were better than that of popular cultivars Kufri Pukhraj and Kufri Bahar. J.93-58 also had better water use efficiency than cultivars Kufri Pukhraj and Kufri Bahar (Table 1).

Associated characters and cultivation practices: This accession is medium maturing and susceptible to late blight and early blight diseases.

Table 1. Water Use Efficiency (q/mm) of advance hybrids/genotypes

Treatment	Water Use Efficiency (q/mm)				Mean
	2012-13	2013-14	2014-15	2015-16	
At wet regime (0.20-0.25 bars)					
J. 93-58	1.198	1.540	1.299	1.373	1.353
K. Bahar	1.132	1.355	1.184	1.105	1.194
K. Pukhraj	1.286	1.379	1.312	1.191	1.292
CD at 5%	0.079	0.077	0.096	0.067	0.048
At moist regime (0.40-0.45 bars)					
J. 93-58	1.319	1.763	1.520	1.434	1.509
K. Bahar	1.260	1.548	1.360	1.145	1.328
K. Pukhraj	1.489	1.678	1.434	1.287	1.472
CD at 5%	0.068	0.105	0.103	0.080	0.037
At semi-dry regime (0.60-0.65 bars)					
J. 93-58	1.609	2.106	1.766	1.641	1.780
K. Bahar	1.421	1.861	1.515	1.358	1.539
K. Pukhraj	1.555	1.981	1.690	1.479	1.676
CD at 5%	0.111	0.138	0.120	0.099	0.047

REFEREES FOR VOLUME 33 (1, 2 & 3) 2020

The Editors gratefully acknowledge the help rendered by following referees in reviewing the manuscripts published during 2020.

A Nirmalakumari
Professor (Plant Breeding and Genetics)
Centre of Excellence in Millets
Tamil Nadu Agricultural University
Athiyandal-606603, Tamil Nadu

AK Parihar
Scientist (Plant Breeding)
Division of Crop Improvement
ICAR- Indian Institute of Pulses Research
Kanpur-208024, Uttar Pradesh

Ajay Kumar Thakur
Senior Scientist
ICAR-Directorate of Rapeseed Mustard Research
Sewar, Bharatpur-321303, Rajasthan

Akarsh Parihar
Associate Professor
Department of Agricultural Biotechnology
Anand Agricultural University (AAU)
Anand-388110, Gujarat

Ambika Baldev Gaikwad
Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus,
New Delhi-110012

Anjula Pandey
Principal Scientist
Division of Plant Exploration and Germplasm Collection
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Avinash Chandra Pandey
Scientist
Tata-Metahelix Life Science Ltd
Plot No 3, KIADB 4th Phase, Bommasandra
Bangalore-560099, Karnataka

B Varalakshmi
Principal Scientist
Division of Vegetable Crops
Indian Institute of Horticultural Research,
Hessaraghatta Lake Post, Bengaluru-560089 Karnataka

Basavaraj
Scientist (Sr. Scale)
Division of Plant Pathology
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Bhaskar Chandra Patra
Principal Scientist & I/c Head
Division of Crop Improvement
ICAR-National Rice Research Institute
Cuttack-753006, Odisha

D Pani
Principal Scientist
ICAR-NBPGR Regional Station
Cuttack-753006,
Orissa

Darshan T Dharajiya
Research Associate
Department of Genetics and Plant Breeding
C.P. College of Agriculture
Sardarkrushinagar Dantiwada Agricultural University
Sardarkrushinagar-385506, Gujarat

Dinesh Chandra Joshi
ICAR-Vivekananda Parvatiya Krishi Anusandhana Sansthan
Almora-263601 Uttarakhand

E Roshini Nayar
Principal Scientist, Retired (ICAR-NBPGR)
41 C, MIG Flats, Sheikh Sarai Phase-I
New Delhi-110017

G Padmavathi
Principal Scientist
ICAR-Indian Institute for Rice Research
Rajendranagar, Hyderabad-500030
Telangana

Gayacharan
Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus
New Delhi-110012

Gunjan Tiwari
Scientist (Genetics & Plant Breeding)
CSIR-Central Institute of Medicinal and Aromatic Plants
Lucknow-226002, Uttar Pradesh

Gururaj Kulkarni
Head
Research & Regulatory Compliance
International Rice Research Institute
Pili Drive, Los Baños, Laguna 4031, Philippines

Jawahar Lal Katara
Scientist (Sr. Scale), Ag. Biotechnology
Crop Improvement Division
ICAR-National Rice Research Institute
Bidyadharpur, Cuttack-753006, Odisha

Jayant Subraya Bhat
Senior Scientist
IARI Regional Research Centre
ICAR-Indian Agricultural Research Institute
UAS Campus, Dharwad-580005, Karnataka

Joseph John K
Principal Scientist & OIC
ICAR-NBPGR, Regional Station
Thrissur-680656, Kerala

K Anitha
Principal Scientist
ICAR-NBPGR, Regional Station
Rajendra Nagar, Hyderabad-500030
Andhra Pradesh

K Sreedevi
Senior Scientist (Agrl. Entomology)
Division of Germplasm Collection and Characterization
National Bureau of Agricultural Insect Resources
Bellary Road, Bengaluru-560024, Karnataka

KC Bhatt
Principal Scientist
Division of Plant Exploration and Germplasm Collection
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

KK Gangopadhyay
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

KS Varaprasad
Former Director, ICAR-IIOR
Plot 87, Road 8
Central Bank Colony
LB Nagar, Hyderabad-500068 Telangana

KV Bhat
Emeritus scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Kuldeep Tripathi
Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

M Latha
Principal Scientist Officer-In-Charge
ICAR-NBPGR Regional Station
Thrissur-680656, Kerala

M Pichaimuthu
Principal Scientist
Division of Vegetable Crops
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bengaluru-560089
Karnataka

M Vignesh
Scientist
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012
Email: pmvignesh@yahoo.co.in

Mamta Arya
Officer-In-Charge
ICAR-NBPGR Regional Station, Bhowali
Nainital-263132, Uttarakhand

Masahiro Kishii
Global Wheat Program, International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico

GS Mohana
Principal Scientist (Genetics and Cytogenetics)
In-charge, Project Coordinating Cell, AICRP on Cashew
In-charge, Agricultural Knowledge Management Unit
ICAR- Directorate of Cashew Research,
Puttur-574202, Karnataka

Mohar Singh
Principal Scientist & Officer-In-Charge
ICAR-NBPGR Regional Station
Shimla-171004, Himachal Pradesh

N Anuradha
Breeder
AICRP on Small Millets
Agricultural Research Station, Gajularega
Vizianagaram-531001, Andhra Pradesh

N Sivaraj
Principal Scientist
ICAR-NBPGR Regional Station
Rajendranagar, Hyderabad-500003, Telangana

M Niranjana
Scientist
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

P Venkata Rami Reddy
Principal Scientist (Agrl. Entomology)
Division of Crop Protection
ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post, Bengaluru-560089 Karnataka

R Parimalan
Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Pidigam Saidaiah
Assistant Professor
Department of Genetics and Plant BreedingCollege of Horticulture (SKLTSHU)
Rajendranagar, Hyderabad-500030, Telangana

Pragya
Principal Scientist
Division of Germplasm Exchange Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Pratibha Brahmi
Principal Scientist
Division of Germplasm Exchange Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Prolay Kumar Bhowmick
Scientist (Plant Breeding)
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

R Balakumbahan
Assistant Professor (Horticulture)
Tamil Nadu Agricultural University
Horticultural College and Research Institute
Periyakulam East-625604, Tamil Nadu

RK Gautam
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

RS Rathi
Principal Scientist
Division of Plant Exploration and Germplasm Collection
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Rajan Sharma
Principal Scientist
International Crops Research Institute for the Semi-Arid Tropics
Patancheru, Hyderabad-502324, Telangana

Rama Chandhrudu
Principal Scientist
ICAR-Indian Institute of Oil Palm Research
Pedavegi-534450, Andhra Pradesh

Ronnie Vernooy
Genetic Resources Policy Specialist
Bioversity International
Via dei Tre Denari, 472/a 00054
Maccarese (Fiumicino), Italy

S Rajkumar
Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

S Velmurugan
Assistant Professor (Horticulture)
Tamil Nadu Agricultural University
Coimbatore-641003, Tamil Nadu

S Vimala Devi
Principal Scientist
Division of Germplasm Conservation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

SB Dandin
Former Vice-Chancellor UHS, Bagalkot
No 21, Vijayashankar,Reshme Nagara,
Behind JUSCO Water Tank,
JP Nagar-Sri Nagar Main Road
Mysuru-570031, Karnataka

SK Kaushik
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

SR Pandravada
Principal Scientist
ICAR-NBPGR Regional Station
Rajendra Nagar, Hyderabad-500030
Andhra Pradesh

SR Yadav
Professor (Retired)
Department of Botany,
Shivaji University
Vidya Nagar
Kolhapur-416004, Maharashtra

Salej Sood
Scientist Senior Scale
Crop Improvement Division
ICAR-Central Potato Research Institute
Shimla-171001, Himachal Pradesh

Sandhya Gupta
Principal Scientist
Tissue Culture and Cryopreservation Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Sanjay Kumar Chetia
Principal Scientist (Plant Breeding)
Regional Agricultural Research Station (RARS)
Assam Agricultural University (AAU)
Titabar, Jorhat-785630, Assam

Satinder Kaur
Asst. Molecular Biologist
School of Agricultural Biotechnology
Punjab Agriculture University (PAU)
Ludhiana-141027, Punjab

Sheikh M Sultan
Officer-In-Charge
ICAR-NBPGR Regional Station
Srinagar-190005, Jammu & Kashmir

Sudhakar Pandey
Principal Scientist
ICAR-Indian Institute of Vegetable Research
Post Bag No. 01; P.O. Jakhini, Shahanshapur
Varanasi-221305, Uttar Pradesh

A Suma
Scientist
ICAR-NBPGR Regional Station
Thrissur-680656, Kerala

Sushil Kumar Sharma
Scientist
ICAR Research Complex for NEH region
Manipur Centre, Imphal-795004, Manipur

T Boopathi
Senior Scientist (Agricultural Entomology)
Division of Crop Protection
ICAR-Indian Institute of Oilseeds Research (IIOR)
Rajendranagar, Hyderabad-500030, Telangana

TS Aghora
Principal Scientist
Division of Vegetable Crops
ICAR-ICAR-Indian Institute of Horticultural Research
Hessaraghatta Lake Post
Bengaluru-560089, Karnataka

V Shridhar
Principal Scientist
ICAR-Indian Institute of Horticultural Research
Hessaraghatta, Bengaluru-560089, Karnataka

Zahoor Dar
Professor (GPB)
SKUAST, Shalimar Campus,
Srinagar-190025, Jammu & Kashmir

GUIDELINES TO AUTHORS

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K. Joseph JOHN
Principal Scientist
ICAR-NBPGR Regional Station – Thrissur
Thrissur, Kerala
joseph.k@icar.gov.in; nbpgrtsr@gmail.com

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

V Celia CHALAM
Principal Scientist
Division of Plant Quarantine
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi
celia.chalam@icar.gov.in

Aditya PRATAP
Principal Scientist
ICAR-Indian Institute of Pulses Research
Kanpur -208024, Uttar Pradesh
Aditya.Pratap@icar.gov.in

N SIVARAJ
Principal Scientist
ICAR-NBPGR Regional Station – Hyderabad
ARI Campus, Rajendra Nagar,
Hyderabad, Telangana
n.sivaraj@icar.gov.in

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

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

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

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

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

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

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

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

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

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

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

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

Kamala VENKATESWARAN
Principal Scientist
ICAR-NBPGR Regional Station – Hyderabad
ARI Campus, Rajendra Nagar,
Hyderabad, Telangana
kamala.Venkateswaran@icar.gov.in

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H-204, ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi–110012, India
E-mail:*ispgr2015@gmail.com*
Publisher website: *www.nbpgr.ernet.in/ispgr*
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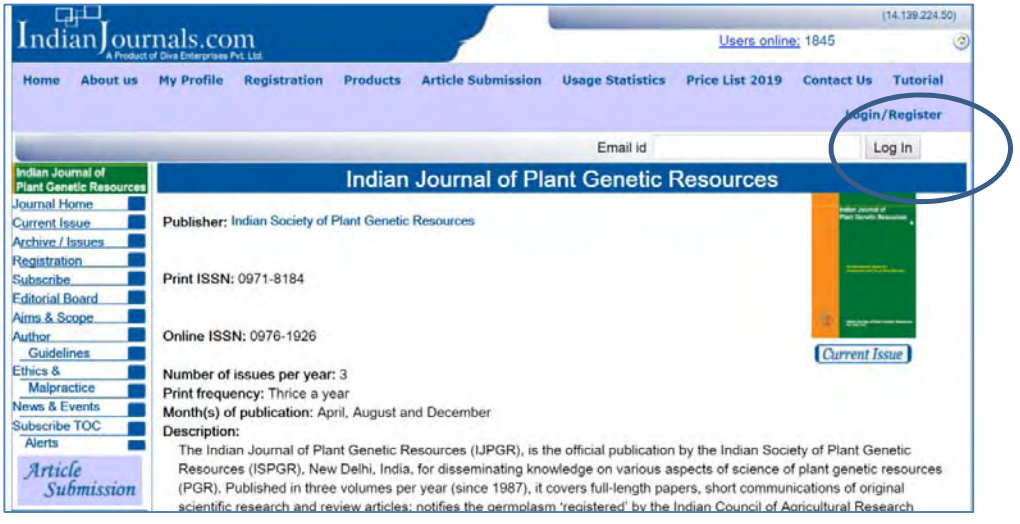

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Print ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

Vol. 34 No.1 2021

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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.