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# Ornamental *Curcuma* Species in Western Ghats of India

**KC Velayudhan**
*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Thrissur-680654, Kerala, India*

(Received: 16 December 2013; Revised: 03 January 2015; Accepted: 17 January 2015)

Efforts for collection, characterization and classification of genetic resources of wild relatives of turmeric in India resulted in sampling a total of 105 accessions devoid of sessile tubers. Of these 40 accessions belonging to 13 identified species, two varieties and three unidentified entities were characterized and assessed in *in situ* and *ex situ* maintenance plots for their ornamental value. Among them *Curcuma mutabilis* and *C. inodora* topped the list with a score of 9 followed by *C. albiflora, C. oligantha* var. *oligantha, C. oligantha* var. *lutea, Curcuma* spp. 1 and 2 with a score of 8 each. *C. karnatakensis* and *C. thalakaveriensis* with a score of 7 each are also ahead of species such as *C. decipiens, C. coriacea, C. pseudomontana, C. neilgherrensis, C. kudagensis* and *Curcuma* sp. 3 with a score of 6. Falling under Sect. *Stolonifera C. vamana* had the lowest score of 5. The subjective assessment of the genetic erosion encountered with respect to the species and future problems and prospectus of their utilization for ornamental purpose is also dealt with, in brief.

**Key Words: *Curcuma* spp., *Eucurcuma*, Germplasm, *Nontuberosa*, Ornamental, *Paracurcuma*, *Stolonifera***

## Introduction

The genus *Curcuma* includes approximately 120 species (Skornickova and Sabu, 2002; Skornickova *et al.*, 2004) which are distributed in tropical and subtropical Asia. In India, the genus is represented by 40 species (Roxburgh 1820; Baker, 1890-1892; Velayudhan *et al.,* 1996; Sabu, 2006). The members are mainly distributed in East, North, East and Southern peninsular region. Based on morphological characters, the Indian *Curcuma* is divided into two subgenera-1) *Eucurcuma* containing three major sections – *Tuberosa, Nontuberosa* and *Stolonifera* (Velayudhan *et al.*, 1996) and *Paracurcuma* of Valeton (1918) containing two species. Western Ghats region lying parallel to Arabian seacoast and lying in states of Kerala, Tamil Nadu, Karnataka, Goa and Maharashtra is rich in *Curcuma* species belonging to the section *Nontuberosa* (characterized by the absence of sessile fingers). Apart from this, *C. vamana* of the section *Stolonifera* and *C. aurantiaca* Zjip and *C. ecalcarata* of the subgenus *Paracurcuma* have been reported from the region. *C. ecalcarata* Sivr. & Balach. is established as synonymous to *C. aurantiaca* Zijp (www.theplantlist org./tpl 1.1/record/kew-235216). While revising the genus *Curcuma* of Peninsular India, Sabu (2006) reported 20 species leaving one established species. Thus, other than eight finger-bearing species, 14 species such as *C. albiflora* Trimen, *C. aurantiaca* Zjip [syn. *C. ecalcarata* Sivar. & Indu], *C. bhatii* (R. M. Sm.) Skornickova & Sabu, *C. oligantha* Trimen, *C. cannanorensis* Ansari, VJ Nair & NC Nair, *C. karnatakensis* Amalraj, Velay. & VK Mural, *C. coriacea* Mangaly & Sabu, *C. decipiens* Dalzell, *C. inodora* Blatter, *C. kudagensis* Velay, Pillai & Amalraj syn. *C. thalakaveriensis* Velay Amalraj & Mural, *C. mutabilis* Skornickova, Sabu & Prasanth, *C. neilgherrensis* Wight, *C. vamana* Mangaly & Sabu and *C. pseudomontana* J Graham have been so far reported from the region (www.theplantlist org./tpl 1.1/record/kew-235216). Among these species though, *C. thalakaveriensis* Velay Amalraj & Mural is considered as a synonym of *C. kudagensis* in the recent working plant list of *Curcuma* species from Kew, these are treated separately here as these are quite different from each other in plant type, leaf shape and inflorescence length. Apart from this, *C. aurantiaca* (Velayudhan *et al.*, 1996) and *C. albiflora* Thwaites (Amlaraj *et al.*, 1991) have been reported from the region. Moreover, few more apparently distinct entities have also been located quite recently about which the present treatise refers them as species no. 1, 2, 3 and 4. The details of the above species without underground fingers as per the available working list of Kew (1994) is presented in Table 1 below.

**Author for Correspondence: E-mail: velagerm@gmail.com*

**Table 1. Taxonomic status of the species collected**

| Subgenus | Section | Species | Distribution |
|---|---|---|---|
| Paracurcuma | – | *Curcuma aurantiaca* Zjip syn. *C. ecalcarata* Sivar. & Balach. | West coast, lower Ghats |
| Eucurcuma | Nontuberosa | *C. albiflora* Thwaites | North Kerala, Karnataka.coast |
| -do- | -do- | C. *bhatii* (R. M. Sm.) Skornockova & Sabu | Udupi, Karnataka |
| -do- | -do- | *C. coriacea* Mangaly & Sabu | Idukki district, Kerala |
| -do- | -do- | *C. decipiens* Dalzell | All over Western Ghats |
| -do- | -do- | *C. oligantha* Trimen syn. *C. oligantha Trimen* var. *oligantha* K. G. Bhat | Konkan, N. Kerala and Karnataka |
| -do- | -do- | *C. cannanorensis* R. Ansari, V. J. Nair & N. C. Nair Syn. *C. oligantha* Trimen var. *lutea* (R. Ansari, V. J. Nair & N. C. Nair) K. G. Bhat | Konkan, N. Kerala and Karnataka |
| -do- | -do- | *C. karnatakensis* Amalraj, Velay & Mural. | Hilly Uttar Kannada |
| -do- | -do- | *C. kudagensis* Velay, Pillai & Amalraj Syn. *C. thalakaveriensis* Velay, Amalraj & Mural. | Coorg district of Karnataka |
| -do- | -do- | *C. mutabilis* Skornockova, M. sabu & Prasanth Kumar | Malappuram and Palakkad, Kerala |
| -do- | -do- | *C. inodora* Blatter | Karnataka and Konkan |
| -do- | -do- | *C. neilgherrensis* Wight | High lands of Western Ghats |
| -do- | -do- | *Curcuma* sp. 1 | Central parts of Kerala |
| -do- | -do- | *Curcuma* sp. 2 | Udupi, Karnataka |
| -do- | -do- | *Curcuma* sp. 3 | Kudremukh, Chikmagalur |
| -do- | -do- | *Curcuma* sp. 4 | |
| -do- | Stolonifera | *C. vamana* Mangaly & Sabu | Lower Ghats in midland Kerala |

Attempts to collect, characterize and conserve the germplasm of *Curcuma longa* L. and its wild relatives in India by ICAR-National Bureau of Plant Genetic Resources in the past has resulted in amassing a total of 1856 accessions belonging to 32 species and several unidentified species. Sizable part of the collections represents the cultivated turmeric and other tuber bearing species of the genus from different parts of India. Usually the species without tubers are generally considered to be not economically useful. Meanwhile, Burch (1998) and Burch *et al.* (1987) reported the commercial use of some Zingiberaceae plants in United States of America. Khumkratok *et al.* (2012) and, Mood and Larsen (2001) reported the ornamental value of some of the South East Asian species of the genus such as *C. alismatifolia, C. aurantiaca, C. cordata, C. inodora, C. parviflora, C. roscoeana, C. alismatifolia, C. rabdota, C. bicolor* and *C. glans* which, have promoted the interest of horticulturists and growers in Thailand, Europe, Australia and United States. Kuehny *et al.* (2002) have also stressed the potential of *Curcuma* and *Kaempferia* for their use as potted plants. Most of these species have fine horticultural attributes and are offered in catalogues and Internet web sites. Though several species of horticultural value occur, these have not yet attracted much attention of horticulturists in India. Collection and preliminary characterization of various members of the genus from the Western Ghats have been carried out in the past pointing to the horticultural value of some of them with beautiful spikes, flowers and other positive attributes which demand more studies in this direction in the immediate future to utilize them (see Fig. 1a, 1b).

## Materials and Methods

A total of 105 accessions belonging to 14 identified species (including two varieties), four unidentified entities (attempts are being made to identify these) without sessile fingers and one species bearing stolons on the rootstock have been collected in the past. Out of these 40 accessions belonging to *Curcuma albiflora* (1), *C. mutabilis* (3), *C. inodora* (6), *C. oligantha* (1), *C. cannanorensis* (2), *C. karnatakensis* (1), *C. thalakaveriensis* (1), *C. decipiens* (3), *C. coriacea* (1), *C. pseudomontana* (1), *C. neilgherrensis* (1), *C. kudagensis* (1), *C. vamana* (4), *C. ecalcarata* (2), *C. aurantiaca* (9) and unidentified species of *Curcuma* (3) have been observed for spike and flower characters (list of characters and states studied furnished below). Species 2 is a new species and is in process of publication. Species 3 is very distinct with better ornamental value; another specimen could not be collected from the locality or anywhere else afterwards. Unidentified *Curcuma* sp. 4 representing a single accession did not flower till the time of submitting the manuscript.

Passport information (descriptor No. 2-13) and qualitative and quantitative characters observed (descriptor No. 14-39) along with overall grade of each species in relation to its ornamental value based on a subjective score (1-9 scale) are furnished in Tables 2 and 3. Presently, a total of 39 accessions belonging to *C. aurantiaca* (9), *C. mutabilis* (4), *C. inodora* (6), *C. vamana* (4), *C. decipiens* (3), *C. pseudomontana* (1),

**Table 2. Parameters, descriptors and descriptor states used**

| S.No. | Passport information | Description |
|---|---|---|
| 1 | Species and varieites | As per the latest taxonomic position |
| 2 | Number of accessions collected | Total number collected by the station from 1978 to 2007 |
| 3 | Number of accessions observed | Accessions observed as when in flowering condition |
| 4 | Distribution | Distribution of the species in Western Ghats and adjoing areas |
| 5 | Subgenus | Subgenus Paracurcuma Val. & Eucurcuma Val. (Valeton, 1917; Velayudhan *et al.,* 1996) |
| 6 | Section | 1- Nontuberosa, 2- Stolonifera |
| 7 | Altitude | In meters from mean sea level |
| 8 | Soil type | 1- Laterite, 2- Sandy loam, 3- Rocky |
| 9 | Rainfall | 1-Low, 2- Medium, 3-High |
| 10 | Ecological niches | 1-Undisturbed forests, 2-Disturbed forests, 3-Orchards & farms, 4-Road sides, 5-Open grasslands, 6-Open river side rocky places, 7-Shola grasslands |
| 11 | Time of Regeneration | Time given in serial number of months |
| 12 | Time of senescence | Time given in serial number of months |
| **Characters observed both *in situ* and *ex situ*** | | |
| 13 | Flowering time | Serial number of months |
| 14 | Spike position | 1-Central, 2-Lateral, 3- Both central & lateral |
| 15 | Spike size | 1-Small, 2-Medium, 3-Large |
| 16 | Presence of coma | 1- Present, 2-Absent |
| 17 | Coma bracts colour | 1- White, 2-Light green, 3-Green, 4-Light purple, 5-Purple, 6-Voilet, 7-Pink, 8-Golden |
| 18 | Flower bracts colour | 2-Light green, 3-Green, 4-Light purple, 5-Purple |
| 19 | Flower exertion | 1-Less exerted, 2- Moderate, 3-High, 4-Very high |
| 20 | Flower size | 1-Small, 2-Medium, 3-Large, 4-Very large |
| 21 | Corolla tube colour | 1-White, 5-Purple, 7-Pink, 10- Cream, 11-Pale yellow, 12-Yellow, 13-Bright yellow |
| 22 | Corolla main lobe colour | 1-White, 5-Purple, 6-Violet, 7-Pink, 9-Rose, 10-Cream, 11-Pale yellow, 12-Yellow, 13-Bright yellow, 14-Greenish white |
| 23 | Staminode colour | 1-White, 4-Light purple, 5-Purple, 13-Bright yellow |
| 24 | Lip shape | 1-Three lobed, 2-Suborbicular |
| 25 | Lip colour | 1-White, 4-Light purple, 5-Purple, 6-Violet, 12-Yellow, 13-Bright yellow |
| 26 | Presence of fruit setting | 1-Present, 2-Absent |
| 27 | Propagation in nature | 1-By vegetative means, 2-By seeds |
| 28 | Spike longevity or life on plant | Given approximately in weeks |
| 29 | Appearance of spike | <1-Satisfactory, 1-Good, 2-Very good, 3-Excellent |
| 30 | Fauna affecting the natural population | 1- Rats, 2-Wild boars |
| 31 | Adaptability to potted and shaded | 1-Adapted, 2-Not easily adapted |
| 32 | Plant height | cm |
| 33 | Spike length | cm |
| 34 | Spike width | cm |
| 35 | Flower length | cm |
| 36 | Lip length | cm |
| 37 | Lip width | cm |
| 38 | Overall grade in relation to ornamental value of the species | 1-9 scale based subjectively on the basis of ornamental value, mainly appearance of spikes and flowers, and adaptability under *ex situ* conditions |

**Table 3. Descriptor and descriptor states of *Curcuma* species of Western Ghats having ornamental value**

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|---|---|---|---|---|---|---|---|---|
| S No | Species | Collected | Observed | Distribution | Subgenus | Section | Altitude (m) | Soil type |
| 1 | C. *albiflora* | 4 | 1 | 1,2 | Eucurcuma | Nontuberosa | 10-600 | 1,2 |
| 2 | *C. mutabilis* | 4 | 3 | 1,2 | Eucurcuma | Nontuberosa | 40-100 | 2 |
| 3 | *C. inodora* | 11 | 6 | 2,4,5 | Eucurcuma | Nontuberosa | 10-101 | 1,2 |
| 4 | *C. oligantha* Trimen var *oligantha* | 6 | 1 | 1,2,4 | Eucurcuma | Nontuberosa | 10-600 | 1,2 |
| 5 | *C. cannanorensis* syn *(Oligantha* var. *lutea)* | 12 | 2 | 1,2 | Eucurcuma | Nontuberosa | 10-600 | 1,2 |
| 6 | C. *karnatakensis* | 9 | 1 | 2 | Eucurcuma | Nontuberosa | 100-600 | 2 |
| 7 | *C. thalakaveriensis** | 4 | 1 | 2 | Eucurcuma | Nontuberosa | 1001 | 3,2 |
| 8 | *Curcuma* sp. 1 | 1 | 3 | 1,2 | Eucurcuma | Nontuberosa | 20-40 | 1 |
| 9 | *Curcuma* sp. 3 | 1 | 1 | 2 | Eucurcuma | Nontuberosa | >1000 | 2 |
| 10 | *Curcuma* sp. 2 | 2 | 1 | 2 | Eucurcuma | Nontuberosa | <10 | 1 |
| 11 | *Curcuma* sp.4 | 1 | 0 | 2 | Eucurcuma | Nontuberosa | 601 | 2 |
| 12 | C. *decipiens* | 6 | 3 | 1,2 | Eucurcuma | Nontuberosa | 20-40 | 1 |
| 13 | *C. coriacea* | 2 | 1 | 1 | Eucurcuma | Nontuberosa | 100-1000 | 2 |
| 14 | *C. pseudomontana* | 10 | 1 | 1,2,3 | Eucurcuma | Nontuberosa | 200-1000 | 2, 3 |
| 15 | *C. neilgherrensis* | 4 | 1 | 1,2,3 | Eucurcuma | Nontuberosa | >1000 | 2 |
| 16 | C. *kudagensis* | 7 | 1 | 2 | Eucurcuma | Nontuberosa | >1000 | 2,3 |
| 17 | *C. vamana* | 6 | 4 | 1 | Eucurcuma | Stolonifera | 40-100 | 1,2 |
| 18 | *C. ecalcarata*** | 2 | 1 | 1 | Paracurcuma | | 10-100 | 1,2 |
| 19 | *C. aurantiaca* | 13 | 8 | 1,2 | Paracurcuma | | 10-800 | 1,2 |
| | | 105 | 40 | | | | | |

| 1 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
|---|---|---|---|---|---|---|---|---|---|
| S No. | Rainfall | Ecological niche | Time of regeneration | Time of senescence | Flowering time | Spike position | Spike size | Presence of coma | Colour of coma bracts |
| 1 | 3 | 1,2,3 | 4,5 | 11 | 4,5,6,7,8 | 3 | 1 | 2 | |
| 2 | 3 | 1,2,3,4 | 5,6 | 10,11 | 4,5,6,7,8,9 | 3 | 3 | 1,2 | 2,4 |
| 3 | 3 | 1,2,4 | 5,6 | 10,11 | 4,5,6,7,8 | 3 | 3 | 1 | 1,5 |
| 4 | 3 | 1,2,3,4 | 4,5 | 10,11 | 4,5,6,7,8 | 3 | 1 | 2 | |
| 5 | 3 | 1,2,3,4 | 4,5,6 | 10,11 | 4,5,6,7,8 | 3 | 1 | 2 | |
| 6 | 3 | 1,2,4 | 5,6 | 10,11 | 5,6,7,8 | 3 | 1 | 2 | |
| 7 | 3 | 5 | 4,5 | 10,11 | 5,6,7,9 | 3 | 1 | 1 | 1,2,5 |
| 8 | 3 | 2,3,4 | 4,5 | 10,11 | 6,7,8 | 1 | 1 | 1 | 1,5,6 |
| 9 | 2 | 4,5 | 5,6 | 10,11 | 5,6,7,8 | 3 | 2 | 1 | 1,7,8 |
| 10 | 3 | 3 | 5,6 | 10,11 | 5,6,7,8,9 | 3 | 2 | 1,2 | 4 |
| 11 | 3 | 6 | 5,6 | 10 | | | | | |
| 12 | 3 | 2,3,4 | 4,5 | 10,11 | 6,7,8 | 1 | 1,2 | 1 | 1,2,4 |
| 13 | 3 | 5 | 4,5 | 10,11 | 4,5 | 2 | 2 | 1 | 1,2,4 |
| 14 | 1,2,3 | 5 | 4,5 | 10,11 | 7,8,9 | 1 | 2 | 1 | 1,2,4 |
| 15 | 1,2,3 | 7 | 4,5 | 10,11 | 4,5 | 2 | 1,2 | 1 | 4,5,7 |
| 16 | 3 | 7 | 4,5 | 10,11 | 4,5 | 2 | 1 | 1 | 2,4 |
| 17 | 3 | 1,2 | 4,5 | 10,11 | 6,7,8 | 1 | <1 | 1 | 2 |
| 18 | 3 | 1,2,4,8 | 4,5 | 10,11 | 6,7,9 | 1 | 2,3 | 1 | 1,2,7,9 |
| 19 | 3 | 1,2,4,8 | 4,5 | 10,11 | 6,7,10 | 1 | 2,3 | 1 | 1,2,7,9 |

| 1 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
|---|---|---|---|---|---|---|---|---|---|
| S No. | Flower bract colour | Flower exertion | Flower size | Corolla tube colour | Corolla colour | Staminode colour | Lip shape | Lip colour | Fruits setting |
| 1 | 2 | 4 | 1 | 10 | 1,7 | 1 | 1 | 1,12 | 1 |
| 2 | 2,4 | 4 | 3 | 10 | 1,13 | 1,12 | 1 | 1,12 | 1 |
| 3 | 2,5 | 3 | 3 | 5 | 5,6 | 4,5 | 1 | 4,5,6,12 | 1 |
| 4 | 2 | 4 | 1 | 10,11 | 14,5 | 1 | 1 | 1,12 | 1 |
| 5 | 2 | 4 | 1 | 11 | 11 | 13 | 1 | 13 | 1 |
| 6 | 2,5, | 4 | 1 | 11 | 10,9 | 1 | 1 | 13 | 1 |
| 7 | 2,4, | 4 | 1 | 12 | 11 | 13 | 1 | 13 | 1 |
| 8 | 1,5 | 3 | 1 | 5 | 5 | 13 | 2 | 13 | 1 |
| 9 | 2,7 | 3 | 2 | 12 | 12 | 13 | 1 | 13 | 3 |
| 10 | 3,4 | 3 | 2 | 1,7 | 1,7 | 1 | 1 | 13 | 1 |
| 11 | | | | | | | | | |
| 12 | 1,2,4 | 2 | 2 | 5 | 5 | 13 | 1 | 13 | 1 |
| 13 | 2,4 | 2 | 2 | 13 | 13 | 13 | 1 | 13 | 3 |
| 14 | 2,4 | 2 | 2 | 12 | 11, 5 | 13 | 1 | 13 | 1 |
| 15 | 2,5,7 | 3 | 2 | 11 | 12 | 12 | 1 | 12 | 1 |
| 16 | 2,5 | 3 | 1 | 11 | 11,5 | 13 | 2 | 13 | 1 |
| 17 | 2 | 1 | 1 | 10 | 10 | 12 | 2 | 12 | 1 |
| 18 | 1,2,8 | 2 | 3 | 11 | 12 | 13 | 1 | 13 | 1 |
| 19 | 1,2,8 | 2 | 3 | 11 | 12 | 13 | 1 | 13 | 1,3 |

| 1 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S.No. | Propagation | Spike survival | Appearance of spike | Biotic factors | Adaptability to pots | Plant height | Spike length | Spike width | Flower length | Lip length | Lip width | Grade |
| 1 | 1,2 | 1 | 2 | 1,2 | 1 | 58.0 | 7.0 | 6.0 | 5.0 | 1.6 | 1.8 | 8 |
| 2 | 1,2 | >2 | 2 | 1,2 | 1 | 78.0 | 8.0 | | 6.5 | 1. | 1.8 | 9 |
| 3 | 1,2 | >2 | 3 | 1,2 | 1 | 77.0 | 14 | 8.5 | 5.5 | 2.0 | 1.8 | 9 |
| 4 | 1,2 | 1 | 3 | 1,2 | 1 | 43.0 | 11.0 | 6.0 | 7.0 | 2.0 | 1.8 | 8 |
| 5 | 1,2 | 1 | 3 | 1,2 | 1 | 60.0 | 5.8 | 2.7 | 5.7 | 1.6 | 1.5 | 8 |
| 6 | 1,2 | >2 | 1 | 1,2 | 1 | 52.0 | 9.0 | 7.5 | 7.6 | 2.6 | 2.2 | 7 |
| 7 | 1,2 | 2 | 1 | 1,2 | 1 | 83.0 | 18.0 | 5.0 | 6.1 | 2.3 | 1.7 | 7 |
| 8 | 1,2 | 2 | 1 | 1,2 | 1 | 51.5 | 10.0 | 4.2 | 5.0 | 1.5 | 1.8 | 7 |
| 9 | 1 | >5 | 3 | 1,2 | 1 | 67.5 | 6.0 | 6.2 | 5.0 | 1.5 | 1.5 | 8 |
| 10 | 1,2 | 2 | 3 | 1,2 | 1 | 70.0 | 12.0 | 9.0 | 7.0 | 1.7 | 1.5 | 8 |
| 11 | | | | 1,2 | 1 | | | | | | | |
| 12 | 1,2 | >2 | 1 | 1,2 | 1 | 60.2 | 7.5 | 4.7 | 5.3 | 3.3 | 1.5 | 7 |
| 13 | 1 | >2 | 1 | 1,2 | 1 | 55.0 | 5.0 | | 6.0 | 2.0 | 2.0 | 6 |
| 14 | 1,2 | >2 | 1 | 1,2 | 1 | 48.0 | 17.0 | 6.5 | 4.8 | 1.8 | 1.7 | 6 |
| 15 | 1,2 | >2 | 1 | 1,2 | 2 | 65.0 | 10.5 | | 5.7 | 2.2 | 2.5 | 7 |
| 16 | | <2 | 1 | 1,2 | 2 | 44.0 | 58.0 | 2.7 | 5.2 | 1.6 | 1.5 | 6 |
| 17 | 1,2 | >2 | <1 | 1,2 | 1 | 72.3 | 5.0 | 3.5 | 2.2 | 0.8 | 0.7 | 5 |
| 18 | 1,2 | >3 | 1 | 1,2 | 1 | 58.0 | 5.4 | 6.2 | 5.3 | 1.7 | 1.5 | 8 |
| 19 | 1,2 | >3 | 1 | 1,2 | 1 | 55.0 | 7.0 | 6.0 | 5.2 | 1.7 | 1.4 | 8 |

* Synonym of *C. kudagensis*; ** Synonym of *C. aurantiaca*

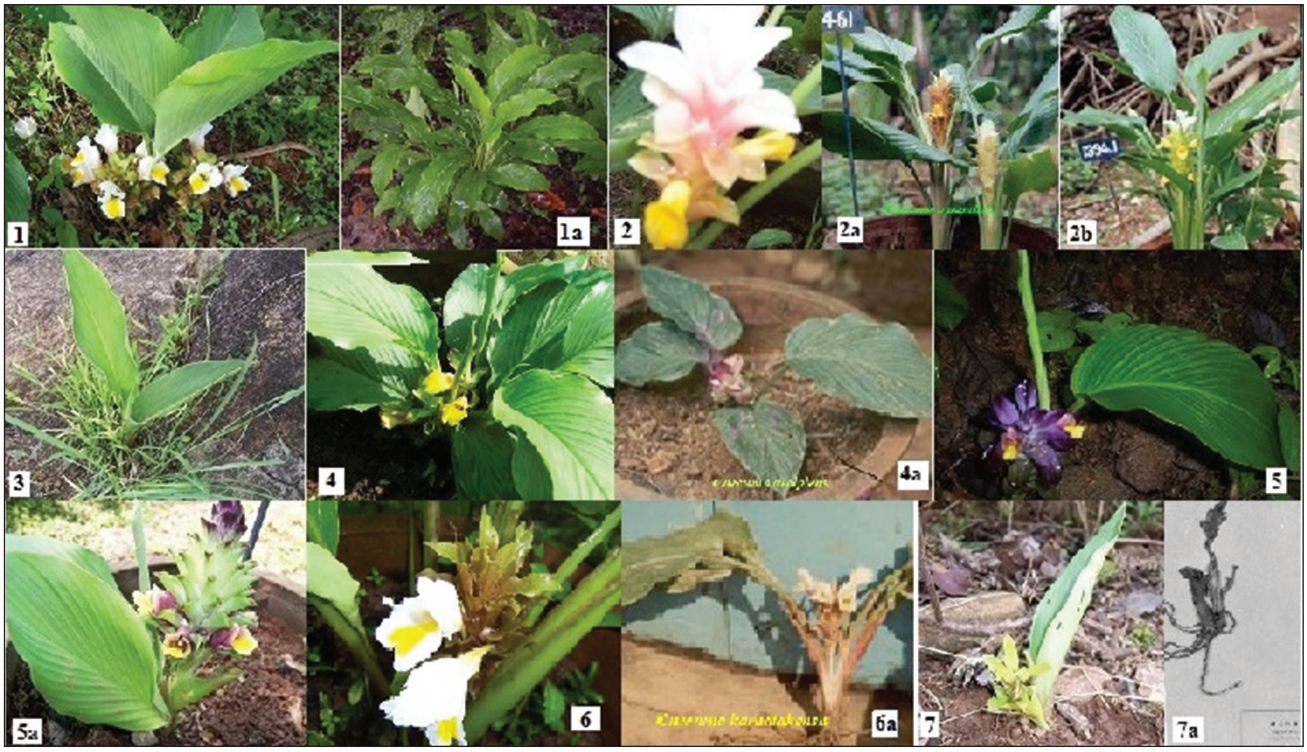


**Fig. 1a.1-*C. albiflora*, 1a-*C. albiflora* (vegetative phase), 2, 2a, 2b-*C. aurantiaca* syn. *C. aurantiaca*, 3-*C. coriacea* (juvenile plant), 4 and 4a-*C. decipiens* (variants), 5 and 5a-*C. inodora* with varying colour of bracts and perianth, 6 and 6a-*C. karnatakensis*, 7 and 7a-*C. kudagensis***

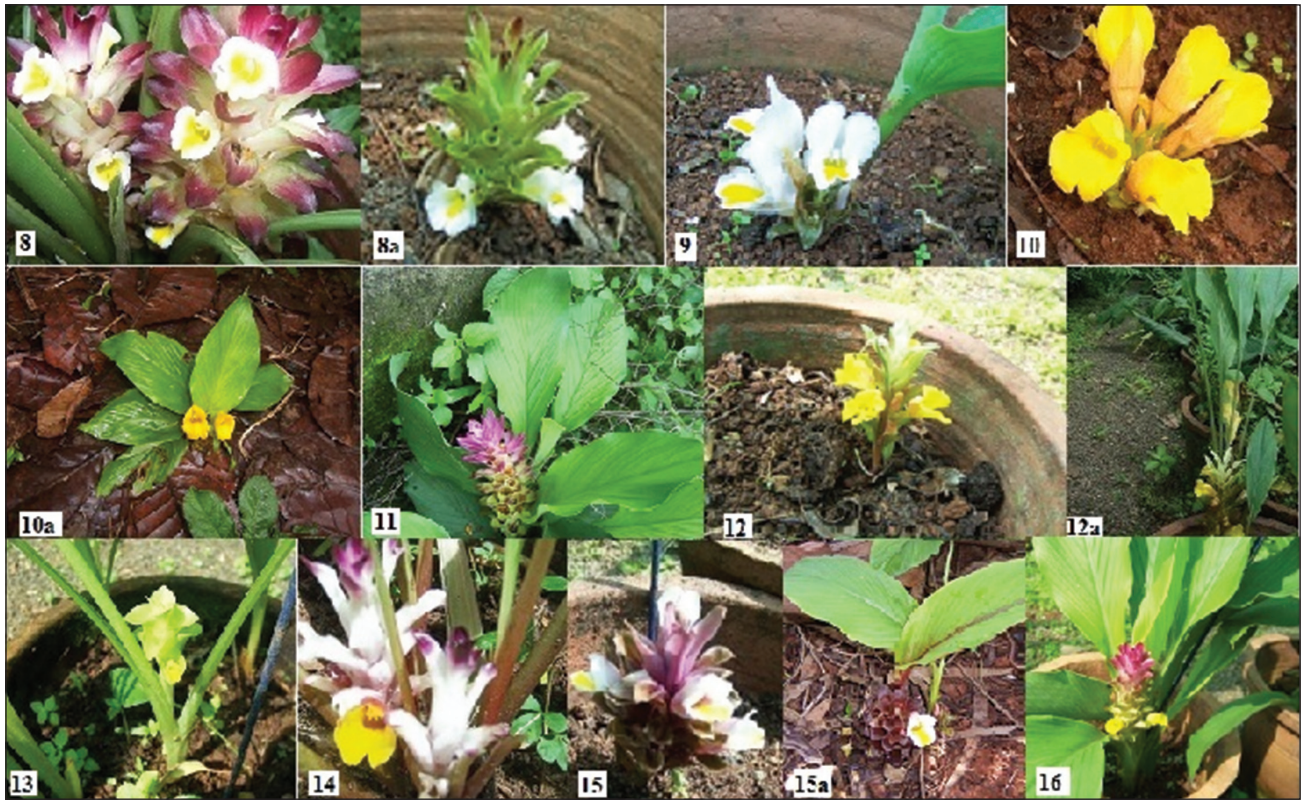


**Fig. 1b.8 and 8a-*C. mutabilis*, 9-*C. oligantha*, 10 and 10a-*C. cannaniorensis*, 11-*C. pseudomotana*, 12 and 12a-*C. thalakaveriensis*, 13-*C. vamana*, 14-*Curcuma* sp.1, 15, 15a-*Curcuma* sp.2 and 16-*Curcuma* sp.**

**Table 3. Collections maintained in pots**

| Species | Collector No. | IC Number |
|---|---|---|
| *Curcuma oligantha* var. *oligantha* | | 248154, 329264 |
| *C. oligantha* var. *lutea* | | 313105 |
| *C. albiflora* | | 329329 |
| *C. mutabilis* | A674 | 313104, 324420 |
| *C. inodora* | VBR/01-1, V/04-38 | 248332, 405356, 248212, 427565 |
| *C. thalakaveriensis* | | 313116 |
| *C. decipiens* | | 248185, 322301 |
| *C. coriacea* | | 210410A |
| *C. karnatakensis* | | 427581 |
| *C. aurantiaca* | VJ/99-102 | 329264, 324455, 324807, 266541, 136936, 248187, 266516 |
| *Curcuma* sp. 1 | V/03-178 | 88952B |
| *Curcuma* sp. 2 (s) | | 329331 |
| *Curcuma* sp. 3 (f) | | 329287 |
| *C. vamana* | | 406444, 324067, 427596, 337513 |

*C. oligantha* var. *oligantha* (1), *C. oligantha* var. *lutea* (2), *C. albiflora* (1), *C. coriacea* (1), C. *thalakkaveriensis* (1), *Curcuma* sp. 1 (3v), *Curcuma* sp. 2 (1f), *Curcuma* sp. 3 (1s) and *Curcuma* sp. 4 (1CTCRI) are maintained in the pots under 25% shade. Also, availability of sample planting materials for research purpose is also furnished. Problems and future prospects of the genetic resources of the genus having potential for use as ornamentals are also discussed.

## Result and Discussion

A total of 40 accessions belonging to 15 species (excluding three synonyms as per Table 1) and 3 unidentified entities were observed. A total of 38 parameters pertaining to passport information and qualitative characters are furnished in Table 2. Out of this, one unidentified entity *Curcuma* sp. 4 did not flower and was not considered here for its ornamental value.

*C. oligantha* Trimen with two varieties (now revised as *C. oligantha* Trimen and *C. cannanorensis* (Table 1) with two flowering seasons in a year, central and lateral spikes, absence of coma bracts, highly exerted, showy and large flowers with white in the first and bright yellow staminodes in the second, respectively and seed setting and good adaptability to potted conditions has wide distribution from North Kerala to Goa and borders of Maharashtra. These varieties possess an excellent potential for development as a tropical ornamental (9 grade) species. However, the short span of the spike in bloom requires further studies to improve them. *Curcuma* sp. 1, 2 and 3 identified as separate entities having some morphological similarities with *C. decipiens*, *C. albiflora* and *C. pseudomontana*, respectively, in some characters are also potential candidates (grade 8). Out of these, species 2 and 3 with very showy spikes and, lateral and central spikes during end of summer and main growing season and with fruit and seed setting may also be potential candidates for development as an ornamental species. *Curcuma* sp. 3 having a long duration of spike bearing and with light pinkish and golden coma and flower bracts bearing yellow showy flowers may be worth looking into. This has very restricted distribution in and around Kudremukh hills in Karnataka. Further exploration and collection in other parts of Karnataka at higher elevations may also be rewarding. *Curcuma* sp. 1 sharing the niches of *C. decipiens* in central Kerala in farmer's compounds, disturbed forests and roadsides on hard laterite soils under partial shade has small to medium central spikes, purple violet tipped coma and flower bracts, exerted flowers with bright yellow staminodes, seed setting, and moderate adaptability to potted condition. This was described as *C. vellanikkarensis* by Velayudhan *et al.* (1996) but is yet to be validated as a species. This entity is less robust and more erect than *C. decipiens* occurring in similar niches which also deserves attention as an ornamental species. The difference between *Curcuma* sp. 1 and *C. decipiens* is in the former as compared to elliptic lanceolate leaves with acute base ovate-elliptic leaves with rounded to cordate base and the extended flowering in latter. The second entity *i.e. Curcuma* sp. 2 is the strikingly beautiful plant having very restricted distribution in gardens and orchards in Udupi of Karnataka state. It has very interesting features such as erect and thin plant type, purple leaf midrib and light purple tint on the base of young leaves, exerted lateral and central spikes without coma bracts, purple flower bracts, exerted and large flowers with purple violet corolla and white large staminodes with bright yellow median band on lip.

*C. karnatakensis* and *C. mutabilis* are two related species as these have spreading semi-erect or horizontal leaf disposition, large elliptic ovate leaves, prominent veins on the leaves, both central and lateral spikes, absence of coma or if present, very obscure and even degenerated in the latter. The former occur in Karnataka especially in Dakshin and Uttar Kannada districts of Karnataka and the later in Palakkad and Malappuram districts of Kerala. These are adapted to lower foothills and occur very seldom in the midlands and never found in coastal areas. Both have white staminodes with rose tint in the former. Sabu (2006) gave two different types with white and yellow satminodes in the later. Both have good ornamental value (8 grade). *C. neilgherrensis*, *C. kudagensis* syn. *C. thalakaveriensis*, *C. coriacea* and *C. pseudomontana* are adapted to open grasslands in Ghats and have comparatively lesser showy spikes as compared to others. All have larger spikes, moderately exerted flowers. However, *C. thalakaveriensis* is more beautiful with tall, thin plants, narrow lanceolate and thicker leaves, very long thin inflorescences bearing flowers with bright yellow staminodes, lips, varying colours of coma bracts is of more ornamental value. Hence this has been treated here as a separate entity. Survey in certain pockets of Ghats at elevations above 1400m has indicated that the population of *C. neilgherrensis* and *C. kudagensis* are dwindling due to habitat destruction. *C. coriacea* has been found to occur at two places. *C. thalakaveriensis* in Thalakkavery of Coorg and in Kudremukh of Chikmagalur in Karnataka. *C. pseudomontana* is very common at 1000 m elevation in pockets of Ghats extending to Pockets in Kolli Hills in Tamil Nadu. Further, adaptability of these species to potted condition under shade in plains is very difficult especially in the case of *C. neilgherrensis* and *C. kudagensis* which usually occur in shola grasslands. Hence, low temperature and mist during the growing season followed by cold spell and then by summer season is needed for better growth of the species. Most of them are adapted to rocky and stony soils in grasslands, which are at times, subject to phenomenon of summer fire. *C. vamana* having the smallest plant type with very small rootstock giving forth branched stolons and bearing smallest green spikes and small yellow flowers is least valuable as an ornamental. However, it is adapted to very shady areas in low altitudes hence can also be considered for development as an ornamental in gardens along with other species. *C. ecalcarata*, a species reported from the coastal areas, midlands and mountainous areas at lower altitudes is similar to *C. aurantiaca* van Zijp in all respects. These entities treated here as separate entities are highly varying in plant height, leaf shape, coma and flower bract colours and, with bright yellow staminosdes and corolla. Both seed setting and non-seed setting plants have been found to occur in nature.

Out of a total of 40 accessions observed, based on the overall grade assigned in relation to ornamental value *C. mutabilis* and *C. inodora* with 3 and 6 accessions, respectively have topped the list with the highest score of 9 followed by *C. albiflora*, *C. oligantha* var. *oligantha*, *C. oligantha* var. *lutea*, *C. aurantiaca*, *C. ecalcarata*, *Curcuma* sp. 2 and 3 with a score of 8, and *C. karnatakensis* and *C. thalakaveriensis* with a score of 7 are also ahead of other species such as *C. decipiens*, *C. coriacea*, *C. pseudomontana*, *C. neigherrensis*, *C. kudageneis* and *Curcuma* sp.1with a score of 6. *C. vamana* had the lowest score of 5. The results indicated clear cut difference between C. *kudagensis* and *C. thalakaveriensis* which is presently considered as a synonym of the earlier.

All the species reported in this communication occur in areas with medium to high rainfall, received mostly from South West monsoon and, to a lesser extent from North East monsoon. Total annual precipitation varies from 1500 mm in Bababudangiri hills to over 4000 mm in Agumbe Ghat in Karnataka. Soil, which is acidic in nature, varies from fine sandy in coastal plains on the West Coast to laterite in midlands and plateaus, and sandy loam in forest areas. Altitude generally varies from 5 m to as high as 2000 m and the latitude from $10^{o}6$ to $16^{o}5$ N lat. and from $72^{o}5$ to $76^{o}4$ E long. where, there is a grater concentration of species without sessile tubers. Maximum concentration of the species can be noticed in North Kerala, Coastal and hilly Karnataka, Goa and Southern districts of Maharashtra and this large area can be considered as the hot-spot for *Curcuma* spp. falling under aforementioned three sections.

### *Genetic Erosion*

Genetic erosion of various species under the treatise is possible in case of highly niche specific population which is either very small or it remains as individuals. There is no threat for many of the species such as *C. aurantiaca*, *C. oligantha*, *C. cannanorensis*, *C. inodora*, *C. mutabilis* and *C. karnatakensis* having very frequent occurrence of large populations in pockets. Some of the species from Karnataka grow rather luxuriantly along the

highways in grassy slopes, under grasses and bushes, and sharp edges of ghat roads and in grasslands on stony soils. However, species such as *C. thalakaveriensis* and *C. kudagensis* having very restricted occurrence in pockets of hilly grasslands in Kudremukh hills, Thalakavery and Bababudangiri hills in Karnataka are under threat of erosion due to habitat destruction. *C. neilgherrensis* and *C. pseudomontana* having wider distribution in sholay grasslands and lower tropical grasslands respectively in Western Ghats are also facing threat of erosion. Ecological niche of *C. vamana*, the only species under the section *Stolonifera* from India, is confined to specific locations under disturbed forests at lower elevations of foothills and midlands in Central Kerala and it is under threat. Similarly, *C. mutabilis* population noticed in lower slopes and along disturbed forest roads in Malappuram and Palakkad districts of Kerala faces threat due to deforestation and plantation activities.

### *Future Problems and Prospects*

Several species such as *C. oligantha*, *C. inodora*, *C. albiflora*, *C. karnatakensis*, *C. mutabilis*, *C. thalakaveriensis* and other entities such as *Curcuma* sp. 1, 2 and 3 have very high potential for their improvement as ornamentals in tropics. Before undertaking any serious attempt in this direction, taxonomic identity of the unidentified entities is a problem as their population is very thin and is represented by few plants at a site posing problem in validating these entities as new species. They flower two times in a year and bear stunningly beautiful spikes and flowers. *Curcuma* sp. 3, the only entity having very long flowering duration, appears to be an ideal genetic base for transfer to others, bearing more beautiful inflorescence. Detailed studies on adaptability and cultural techniques based on the ecology, physiology, seed setting and germination, studies on vegetative regeneration and mass propagation, cultural techniques are to be immediately worked out in these species as done by Kuehny *et al.* (2002) in some ornamental gingers. These species are adapted to different temperature regimes, altitudes and rain fall pattern in tropics and may be useful in developing exquisitely beautiful garden plants under different climatic regimes. Use of the spikes as cut flowers in some of these may be worked out as the flowers remain only for a day or two but flowers are produced continuously for a period varying from one week to over one month.

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# Characterization and Evaluation of Asian Mustard (*Brassica tournefortii* Gouan.) – An Endangered Oilseed Crop of Northwestern India

**Ranbir Singh, DP Semwal and KC Bhatt***
*Division of Plant Exploration and Germplasm Collection, ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India*

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Asian mustard (*Brassica tournefortii* Gouan.), an endangered oilseed crop, is cultivated in the parts of north-western India. This crop is known to have genes for resistance to biotic and abiotic stresses, therefore, attempts were made to collect, evaluate and conserve its genetic resources for further utilization. A total of 18 accessions were grown consecutively for three crop seasons in randomized block design for characterization and evaluation using twelve minimal morpho-agronomic traits. Promising accessions were identified for different economic traits, which may be useful for developing disease, pest and drought resistant varieties, cytoplasmic male sterile (CMS) lines as well as for developing hybrids. Moreover, Geographical Information System (GIS) tools were also used to understand distribution of diversity/ variability in the collected germplasm.

**Key Words: Asian mustard, *Brassica tournefortii*, Characterization, Endangered, Genetic diversity, GIS tools, Under-utilized**

## Introduction

Asian mustard (*Brassica tournefortii* Gouan.), also known as Saharan mustard, is a member of mustard family Brassicaceae. It is an endangered, underexploited oilseed crop, which has become naturalized under tropical and subtropical regions of Asia, Africa, Australia and USA. In India, it is localized in drier parts of North-western states (Rajasthan, Punjab and Haryana). It is cultivated under rainfed conditions either as a sole or mixed crop on marginal lands and sand dunes as a source of edible oil and forage (Fig. 1a & b). Asian mustard was a common oilseed crop of Indian arid region (Rana and Singh, 1992) but due to low yield, shattering habit and development of high yielding varieties of rapeseed-mustard, its cultivation has declined and gradually it became an endangered oilseed crop in the region. Presently, this crop is confined only to sand dunes of uninhabited remote localities in Haryana and Rajasthan (Duhoon and Koppar, 1998; Kumar *et al.,* 2004; Singh 1996; Singh and Sharma, 2007). It has been observed that its seeds generally grow as weed from the shattered seeds of previous season crop.

Inter-specific hybridization is considered as an important tool for transferring resistance genes from wild to cultivated brassicas in order to improve rapeseed-mustard crop. Asian mustard is known to have resistance genes against biotic and abiotic stresses and, therefore, it can play an important role in development of tolerant lines against *Alternaria* blight, white rust, aphids and drought under changing climatic conditions (Chander *et al.,* 2013; Prakash and Bhat, 2007; Singh *et al.,* 1965). Successful inter-specific hybridization has been reported between *B. tournefortii* and *B. rapa* in India for resistance against diseases and pests (Rawat and Anand, 1979). Its germplasm resource has also been utilized for resistance breeding through development of cytoplasmic male sterile (CMS) restorer lines to generate inter-specific hybrids. Considering the importance of this endangered under-utilized oilseed, attempts have been made to collect, evaluate and conserve the genetic diversity of *B. tournefortii*.

## Materials and Methods

A total of 18 accessions of *B. tournefortii* were collected from drier parts of north-western states of India covering Alwar, Jhunjhunu, Sikar, Jodhpur and Bikaner districts of Rajasthan; and Bhiwani, Mahendragarh and Hisar districts of Haryana (Fig. 2). During field survey, information pertaining to areas under cultivation, time of harvesting/ maturity, its uses, and factors responsible for genetic erosion were also recorded, besides passport data. The assembled germplasm was grown in three replications for three consecutive years (2009-10, 2010-11 and 2011-12) at NBPGR, Experimental Farm, New Delhi, in randomized block design (RBD), keeping recommended

*Author for Correspondence: E-mail: kcbhatt@nbpgr.ernet.in

**Fig. 1a. *B. tournefortii* on sand dune**

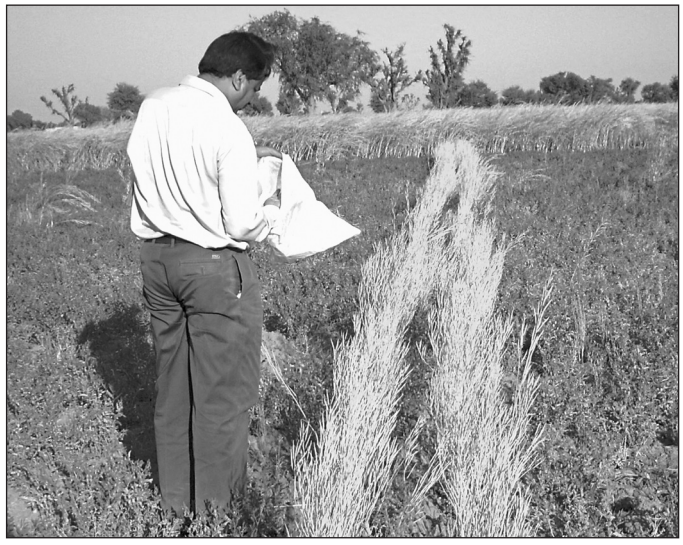

**Fig. 1b. *B. tournefortii* growing as mixed crop**

three rows of 3 m length, row to row distance of 45 cm and plant to plant distance of 10-15 cm. Characterization and evaluation data were recorded on five randomly selected plants using twelve important morpho-agronomic and yield contributing traits. Oil content (%) was estimated using non-destructive Nuclear Magnetic Resonance (NMR) technique. Mean and coefficient of variation were computed for pooled data using standard statistical methods (Gomez and Gomez 1984). DIVA-GIS tool was used for mapping diversity distribution (Semwal *et al.* 2013). For GIS based grid mapping, grid of $0.5^0$ x $0.5^0$ (55.5 Km) cells and a circular neighborhood method was used in the present study. Variability mapping was done using diversity indices (Shannon and Weaver, 1963). At maturity, the dehydrated seed samples were sealed in airtight three layered aluminium packets for long-term conservation at -18°C in the National Genebank at NBPGR, New Delhi.

## Results and Discussion

*B. tournefortii* (18 acc.) germplasm accessions were grown for characterization and evaluation for three consecutive years. Evaluation data were recorded on 12 morpho-agronomic traits. Among the traits studied, the highest variability was observed for seed weight per plot (CV=58.57%) followed by beak length (CV=30.73%), main fruiting branch length (CV=17.36%) and number of primary branches (CV= 16.54%) as given in Table 1.

Based on characterization and evaluation of germplasm, promising accessions identified for various morpho-agronomic traits have been given in Table 2 along with source of collection. Maximum promising accessions were identified from Bhiwani district of Haryana and Jodhpur district of Rajasthan. An accession (IC 560703) collected from Alwar (Rajasthan) was found highly tolerant to mustard aphid (*Lipaphis erisimi*) under field condition (Chander *et al.,* 2013).

Among the promising accessions, IC560709 was identified as useful donors for length of main fruiting branch (>50.0 cm) from Jhunjhunu (Rajasthan); RBT2003 for number of siliquae on main fruiting branch (>30) from Jodhpur (Rajasthan); IC560711 for number of

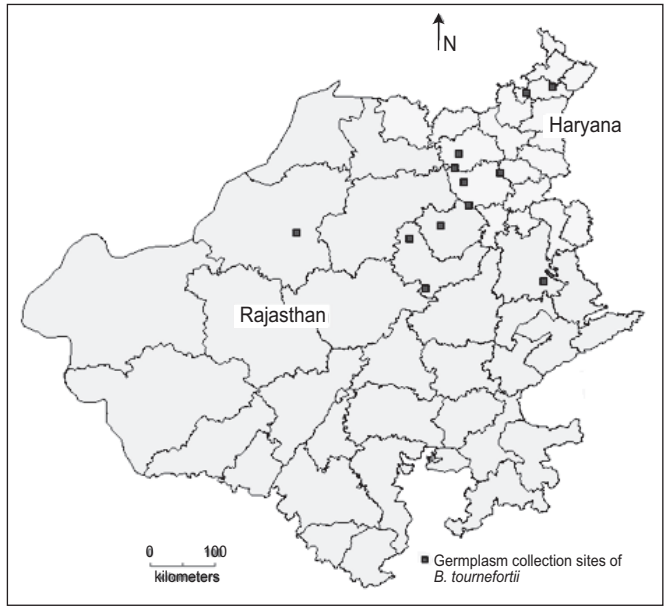


**Fig. 2. Germplasm collection sites of *B. tournefortii***

**Table 1. Range, mean, standard error (SE) and coefficients of variation (CV) for different agro-morphological traits of *B. tournefortii***

| S.No. | Traits/Variables | Code | Minimum | Maximum | Mean | SE | Mean CV (%) |
|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | PLH | 70.6 | 110.0 | 88.8 | 3.20 | 12.49 |
| 2 | No. of primary Branches | NPB | 8.80 | 15.6 | 10.5 | 0.50 | 16.54 |
| 3 | Length of main fruiting branch | LFB | 32.0 | 56.0 | 40.8 | 2.04 | 17.36 |
| 4 | Pods on main fruiting branch | PFB | 15.0 | 29.2 | 24.3 | 1.10 | 15.64 |
| 5 | Pod length (cm) | PDL | 3.1 | 4.3 | 3.6 | 0.12 | 11.35 |
| 6 | Beak length (cm) | BKL | 0.7 | 1.8 | 1.27 | 0.11 | 30.73 |
| 7 | No. of seeds/pod | NSP | 13.0 | 17.8 | 15.07 | 0.49 | 11.41 |
| 8 | Days to first flower | DFF | 64.0 | 69.0 | 66.9 | 0.48 | 2.51 |
| 9 | Days to first maturity | DFM | 122.0 | 127.0 | 124.58 | 0.53 | 1.47 |
| 10 | Days to mean maturity | DMM | 128.0 | 134.0 | 130.75 | 0.55 | 1.46 |
| 11 | Oil content (%) | OIL | 28.39 | 31.7 | 29.5 | 0.18 | 3.74 |
| 12 | Seed weight/plot (g) | SWP | 30.0 | 470.0 | 252.08 | 4.30 | 58.57 |

seeds per silique (>17.0) from Jodhpur (Rajasthan) and IC560724 for high oil content (31.7%) from district Jodhpur (Rajasthan).

Morpho-agronomic traits were mapped using GIS tools for showing variability distribution in the germplasm accessions. On the basis of areas identified (Table 2) for collection of trait-specific germplasm, area no. 0.97-2.0 and 1.28-2.0 in grid map representing regions with high diversity/variability (Fig. 3) while green areas represent regions with low diversity/variability. Colours of the grids are indicating the extent of diversity in the germplasm accessions. Analysis for richness in oil content using diversity indices method of DIVA-GIS showed that Jodhpur district of Rajasthan is potential area for collection of *B. tournefortii* germplasm with high oil content.

## Conclusions

Although limited germplasm of Asian mustard is available in India but good variability has been present for plant height, number of primary branches per plant, oil content (%) and number of seeds per siliquae. Most of the promising accessions identified as useful donors were from Alwar and Jodhpur districts of Rajasthan; and Bhiwani district of Haryana mainly for traits like

**Table 2. Promising donor genotypes of *B. tournefortii* germplasm identified for important traits**

| S.No. | Traits | Promising value | Promising donor genotypes | | |
|---|---|---|---|---|---|
| | | | Accessions | Value | Source of collection |
| 1 | Dwarf plant height | < 80.0 cm | IC560717 | 78.8 | Sikar, Rajasthan |
| | | | IC560720 | 70.6 | Hisar, Haryana |
| | | | IC560722 | 76.2 | Bhiwani, Haryana |
| 2 | Number of primary branches | >12.0 | IC560703 | 15.6 | Alwar, Rajasthan |
| | | | BT Yellow | 13.0 | Jodhpur, Rajasthan |
| | | | IC342758 | 13.0 | |
| 3 | Length of main fruiting branch (cm) | >50.0 cm | IC560709 | 56.0 | Jhunjhunu, Rajasthan |
| | | | BT Yellow | 53.6 | |
| | | | IC560703 | 52.0 | Alwar, Rajasthan |
| 4 | No of siliquae on main fruiting branch | >30.0 | RBT2003 | 32.0 | Jodhpur, Rajasthan |
| | | | RBT2001A | 31.2 | |
| | | | BT Yellow | 30.8 | |
| 5 | Siliquae length (cm) | >4.0 cm | IC560709 | 4.3 | Jodhpur, Rajasthan |
| | | | RBT2001A | 4.1 | |
| 6 | No. of seeds/siliquae | >17.0 | RBT2002 | 18.6 | Jodhpur, Rajasthan |
| | | | IC560711 | 17.8 | |
| | | | IC560705 | 17.6 | |
| 7 | Days to first flowering (early flowering) | < 65 | RBT2003 | 63 | Jodhpur, Rajasthan |
| | | | IC560722 | 64 | Bhiwani, Haryana |
| 8 | Oil content (%) | >31.0 | IC560724 | 31.7 | Jodhpur, Rajasthan |
| 9 | Seed weight/plot (SWP) g | >12 | IC560708 | 12.5 | Mahendragarh, Haryana |

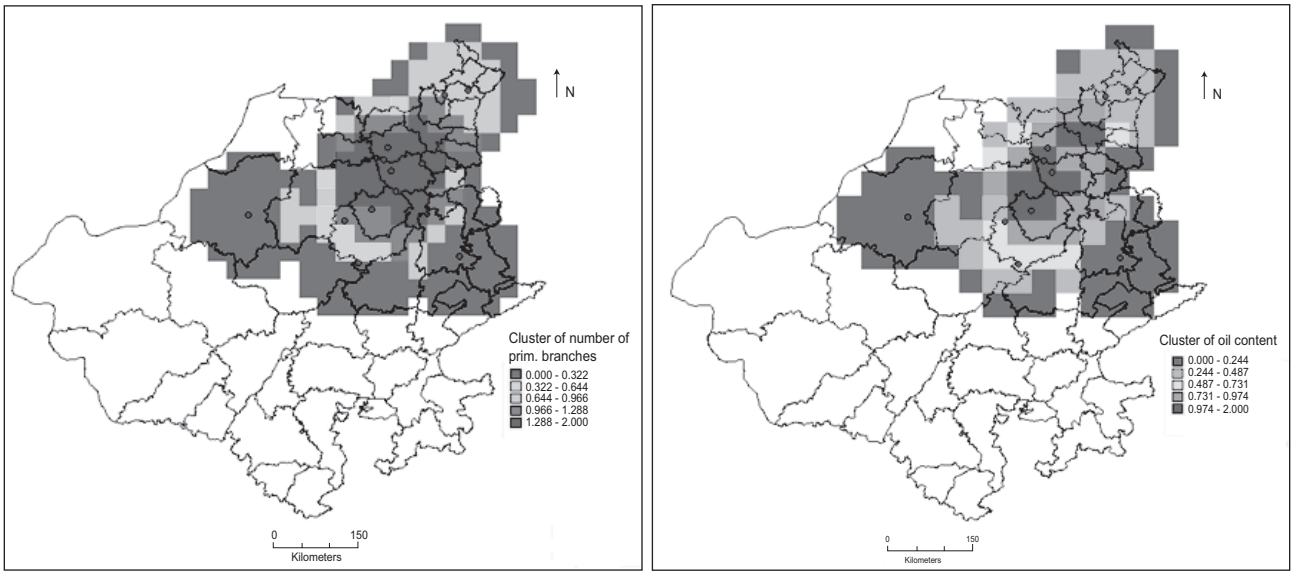


**Fig. 3. Grid map showing diversity in number of primary branches and richness value of oil content**

dwarf plant height, early maturity, high yield and high oil content. Such pockets need to be surveyed intensively for more number of germplasm to broaden genetic base and to utilize in breeding programmes of the crop. The development of improved cultivars through hybridization combining with high seed yield potential and specific fatty acid composition, disease, pest and drought resistance as well as low levels of glucosinolates would allow expanded production of spring grown *Brassica rapa* will be improved using *B. tournefortii* as oilseed crop across the northwestern parts of India.

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# Genetic Variability for Physiological Characters and their Relationships with Seed Yield and its Components in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.] under Drought

**Raju Lal Meena[1], JS Chauhan[2]*, KH Singh[1] and SS Rathore[1]**
[1] *ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur-321303, Rajasthan, India*
[2] *Indian Council of Agricultural Research, Krishi Bhawan, Dr. Rajendra Prasad Road, New Delhi-110001, India*

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Twenty-two genotypes of Indian mustard were grown in a randomized complete block design with three replications. Analysis of variance indicated presence of variability in the experimental genotypes for all the physiological characters investigated except specific leaf weight (SLW) at 35 DAS and seed: husk ratio. Phenotypic (PCV) and genotypic (GCV) variability was substantial for leaf growth rate (LGR), leaf area index (LAI), leaf area ratio (LAR), crop growth rate (CGR), relative growth rate (RGR), net assimilation rate (NAR), transpiration quotient (TQ) and SPAD chlorophyll meter reading (SCMR). All the physiological parameters except LGR between 35 and 75 DAS, TDM at 35 DAS and SCMR at 35 and 75 DAS had high heritability and moderate to high genetic advance implying that additive gene effects were mainly responsible for the expression of these characters. Seed yield/plant was positively and significantly correlated at phenotypic and genotypic levels with LAI, CGR and biological yield/plant. It had negative genotypic correlations of moderate strength (r=-0.599–(-) 0.394) with TQ at 35 and 75 DAS indicating its positive relationship with water use efficiency. Dry matter production, early growth and development of the crop are important under drought stress due to continuous decline in available soil moisture. Since LAI, LGR, CGR, RGR and NAR are the functions of dry matter production and/or leaf area, therefore, selection on the basis of high biological yield and large LAI at 50% flowering should be quite effective in improving seed yield under drought. An increase in LAI might increase radiation load resulting in to high transpiration. Therefore, genotypes having high LAI with erect leaves and low TQ should be accorded priority in the selection programme.

**Key Words:** ***Brassica juncea* L., Drought, Genetic variability, Genotypes, Physiological parameters, Seed yield**

## Introduction

Rapeseed and mustard are important group of oilseed crops contributing 26.1% and 23.9% to the total oilseeds production and acreage, respectively, in India (Anonymous, 2014). Of these, Indian mustard (*Brassica juncea*) is the major crop. Nearly 27% of the total cropped area is rainfed where drought affects growth and development of the crop and consequently, the seed yield, depending upon time of its occurrence, duration and intensity. The yield reduction under drought in Indian mustard ranged from 17 to 94 % (Mohamed Ali *et al*., 1990, Chauhan *et al*., 2007) due to considerable effects on yield components (Chauhan *et al*., 2007; Sharma and Pannu, 2007). Reduced leaf area index, crop growth rate, net assimilation rate, total dry matter, harvest index, partitioning coefficient (Shiv Ratan *et al*., 2005); $N_2$ assimilatory enzymes activity and plant water relation have been reported as a consequence of drought (Singh *et al*., 2003; Gunasekra *et al*., 2004). Singh *et al.* (1988) reported that mustard genotypes with drought tolerance trait(s) yielded better than those without such trait(s) under water stress. Transpiration efficiency (TE), defined as the amount of dry matter produced/unit amount of water transpired is one such trait, which influenced the performance of crop under water-limited conditions.The negative effects of drought during seed development may be mitigated by remobilization of assimilates that is by increasing harvest index. Exploitation of germplasm for improved TE and other physiological trait(s) would depend on the available variability in the germplasm as well as heritability of the traits. The information on nature and magnitude of variability for these characters is scanty in Indian mustard. The present investigation was under taken to assess extent and nature of variability for growth parameters and their interrelationships with seed yield and other related traits.

**Author for Correspondence: E-mail: adgseedicar@gmail.com*

## Materials and Methods

The materials for the present investigation comprised 18 advanced breeding lines and four varieties of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. These were grown in a randomized complete block design with three replications under rainfed conditions during *rabi* season of 2007-08 using only pre-sowing irrigation. There were four rows of 4 m length for each entry in a block. The row spacing was 30 cm and plant spacing with in a row was maintained at 10 cm by thinning. A fertilizer dose of 40:20:20 kg/ha ($N:P_2O_5:K_2O$) was applied at the time of sowing. Soil moisture content was recorded from the time of sowing till maturity at an interval of 15 days at three depths (15, 30 and 60 cm) using gravimetric method. The soil samples were dried in an oven at $75^o \pm 2^0$ C for at least 72 hr till constant weight was achieved. The soil moisture content was expressed in percentage on wet basis.

To study different growth parameters, the plant samples from 50 cm running row length were harvested above ground level at 35,75, 95 days after sowing (DAS). The shoot and leaves were separated and leaf area was recorded. Plant samples (shoot and leaves) were dried separately in an oven at 65 ± 2°C for at least 72 hours till constant weight was achieved. The samples were weighed using an electronic balance and dry matter of leaves, shoot as well as shoot + leaves was expressed in $g/m^2$. For recording photosynthesis, transpiration and SPAD chlorophyll meter readings (SCMR), 3rd and 4th fully expanded leaf from the top was used from three randomly selected plants in each replication. Growth parameters were computed using leaf area and dry weight of leaves as well as total dry matter as per the methods of Radford (1967). Photosynthesis and transpiration rate were measured with the help of portable Photosynthesis system (CIRAS-2). Transpiration quotient (TQ), ratio of transpiration and photosynthesis was expressed as mmoles/µ mole. The SCMR measurements were obtained from the SPAD chlorophyll meter. Days to maturity were computed on plot basis. At the time of harvest, ten random competitive plants from each replication were taken from the two central rows to record seed yield/plant, yield components, biological yield/plant and harvest index.

The character means for each replication were subjected to analysis of variance according to the procedure outlined by Panse and Sukhatme (1967). Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated following the method of Burton (1952). Heritability in broad sense ($h^2_b$) and expected genetic advance at 5% selection intensity were calculated following the methods of Hanson (1963) and Johnson *et al.* (1955), respectively. The correlation coefficients at phenotypic ($r_{pxy}$) and genotypic ($r_{gxy}$) level among different characters were computed according to the methods suggested by Searle (1971).

## Results and Discussion

The soil moisture content at the time of sowing varied from 9.0-12.8% at 15 cm, 9.0-12.5% at 30 cm and 10.0-13.5% at 60 cm depth. There was a steady and rapid decline in soil moisture content at all the three soil depths up to 65 days after sowing (DAS) coinciding with 50% flowering in majority of the genotypes. The soil moisture content at this time reached 4.6%, 5.6% and 7.4% at 15, 30 and 60 cm, respectively. Thereafter, the moisture content stabilized and showed gradual decline. The reduction in soil moisture content from 65 DAS till the time of harvest was only 1.6% at 15 cm, 0.6% at 30 cm and 1.4% at 60 cm.

Highly significant genotypic differences were observed for leaf area index (LAI) and total dry matter (TDM) at 35, 75 and 95 DAS. However, TQ and SCMR showed highly significant genotypic differences at 35 and 75 DAS. The specific leaf weight (SLW) did not exhibit significant genotypic differences at 35 DAS but genotypes had highly significant differences at 75 and 95 DAS (Table 1). The genotypic differences were also highly significant for leaf area ratio (LAR), leaf growth rate (LGR), crop growth rate (CGR), relative growth rate (RGR) and net assimilation rate (NAR) during 35-75 and 75-95 DAS.

### *Variability*

All the physiological characters investigated, *viz.*, LAI, LAR, LGR, SLW, CGR, RGR, NAR, TQ and SCMR had wide variation at both the phenotypic and genotypic levels. The range for phenotypic and genotypic coefficients of variability was 10.7 (SCMR at 35 DAS)-67.7% (LGR during 35-75 DAS) and 10.6 (SCMR at 35 DAS)-57.8 % (NAR during 75-95 DAS), respectively (Table 2). The PCV>35 %, 25-35%, 15-24% and <15% were classified as very high, high, moderate and low, respectively and GCV>20%, 10-20% and <10% were classified as high, moderate and low, respectively. The genotype BPR-538-12 and Rohini had the highest and lowest LAI at 35 DAS with high PCV and GCV. The minimum (0.4)

**Table 1. Analysis of variance for physiological characters in Indian mustard under drought**

| Characters/degree of freedom | Source of variation (Mean sum of squares) | | | | |
|---|---|---|---|---|---|
| | Replication | Genotype | Error | SEM (±) | CD (5%) |
| **Leaf area index** | | | | | |
| 35 DAS* | 0.020 | 0.095** | 0.010 | 0.055 | 0.161 |
| 75 DAS | 0.012 | 0.553** | 0.029 | 0.097 | 0.282 |
| 95 DAS | 0.004 | 0.031** | 0.002 | 0.026 | 0.076 |
| **Leaf area ratio** | | | | | |
| 35 - 75 DAS | 1.918 | 9.227 ** | 3.039 | 1.007 | 2.877 |
| 75 - 95 DAS | 0.118 | 6.702 ** | 0.229 | 0.276 | 0.790 |
| **Leaf growth rate** | | | | | |
| 35 - 75 DAS | 0.006 | 0.216** | 0.069 | 0.152 | 0.435 |
| 75 - 95 DAS | 0.394 | 0.535** | 0.295 | 0.314 | 0.896 |
| **Specific leaf weight** | | | | | |
| 75 DAS | 0.351 | 4.307** | 0.280 | 0.299 | 0.873 |
| 95 DAS | 0.153 | 2.154** | 0.317 | 0.317 | 0.927 |
| **Total dry matter** | | | | | |
| 35 DAS | 54.327 | 260.888** | 62.746 | 4.468 | 13.052 |
| 75 DAS | 56.096 | 22007.324** | 466.636 | 12.185 | 35.594 |
| 95 DAS | 1367.050 | 35736.899** | 492.510 | 12.518 | 36.568 |
| **Crop growth rate** | | | | | |
| 35 - 75 DAS | 0.346 | 21.469** | 1.155 | 0.606 | 1.771 |
| 75 - 95 DAS | 1.716 | 66.401** | 0.905 | 0.537 | 1.568 |
| **Relative growth rate** | | | | | |
| 35 -75 DAS | 4.012 | 53.897** | 3.940 | 1.119 | 3.271 |
| 75 - 95 DAS | 3.178 | 134.777** | 4.128 | 1.146 | 3.347 |
| **Net assimilation rate** | | | | | |
| 35-75 DAS | 0.149 | 1.441** | 0.185 | 0.248 | 0.710 |
| 75 - 95 DAS | 5.913 | 47.517** | 1.434 | 0.691 | 1.976 |
| **Transpiration quotient** | | | | | |
| 35 DAS | 0.001 | 0.040** | 0.001 | 0.021 | 0.061 |
| 75 DAS | 0.002 | 0.045** | 0.026 | 0.026 | 0.075 |
| **SCMR** | | | | | |
| 35 DAS | 0.210 | 79.618** | 0.069 | 0.148 | 0.432 |
| 75 DAS | 0.136 | 117.384** | 0.056 | 0.133 | 0.389 |

*DAS: Days after sowing ; ** Significant at 1% probability level

and maximum (2.2) LAI at 75 DAS was recorded for the genotype RLM-619 and RCC-4, respectively, and the PCV and GCV were high. The range for LAI among the genotypes at 95 DAS was 0.12 (RLM-619)-0.45 (BPR 539-4) with an overall mean 0.26 ± 0.03 and the PCV and GCV were high.

The PCV was moderate and GCV was high for LAR during 35-75 DAS. The LAR was 3.23 and 20.28 for Rohini and BPR-541-5, respectively. LAR during 75-95 DAS varied from –8.91 (Rohini) to –1.50 (RLM-619). The mean LAR was –2.94 ± 0.31 with high PCV and GCV (Table 2). The LGR ($mm^2$/day) was minimum (0.35) for the genotype RLM-619 and maximum (3.09) for the genotype RCC-4. The character showed high GCV and PCV. The LGR during 75-95 DAS also had similar trend of variability but mean value was negative. SLW (mg/$cm^2$) had an appreciable range of variation at 75 and 95 DAS, respectively, and had moderate GCV and PCV. Total dry matter (g/$m^2$) increased consistently from 35 DAS to 95 DAS, respectively. The genotype Varuna had the highest TDM at 35 DAS whereas; RCC-4 recorded the highest value at 75 and 95 DAS. This character had moderate to high variability.

Crop growth rate (g/day/$m^2$) had substantial genetic and phenotypic variation at both the growth stages (Table 2). The range was 1.69 (Rohini)-12.79 (Urvashi)

**Table 2. Range, mean, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability in broad-sense ($h^2$) and genetic advance (as % of mean) for physiological characters in Indian mustard under drought**

| Character | Range | Mean ± SEM | PCV (%) | GCV (%) | $h^2$ (%) | Genetic advance |
|---|---|---|---|---|---|---|
| Leaf area Index | | | | | | |
| 35 DAS* | 0.34 - 1.07 | 0.64 ± 0.06 | 30.5 | 26.4 | 74.9 | 47.1 |
| 75 DAS | 0.42 - 2.17 | 0.99 ± 0.10 | 45.8 | 42.3 | 85.6 | 80.7 |
| 95 DAS | 0. 12 - 0.45 | 0.26 ± 0.03 | 41.8 | 37.8 | 81.8 | 70.3 |
| Leaf area ratio | | | | | | |
| 35-75 DAS | 3.23 - 20.28 | 10.31 ± 1.01 | 32.7 | 28.0 | 73.3 | 49.3 |
| 75-95 DAS | (-) 8.91- (-) 1.50 | (-) 2.55 ± 0.28 | 60.6 | 57.6 | 90.4 | 113.2 |
| Leaf growth rate ($mm^2$/day) | | | | | | |
| 35-75 DAS | 0.35 - 3.09 | 0.510 ± 0.15 | 67.7 | 43.6 | 41.4 | 57.8 |
| 75-95 DAS | (-) 5.08 - (-) 0.793 | (-) 2.94 ± 0.31 | 40.0 | 35.4 | 78.3 | 64.2 |
| Specific leaf weight (mg/$cm^2$) | | | | | | |
| 75 DAS | 5.34 - 9.52 | 6.92 ± 0.30 | 18.4 | 16.7 | 82.7 | 31.4 |
| 95 DAS | 4.33 - 7.87 | 6.11 ± 0.32 | 15.8 | 12.8 | 65.9 | 21.4 |
| Total dry matter (g/$m^2$) | | | | | | |
| 35 DAS | 35.50 - 67.14 | \49.74 ± 4.47 | 22.8 | 16.3 | 51.3 | 24.1 |
| 75 DAS | 123.05 - 464.58 | 256.93 ± 12.19 | 34.0 | 33.0 | 93.9 | 65.8 |
| 95 DAS | 237.94 - 683.22 | 481.84 ± 12.52 | 23.0 | 22.5 | 96.0 | 45.4 |
| Crop growth rate (g/$m^2$/day) | | | | | | |
| 35-75 DAS | 1.69 – 12.77 | 5.62 ± 0.61 | 50.1 | 46.3 | 85.4 | 88.2 |
| 75- 95 DAS | 3.42 - 20.74 | 10.83 ± 0.54 | 44.0 | 43.7 | 96.0 | 87.1 |
| Relative growth rate (mg/g/day) | | | | | | |
| 35 - 75 DAS | 10.13 - 24.87 | 18.41 ± 1.12 | 24.7 | 22.2 | 80.9 | 41.1 |
| 75 - 95 DAS | 5.48 - 27.74 | 15.10 ± 1.15 | 45.8 | 43.7 | 91.3 | 86.1 |
| Net assimilation rate (mg/$cm^2$/day) | | | | | | |
| 35 - 75 DAS | 0.56 – 5.72 | 2.00 ± 0.25 | 38.9 | 32.4 | 69.4 | 50.1 |
| 75 - 95 DAS | (-) 19.01 - (-) 2.76 | (-) 6.78 ± 0.69 | 60.5 | 57.8 | 91.5 | 114.0 |
| Transpiration quotient (m moles/µ mole) | | | | | | |
| 35 DAS | 0.23 - 0.66 | 0.33 ± 0.02 | 35.6 | 33.9 | 90.3 | 66.3 |
| 75 DAS | 0.23 - 0.68 | 0.34 ± 0.03 | 37.0 | 34.7 | 87.3 | 66.7 |
| SCMR | | | | | | |
| 35 DAS | 40.48 - 58.13 | 48.70 ± 0.15 | 10.7 | 10.6 | 99.7 | 21.8 |
| 75 DAS | 30.45 - 51.76 | 41.83 ± 0.13 | 15.0 | 14.9 | 99.9 | 30.8 |

*DAS: Days after sowing

during 35-75 and 3.42 (Rohini)-20.74 (BPR-542-14) during 75-95 DAS. The overall mean value was more during 75-95 DAS (10.8g). RGR (mg/g/day) was the highest for the genotype BPR-537 (24.87) and RLM-619 (27.74) during 35-75 and 75-95 DAS, respectively. The mean RGR reduced during 75-95 DAS but showed more variation as compared to that of 35-75 DAS (Table 2). The genotype RLM-619 and Rohini showed the maximum and minimum NAR of 5.72 and -2.76 (mg/$m^2$/day), respectively. The mean NAR was negative between 75-95 DAS. The NAR had substantial genotypic and phenotypic variability. Transpiration quotient had the range 0.23-0.66 and 0.23-0.68 at 35 and 75 DAS. The genotype BPR-542-6 and Rohini had the maximum TQ at 35 and 75 DAS, respectively. TQ was highly variable at both the stages with high PCV and GCV. The SCMR values were the maximum for the genotype Rohini at both the stages with reduction in mean at 75 DAS. The character had low GCV and PCV at both the stages (Table 2).

### *Heritability and Genetic Advance*

The heritability estimates varied substantially from 41.4% for LGR during 35-75 DAS to 99.9% for SCMR at 75 DAS. The genetic advance was the highest (88.2%) for CGR during 35-75 DAS and the lowest (21.4%) for SLW at 95 DAS. The heritability >80%, 60-80% and <60% were classified as high, moderate and low, respectively. The genetic advance was categorized as high (>50%), moderate (25-50%) and low (<25%). The LAI at 75 and 95 DAS had high heritability and genetic advance, but such estimates were low and moderate at 35 DAS. Both heritability and genetic advance were also high for LAR during 75-95 DAS. The heritability and genetic advance estimates were moderate during 35-75 DAS. The LGR had low and moderate heritability during 35-75 DAS

and 75-95 DAS, respectively. Nevertheless, the genetic advance for LGR was high during both the stages. Moderate heritability for SLW at 75 and 95 DAS was accompanied by moderate genetic advance (Table 2). Heritability estimates for TDM ranged from 51.3% (35 DAS) to 96% (95 DAS). The genetic advance was high, moderate and low at 75, 95 and 35 DAS, respectively.

High heritability estimates coupled with high genetic advance were recorded for CGR at both the stages. Estimates of heritability and genetic advance were high for RGR during 75-95 DAS. However, high heritability was associated with moderate genetic advance during 35-75 DAS for this character. NAR during 35-75 and 75-95 DAS exhibited moderate to high heritability (69.4-91.5 %) coupled with high genetic advance (>50%). High estimate for heritability was associated with high genetic advance for TQ while SCMR had high heritability coupled with low to moderate genetic advance.

### *Correlations*

*Phenotypic Level*

The leaf area index at 75 and 95 DAS was positively and significantly correlated with days to maturity, the correlation coefficients were 0.540** and 0.559**, respectively. Positive and significant association of days to maturity with LGR during 35-75 DAS ($r_{pxy}$ = 0.445*) and TDM at 75 DAS ($r_{pxy}$ = 0.556 **) was observed. The relationship of plant height with LAI at 35 DAS and TDM at 75 DAS was positive and significant. The correlation of LAI at 75 DAS and plant height was positive and highly significant ($r_{pxy}$ = 0.588**). The LAI at 35 DAS positively and significantly influenced secondary branches/plant and siliquae on main shoot. A similar trend of association was recorded for LAI at 75 DAS and siliquae on main shoot. Biological yield/plant and seed yield/plant were positively and significantly related with LAI at 35 and 75 DAS.

Days to maturity recorded positive and highly significant association with TDM at 95 DAS, CGR and RGR during 35-75 DAS. The CGR during 35-75 DAS exhibited positive and significant association with plant height ($r_{pxy}$ = 0.540**), siliquae on main shoot ($r_{pxy}$ = 0.446*), biological yield/plant ($r_{pxy}$ = 0.540**) and seed yield/plant ($r_{pxy}$ = 0.480*). The inter-relationship of the RGR during 35-75 DAS was positive and significant with 1000-seed weight. However, the association between 1000-seed weight and RGR during 75-95 DAS was significant and negative ($r_{pxy}$ = -0.452*). Reddy (1991) also reported positive and significant association of seed yield and LAI.

The leaf area index at 35 DAS had positive correlation with LAI at 75 DAS, LGR during 75-95 DAS, TDM at 35 and 75 DAS and CGR during 35-75 DAS. Mathur and Wattal (1996) also observed a positive association of LAI with TDM till 100 % flowering. The association between RGR (75-95 DAS) and LAI (35 DAS) was negative and significant ($r_{pxy}$ = - 0.492*). Similarly, LAI at 75 DAS exhibited positive relationship with LGR between 35-75 and 75-95 DAS, TDM at 75 and 95 DAS, CGR and RGR between 35-75 DAS (Table 3.). Negative and significant association of LAI at 75 DAS was observed with RGR, NAR between 75-95 DAS and SCMR at 35 DAS. The LGR (75-95 DAS), SLW (95 DAS) and TQ (35 DAS) exhibited negative and significant associations with LAI at 95 DAS. The association of SLW (75 DAS), TDM (95 DAS), CGR and RGR (35-75 DAS) were positive and significant with LAI at 95 DAS. Negative and significant associations of NAR during 35-75 DAS (r = - 0.759**) and SCMR at 35 DAS ($r_{pxy}$ = - 0.514*) were recorded. The LAR (35-75 DAS) and LGR (75-95 DAS) were positively and significantly interrelated ($r_{pxy}$ = 0.482*). TQ at 35 and 75 DAS exhibited significant and positive correlation with LAR during 75-95 DAS. The LGR (35-75 DAS) had positive and significant association with CGR (35-75 DAS) and TDM at 35 DAS. The association between LGR (35-75 DAS) and SLW at 75 DAS was negative and significant ($r_{pxy}$ = - 0.431*). SLW at 75 DAS showed negative and highly significant relationship with TDM at 75 and 95 DAS and CGR during 35-75 DAS. However, the correlation of SLW at 75 DAS was positive and highly significant with RGR during 35-75 DAS (Table 3).

Total dry matter at 75 and 95 DAS was positively and significantly related with CGR and RGR during 35-75 DAS. TDM at 75 DAS also showed positive association with NAR (35-75 DAS). The relationship of RGR and NAR (75-95 DAS) was significant and negative with TDM at 75 DAS. The TQ at 75 DAS and TDM at 95 DAS were negatively associated ($r_{pxy}$ = - 0.578**). The TDM at 95 DAS exhibited positive and significant relationship with CGR (75-95 DAS). The CGR and RGR between 35-75 DAS were positively and significantly correlated with each other (Table 4). The association of CGR (35-75 DAS) was negative and significant with RGR and NAR during 75-95 DAS. The CGR, NAR and RGR during 75-95 DAS were positively and significantly interrelated

**Table 3. Relationship among physiological character at phenotypic (light) and genotypic (bold) level in Indian mustard under drought**

| Character | LAI | | LAR | | LGR | | SLW | | TDM | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 75 DAS | 95 DAS | 35-75 DAS | 75-95 DAS | 35-75 DAS | 75-95 DAS | 75 DAS | 95 DAS | 35 DAS | 75 DAS | 95 DAS |
| LAI (35 DAS) | 0.521* | 0.028 | 0.294 | -0.275 | 0.099 | 0.499* | -0.180 | -0.079 | 0.606** | 0.509* | 0.363 |
| | **0.620** | **-0.005** | **0.230** | **-0.385** | **0.328** | **0.628** | **-0.209** | **-0.057** | **0.868** | **0.626** | **0.451** |
| LAI (75 DAS ) | | 0.287 | 0.384 | 0.021 | 0.592** | 0.495* | -0.422 | -0.018 | 0.400 | 0.674** | 0.492* |
| | | **0.343** | **0.378** | **-0.008** | **0.890** | **0.567** | **-0.504** | **-0.037** | **0.559** | **0.722** | **0.558** |
| LAI (95 DAS ) | | | -0.129 | -0.070 | 0.360 | -0.537** | 0.539** | -0.430* | -0.083 | 0.384 | 0.575** |
| | | | **-0.202** | **-0.129** | **0.712** | **-0.543** | **-0.636** | **-0.565** | **-0.002** | **-0.466** | **0.665** |
| LAR (35-75 DAS ) | | | | -0.227 | 0.030 | 0.482* | 0.141 | 0.274 | 0.033 | -0.242 | -0.045 |
| | | | | **-0.341** | **0.064** | **0.525** | **0.196** | **0.459** | **0.139** | **-0.260** | **-0.011** |
| LAR (75-95 DAS ) | | | | | 0.279 | 0.089 | 0.049 | 0.071 | -0.036 | 0.002 | -0.318 |
| | | | | | **0.414** | **0.120** | **0.045** | **0.091** | **-0.056** | **0.013** | **-0.311** |
| LGR (35 -75 DAS ) | | | | | | 0.246 | -0.431* | -0.100 | 0.132 | 0.497* | 0.352 |
| | | | | | | **0.261** | **-0.709** | **-0.303** | **0.497** | **0.825** | **0.582** |
| LGR (75-95 DAS ) | | | | | | | 0.065 | 0.326 | 0.424* | 0.214 | -0.40 |
| | | | | | | | **0.068** | **0.394** | **0.601** | **0.257** | **-0.052** |
| SLW (75 DAS ) | | | | | | | | 0.320 | -0.025 | -0.608** | -0.685** |
| | | | | | | | | **0.515** | **-0.169** | **-0.680** | **-0.760** |
| SLW (95 DAS ) | | | | | | | | | -0.075 | -0.389 | -0.150 |
| | | | | | | | | | **-0.035** | **-0.522** | **-0.189** |
| TDM (35 DAS ) | | | | | | | | | | 0.350 | 0.195 |
| | | | | | | | | | | **0.525** | **0.241** |
| TDM (75 DAS ) | | | | | | | | | | | 0.578* |
| | | | | | | | | | | | **0.590** |

(Table 4). Negative and significant relationship between CGR (75-95 DAS) and TQ at 75 DAS was also observed ($r_{pxy}$ = - 0.457*). The relative growth rate (35-75 DAS) showed negative and significant association with RGR (75-95 DAS), positive and significant relationship with NAR during 35-75 DAS ($r_{pxy}$ = 0.464*) and TQ at 35 DAS ($r_{pxy}$ = 0.500*). The RGR and NAR during 75-95 DAS were significantly correlated ($r_{pxy}$ = 0.713**). TQ and SCMR at 35 DAS were positively and significantly associated with those of 75 DAS (Table 5).

*Genotypic Level*

The genotypic correlations were invariably higher than the phenotypic correlations. The genotypic and phenotypic correlations were in the same direction for all the characters except association of days to maturity with SCMR. Days to maturity had positive and moderate correlation with majority of the physiological characters studied, except LAR during 35-75 and 75-95 DAS, LGR during 75-95 DAS, TDM at 35 DAS, CGR during 75-95 DAS and SCMR at 75 DAS. However, SLW at 75 DAS was negatively correlated with days to maturity ($r_{gxy}$ = - 0.760).

Plant height had high and positive correlation with LAI at 35 and 75 DAS, LGR (35-75 and 75-95 DAS), CGR and RGR (35-75 DAS). The association of plant height with LAR (35-75 DAS), TDM at 35 and 95 DAS was positive but moderate. Low to moderate and negative relationship of plant height with LAR (75-95 DAS), SLW at 75 DAS, RGR (75-95 DAS), NAR (75-95 DAS), TQ and SCMR at 35 and 75 DAS were observed. Primary branches/plant had positive and high genotypic correlation with LAI at 35 DAS ($r_{gxy}$= 0.722) whereas; its association with LAI at 75 DAS, LAR (35-75 DAS), LGR (75-95 DAS) and TDM (35 DAS) was positive and moderate. The relationship of primary branches/ plant with NAR during 35-75 DAS ($r_{gxy}$ = -0.683), TQ ($r_{gxy}$ = - 0.433) and SCMR at 35 DAS ($r_{gxy}$ = -0.414) was negative and moderate. The association of secondary

**Table 4. Relationship among physiological characters at phenotypic (light) and genotypic (bold) level in Indian mustard under drought**

| Character | CGR | | RGR | | NAR | | TQ | | SCMR | |
|---|---|---|---|---|---|---|---|---|---|---|
| | 35-75 DAS | 75-95 DAS | 35-75 DAS | 75-95 DAS | 35-75 DAS | 75-95 DAS | 35 DAS | 75 DAS | 35 DAS | 75 DAS |
| LAI (35 DAS) | 0.529* | 0.151 | 0.317 | -0.492* | -0.202 | -0.326 | -0.330 | -0.161 | -0.280 | -0.291 |
| | **0.671** | **-0.177** | **0.473** | **-0.603** | **-0.130** | **-0.336** | **-0.408** | **-0.189** | **-0.325** | **-0.334** |
| LAI (75 DAS) | 0.701** | -0.213 | 0.440* | -0.438* | -0.065 | -0.490* | -0.215 | -0.022 | -0.530* | -0.350 |
| | **0.750** | **-0.233** | **0.532** | **-0.468** | **0.018** | **-0.499** | **-0.230** | **-0.014** | **-0.573** | **-0.381** |
| LAI (95 DAS) | 0.492* | 0.241 | 0.545** | -0.171 | -0.399 | -0.196 | -0.429* | -0.331 | -0.073 | -0.045 |
| | **0.531** | **0.262** | **0.654** | **-0.212** | **0.534** | **-0.194** | **-0.483** | **-0.401** | **-0.080** | **-0.053** |
| LAR (35-75 DAS) | -0.017 | 0.202 | -0.083 | 0.059 | -0.759** | -0.006 | -0.113 | -0.356 | -0.514* | -0.403 |
| | **-0.075** | **0.234** | **-0.116** | **0.059** | **-0.798** | **0.076** | **-0.175** | **-0.424** | **-0.603** | **-0.472** |
| LAR (75-95 DAS) | -0.246 | -0.341 | -0.419 | 0.282 | 0.196 | 0.368 | 0.560** | 0.484* | 0.272 | 0.262 |
| | **-0.324** | **-0.354** | **-0.453** | **0.279** | **0.279** | **-0.343** | **0.622** | **0.530** | **0.285** | **0.270** |
| LGR (35 -75 DAS) | 0.436* | -0.154 | 0.318 | 0.196 | 0.287 | -0.416 | 0.045 | 0.153 | -0.093 | -0.68 |
| | **0.727** | **-0.262** | **0.504** | **-0.388** | **0.422** | **-0.666** | **0.044** | **0.210** | **-0.142** | **-0.115** |
| LGR (75-95 DAS) | 0.168 | 0.335 | -0.096 | -0.181 | -0.399 | -0.251 | 0.190 | 0.224 | -0.323 | -0.246 |
| | **0.201** | **-0.377** | **-0.112** | **-0.227** | **-0.464** | **-0.292** | **0.214** | **0.289** | **-0.366** | **-0.276** |
| SLW (75 DAS) | -0.596** | -0.131 | 0.599** | 0.181 | -0.425* | -0.143 | 0.369 | 0.178 | 0.215 | 0.201 |
| | **-0.711** | **-0.142** | **-0.676** | **0.219** | **-0.547** | **0.157** | **0.434** | **0.208** | **0.234** | **0.221** |
| SLW (95 DAS) | -0.351 | 0.170 | -0.398 | 0.397 | -0.383 | 0.308 | 0.253 | 0.228 | -0.010 | -0.019 |
| | **-0.459** | **0.256** | **-0.556** | **0.499** | **-0.632** | **0.409** | **0.437** | **0.266** | **-0.002** | **-0.021** |
| TDM (35 DAS) | 0.232 | -0.212 | -0.135 | -0.301 | -0.182 | -0.277 | -0.072 | 0.023 | -0.071 | 0.003 |
| | **0.463** | **-0.332** | **0.153** | **-0.475** | **-0.126** | **-0.416** | **-0.057** | **0.115** | **-0.102** | **0.016** |
| TDM (75 DAS) | 0.883** | -0.406 | 0.443* | -0.701** | 0.517** | -0.586** | -0.275 | 0.050 | -0.193 | -0.197 |
| | **0.932** | **-0.416** | **0.797** | **-0.703** | **0.598** | **-0.620** | **-0.308** | **0.057** | **-0.199** | **-0.204** |

branches/plant with other physiological characters, by and large, followed the trend of association as that of primary branches/plant.

The association of siliquae on main shoot was positive and high with LAI and TDM at 35 DAS and LGR during 35-75 DAS ($r_{gxy}$ = 0.718). The association was positive and moderate with LAI at 75 DAS, LAR (35-75 DAS), LGR (75-95 DAS), TDM at 95 DAS, CGR and RGR (35-75 DAS). The LAR during 75-95 DAS had negative ($r_{gxy}$ = - 0.596) correlation with siliquae on main shoot, RGR during 75-95 DAS($r_{gxy}$ = - 0.421), TQ and SCMR at 35 and 75 DAS. Positive association of low to moderate strength of siliqua length with LAI at 35, 75 and 95 DAS, CGR and RGR during 35-75 DAS was observed. SLW had negative relationship with siliqua length ($r_{gxy}$ = - 0.671). The RGR and NAR (75-95 DAS), TQ at 35 and 75 DAS and SCMR at 35 DAS exhibited negative correlation with siliqua length. Moderate and negative relationship of siliqua length with LGR (75-95 DAS) and TDM at 75 DAS was observed. However, LGR (35-75 DAS) exhibited positive association of moderate strength with siliqua length.

The association of seeds/siliqua was positive with SLW at 75 DAS ($r_{gxy}$=0.488) and SCMR at 75 DAS ($r_{gxy}$=0.435). The RGR during 35-75 DAS ($r_{gxy}$=0.557) and LAI at 95 DAS ($r_{gxy}$=0.453) were positively correlated with 1000-seed weight but RGR during 75-95 DAS showed negative and moderate association with 1000-seed weight ($r_{gxy}$=-0.535). High and positive genotypic relationship of biological yield/plant was observed with LAI (35 and 75 DAS), LGR (35-75 DAS), TDM (35, 75 and 95 DAS), CGR and RGR during 35-75 DAS (Table 5). Specific leaf weight at 75 DAS, RGR and NAR during 75-95 DAS and TQ at 35 DAS exhibited negative correlations with biological yield/plant.

Seed yield/plant had high and positive relationship with LAI at 35 ($r_{gxy}$=0.861) and 75 DAS ($r_{gxy}$=0.747), CGR ($r_{gxy}$=0.679) and LGR during 35-75 DAS ($r_{gxy}$=0.857). It also exhibited positive association of moderate strength with LAI at 95 DAS, TDM at 35, 75

**Table 5. Relationship among physiological characters at phenotypic (light) and genotypic (bold) level in Indian mustard under drought**

| Character | CGR | | RGR | | NAR | | TQ | | SCMR | |
|---|---|---|---|---|---|---|---|---|---|---|
| | 35-75 DAS | 75-95 DAS | 35-75 DAS | 75-95 DAS | 35-75 DAS | 75-95 DAS | 35 DAS | 75 DAS | 35 DAS | 75 DAS |
| TDM (95 DAS) | 0.618** | 0.475* | 0.595** | -0.065 | 0.268 | 0.150 | -0.578** | -0.288 | -0.228 | -0.251 |
| | **0.684** | **0.473** | **0.677** | **-0.066** | **0.316** | **0.129** | **-0.627** | **-0.321** | **-0.233** | **-0.255** |
| CGR (35-75 DAS) | | -0.257 | 0.850** | -0.730** | 0.351 | -0.456* | -0.409 | -0.105 | -0.341 | -0.293 |
| | | **-0.270** | **0.920** | **-0.751** | **0.456** | **-0.483** | **-0.481** | **-0.116** | **-0.367** | **-0.318** |
| CGR (75-95 DAS) | | | -0.088 | 0.661** | -0.247 | 0.770** | -0.388 | -0.457* | -0.009 | -0.071 |
| | | | **-0.073** | **0.679** | **-0.250** | **0.794** | **-0.423** | **-0.519** | **-0.009** | **-0.071** |
| RGR (35-75 DAS) | | | | -0.661** | 0.464* | -0.316 | 0.500* | -0.278 | -0.294 | -0.326 |
| | | | | **-0.682** | **0.504** | **-0.363** | **-0.624** | **-0.330** | **-0.327** | **-0.366** |
| RGR (75-95 DAS) | | | | | -0.239 | 0.713** | 0.137 | 0.003 | 0.191 | 0.122 |
| | | | | | **-0.263** | **0.769** | **0.160** | **-0.019** | **0.202** | **0.127** |
| NAR (35-75 DAS) | | | | | | -0.234 | -0.044 | 0.142 | 0.331 | 0.101 |
| | | | | | | **-0.309** | **-0.052** | **0.212** | **0.397** | **0.116** |
| NAR (75-95 DAS) | | | | | | | -0.198 | -0.168 | 0.144 | 0.075 |
| | | | | | | | **-0.217** | **-0.217** | **0.150** | **0.082** |
| TQ (35 DAS) | | | | | | | | 0.780** | 0.410 | 0.395 |
| | | | | | | | | **0.865** | **0.429** | **0.415** |
| TQ (75 DAS) | | | | | | | | | 0.326 | 0.357 |
| | | | | | | | | | **0.351** | **0.384** |
| SCMR (35 DAS) | | | | | | | | | | 0.719** |
| | | | | | | | | | | **0.721** |

*, **: Significant at 5% and 1% probability level, respectively.

and 95 DAS and RGR (35-75 DAS). However, TQ at 35 DAS and RGR (75-95 DAS) had negative relationship with seed yield.

High positive correlation of LAI and TDM at 35 DAS was observed. LAI at 35 DAS also had positive association with LAI at 75 DAS, LGR during 75-95 DAS, CGR during 35-75 DAS, TDM at 75 and 95 DAS (Table 4). RGR (75-95 DAS) recorded negative association of moderate magnitude with LAI at 35 DAS. LAI at 75 and 95 DAS had high and positive association with LGR during 35-75 DAS. Moderate to high positive relationship of LAI at 75 DAS with LGR during 75-95 DAS, TDM at 75 and 95 DAS, CGR and RGR between 35-75 DAS were also observed (Table 3). The LAI at 75 DAS had negative association of moderate magnitude with SLW at 75 DAS, RGR and NAR during 75-95 DAS and SCMR at 35 DAS. The LAI at 95 DAS exhibited negative and moderate relationship with LGR (75-95 DAS), SLW at 75 and 95 DAS, TDM at 75 DAS and TQ at 35 and 75 DAS. However, TDM at 95 DAS was positively correlated with LAI at 75 ($r_{gxy}$ = 0.558) and 95 DAS ($r_{gxy}$ = 0.665). The relationship of LAR (35-75 DAS) was negative and high with NAR (35-75 DAS), negative and moderate with SCMR (35 DAS), positive and moderate with LGR during 75-95 DAS and SLW at 95 DAS (Table 4).

Positive correlations of moderate magnitude were observed between LAR (75-95 DAS) and TQ (35 and 75 DAS). The LAR (75-95 DAS) also showed positive and negative association with LGR (35-75 DAS) and RGR (35-75 DAS). Highly positive association of LGR (35-75 DAS) was observed with TDM at 75 DAS and CGR during 35-75 DAS (Table 4). A negative and strong relationship was recorded between LGR (35-75 DAS) and SLW at 75 DAS. Relationship of LGR (75-95 DAS) with TDM at 35 DAS was positive and moderate ($r_{gxy}$ = 0.601).

The SLW at 75 DAS showed highly negative association with TDM at 75 and 95 DAS, CGR and RGR during 35-75 DAS. The NAR (35-75 DAS) was also negatively associated with SLW (75 DAS). The associations of SLW at 95 DAS were negative and

moderate with TDM at 75 DAS, CGR, RGR and NAR during 35-75 DAS (Table 3).TQ at 35 DAS, RGR and NAR during 75-95 DAS were positively associated with SLW at 95 DAS. The relationship of TDM at 35 DAS with CGR during 35-75 DAS was positive ($r_{gxy}$ = 0.463). Negative associations of moderate magnitude were observed for TDM at 35 DAS with RGR and NAR (75-95 DAS). The genotypic correlations of TDM at 95 DAS were 0.684, 0.473 and 0.677, respectively, with CGR (35-75 and 75-95 DAS) and RGR (35-75 DAS).

The CGR and RGR (35-75 DAS) were positively correlated with each other while CGR (35-75 DAS) and RGR (75-95 DAS) were negatively correlated (Table 5). The association of CGR (35-75 DAS) was positive and negative with NAR during 35-75 and 75-95 DAS, respectively. The correlation of CGR (35-75 DAS) and TQ at 35 DAS was positive. CGR, RGR and NAR between 75-95 DAS were positively correlated (Table 5). Similarly, NAR (75-95 DAS) and SCMR (75 DAS) were positively associated with each other. TQ and SCMR at 35 DAS also had high positive genotypic correlation with that of 75 DAS (Table 5).

## Conclusions

Physiological characters determining the growth and development of the crop such as LAI, LAR, LGR, SLW, TDM, CGR, RGR, NAR and TQ had moderate to high genetic variability. Except LGR between 35 and 75 DAS, TDM at 35 DAS and SCMR at 35 and 75 DAS all the growth parameters had high heritability and moderate to high genetic advance implying that additive gene effects were mainly responsible for the expression of these characters. Moderate to high variability available in the present materials could be quite useful for selection. The LAI and CGR also had positive correlations with seed yield. The relationship of days to maturity with LAI at 75 and 95 DAS, LGR, CGR, RGR between 35 and 75 DAS and TDM at 35, 75 and 95 DAS were positive and significant suggesting that days to maturity is directly related to characters influencing total dry matter production. LAI and TDM were also positively correlated at 35 and 75 DAS. The results suggested that under drought stress, 1000-seed weight, LAI, CGR. RGR, NAR and TQ could be the reliable selection criteria for yield enhancement. Negative genotypic correlation of moderate to high strength of TQ with plant height, primary branches/plant, siliquae on main shoot, siliqua length, biological yield and seed yield suggested that genotypes with low TQ conversely high water use efficiency (WUE) should be selected in the breeding programme to improve seed yield under drought stress.

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# Genetic Parameters, Character Association and Path Analysis for Fruit Yield and its Component Characters in Mango (*Mangifera indica* L.)

**Mandeep Singh Gill[1] and S Navprem[2]**
[1]*Punjab Agricultural University, Regional Research Station, Bathinda-151001, Punjab, India*
[2]*Department of Fruit Science, Punjab Agricultural University, Ludhiana-141004, Punjab, India*

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The nature and genetic parameters were assessed to select superior genotypes of mango (*Mangifera indica* L.) for sub-mountain region of Punjab (India). The moderate estimates (>7.0%) of genotypic co-efficient of variation (GCV) recorded for fruit yield/plant (11.70), fruit weight (7.18), pulp weight (8.73) and peel weight (9.69) signified the presence of adequate variation among the genotypes. Physical fruit attributes *viz.* fruit yield/tree, fruit weight, pulp weight and peel weight had substantially higher heritability estimates coupled with high genetic advance and confirmed that these traits are under the control of additive gene action hence phenotypic selection for their improvement may be effective. Estimates of correlation co-efficient showed positive significant association of fruit yield/plant with fruit breadth (0.72) and fruit weight (0.66), while it was negatively associated with acidity (-0.076). Path analysis revealed that fruit weight (1.60) and fruit breadth (0.41) had moderately higher direct effects on fruit yield. Fruit weight showed indirect contribution via all the traits except fruit juice acid content signifying that fruit weight is the major contributor towards fruit yield/plant. The scope of further improvement of mango cultivars under Punjab conditions has been discussed.

**Key Words: GCV, Genetic advance, Heritability, *Mangifera*, Mango, Path analysis, PCV**

## Introduction

The mango (*Mangifera indica* L.), commonly called as the 'King of fruits' in India is acclaimed an important tropical and sub-tropical fruit in the world due to its excellent flavour, delicious taste, attractive colour and nutraceutical properties (Nayak *et al*., 2013, Rathore *et al*., 2007). In India, primarily thirty mango cultivars are commercially cultivated; and also seedlings originated from seeds as well as indigenous strains/genotypes are grown on an area of 2516 thousand hactares with an annual production of 18431 thousand million tonnes (NHB, 2014). A wide variability in fruit shape, size, skin colour, time of maturity, stone size, pulp content and its quality attributes has been observed in the naturally growing population of seedling mangoes (Singh *et al*., 2012). The choice of a suitable cultivar is of paramount importance for its successful cultivation. The knowledge of genetic parameters such as heritability and correlation among characters under selection is very useful for predicting genetic progress in breeding programme and developing efficient breeding strategies (Falconer and Mackay, 1996). Knowledge of the magnitude of genetic variation among fruit characters and their heritability is utmost important particularly in highly out crossing species like mango (Rajan *et al*., 2009). The breeding strategy for the genetic improvement of fruit yield and its components depends upon the genetic diversity for different traits. The assessment of genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ($h^2$) and genetic advance is a pre-requisite for making effective selection and improvement in the base population. Path analysis based on phenotypic correlation coefficients further unravels the contributions of different traits towards fruit yield. Hence, the present investigation was carried out to assess the nature and magnitude of genetic parameters and their utilization for the development of superior genotypes of mango suitable for sub mountain regions of Punjab.

## Materials and Methods

The studies were conducted at PAU-Fruit Research Station, Gangian (Hoshiarpur), Punjab, on 35-year-old indigenous genotypes/promising cultivars of north India during 2010-13. The experimental material comprised of $GN_1$ (Gurmail da Amb), $GN_2$ (Samrali), $GN_3$ (Kukian de Chhalli), $GN_4$ (Bijrore de Bud), $GN_5$ (Hariana Kanghi), $GN_6$ (Punjab Beauty), $GN_7$ (Mallian de Chhalli), $GN_{12}$ (Bijrore de Chhalli), $GN_{19}$ (Chhauni Kalan de Chhalli),

*Author for Correspondence: E-mail: mandeepgill21@pau.edu

Langra, Dushehari, SB Rampur, SB Chausa, Alphonso, Mallika, Fazri, Malda, Amrapalli and Kishan Bhog planted at 9m × 9m spacing and all the recommended package of practices like fertilizers, irrigation and plant protection measures were followed (Anonymous, 2014). The region is situated in the sub montane and undulated tract of 31.82° North latitude and 75.66° East longitudes in district Hoshiarpur (Punjab) in North western part of India. The average elevation is about 239 meters from the mean sea level. The annual rainfall is around 800-1000 mm, where 75 per cent of the total rainfall is received during months of July to September and 15 per cent in the winter months from December to February. Fruit yield was recorded from the whole fruit weight per tree. Data was recorded from randomly selected ten fruits per genotype per replication at physiological maturity ('*Tapka* stage' having specific gravity > 1.0) and analyzed for various fruit physico-chemical quality attributes viz. fruit weight (g), fruit size (cm), pulp weight (g), peel weight (g), stone weight (g), total soluble solids, fruit juice acid content and reducing sugars. Fruit juice was extracted from the pulp by straining through a muslin cloth for determining various bio-chemical characteristics. Total soluble solids were noted with Bausch and Lamb hand refractometer and values were corrected at 20°C. Fruit juice acid content and reducing sugars were determined with standard methods (AOAC, 1980). The pooled data recorded was subjected to biometrical analysis. The genotypic and phenotypic co-efficients of variation and heritability were calculated according to Singh and Choudhary (1985), while phenotypic correlation co-coefficients and genetic advance were estimated as per the procedure described by Johnson *et al*. (1955). The path analysis was carried out according to the method suggested by Dewey and Lu (1959).

## Results and Discussion

The analysis of variance showed significant differences among the cultivars for all the traits. The moderate estimates (>7.0%) of genotypic co-efficient of variation (GCV) (Table 1) recorded for fruit yield/plant, fruit weight, pulp weight and peel weight indicated the presence of adequate genetic variation among different genotypes which showed that these attributes may be improved through selection procedure. The data revealed that high phenotypic co-efficient of variation (PCV) along with high genotypic co-efficient of variation (GCV) were recorded for fruit yield, fruit weight, peel weight and pulp weight and medium to low for other traits. The magnitude of PCV was higher than GCV for all the traits indicating that they are highly influenced by environmental components. Rai *et al*. (2001) found high range of variation for peel, pulp and stone weight in mango. GCV alone is not sufficient to determine the extent of heritable variation. Hence, heritability in broad sense was estimated for all the traits.

The heritability estimates were high for all the traits except total soluble solids (Table 1). As characters like fruit yield per plant, fruit weight, pulp weight and peel weight showed high heritability estimates coupled with high genetic advances, indicating that these traits are under the control of additive gene action. Rajan *et al*. (2009) also reported high heritability estimate accompanied with greater genetic advance on the basis of per cent mean for fruit yield/plant, fruit weight, pulp and peel weight indicating that these characters are additive gene action effect and, therefore, have more role in proficient selection. In present study high genetic advance was found for fruit yield and peel weight. Relatively moderate genetic advance was observed for pulp weight and fruit weight, while extremely low genetic advance was recorded for total soluble salts. The result pertaining to genetic advance coupled with $h^2$ clearly depicted that environmental effects might not be contributing much to the total phenotypic variation for fruit yield and pulp weight and could have moderate to high influence on fruit and pulp weight. Relationship of heritability and genetic advance also give an idea about the type of gene action. According to Johnson *et al.* (1955), an estimated heritability associated with genetic advance is more reliable than heritability alone for prognosticating the impact of selection. High heritability accompanied with high genetic advance is mainly referred to the action of additive genes (Panse, 1957). A low genetic advance implies that heritability of a particular trait in a specific environment was mainly due to non-additive gene action, whereas, if the heritability was due to additive gene effect, it would be associated with high genetic advance (Shadakshari *et al.,* 1995). So, it can be concluded that different characters specially fruit yield/plant and pulp weight under study can be improved through phenotypic selection.

The estimates of correlation coefficients showed significant positive association of fruit yield per plant with all the traits except total soluble solids and acidity (Table 2). Among the other components fruit weight was positively correlated with the quantitative traits.

**Table 1. Estimation of genetic parameters for fruit yield and its components in mango**

| Character | GCV | PCV | Heritability ($h^2$) | Genetic advance | GA (%) | Mean | CV (%) |
|---|---|---|---|---|---|---|---|
| Fruit yield/plant (kg) | 11.70 | 12.15 | 96.31 | 9.59 | 11.27 | 58.05 | 19.63 |
| Fruit weight (g) | 7.18 | 7.73 | 92.81 | 12.24 | 6.66 | 183.78 | 17.28 |
| Fruit length (cm) | 4.98 | 5.34 | 93.19 | 0.43 | 4.64 | 9.28 | 11.63 |
| Fruit breadth (cm) | 3.92 | 4.29 | 91.30 | 0.24 | 3.58 | 6.67 | 10.51 |
| Stone weight (g) | 5.18 | 5.74 | 90.27 | 1.61 | 4.68 | 34.37 | 14.82 |
| Pulp weight (g) | 8.73 | 8.86 | 98.6 | 10.29 | 8.61 | 119.57 | 9.01 |
| Peel weight (g) | 9.69 | 9.94 | 97.48 | 2.97 | 9.45 | 31.48 | 13.31 |
| Total soluble solids (%) | 1.76 | 2.86 | 61.46 | 0.19 | 1.08 | 17.87 | 13.54 |
| Acidity (%) | 6.75 | 7.27 | 92.85 | 0.02 | 6.26 | 0.395 | 16.18 |
| Reducing sugars (%) | 4.63 | 5.26 | 88.05 | 0.18 | 4.08 | 4.50 | 14.96 |

However, qualitative characters had no association with yield attributing traits. Among the quality traits, there was no inter-relationship but stone weight showed positive association with juice acidity and negative with pulp weight. Chadha *et al*. (1993) and Pareek and Dhaka (2003) also observed that fruit length, fruit breadth, fruit weight and pulp weight had significant positive association with fruit yield in mango and ber, respectively. Significant association among fruit yield components indicated that correlated response to selection for these traits will increase improvement of fruit yield.

Path analysis carried out to estimate the direct and indirect contributions of various component traits for recommending a reliable selection criterion revealed that fruit weight (1.6026) followed by fruit breadth (0.4052) and peel weight (0.3555) had direct effect on fruit yield (Table 3). Highest direct effect of fruit length towards fruit yield was also reported by Prasad (1987) and Pareek and Dhaka (2003) in mango and ber, respectively. Though pulp weight is more desirable trait in mango but its contribution directly and indirectly to the productivity is negative, likewise stone weight had also negative contribution towards fruit yield. It is desirable to give due consideration to stone weight and pulp weight while selecting mango cultivars for higher productivity. Higher pulp: stone ratio is desirable while selecting mango cultivars for pickle purposes (Singh *et al*., 2012). Among the quality traits *viz.* total soluble

**Table 2 Phenotypic correlation coefficients of fruit yield and component characters in mango**

| Character | Fruit weight | Fruit length | Fruit breadth | Pulp weight | Peel weight | Stone weight | TSS (%) | Acidity (%) | Reducing sugars | Fruit yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|
| Fruit weight | 1.0000 | | | | | | | | | |
| Fruit length | 0.8681** | 1.0000 | | | | | | | | |
| Fruit breadth | 0.8035** | 0.5688** | 1.0000 | | | | | | | |
| Pulp weight | 0.9365** | 0.7754** | 0.7682** | 1.0000 | | | | | | |
| Peel weight | 0.9171** | 0.7989** | 0.7162** | 0.8027** | 1.0000 | | | | | |
| Stone weight | 0.6031** | 0.5889** | 0.4104** | 0.3284* | 0.7172** | 1.0000 | | | | |
| Total soluble solids (%) | 0.1533* | 0.2747 | 0.0048 | -0.0482 | 0.0366 | 0.2781* | 1.0000 | | | |
| Acidity (%) | -0.0548 | -0.0077 | -0.0053 | -0.3292* | 0.1036* | 0.5732** | 0.2832 | 1.0000 | | |
| Reducing sugars | 0.3718** | 0.3700* | 0.4067** | 0.3903** | 0.1456* | -0.0308 | 0.2991 | -0.2565 | 1.0000 | |
| Fruit yield/ plant | 0.6593** | 0.5153** | 0.7210** | 0.6181** | 0.6217** | 0.3094* | 0.0149 | -0.0758 | 0.4264** | 1.0000 |

* Significant at 5% level of probability
** Significant at 1% level of probability

**Table 3. Path coefficient analysis of fruit yield versus component characters in mango**

| Character | Fruit weight | Fruit length | Fruit breadth | Pulp weight | Peel weight | Stone weight | TSS (%) | Acidity (%) | Reducing sugars | PCC*with fruit yield/plant |
|---|---|---|---|---|---|---|---|---|---|---|
| Fruit weight | **1.6026** | -0.0187 | 0.3255 | -1.3509 | 0.3260 | -0.2749 | -0.0317 | 0.0069 | 0.0745 | 0.6593 |
| Fruit length | 1.3911 | **-0.0215** | 0.2305 | -1.1186 | 0.2840 | -0.2685 | -0.0568 | 0.0010 | 0.0741 | 0.5153 |
| Fruit breadth | 1.2876 | -0.0122 | **0.4052** | -1.1082 | 0.2546 | -0.1871 | -0.0010 | 0.0007 | 0.0815 | 0.7210 |
| Pulp weight | 1.5007 | -0.0167 | 0.3113 | **-1.4426** | 0.2853 | -0.1497 | 0.0099 | 0.0416 | 0.0782 | 0.6181 |
| Peel weight | 1.4696 | -0.0172 | 0.2902 | -1.1579 | **0.3555** | -0.3269 | -0.0076 | -0.0131 | 0.0292 | 0.6217 |
| Stone weight | 0.9665 | -0.0127 | 0.1663 | -0.4737 | 0.2549 | **-0.4558** | -0.0575 | -0.0724 | -0.0062 | 0.3094 |
| Total soluble solids (%) | 0.2457 | -0.0059 | 0.0020 | 0.0695 | 0.0130 | -0.1268 | **-0.2066** | -0.0358 | 0.0599 | 0.0149 |
| Acidity (%) | -0.0879 | 0.0002 | -0.0022 | 0.4749 | 0.0368 | -0.2613 | -0.0585 | **-0.1264** | -0.0514 | -0.0758 |
| Reducing sugars | 0.5959 | -0.0080 | 0.1648 | -0.5631 | 0.0518 | 0.0140 | -0.0618 | 0.0324 | **0.2003** | 0.4264 |

Residual effect: 0.3823 * PCC stands for phenotypic correlation coefficient
Bold figures are direct effects

solids, acidity and reducing sugars are the desirable attributes for fruit flavour and taste but these do not affect the production. Mango cultivars having excellent flavour and taste may be selected without compromising total productivity of the crop.

It is concluded that fruit weight, fruit breadth and peel weight are the major yield contributing characters and hence during selection, weightage should be given to these characters for the development of high yielding cultivars of mango for sub-mountain region of Punjab.

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# Performance of Certain Mango Varieties and Hybrids in East Coast of India

**Kundan Kishore[1]*, HS Singh[1], RM Kurian[2], P Srinivas[1] and Deepa Samant[1]**
[1] *Central Horticultural Experiment Station, Indian Institute of Horticultural Research, Bhubaneswar-751019, Odisha, India*
[2] *Division of Fruit Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru-560089, Karnataka, India*

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Mango varieties and hybrids were evaluated for flowering behaviour, fruit maturity, yield and physico-chemical properties during 2011-14 at the research farm of Central Horticutural Experiment Station, Bhubaneswar. December was the critical month for panicle initiation, whereas January was the major period for peak bloom under the eastern tropical coastal region. In Dashehri, Langra, Mallika, Neelgoa and Sabri there was a marginal deviation in panicle initiation during the study period whereas, Arka Neelachal Kesari, Arka Neelkiran, AU-Rumani, Totapuri, and Sindhu showed wide deviation. Manjeera had the highest flowering intensity (85.3 per cent) whereas Amrapali, PKM-2, Arka Aruna and Arka Puneet had moderate intensity. Zardalu had the lowest flowering intensity. The maximum percentage of perfect flower (34.03) was recorded in Neelgoa followed by Arka Anmol and Lat Sundari. Arka Neelachal Kesari was the extra early mango with shortest fruit maturity period (88.3 days), whereas Totapuri had the longest fruit maturity period (142.3 days). Manjeera, Amrapali, Mallika and Lat Sundari were observed to be heavy bearer, whereas Alphonso, Zardalu, Bombay Green and Ratna showed poor yield potential. Sindhu recorded the highest pulp percentage. Amrapali was the sweetest variety with maximum TSS and TSS/acid ratio.

**Key Words: Evaluation, Flowering intensity, Mango, Panicle, Perfect flower, Pulp content, Varieties**

## Introduction

Mango (*Mangifera indica* L.), the fifth most important fruit in the world, is being cultivated in more than 90 tropical and subtropical countries situated in different continents *viz.* Asia, Africa, Australia, North America and South America (Litz, 1997). Mango has been the most important fruit of India due to its wide range of adaptability, diversity, delicacy and nutritive value. It is cultivated in 2.37 million hectares area with the production of 16.19 million metric tonnes and productivity of 6.8 t/ha (Anonymous, 2012). In spite of high demand of fresh mango in the international markets the area, production and productivity of mango have marginally increased during the last five years.

The flowering behaviour, sex expression, yield and fruit quality of mango are primarily influenced by climate, cultivars, rootstock and tree physiology (Reddy *et al*., 2003; Padhiar *et al*., 2011; Parmar *et al*., 2012; Singh *et al*., 2012, 2013; Kumar *et al*., 2014). It has been observed that the flowering pattern of mango varieties expresses differentially under tropical and subtropical conditions (Davenport, 2003). Even in the same region, different weather conditions during different years can affect flowering behaviour. The flowering pattern in tropical climate of India is distinctly different as flowering starts in November and extends up to February. Variation in the flowering pattern under different climatic conditions is attributed to physiology of flowering. Under tropical condition emergence of flowering flushes depend on shoot age, whereas low temperature induces flowering in sub-tropics (Davenport and Nunz-Elisea, 1997). Mango is andromonoecious as plant bears both perfect and male flowers in the same panicle. The distribution pattern and intensity of both types of flowers vary with cultivar, bloom time and environmental factors (Singh, 1960).

Flowering behaviour, sex expression, yield and physico-chemical attributes of mango varieties are important determinants of assessing their performance. Since these attributes are influenced by climate, an evaluation programme of mango varieties was conducted to compare their relative performance so that the best performating varieties/hybrids could be recommended for the eastern coastal region of India.

**Author for Correspondence: E-mail: kkhort12@gmail.com*

## Materials and Methods

Studies were conducted on 12-15 years old mango varieties and hybrids during 2011-12, 2012-13 and 2013-14 at the research farm of Central Horticultural Experiment Station, Bhubaneswar, Odisha. The research site is situated at an altitude of 45m between 20°27' N latitude and 85°40' E longitude. The climate of the location is tropical, hot and humid with the average minimum and maximum temperature of 22.2 and 33.7 °C, respectively. The average annual rainfall was 1650 mm and the average relative humidity was 76%. The soils are sandy loam, strongly acidic (pH 4.0-4.5) and low in organic carbon content (0.38-0.47%). The site has hardly 0.5-0.7 m soil depth. The mango block has low N (<200 kg/ha), medium P (10-15 kg/ha) and K contents (150-200 kg/ha). Thirty mango hybrids (Alfazli, Amrapali, Arka Anmol, Arka Aruna, Arka Neelkiran, Arka Puneet, AU Rumani, Ambika, Arunika, H-949, H-1084, H-1739, Pusa Arunima, Mahmud Bahar, Mallika, Manjeera, Neeleshan, Neeleshwari, Neelgoa, Neelphonso, Neeluddin, PKM-1, PKM-2, Prabha Shankar, Ratna, Sabri, Sai Sugandh, Sindhu, Sundar Langra, Swarna Jehangir) and fifteen varieties [Arka Neelachal Kesari, Alphonso, Banganapalli, Bombay Green, Dashehari, Himsagar, Janardan Pasand, Kesar, Langra, Lat Sundari, Navneetham, Pusa Surya (selection), Rajapuri, Suvarnarekha and Totapuri] were evaluated for their flowering behaviour, yield and physico-chemical properties. Flower initiation and full bloom (75% flowering) were observed on four tagged branches (one each towards east, west, north and south directions) in five trees of individual variety. The number of perfect (hermaphrodite) flowers per panicle was recorded at the full bloom in four panicles on each replicate for all the varieties. Reproductive shoots (panicle bearing) per square meter canopy were counted in all the directions in the replicates and flowering intensity was worked out with the following formula:

$$\text{Flowering intensity} = \frac{\text{No. of flowering shoots} \times 100}{\text{Total no. of shoots}}$$

The days between the initial fruit set (mustard stage) and physiological fruit maturity was considered as the maturity period of mango varieties and for this twenty panicles were tagged just after initial fruit set in all the replicates and days were recorded as fruits matured. The average fruit yield was worked out in kg/tree by taking the average fruit yield of six plants each year. Fruits were randomly collected from marked trees at the time harvesting period and analysed for various physico-chemical attributes. Average fruit weight (g), pulp weight (g), stone weight (g) and pulp/stone ratio were determined using standard methods. The pulp percentage was calculated by using following formula:

$$\text{Pulp percentage} = \frac{\text{Fruit wt.} - (\text{peel wt.} + \text{stone wt.}) \times 100}{\text{Fruit wt.}}$$

The TSS was measured with the digital refractometer (0-85%) and acidity was estimated by 0.1N NaOH method and TSS/acid ratio was worked out (AOAC, 1984). Data were subjected to factor analysis (ANOVA) by using OPSTAT package HAU, Hisar and critical difference (CD) and standard error of mean were calculated. The weather data were obtained from the meteorological unit of Odisha University of Agricultural Technology, Bhubaneswar.

## Results and Discussion

December and January were the most crucial period for panicle initiation and peak flowering, respectively in majority of the mango varieties. However, Arka Nelachal Kesari had the earliest panicle initiation and peak flowering and Langra, PKM-2, H-1084, H-1739 and Dashehari showed late panicle initiation and peak flowering (Table 1). There was a variation in the date of panicle initiation and peak flowering in mango varieties (data not shown) during the study period. However, the months were remained unchanged. Tandel and Patel (2011) also observed full bloom in Alphonso, Kesar and Rajapuri in January under Gujarat conditions. Peak flowering (full bloom) was observed after 35-42 days of panicle initiation across the varieties. It was observed that except Arka Neelachal Kesari, varieties known for early fruit maturity like Himsagar, Sabri and Prabha Sankar were not necessarily early in flowering but their fruit maturity was relatively faster.

There was a significant variation in flowering intensity among mango varieties (Table 1). Manjeera had the highest intensity and Zardalu had the lowest. Arka Anmol, Arka Puneet, Neeleshan, Amrapali, and Arka Aruna had relatively high intensity of flowering. Alphonso, Alfazli, Ambika, Arunika, Bombay Green, H-1084, Janardan Pasand, Langra, Neeleswari, Pusa Arunima and Ratna had low flower intensity. Remaining varieties had moderate flowering intensity. Kumar *et al.* (2014) also reported variation in flowering intensity

**Table 1. Flowering behaviour and fruit maturity in mango varieties and hybrids**

| Varieties | Panicle initiation | Peak flowering | Flowering intensity (%) | Flowers/ panicle | Perfect flower (%) | Fruit maturity period (days) | Fruit maturity |
|---|---|---|---|---|---|---|---|
| Alfazli | January | February | 10.06 | 384.67 | 10.92 | 132.5 | May |
| Alphonso | December | January | 19.20 | 520.50 | 4.23 | 123.4 | May |
| Ambika | December | January | 21.01 | 668.67 | 9.02 | 121.5 | May |
| Amrapali | December | January | 67.08 | 929.67 | 15.45 | 117.8 | May |
| Arka Anmol | December | January | 72.58 | 610.20 | 27.63 | 134.6 | May |
| Arka Aruna | December | January | 62.05 | 1185.67 | 3.71 | 127.5 | May |
| Arka Neelachal Kesari | November | December | 45.35 | 912.50 | 16.16 | 88.3 | April |
| Arka Neelkiran | December | January | 83.44 | 815.33 | 4.78 | 124.6 | May |
| Arka Puneet | December | January | 76.82 | 635.33 | 5.61 | 125.5 | May |
| Arunika | January | February | 24.64 | 946.30 | 19.45 | 123.6 | May |
| AU Rumani | December | January | 21.54 | 1100.50 | 27.58 | 128.6 | May |
| Banganapalli | December | January | 58.91 | 770.80 | 9.60 | 137.6 | May |
| Bombay Green | December | January | 16.08 | 334.50 | 26.00 | 116.4 | May |
| Dashehari | January | February | 25.98 | 531.67 | 27.50 | 106.5 | May |
| Himsagar | December | January | 14.86 | 337.51 | 4.30 | 93.6 | April |
| H-949 | December | January | 56.59 | 1007.27 | 19.40 | 125.4 | May |
| H-1084 | January | February | 17.59 | 622.33 | 3.34 | 134.4 | June |
| H-1739 | January | February | 41.71 | 1380.00 | 14.5 | 123.4 | May |
| Janardan Pasand | December | January | 12.97 | 574.33 | 13.90 | 129.2 | May |
| Kesar | December | January | 49.61 | 609.67 | 9.73 | 118.3 | May |
| Langra | January | February | 15.44 | 1019.00 | 26.86 | 112.3 | May |
| Lat Sundari | December | January | 55.63 | 1141.67 | 27.33 | 124.6 | May |
| Mahmud Bahar | December | January | 21.90 | 1463.67 | 17.37 | 114.2 | May |
| Mallika | December | January | 53.98 | 449.00 | 3.29 | 124.4 | May |
| Manjeera | December | January | 85.37 | 709.33 | 4.62 | 132.4 | May |
| Navneetham | December | January | 32.50 | 725.60 | 11.30 | 115.4 | May |
| Neeleshan | December | January | 49.32 | 2159.33 | 8.92 | 124.6 | May |
| Neeleswari | December | January | 4.54 | 499.60 | 8.96 | 127.8 | May |
| Neelgoa | December | January | 57.76 | 628.67 | 34.03 | 129.4 | May |
| Neelphonso | December | January | 31.40 | 866.00 | 17.50 | 131.2 | May |
| Neeluddin | December | January | 33.89 | 546.20 | 17.25 | 130.4 | May |
| PKM-1 | December | January | 37.44 | 822.40 | 18.41 | 123.4 | May |
| PKM-2 | January | February | 65.61 | 530.67 | 13.32 | 118.4 | May |
| Prabha Sankar | December | January | 45.05 | 1019.33 | 12.13 | 95.4 | April |
| Pusa Arunima | December | January | 5.72 | 920.30 | 5.79 | 125.4 | May |
| Pusa Surya | December | January | 20.73 | 1270.33 | 7.90 | 126.3 | May |
| Ratna | December | January | 12.56 | 658.80 | 9.68 | 122.8 | May |
| Sabri | December | January | 59.55 | 605.67 | 17.0 | 97.5 | May |
| Sai Sugandh | December | January | 54.67 | 1087.33 | 16.84 | 140.3 | June |
| Sindhu | December | January | 26.69 | 1169.33 | 9.04 | 112.6 | May |
| Sundar Langra | December | January | 59.55 | 2395.60 | 7.98 | 98.4 | May |
| Swarna Jehangir | December | January | 54.49 | 1249.62 | 7.50 | 136.5 | May |
| Suvarnarekha | December | January | 46.13 | 496.80 | 14.72 | 122.5 | May |
| Totapuri | December | January | 48.64 | 721.67 | 4.19 | 142.3 | June |
| Zardalu | December | January | 2.90 | 799.00 | 9.93 | 125.4 | May |
| **CD *(P=0.05)*** | **–** | **–** | **2.86** | **137.24** | **2.40** | **2.87** | **–** |
| **SE(m)** | **–** | **–** | **1.01** | **48.75** | **0.85** | **1.02** | **–** |

**Table 2. Physico-chemical attributes of mango varieties and hybrids**

| Varieties | Fruit weight (g) | Pulp content (%) | Pulp/stone ratio | TSS/acid ratio |
|---|---|---|---|---|
| Alfazli | 445.0 | 77.5 | 6.9 | 35.5 |
| Alphonso | 280.5 | 65.7 | 4.8 | 49.4 |
| Ambika | 325.4 | 69.5 | 3.4 | 52.2 |
| Amrapali | 224.6 | 74.2 | 5.8 | 72.3 |
| Arka Anmol | 225.4 | 64.5 | 3.3 | 20.3 |
| Arka Aruna | 440.3 | 76.2 | 6.0 | 39.1 |
| Arka Neelachal Kesari | 220.6 | 67.5 | 4.1 | 43.5 |
| Arka Neelkiran | 251.2 | 69.0 | 4.3 | 42.3 |
| Arka Puneet | 210.9 | 64.2 | 3.2 | 40.5 |
| Arunika | 190.2 | 65.4 | 4.4 | 70.6 |
| AU Rumani | 187.6 | 72.5 | 5.6 | 42.2 |
| Banganapalli | 380.6 | 68.7 | 4.3 | 45.3 |
| Bomabay Green | 300.4 | 74.7 | 5.8 | 37.1 |
| Dashehari | 182.4 | 70.4 | 4.7 | 52.6 |
| Himsagar | 360.2 | 71.6 | 5.2 | 52.8 |
| H-949 | 220.3 | 72.2 | 5.7 | 42.7 |
| H-1084 | 230.5 | 65.2 | 3.3 | 37.2 |
| H-1739 | 231.2 | 68.4 | 4.1 | 63.4 |
| Janardan Pasand | 220.3 | 68.7 | 4.4 | 23.8 |
| Kesar | 250.4 | 67.8 | 4.2 | 34.2 |
| Langra | 310.4 | 75.8 | 6.7 | 46.2 |
| Lat Sundari | 220.6 | 68.2 | 3.7 | 26.4 |
| Mahmud Bahar | 268.4 | 67.4 | 3.5 | 50.8 |
| Mallika | 381.4 | 76.8 | 6.7 | 55.9 |
| Manjeera | 389.5 | 74.2 | 5.4 | 40.5 |
| Navneetham | 234.6 | 74.5 | 6.4 | 34.5 |
| Neeleshan | 380.6 | 72.6 | 6.3 | 43.6 |
| Neeleswari | 230.7 | 76.5 | 6.8 | 37.2 |
| Neelphonso | 370.5 | 63.2 | 4.4 | 39.7 |
| Neelgoa | 305.7 | 75.1 | 6.5 | 37.5 |
| Neeluddin | 435.2 | 69.4 | 5.5 | 40.8 |
| PKM-1 | 295.7 | 68.2 | 4.9 | 40.2 |
| PKM-2 | 180.6 | 66.3 | 4.1 | 40.9 |
| Prabha Sankar | 192.4 | 68.2 | 4.2 | 45.5 |
| Pusa Arunima | 285.7 | 76.4 | 6.6 | 55.4 |
| Pusa Surya | 360.7 | 76.0 | 6.5 | 40.5 |
| Ratna | 300.4 | 76.5 | 6.8 | 65.3 |
| Sabri | 185.9 | 70.4 | 5.4 | 36.4 |
| Sai Sugandh | 306.2 | 72.3 | 5.7 | 30.4 |
| Sindhu | 260.7 | 78.8 | 7.1 | 51.2 |
| Sundar Langra | 292.4 | 75.6 | 6.6 | 48.5 |
| Swarna Jehangir | 432.4 | 77.2 | 6.8 | 29.4 |
| Suvanarekha | 380.6 | 75.0 | 6.6 | 27.9 |
| Totapuri | 450.7 | 74.1 | 5.4 | 30.4 |
| Zardalu | 230.4 | 66.6 | 4.1 | 33.5 |
| **CD (*P=0.05*)** | **21.7** | **1.47** | **0.29** | **1.95** |
| **SE(m)** | **7.71** | **0.52** | **0.10** | **0.69** |

in mango varietes under tropical condition. The high intensity of flowering in some of the mango varieties may be due to the synchronization in the shoot maturity as flowering in the tropics is primarily regulated by the age of the initiating shoots as well as high level of florigenic promoter (Davenport, 2003).

Significant variation was observed in the number of flowers per panicle and intensity of occurrence of

perfect flowers (Table 1). Number of flowers per panicle varied from 384.67 in Alfazli to 2395.60 in Sundar Langra. Arka Aruna, H-1739, H-949, Langra, Latsundari, Mahmud Bahar, Prabha Sankar, Pusa Surya, Sai Sugandh, Sindhu and Swarna Jehangir also had high number of flowers per panicle. In contrast, Swarnarekha, Mallika, AU-Rumani and Neeleshan Gujarat had fewer flowers in their panicles. Mango bears male and perfect flowers in the same panicle; however their intensities vary with the varieties, position of panicle and climatic conditions. The per cent of perfect flower varied between 3.72–34.03 per cent in different mango varieties. The maximum percentage of perfect flower was observed in Neelgoa followed by Arka Anmol and Lat Sundari. Arka Aruna, Alphonso, Arka Neelkiran, H-1084, Mallika, Manjeera and Totapuri had relatively less number of perfect flowers. The remaining varieties had moderate intensity perfect flower. The varieties with high per cent of perfect flower would have high sex ratio and vice versa as the sex ratio is the ratio between perfect and male flowers. Studies indicated the varietal difference in the intensity of flower and perfect flower per panicle. Flowering behaviour and sex expression are vital indicators for assessing the potential of varieties under particular climatic conditions. Under tropical eastern region, mango flowering was earlier than subtropical region which indicated role of climate in influencing flowering behaviour (Ravishankar *et al*., 1979). Mango responds to temperature variations more critically than to photoperiods as is evident from variation in flowering behaviour at different places in India (Kumar *et al*., 2014). Many reports substantiate the findings on the variation in perfect flowers with the varieties and growing conditions (Singh and Rajput, 1990; Vijayalakshmi and Srinivasan, 2002; Sweidan *et al.,* 2007; Abourayya *et al*., 2011).

A significant variation in the fruit maturity of mango varieties was observed (Table 1). Arka Neelachal Kesari had the shortest maturity period followed by Himsagar and Prabha Sankar and these varieties mature in April. On the other hand, Totapuri and Sai Sugandh matured in June with the fruit maturity period of more than 140 days. Most of the varieties matured in May with the maturity period of 120-30 days. It is evident that early variety had short fruit maturity period.

Mango varieties varied in their yield potential (Fig 1). Under the tropical coastal climate Manjeera was the most productive variety followed by Lat Sundari, Amrapali, and Mallika. Arka Anmol and Totapuri were also prolific bearers. Data clearly indicated that Alphonso, Zardalu, Bombay Green, Ratna and Kesar were less suited to this climate as they had consistently poor fruit yield. Other mango varieties had average to modium yield potential. Under Gujarat condition Kesar, Totatpuri and Mallika were prolific bearers wheras under Punjab Condition Mallika and Dashehari were relatively more productive mango varieties (Gunjate *et al*., 2009; Chanana *et al*., 2005). Among mango varieties, Alfazli, Arka Anmol, Neeluddin and Totapuri had large fruits weighing more than 400g, whereas Dashehari, Prabha Sankar, AU Rumani, and Arunika had small fruits of less than 200g. The fruit weight of remaining varieties and hybrids varied from 210.9 to 389.5 g. The pulp content and pulp to stone ratio are important characters of table varieties of mango. The highest pulp content (78.8%) and pulp stone ratio (7.1) were recorded in Sindhu followed by Alfazli, Ratna, Neeleswari and Swarna Jehangir. High pulp content and pulp/stone ratio were also recorded in Langra, Mallika, Pusa Arunima and Pusa Surya. Whereas, Arka Anmol, Arka Puneet, H1084, Lat Sundari and Mahmud Bahar had low pulp and pulp/stone ratio. Varieties show variation in pulp content with the growing conditions. The pulp content of mango varieties varied with the climatic conditions (Anil and Radha, 2003; Padhiar *et al*., 2011). The TSS and TSS/acid ratio are the most important parameters to measure the fruit maturity and fruit quality. The highest TSS (21.9 °Brix) and TSS/acid ratio (72.3) were recorded in Amrapali (Fig. 1). However, Arunika, Himsagar, H1739, Mallika, Ratna and Sindhu also had high TSS and TSS/acid ratio (Table 1). Data clearly indicated that Arka Anmol, AU Rumani, Lat Sundari, Totapuri and Alfazli had low TSS (< 15 °Brix) and TSS/acid ratio which indicate that these varieties are not suitable for table purpose. The variation in TSS is climate dependent as Dashehari and Langra had high TSS in the plateau of Madhya Pradesh (Singh *et al*., 2013).

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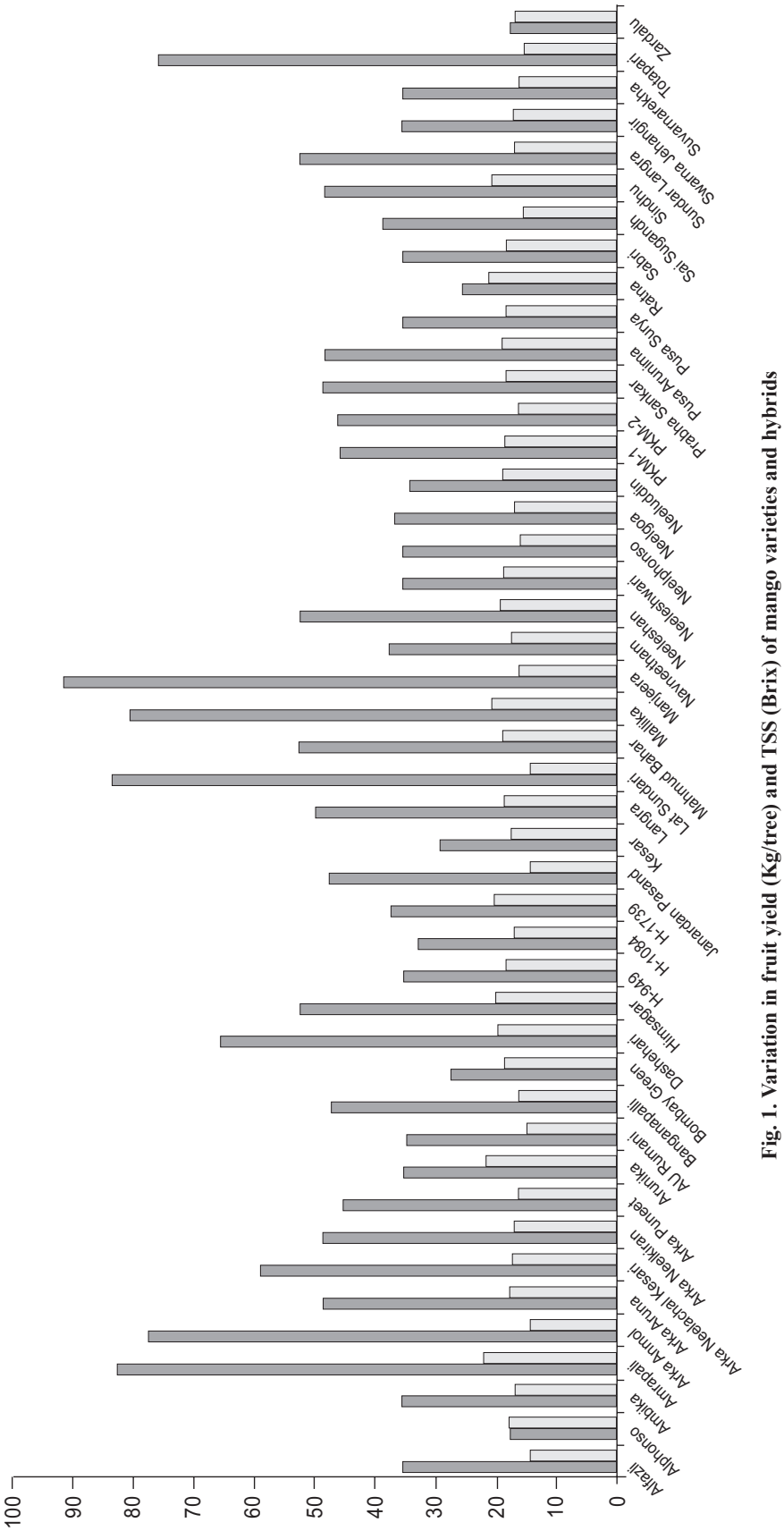


**Fig. 1. Variation in fruit yield (Kg/tree) and TSS (Brix) of mango varieties and hybrids**

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# Field Screening of Mungbean Genotypes and the Role of Total Soluble Sugars and Phenols against Powdery Mildew Resistance

**Nidhi Pathak[1]*, MN Singh[2], MK Mishra[1], DK Singh[2], Yash Pal[2], SY Dhurai[2] and Rishi Pathak[3]**

[1] *College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Tikamgarh-472001, Madhya Pradesh, India*

[2] *Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221002, Uttar Pradesh, India*

[3] *College of Agricultural Engineering, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur-482004, Madhya Pradesh, India*

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Powdery mildew of mungbean caused by *Erysiphe polygoni* DC may cause yield loss up to 20-40%. Mungbean (51) genotypes were screened in three consecutive seasons under natural epiphytotic conditions. Out of 51 genotypes, TM-96-2 exhibited highly resistance, nine as resistance, five as moderately resistance, 16 as susceptible and 20 as highly susceptible reactions for powdery mildew. On the basis of field screening, two resistant and 10 susceptible genotypes were selected for the study of relationship between induced resistance mechanism with total soluble sugars and phenol contents in plants. The resistant genotypes contained high level of phenols than the susceptible genotypes while, susceptible genotypes contained high level of total soluble sugars than the resistant genotypes.

**Key Words: Mungbean, Powdery mildew, Total phenols, Total soluble sugars**

## Introduction

Mungbean [*Vigna radiata* (L.) Wilckzek], $2n = 2x = 22$ is one of the important pulse crops in India. In north India, it is grown in *summer* and *rainy* seasons and in southern India; it is grown in *winter* season. Mungbean is susceptible to various diseases like yellow mosaic virus, powdery mildew, Cercospora leaf spot and Rhizoctonia blight etc. among which powdery mildew is very serious. Powdery mildew of mungbean is caused by *Erysiphe polygoni* DC and causes yield loss up to 20-40% (Khare *et al.,* 1998). It is considered as disease of South East Asia (Park and Yang 1978), being more prevalent in southern and central India. A wide range of chemicals are being used to control the disease but these chemicals are not effective under heavy infection and produce health hazards. Development of resistant variety is a cheap, viable and environment friendly approach to overcome this problem. Anatomical and biochemical features of the host are involved in disease resistance mechanism. Phenols are secondary metabolites of plants involved in several biological process of plant such as pigmentation, growth, reproduction and resistance to pathogens. At the time of disease infection, rate of production of phenols are more in resistant genotypes as compared to susceptible one (Dakshayani *et al.*, 2005). After the infection of pathogen into the host tissue a rapid accumulation of phenols at the infection site, restricts or reduce the growth of the pathogen (Matern and Kneusal, 1988). Sugars as signalling molecules in plants (Rolland *et al.,* 2006) play an important role in defence mechanism of the host plant against diseases. Low levels of total and reducing sugars were observed in groundnut genotypes resistant to tikka disease when compared to the susceptible ones (Sindhan and Jaglan, 1987). Thus, total phenol and sugar status of mungbean plant could be correlated with host resistance.

The present experiment was aimed to identify the genotypes resistant to powdery mildew and compare changes in total soluble sugars and phenols in selected resistant and susceptible genotypes.

## Materials and Methods

### *Field Screening of Powdery Mildew*

A total of 51 diverse genotypes of mungbean obtained from AICRP on Pulses of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India which is located in the South-Eastern part of Varanasi city at 25′ 18″ N latitude, 83′ 03″ E longitude and at

*Author for Correspondence: E-mail: nidhijnkvv@gmail.com

**Table 1. Methodology for scoring mungbean genotypes for powdery mildew**

| Grade | Disease severity (%) | Reaction | Symptom description |
|---|---|---|---|
| 0 | Nil | Free/highly resistant (HR) | No infection |
| 1 | 0.1-5 | Resistant (R) | Infection in traces only |
| 2 | 5.1-25 | Moderately resistant (MR) | Roughly one in every four leaves showing fine coating of powdery growth on upper surface of leaves |
| 3 | 25.1-50 | Moderately susceptible (MS) | Nearly 50% of the leaves infected, stem infection slight, plant size normal |
| 4 | 50.1-75 | Susceptible (S) | Nearly 75% of the foliage including stem appears to be covered with white powdery coating, plant slightly stunted |
| 5 | >75 | Highly susceptible (HS) | Entire plant including pods and floral parts are infected, leaves turn pale green to yellow and start drying up, the affected plants are conspicuous because of stunted growth |

altitude of 75.7 meters above the mean sea level were screened against powdery mildew disease. The field screening trials were laid in randomised complete block design with three replications in three consecutive late *kharif* (rainy) seasons of 2009, 2010 and 2011 and date of sowing was 20$^{th}$ September every year. Each plot consisted of two rows of 2m length with 40 cm and 10 cm row to row and plant to plant spacing, respectively. Standard agronomic practices recommended for the mungbean crop were followed (Park and Yang, 1978). To ensure sufficient source of inoculum and uniform spread of disease, one row of HUM 26 (highly susceptible to powdery mildew) was planted as infector row after every two rows of the test entries. Further, two infector rows were also raised around the experimental plots to maintain the sufficient load of inoculum. The entire experimental material in the trial were also inoculated twice *i.e.*, 32 days after sowing and 42 days after sowing by spraying the spore suspension ($3.5\times10^6$ conidia/ml) of *E. polygoni* (Reddy *et al.,* 1987) obtained from the infected crop of mungbean of another field. Observation of powdery mildew severity was recorded 55 days after sowing on 10 randomly selected plants from each genotype in each replication. Disease severity (%) in the plant was recorded on the basis of the visual observation of the per cent leaf area infected. The reaction of genotypes against powdery mildew was categorized by using 0-5 scale given by Reddy *et al.* 1987 (Table1). Each plot of a genotype was scored separately and genotypes were classified according to mean grade. Three years grade of the genotypes were pooled. The cumulative scores (0=HR, 0.1-1=R, 1.1-2=MR, 2.1-3=MS, 3.1-4=S, 4.1-5=HS) were calculated and genotypes classified accordingly.

Finally, on the basis of field screening genotypes in three consecutive seasons, two powdery mildew resistant genotypes *viz*., ML-713 and TM -96-2 and 10 susceptible genotypes *viz.,* HUM-7, HUM-8, HUM-9, HUM-12, HUM-26, PUSA-0672, PUSA-0871, ML-515, ML-5 and IPM-02-17 were selected.

### *Biochemical Studies*

Total soluble sugars and phenols were estimated in two powdery mildew resistant (ML-713, TM -96-2) and three susceptible (HUM-7, HUM-8, HUM-9) and seven highly susceptible (HUM-12, HUM-26, PUSA-0672, PUSA-0871, ML-515, ML-5 and IPM-02-17) genotypes.

The amount of total soluble sugars was estimated by Phenol sulphuric acid reagent method (Dubois *et al.*, 1951) and the total phenols were measured by Folin Ciocalteu reagent method (McDonald *et al.,* 2001). Five plants from each of the genotypes were tested twice, in three replications before infection (30 DAS) and after infection (55 DAS) because the severity of disease was high during this period.

## Results and Discussion

### *Field Screening of Powdery Mildew*

Among the 51 genotypes, one genotype TM 96-2 exhibited highly resistance, nine genotypes as resistance, five genotypes as moderately resistance, 16 genotypes as susceptible and 20 genotypes as highly susceptible reaction. None of the genotypes were moderately susceptible to powdery mildew (Table 2).

### *Level of Biochemical Constituents in Relation to Powdery Mildew Resistance*

In the present investigation total soluble sugars were lowest in resistant genotypes ML-713 and TM-96-2 while, maximum in highly susceptible genotype ML-5 before and after infection (Table 3). After infection, total

**Table 2. Mungbean germplasm lines, cultivars and mutants screened against to powdery mildew disease**

| Disease reaction | No. of genotypes | Name of genotypes | Score range |
|---|---|---|---|
| Highly resistant | 1 | TM-96-2 | 0.0 |
| Resistant | 9 | COGG-912, DBG-1030, DBG-1045, DPM-90-1, IPM-02-3, ML-713, ML-717, TARM-1, TARM-18 | 0.3-1.0 |
| Moderately resistant | 5 | BDYR-1, MH-521, IPM- 02-19, TM-2000-1, UPM-98-1 | 1.3-2.0 |
| Moderately susceptible | 0 | — | |
| Susceptible | 16 | HUM-2, HUM-8, HUM-9, HUM-7, PUSA-9531, ML-1296, ML-1294, ML-1465, PUSA RATNA, PDM-54, VRMGG-1, PDM-11, K-851, RMG-991, UPM-98-1, V. *Trilogata* | 3.3-4.0 |
| Highly susceptible | 20 | AKM-9904, HUM-1, HUM-6, HUM-12, HUM-15, HUM-16, HUM-26, IPM- 02-17, ML-515, ML-1451, MH-318, ML-5, PS-16, PUSA-105, Pusa-0672, Pusa-0871, PUSA VISHAL, SML-668, T-44, T-9 | 4.3-5.0 |

**Table 3. Biochemical studies of powdery mildew disease before and after infection in resistant and susceptible genotypes**

| Genotypes | Total soluble sugar (mg/g dry weight) | | Reduction (%) | Total phenols (mg/g fresh weight) | | Reduction (%) |
|---|---|---|---|---|---|---|
| | Before infection | After infection | | Before infection | After infection | |
| HUM- 7 | 9.81 | 8.41 | 14.24 | 11.67 | 9.65 | 17.28 |
| HUM-8 | 9.79 | 8.95 | 8.65 | 11.19 | 9.35 | 16.44 |
| HUM-9 | 9.65 | 8.86 | 8.19 | 11.73 | 9.08 | 22.57 |
| HUM- 12 | 9.82 | 8.56 | 12.83 | 11.74 | 9.29 | 20.87 |
| HUM- 26 | 9.65 | 7.83 | 18.80 | 11.22 | 9.22 | 17.80 |
| IPM- 02-17 | 9.65 | 8.31 | 13.92 | 11.64 | 9.48 | 18.56 |
| ML- 515 | 10.58 | 8.46 | 20.07 | 10.85 | 8.46 | 22.08 |
| ML- 5 | 11.31 | 9.04 | 20.12 | 10.73 | 8.15 | 24.01 |
| ML- 713 | 8.49 | 7.75 | 8.71 | 13.17 | 9.87 | 25.04 |
| PUSA- 0672 | 10.29 | 8.91 | 13.41 | 11.28 | 9.40 | 16.66 |
| PUSA- 0871 | 9.83 | 8.88 | 9.60 | 10.64 | 8.62 | 19.01 |
| TM-96-2 | 8.42 | 7.55 | 10.30 | 14.27 | 10.39 | 27.19 |
| SEm_± | 0.20 | 0.35 | | 0.28 | 0.25 | |
| CD (P=0.05) | 0.56 | 1.01 | | 0.81 | 0.72 | |

soluble sugars decreased in all genotypes, particularly in highly susceptible genotype ML-5. These results supported by the finding of Gawande and Patil (2004). The findings indicated that the pathogen uses more sugars for establishment in the host and also decreases photosynthesis (data not shown) in susceptible genotypes as compared to resistant genotypes as the large area of leaves was covered by the pathogen. Total phenols were maximum in resistant genotype TM-96-2 followed by ML-713, whereas, minimum in susceptible genotype PUSA- 0871 before infection. The levels of total phenols content decreased after infection in all the genotypes. Similar findings were observed by Sharma *et al.* (1982) and Guleria *et al*. (1998). After infection, total phenols content was maximum in resistant genotypes TM-96-2 and ML-713 whereas, minimum in susceptible genotype ML-5. It was also observed that reduction of total phenols content was more in resistant genotypes due to higher activities of polyphenol oxidase enzymes in resistant genotypes than in susceptible ones (Gawande and Patil, 2006). Different studies showed that phenolics compounds are involved in natural resistance mechanism of plants.

Therefore, it may be concluded that total soluble sugars and total phenols and their accumulation pattern decide the degree of resistance to powdery mildew in mungbean. These biochemical parameters can be used for screening of mungbean genotypes for powdery mildew resistance.

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# Assessment of Genetic Architecture of Grain Yield and its Component Traits in Barley (*Hordeum vulgare* L.) through Generation Mean Analysis

**SS Bornare, LC Prasad and R Prasad***
*Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India*

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The suitable breeding procedure for crop improvement mainly depends on knowledge of the genetic make-up of the character to be selected. Unique architectural phenotypes have the vast potential for increasing the yield of the crop. Therefore, the investigation was carried out during three successive seasons *Rabi* 2009-10, 2010-11 and 2011-12 at Agriculture Research Farm, Banaras Hindu University, U.P. India with objective to estimate the main genetic effects including digenic non-allelic interactions controlling yield and yield component traits as-well-as to determine the yield component that affects yield to a greater extent. The generation mean analysis was carried out on six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$) in six crosses involving two tester (LAKHAN and BH-902) and three exotic lines (MOROC-9-75, BEECHER and HARMAL) of barley. Duplicate type of epistasis was found for most of the traits in certain cross combinations, whose effect can be wiped out by following sophisticated selection procedure such as reciprocal recurrent selection and/or biparental mating in early segregating generations for the development of high yielding barley varieties with desirable yield contributing traits.

**Key Words: Barley, Epistasis, Generation mean analysis, *Hordeum vulgare*, Yield traits**

## Introduction

Barley (*Hordeum vulgare* L.) is one of the principal crop species grown in the world (Eshghi and Akhundova, 2010), ranking fourth after wheat, rice and maize (Bengtsson, 1992; FAO, 2005; Kakani *et al.,* 2007; Raikwar, 2013) with a great adaptation potential. It has been widely used for different purposes such as staple food for mankind in few countries, cheap ingredient in whisky and beer production, and feed for animals. It can grow on wide range of environmental conditions compared to any other cereal and spreads in tropical to sub-tropical areas. With the economic development, more and more barley will be needed for beer processing and animal feed. Hence, improvement of yield potential of the crop has been a major objective in barley breeding programmes (Xue *et al.,* 2008).

Progress in yield improvement or even for quality traits of a crop requires information about the nature of combining ability of parents to be involved in the hybridization programme along with the nature of gene effects operative in the inheritance of different traits (Singh *et al*., 2013). The generation mean analysis is one of the most appropriate methods for genetic analysis of quantitative traits (Eshghi and Akhundova, 2010). In this method, epistatic effects as-well-as additive and dominance effects can be estimated.

The present study was undertaken to estimate the main genetic effects including digenic non-allelic interactions controlling yield and yield components in six cross combinations comprising two indigenous and three exotic barley genotypes. The other aim was to determine the yield component that affects yield to a greater extent in order to define efficient selection strategy for increasing the yielding ability in barley crop.

## Materials and Methods

Experimental material consisted of six generations *viz.,* $P_1$, $P_2$, $F_1$, $F_2$ and two backcrosses ($B_1$ and $B_2$) relating to six crosses involving two tester (LAKHAN and BH-902) and three exotic lines (MOROC-9-75, BEECHER and HARMAL) (Table 1). The genotypes were intercrossed in Line x Tester design during the *Rabi* season of 2009-10 in order to produce $F_1$ hybrids. In the next year by selfing of $F_1$, the $F_2$ generation was obtained and also the backcrosses ($B_1$ and $B_2$) were made. Comparative field trial involving six generations of each of the six crosses were grown during *Rabi* 2011-2012 in Randomized Block Design with three replications at Agriculture Research Farm, Banaras Hindu University.

*Author for Correspondence: E-mail: rsprasadbhugpb@gmail.com

The row-length was 2.5 metre and distance between two rows was 0.25 metre. The plants were spaced at 10 cm from each other. Each parent and $F_1$ had 3 rows/plot, while, 10 and 7 rows/plot, respectively, were for each $F_2$ and backcross populations. Data on yield and other five traits on 10 randomly selected plants in parents and their $F_1$s were recorded. In each $F_2$ population data was recorded on 50 plants and in the backcross population data on 20 plants were recorded.

The type of interactions in crosses was sorted out with the help of scaling test (Mather, 1949) as well as joint scaling tests by Cavalli (1952) and the gene effects were estimated using the model as suggested by Hayman (1958) and Jinks and Jones (1958).

## Results and Discussion

The incorporation of derived traits from the donor parent in the background of cultivated varieties is often not profuse direction owing interaction at genetic level. This requires the need to understand the gene effects controlling yield and its component traits. The scaling test (A, B, C and D) were applied to detect the presence or absence of non-allelic gene interaction for the eight quantitative traits (Table 2). Presence of gene action and inter-allelic interaction varied cross-wise as-well-as trait-wise. Most of the crosses revealed presence of duplicate type of inter-allelic interaction.

Two crosses namely LAKHAN × MOROC-9-75 and BH-902 × BEECHER showed absence of non-allelic interactions, revealing additive (d) and dominance gene effect (h) for plant height (Table 2). The dominance gene effect for plant height was in agreement with findings of Taleei *et al*., 2004. Crosses *i.e.,* LAKHAN × BEECHER and LAKHAN × HARMAL exhibited duplicate type of epistasis while, cross BH-902 × MOROC-9-75 showed complementary gene effects. In cross BH-902 × HARMAL additive x dominance (j) and dominance × dominance (l) interaction was found significant.

The LAKHAN × HARMAL and BH-902 × BEECHER revealed absence of non allelic interaction for peduncle length. In the cross LAKHAN × HARMAL dominance gene effect (h) was significant, whereas, in BH-902 × BEECHER cross, both additive as well as dominance gene effects were significant. In cross, BH-902 × MOROC-9-75 peduncle length revealed duplicate type of gene action while BH-902 × HARMAL revealed complementary type of gene action.

The crosses such as LAKHAN × MOROC-9-75, BH-902 × MOROC-9-75 and BH-902 × HARMAL indicated absence of non-allelic interactions for number of tiller/plant. The dominance gene effect (h) was significant in all these three crosses. Duplicate type of gene action was revealed significant for LAKHAN × BEECHER and LAKHAN × HARMAL, whereas, dominance × dominance (l) was significant for BH-902 × BEECHER.

Complement type of gene action was significant in BH-902 × MOROC-9-75 and BH-902 × HARMAL for number of grain/ear, whereas, duplicate gene action was revealed in LAKHAN × Moroc-9-75 and BH-902 × BEECHER. In crosses LAKHAN × BEECHER and LAKHAN × HARMAL both additive gene effect (d) and dominance (h) gene effects were found significant.

1000-grain weight was under the control of duplicate type of gene action in LAKHAN × BEECHER, whereas, LAKHAN × HARMAL, BH-902 × BEECHER and BH-902 × HARMAL revealed both additive (d) and dominance (h) gene effect. The cross BH-902 × MOROC-9-75 showed dominance gene effect (h)

**Table 1. Experimental material (genotypes) used in the study with their special feature**

| Lines | Special Features |
|---|---|
| MOROC-9-75 | 2-rowed, rainfed, prostrate, vigour- medium, spread bushy, sensitive to drought stress (exotic) |
| BEECHER | 6-rowed, cross between Atlas and Vaughn received in Kansas in 1934 from Aberdeen, Idaho, tolerant to spot blotch, erect ear, prostrate, earlier maturity, long awn (exotic) |
| HARMAL | 2-rowed, irrigated, prostrate, improved cultivar from Syria (exotic) |
| Testers | |
| LAKHAN | Spike 6-rowed, parentage: K-12/IB-226, plant semi erect, medium tall, good tillering, rachis non-fragile, non-shattering, seed medium bold, ear medium long, mid-lax awns, long serate semi-spreading at top and seed semi uniform well developed medium bold light blue in colour. |
| BH-902 | Spike 6-rowed, parentage: BH-495/RD-2552, medium plant height, erect growth habit, green leaf sheath, dark green foliage colour (boot stage) and medium leaf width (boot stage). |

**Table 2. Scaling test, estimate of gene effects from analysis of generation mean for various traits studied in six crosses of barley**

| Cross/trait | A | B | C | D | [m] | [d] | [h] | [i] | [j] | [l] | Epistasis |
|---|---|---|---|---|---|---|---|---|---|---|---|
| LAKHAN × MOROC-9-75 | | | | | | | | | | | |
| Plant height | -1.23 | 1.11 | 1.37 | 1.54 | 110.20** | 3.66** | 1.96 | - | - | - | - |
| Peduncle length | -2.20* | 1.50 | -0.29 | -0.09 | 12.26** | -0.33 | 7.86** | 0.66 | -3.73** | 0.53 | - |
| Ear length with awn | -1.83 | 0.54 | 0.93 | 0.98 | 33.60** | 0.33 | -50.70** | - | - | - | - |
| Ear length without awn | -2.76** | -0.98 | 0.57 | 1.76 | 10.00** | 0.19 | -6.06** | -7.60** | -0.86 | 12.66** | D |
| Number of tiller/plant | -1.70 | -0.86 | 0.06 | 1.51 | 10.33** | -0.39 | -5.16** | - | - | - | - |
| Number of grain/ear | -0.09 | 0.82 | -5.03** | -1.38 | 27.60** | 7.20** | 32.93** | 45.60** | -9.66** | -60.00** | D |
| 1000-grain weight | -2.07* | 2.23* | -0.46 | -0.18 | 48.76** | -8.15** | 19.38** | 3.38** | -13.03** | 1.10 | - |
| Grain yield/plant | -2.09* | -1.64 | -2.39* | -1.27 | 9.02** | 5.27** | 14.87** | 13.43** | 0.38 | -0.80 | - |
| LAKHAN × BEECHER | | | | | | | | | | | |
| Plant height | 2.69* | 1.99 | 1.41 | -3.17** | 108.26** | 5.53** | 16.06** | 14.26** | 0.66 | -45.20** | D |
| Peduncle length | 0.01 | 2.47* | -0.05 | -1.41 | 10.00** | -0.39 | 5.70** | 6.40** | -2.96** | -12.46** | D |
| Ear length with awn | 2.22* | 0.82 | 1.71 | -0.58 | 20.66** | 0.40 | 0.66 | 2.40* | 0.53 | -9.33** | - |
| Ear length without awn | 0.36 | 1.25 | -0.47 | -1.26 | 7.26** | -0.66 | 2.76** | - | - | - | - |
| Number of tiller/plant | 0.67 | 3.34** | 0.20 | -1.32 | 7.66** | -2.00 | 7.13** | 7.20** | -1.73 | -15.33** | D |
| Number of grain/ear | 0.63 | 0.91 | 1.43 | 1.35 | 87.26** | -2.20* | -108.03** | - | - | - | - |
| 1000-grain weight | -0.00 | 2.73** | -1.03 | -2.89** | 39.45** | 3.27** | 20.71** | 16.86** | -5.20** | -27.22** | D |
| Grain yield/plant | 0.87 | 1.39 | -0.50 | -1.25 | 10.67** | 1.84 | 16.68** | - | - | - | - |
| LAKHAN × HARMAL | | | | | | | | | | | |
| Plant height | 2.50* | 0.03 | -0.85 | -1.10 | 101.13** | 5.26** | 34.86** | 31.33** | 2.79** | -37.46** | D |
| Peduncle length | 0.48 | 0.77 | -0.36 | -0.80 | 10.13** | 0.66 | 7.53** | - | - | - | - |
| Ear length with awn | 1.13 | 1.22 | 0.84 | -0.08 | 20.53** | 1.40 | 0.96 | - | - | - | - |
| Ear length without awn | 0.71 | 0.44 | 0.51 | -0.14 | 8.93** | 0.80 | 1.59 | - | - | - | - |
| Number of tiller/plant | -0.53 | -3.34** | 0.64 | 1.70 | 9.06** | 1.20 | -5.56** | -7.20** | 1.43 | 11.66** | D |
| Number of grain/ear | -0.87 | 0.73 | 0.51 | 0.41 | 51.13** | -6.80** | -42.26** | - | - | - | - |
| 1000-grain weight | 0.66 | 0.86 | 0.32 | -0.87 | 49.54** | -12.67** | 34.31** | - | - | - | - |
| Grain yield/plant | -0.78 | -1.20 | -1.97 | -0.45 | 11.91** | 2.80** | 0.30 | - | - | - | - |
| BH-902 × MOROC-9-75 | | | | | | | | | | | |
| Plant height | 3.94** | 0.88 | 2.87** | 1.15 | 97.06** | 10.26** | -14.63** | -20.80** | 3.76** | -5.39** | C |
| Peduncle length | -0.21 | -0.51 | 3.81** | 4.07** | 12.80** | 1.46 | -18.76** | -20.26** | 0.23 | 21.80** | D |
| Ear length with awn | 3.25** | -0.34 | -0.03 | -1.32 | 18.06** | -0.13 | -1.63 | 5.06** | 5.90** | -9.80** | - |
| Ear length without awn | 0.73 | 0.43 | 0.00 | -0.69 | 7.80** | -6.66** | 3.20** | - | - | - | - |
| Number of tiller/plant | -1.02 | 0.09 | 0.59 | 0.76 | 9.00** | 0.19 | -6.09** | - | - | - | - |
| Number of grain/ear | -2.00 | -5.45** | -22.22** | 0.15 | 28.26** | 15.60** | 14.49** | -2.66* | -0.16 | 67.54** | C |
| 1000-grain weight | -1.30 | 2.57* | 1.54 | 0.78 | 48.18** | -4.65** | 3.55** | -6.98 | -12.57** | -1.22 | - |
| Grain yield/plant | -1.98 | -0.41 | 0.67 | 1.31 | 11.84** | -84.66** | -12.72** | - | - | - | - |
| BH-902 × BEECHER | | | | | | | | | | | |
| Plant height | 1.49 | 0.04 | 0.75 | 0.11 | 95.2**0 | 1.33 | 4.66** | - | - | - | - |
| Peduncle length | 0.93 | -0.16 | 0.27 | -0.80 | 8.93** | 14.90** | 28.16** | - | - | - | - |
| Ear length with awn | 1.85 | 0.39 | -0.96 | -1.89 | 16.73** | 1.13 | 10.31** | - | - | - | - |
| Ear length without awn | 0.92 | 0.68 | 0.65 | -0.48 | 7.46** | 0.46 | 1.30 | - | - | - | - |
| Number of tiller/plant | 3.59** | 1.97 | 2.20* | 0.21 | 10.86** | 0.00 | -0.29 | -1.59 | -0.10 | -11.13** | - |
| Number of grain/ear | 3.11** | 2.29* | 0.30 | -1.72 | 54.00** | -1.63 | 19.86** | 26.46** | 4.16** | -58.13** | D |
| 1000-grain weight | 0.15 | -0.72 | -1.37 | -1.32 | 33.61** | 7.54** | 38.70** | - | - | - | - |
| Grain yield/plant | -2.52* | -0.62 | -0.64 | 0.10 | 11.08** | -0.49 | -5.35** | -1.29 | -3.17** | 10.59** | D |
| BH-902 × HARMAL | | | | | | | | | | | |
| Plant height | 2.04* | 3.60** | 2.06* | -0.09 | 98.86** | -3.80** | 1.40 | 1.20 | 3.73** | -25.46** | - |
| Peduncle length | 23.72** | 3.80** | 9.66** | 2.70** | 12.06** | 1.33 | -5.76** | -6.13** | 1.16 | -7.66** | C |
| Ear length with awn | 1.78 | 2.14* | 2.45* | 0.04 | 17.60** | -0.33 | -0.83 | -0.13 | 3.33** | -6.33** | - |
| Ear length without awn | 0.11 | 0.14 | 2.64* | 2.96** | 9.40** | -0.73 | -6.73** | -6.80** | 0.00 | 6.53** | D |
| Number of tiller/plant | -0.14 | -0.02 | 0.85 | 0.92 | 14.06** | -0.40 | -10.86** | - | - | - | - |
| Number of grain/ear | -1.73 | -1.04 | -2.46* | -0.63 | 32.80** | 5.00** | 12.86** | 10.53** | -6.26** | 19.33** | C |
| 1000-grain weight | 0.06 | 0.20 | 0.38 | 0.33 | 47.67** | -4.21** | -13.29** | - | - | - | - |
| Grain yield/plant | 1.12 | 3.46** | 1.27 | -1.25 | 13.55** | -6.85** | 1.45 | 10.53** | -7.02** | -31.91** | - |

* Significant at 5% and ** significant at 1% level of significance; A, B, C and D are scaling test; C and D are complementary and duplicate type of epistasis, respectively.

as well as additive × dominance (j) type of interaction. The cross LAKHAN × MOROC-9-75 revealed dominance gene effect (h), additive × dominance (j) and dominance × dominance (l) type of interaction. These results corroborate the findings of Soyhu *et al*. (2002).

Duplicate type of gene action was significant in BH-902 × BEECHER for grain yield/plant while, LAKHAN × MOROC-9-75 showed dominance gene effect (h) as well as additive × dominance (j) type of interaction. BH-902 × HARMAL revealed significant effect for three types of interactions *viz.,* additive × additive (i), additive × dominance (j) and dominance × dominance (l). The crosses LAKHAN × BEECHER, LAKHAN × HARMAL and BH-902 × MOROC-9-75 showed absence of non-allelic interaction; additive gene effect (d), dominance gene effect (h) and both additive gene effect (d) and dominance gene effect (h). These results were similar with the findings of Verma *et al*. (1981). The generation mean analysis for most of the traits showed the importance of both additive and dominant type of gene effects. In presence of epistasis, almost all the crosses revealed duplicate type of gene interaction. Only four crosses showed complementary type; in such situation additive component is often underestimated, while dominance effect tends to be overestimated (Pathak and Singh, 1970).

The present investigation revealed that epistasis as basic mechanism cannot be ignored and epistasis must be included in a model for the unprejudiced estimation of genetic components. Thus, formulating breeding policies on the basis of only main effects *i.e.* additive and dominance could be ambiguous. The results showed presence of gene action, and inter-allelic interaction varied cross-wise as well as trait-wise. Hence, specific breeding strategy has to be adopted for a particular cross to get improvement in grain yield along with desirable yield contributing traits. Most of the traits revealed presence of duplicate type of inter-allelic interaction, as a consequence of higher magnitude of interactions; the non-fixable gene effects were higher than the fixable. Moreover, duplicate type of epistasis was also found in majority of traits in one or the other cross combinations. In such crosses, the selection intensity should be more intense in the later generations because it marks the progress through selection. Hence, selection procedure such as reciprocal recurrent selection and/or biparental mating in early segregating generations for the development of high yielding barley varieties with desirable yield contributing traits would be rewarding.

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# A Study on Variability of Elite Landraces of Small Cardamom (*Elettaria cardamomum* Maton)

**TK Hrideek[1], VV Radhakrishnan[2], KM Kuruvilla[3] and KV Mohanan[2]**
[1] *Kerala Forest Research Institute, Peechi-680653, Kerala, India*
[2] *Department of Botany, University of Calicut-673635, Kerala, India*
[3] *Indian Cardamom Research Institute, Myladumpara-685553, Kerala, India*

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Even though over one dozen improved varieties of small cardamom are made available to farmers, many farmers still depend on promising landraces for cultivation. Being a crop that is mainly propagated clonally by suckers, evaluation of such landraces in order to select promising genotypes from them has immense scope in the crop improvement of cardamom. With this objective, a field experiment for the evaluation of ten elite landraces of cardamom based on genetic variability, heritability and genetic advance was undertaken. Sixty-three characters including seven growth characters, nine yield characters, sixteen quality characters and thirty-one biophysical/ chemical characters were recorded. Among the growth characters, highest GCV and PCV were shown by tillers per clump; highest heritability was shown by leaf length and highest genetic advance by tillers per clump. This shows that number of tillers per clump is the most important growth character. Among the yield characters highest GCV and genetic advance were shown by internodal length, PCV by panicles per clump and heritability by racemes per panicle. In quality characters, GCV and PCV were the highest in dry seed weight and heritability in percentage of 7 mm and above sized capsules which is a very desirable phenomenon. With regard to the biophysical/biochemical characters, acid insoluble ash showed the highest GCV; PCV was shown by chlorophyll b content of leaf; heritability by acid insoluble ash in capsule. The characters analyzed showed genetic advance ranging from 0.006 to 0.58. Characters with high genetic advance could be utilized for selection.

**Key Words: Cardamom, *Elettaria cardamomum*, Landraces, Variability**

## Introduction

Small cardamom, often referred to as the 'queen of spices' is the commercial product obtained from the zingiberaceous, perennial, rhizomatous plant species *Elettaria cardamomum* Maton. It is grown on plantation scale in the Western Ghat region of South India at an elevation of 800-1300 m as an undercrop in forest lands. It is also grown in countries like Guatemala, Sri Lanka, Papua New Guinea and Tanzania. Cardamom is native to the moist evergreen forests of Western Ghats of South India (Ravindran, 2002).

Till date only a few hybrids have been released in cardamom and hence hybridization and selection of promising genotypes from the resultant segregating populations also can be used as an important tool in cardamom improvement. Cardamom genotypes are highly niche specific and hence evaluation of suitable genotypes adaptable to different growing regions is also necessary.

## Materials and Methods

The experiments consist of analysis of ten elite landraces of cardamom collected from the Idukki district of Kerala, India in comparison with a released variety ICRI-2 based on genetic variability, heritability and genetic divergence. The experiment was designed to study the variability of promising landraces identified by farmers. The investigations were carried out in the experimental farm of Indian Cardamom Research Institute, Myladumpara, Idukki, Kerala, during 2002-2006. The experimental farm is located at an altitude of 1,068 m above MSL at 9° 53'N latitude and 77° 09' E longitude. The location enjoyed humid tropical climate. The soil is forest loam with a pH of 5-6. The experiment was laid out in randomized block design with three replications and 12 plants per plot at a spacing of 3 m × 3 m. The materials used for the study included ten landraces and ICRI-2, a released variety as control. Package of practices recommendation of the Spices Board, India was followed for cultivation.

*Author for Correspondence: E-mail: dr.kvmohanan@rediffmail.com

The details of the landraces studied and the control are furnished in Table 1.

Sixty-three characters including seven growth characters, nine yield characters, sixteen quality characters and thirty one biophysical/chemical characters of the landraces studied and control were observed consecutively for three years starting from the fourth year of planting onwards and subjected to analysis of variance (ANOVA) to test the significance of variations between the accessions with reference to standard F table (Fisher and Yates, 1963). Phenotypic variance, genotypic variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense) and genetic advance were analyzed to study the extent of variation in the case of each character. Phenotypic and genotypic coefficients of variation were estimated following Burton and Devane (1953). Heritability (broad sense), the fraction of the total variance that is heritable was estimated as the percentage of genotypic variance over phenotypic variance (Jain, 1982). Genetic advance under selection was calculated using the formula proposed by Abraham (2000).

## Results and Discussion

Among the growth characters, highest GCV and PCV were shown by tillers per clump; highest heritability was shown by leaf length and highest genetic advance by tillers per clump. This shows that tillers per clump is the most important growth character with the highest GCV, PCV and genetic advance. This character shows 75.42 percentage of heritability (broad sense) also. Among the yield characters studied, the highest GCV and genetic advance were shown by internodal length, highest PCV by panicles per clump and the highest heritability by racemes per panicle. Among the quality characters, GCV and PCV were the highest in dry seed weight, highest heritability was in the case of percentage of 7 mm and above sized capsules and highest genetic advance in the case of percentage of 7 mm and above capsules, seed weight-dry and husk weight-fresh (Table 2).

Among the biophysical/biochemical characters, acid insoluble ash content showed the highest GCV. Highest PCV was shown by chlorophyll b content of leaf. Highest heritability was shown by acid insoluble ash content in capsule followed by soluble protein in leaf, crude protein in capsule, tannin in capsule and reducing sugar in capsule. In all the characters that were statistically significant, PCV was found to be higher than GCV indicating polygenic control of characters and additive gene action. Differential variability of quantitative characters has been reported by earlier workers in cardamom (Prasath and Venugopal, 2002; 2004; Radhakrishnan *et al.*, 2006; Prasath *et al.*, 2009; Prasath and Venugopal, 2009), rice (Mini, 2006), coffee (Nikhila *et al.*, 2002; Raghu *et al.*, 2003), medicinal plants (Misra *et al.*, 1998; Jayasree *et al.*, 2006) and vanilla (Umamaheswari and Mohanan, 2004). Study of variability of the genetic resources of a crop is the first step towards the understanding of the genetic diversity of the genetic stock so as to use them in crop improvement programmes.

Most of the agronomic characters of the crop plants are polygenic and cardamom is no exemption. Polygenic characters show different levels of heritability based on their response to environmental factors. Among the growth characters heritability (broad sense) was found to be the highest in the case of leaf length followed by tillers per clump (Table 2). Among the yield characters, racemes per panicle showed the highest heritability. In case of quality characters the highest heritability was shown by percentage of 7 mm and above sized capsules which is a very desirable phenomenon. In case of biochemical characters, the highest heritability was shown by acid insoluble ash, soluble protein- leaf, crude protein-capsule and reducing sugar-capsule in that order.

Highest heritability of characters indicates the limited influence of environment on these characters. Characters like panicles per clump, panicle length, fruit set percentage, fresh seed weight, litre weight of fresh capsules, oleoresin content, chlorophyll b content of leaf and chlorophyll a/b ratio of leaf and capsules show heritability below 50%, where as all other statistically significant characters showed above 50% of heritability. The reason for low heritability in the case of some characters is the influence of environment on them as suggested by earlier workers (Tripathy *et al.*, 2000; Radhakrishnan, 2003).

Genetic advance of characters in percentage of mean is a very effective indicator of the characters that could be utilized in selection programmes. It is a measure derived from heritability. Statistically significant characters analyzed presently showed genetic advance ranging from 0.006 to 0.58. Total chlorophyll content-fresh capsule showed the maximum genetic advance and this is a very desirable condition since green colour of capsules is determined by their chlorophyll content and green dry capsules are preferred highly in the internal and

**Table 1. Description of the landraces and control used for the study of variability of landraces.**

| Landrace | Description |
|---|---|
| Panikulangara-1 | It is a *Vazhukka* type cardamom with oval shaped and green coloured capsules. This plant performs well under rainfed conditions. |
| Panikulangara-2 | The plants are bushy in nature with vigorous growth. Branched panicles are also seen in this type. The capsules are oblong and deep green in colour. |
| Njallani Green Gold | It is a *Vazhukka* type cardamom. The plants are robust in nature with tall tillers with purple coloured swollen base. It has simple unbranched inflorescence. Capsules are extra bold, dark green and thick skinned. |
| Vali Green Bold | It is a *Vazhukka* type cardamom. The plants are robust in nature and the rhizome is fleshy and very stout with the nodes and internodes crowded. Panicles are unbranched and capsules are extra bold and dark green. |
| Palakkudi | It is a *Malabar* type cardamom. Plants are robust in nature and rhizomes stout and fleshy. Each tiller has 2-3 unbranched panicles. Capsules are round bold and deep green in colour. |
| PNS Vaigai | Plants are robust in nature with tall tillers. The dark green coloured non-pubescent leaves and the prominent ligules with light pale green colour are the striking features of this landrace. It has simple unbranched inflorescence. Capsules are extra bold with parrot green colour and thick skin. |
| Vander Cardamom | It is a *Vazhukka* type cardamom. Plants are robust and bushy in nature with very long shoots and deep green foliage. Branched panicles are also seen in this plant. The capsules are extrabold in size and deep green in colour. |
| Ela Rani -1 | It is a *Vazhukka* type cardamom. Plants are robust and bushy in nature with very stout pseudostem base. Capsules are round oblong and pale green in colour. |
| Ela Rani -2 | It is a *Vazhukka* type cardamom. Plants show only average growth and size with average sized tiller base. Capsules are round, slightly oblong and pale green in colour. |
| Ela Rani-3 | It is a *Vazhukka* type cardamom. Plants are robust and bushy in nature with vigorous growth and strong tiller base. Capsules are medium sized, round oblong in shape with light green colour. |
| ICRI-2 (control) | This variety was released by the Indian Cardamom Research Institute (ICRI), Myladumpara, Idukki, Kerala. It is a *Mysore* type cardamom. Plants are robust in nature. Capsules are oblong and bold with parrot green colour. |

**Table 2. Genotypic variance, phenotypic variance, GCV, PCV, heritability (broad sense) and genetic advance of the characters studied in the case of the landraces of cardamom**

| Characters | Mean | Genotypic variance | Phenotypic variance | GCV | PCV | Heritability (broad sense) (%) | Genetic advance |
|---|---|---|---|---|---|---|---|
| **Growth characters** | | | | | | | |
| Tillers/ clump** | 82.31 | 139.2 | 182.14 | 14.33 | 16.38 | 75.42 | 0.19 |
| Tiller height ** | 341.58 cm | 565.77 | 981.87 | 7.00 | 9.17 | 57.80 | 0.11 |
| Leaves/ tiller$^{NS}$ | 20.44 | 0.23 | 2.40 | – | – | – | – |
| Leaf length ** | 61.74 cm | 20.64 | 24.17 | 7.30 | 7.91 | 85.00 | 0.14 |
| Leaf breadth ** | 11.55 cm | 1.19 | 2.07 | 9.71 | 12.81 | 57.00 | 0.15 |
| Number of vegetative buds$^{NS}$ | 3.83 | 0.08 | 1.19 | – | – | – | – |
| Number of bearing tillers$^{NS}$ | 47.74 | 18.56 | 76.17 | – | – | – | – |
| **Yield characters** | | | | | | | |
| Panicles per clump* | 89.35 | 118.31 | 361.25 | 12.17 | 21.30 | 32.75 | 0.14 |
| Panicle length * | 80.45 cm | 117.64 | 279.4 | 13.48 | 20.77 | 42.10 | 0.18 |
| Racemes per panicle** | 25.51 | 7.79 | 10.96 | 10.93 | 12.95 | 71.00 | 0.19 |
| Capsules per raceme** | 8.04 | 0.30 | 0.59 | 6.58 | 9.57 | 50.85 | 0.10 |
| Fruit set % ** | 69.30 | 30.76 | 70.59 | 8.01 | 12.12 | 43.58 | 0.11 |
| Seeds/ capsule$^{NS}$ | 19.03 | 1.67 | 5.82 | – | – | – | – |
| Internodal length ** | 4.36 cm | 0.39 | 0.68 | 14.19 | 18.76 | 57.00 | 0.22 |
| Yield per plant fresh $^{NS}$ | 4.19 kg | 0.02 | 0.91 | – | – | – | – |
| Yield per plant dry $^{NS}$ | 0.88 kg | 0.01 | 0.04 | – | – | – | – |

| Characters | Mean | Genotypic variance | Phenotypic variance | GCV | PCV | Heritability (broad sense) (%) | Genetic advance |
|---|---|---|---|---|---|---|---|
| **Quality characters** | | | | | | | |
| Recovery %* | 20.95 | 0.47 | 1.12 | 3.29 | 5.05 | 51.09 | 0.05 |
| % of 7 mm and above capsules** | 73.43 | 47.29 | 47.81 | 9.38 | 9.43 | 98.93 | 0.19 |
| Seed wt.– fresh** | 0.43 g | 0.0001 | 0.0043 | 7.18 | 14.90 | 2.32 | 0.006 |
| Seed wt.– dry** | 0.21 g | 0.0008 | 0.0015 | 12.85 | 17.60 | 53.3 | 0.19 |
| Husk wt.–fresh* | 0.92 g | 0.013 | 0.022 | 12..39 | 16.12 | 59.09 | 0.19 |
| Husk wt–dry * | 0.06 g | 0.0543 | 0.0544 | – | – | – | – |
| Seed : Husk ratio fresh$^{NS}$ | 48.78:1 | 31.64 | 111.76 | – | – | – | – |
| Litre wt. of fresh capsules * | 560.78 g | 54.07 | 130.31 | 1.306 | 2.03 | 41.49 | 0.017 |
| Number of fresh capsules per litre** | 558.24 | 1226.57 | 1913.60 | 6.27 | 7.83 | 64.09 | 0.103 |
| 100 capsule wt.– fresh** | 130.16 g | 60.6 | 76.03 | 5.98 | 6.69 | 79.71 | 0.11 |
| Litre wt of dry capsules** | 344.33 g | 124.26 | 131.81 | 3.23 | 3.33 | 94..27 | 0.064 |
| Number of dry capsules/litre** | 2158.03 | 20610.24 | 38543.54 | 6.65 | 9.09 | 53.47 | 0.10 |
| 100 capsule wt dry** | 21.52 g | 5.12 | 9.12 | 10.5 | 14.04 | 56.14 | 0.16 |
| Volatile oil content (%)$^{NS}$ | 8.89 | 0.083 | 0.28 | – | – | – | – |
| Oleoresin content (%)** | 6.80 | 0.23 | 0.50 | 7.05 | 10.30 | 46.00 | 0.10 |
| Moisture content (%)** | 10.88 | 0.81 | 0.92 | 8.24 | 8.78 | 88.04 | 0.14 |
| **Biochemical characters** | | | | | | | |
| Chlorophyll a content– leaf ** | 2.06 mg/g fresh tissue | 0.25 | 0.29 | 24.27 | 26.14 | 86.21 | 0.46 |
| Chlorophyll b content– leaf * | 0.42 mg/g fresh tissue | 0.007 | 0.019 | 19.05 | 33.33 | 36.84 | 0.23 |
| Total chlorophyll– leaf* | 1.83 mg/g fresh tissue | 0.32 | 0.37 | 30.76 | 33.23 | 85.67 | 0.58 |
| Chlorophyll a/ b ratio Leaf* | 4.73 | 0.63 | 1.46 | 16.67 | 25.53 | 43.15 | 0.23 |
| Chlorophyll a content fresh capsule$^{NS}$ | 1.30 mg/g fresh tissue | 0.027 | 0.089 | – | – | – | – |
| Chlorophyll b– fresh capsule** | 0.94 mg/g fresh tissue | 0.07 | 0.09 | 30.68 | 34.1 | 77.78 | 0.05 |
| Total chlorophyll fresh capsule** | 0.97 mg/g fresh tissue | 0.08 | 0.09 | 31.1 | 33.3 | 88.00 | 0.61 |
| Chlorophyll a/ b ratio–fresh capsule** | 1.57 | 0.25 | 0.8 | 31.21 | 56.69 | 31.25 | 0.36 |
| Chlorophyll a –dry capsule** | 2.84 mg/g | 0.053 | 0.123 | 8.07 | 12.30 | 43.00 | 0.11 |
| Chlorophyll b– dry capsule** | 2.66 mg/g | 0.14 | 0.20 | 14.16 | 16.66 | 72.00 | 0.24 |
| Total chlorophyll– dry capsule** | 2.39 mg/g | 0.10 | 0.20 | 12.92 | 18.75 | 50.00 | 0.19 |
| Chlorophyll a/ b ratio– dry capsule** | 1.43 | 0.01 | 0.01 | 6.48 | 9.26 | 50.00 | 0.01 |
| Relative water content– leaf** | 71.26% | 54.94 | 103.20 | 10.39 | 14.25 | 53.24 | 0.16 |
| Stomatal frequency** | 26.85% | 5.59 | 11.04 | 8.80 | 12.37 | 50.63 | 0.47 |
| Stomatal index$^{NS}$ | 5.00 | 0.16 | 0.45 | – | – | – | – |
| Leaf proline** | 1.98 µmoles/g | 0.20 | 0.23 | 22.73 | 24.24 | 86.96 | 0.43 |
| Epicuticular wax** | 9.39 µg/cm$^2$ | 0.91 | 1.13 | 10.11 | 11.28 | 80.53 | 0.19 |
| Reducing sugar– leaf** | 4.49 g 100/g fresh tissue | 0.68 | 1.09 | 18.26 | 23.16 | 62.39 | 0.30 |

| Characters | Mean | Genotypic variance | Phenotypic variance | GCV | PCV | Heritability (broad sense) (%) | Genetic advance |
|---|---|---|---|---|---|---|---|
| Soluble protein– leaf** | 7.58 g 100/g fresh tissue | 3.80 | 3.87 | 25.69 | 25.96 | 98.19 | 0.52 |
| Insoluble protein– leaf** | 17.11 g 100/g fresh tissue | 7.63 | 9.18 | 16.13 | 17.71 | 83.12 | 0.30 |
| Crude protein– capsule** | 11.55 g 100/g capsule flour | 0.94 | 0.97 | 8.39 | 8.48 | 96.91 | 0.17 |
| Crude lipid– capsule$^{NS}$ | 3.05 g 100/g capsule flour | 0.06 | 0.53 | – | – | – | – |
| Crude fibre(%)– capsule** | 23.72 | 5.12 | 6.19 | 9.54 | 11.08 | 74.10 | 0.17 |
| Ash– capsule (%)** | 8.80 | 0.39 | 0.50 | 7.79 | 8.82 | 78.00 | 0.14 |
| Acid insoluble ash– capsule** | 0.34g 100/g capsule flour | 0.02 | 0.02 | 48.76 | 48.76 | 100.00 | 0.14 |
| Carbohydrate– capsule** | 53.93g 100/g capsule flour | 7.30 | 10.74 | 5.0 | 6.07 | 67.97 | 0.08 |
| Calorific value of capsule$^{NS}$ | 288.42Kcal 100/g DM | 12.29 | 312.99 | – | – | – | – |
| Phenol– capsule** | 0.26 g 100/g capsule flour | 0.0020 | 0.0023 | 17.2 | 18.44 | 86.86 | 0.32 |
| Tannins– capsule** | 0.19 g 100/g capsule flour | 0.0023 | 0.0024 | 23.97 | 24.49 | 95.83 | 0.46 |
| Amino acids– capsule** | 0.23 g 100/g capsule flour | 0.0008 | 0.001 | 11.78 | 13.18 | 80.00 | 0.21 |
| Reducing sugar– capsule** | 5.40 g 100/g capsule flour | 2.27 | 2.38 | 27.9 | 28.6 | 92.43 | 0.54 |

**: significant at 1% level; *: significant at 5% level.

international markets. Total chlorophyll content in leaf showed high genetic advance also. Among the growth characters, total tillers per clump showed the highest genetic advance and among the yield characters internodal length of panicles and racemes per panicle showed the highest genetic advance in that order. Among the quality characters percentage of 7 mm and above sized capsules, dry seed weight and fresh husk weight showed the highest genetic advance. Characters with highest genetic advance could be utilized for selection programmes as reported by earlier workers in cardamom (George *et al*., 1981; Radhakrishnan *et al.*, 2006) and other crops (Jayasree *et al.* 2006). Studies by Korikanthimath *et al.* (1998) and Korikanthimath *et al*. (2000) showed significant treatment differences for yield and morphological characters.

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# Studies on Variability, Correlation and Path Analysis of Traits Contributing to Fruit Yield in Grapes

**Navjot Gupta[1]*, KS Brar[2], MIS Gill[1] and NK Arora[1]**
[1] *Punjab Agricultural University Regional Research Station, Bathinda-151001, Punjab, India*
[2] *Punjab Agricultural University, Ludhiana-141001, Punjab, India*

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The present investigation was conducted to estimate genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) along with correlations and path coefficients from the data collected on 20 grape cultivars during 2000-09. The high estimates of GCV and PCV recorded for bunch weight, berry weight, bunch number and fruit yield per vine indicated the presence of adequate genetic variation among the genotypes and suitability of these traits for further improvement by selection. High heritability estimates coupled with high genetic advances for these traits confirmed that these traits are under the control of additive gene action and phenotypic selection for their improvement will be effective. Fruit yield per vine showed significant positive association with bunch length, bunch width, bunch weight and bunch number while significant negative association of berry length, berry diameter and berry weight with acidity percentage indicated that improvement of these traits through selection will also improve quality of table grapes by reducing acidity. Number of bunches per vine had maximum direct effect on fruit yield per vine followed by bunch weight. Bunch length as well as bunch width contributed to fruit yield per vine indirectly via bunch weight. Hence, the number of bunches per vine and bunch weight are identified as key traits for developing high fruit-yielding cultivars of grapes.

**Key Words: Fruit yield, GCV, Grapes, Path analysis, PCV**

## Introduction

Grape cultivation is one of the most remunerative farming enterprises in India. Grape is grown under a variety of soil and climatic conditions in three distinct agro-climatic zones namely sub-tropical, semi arid tropical and mild humid-tropical climatic regions in India. Punjab comes under sub-tropical region, which covers the North western plains corresponding to 28$^{o}$ and 32$^{o}$ N latitude. In South western Punjab, area under grapes has been reducing since last decade due to fluctuations in temperature, erratic rainfall and short shelf life. 'Perlette' is the only early ripening variety quite successful in this region, occupying more than 90% of total area under grapes, whereas, other varieties like Beauty Seedless, Thompson Seedless and Anab-e-Shahi are being cultivated in small areas. Punjab state has a great potential for grapes cultivation for table and wine purposes. Hence, the availability of a suitable high-yielding grapes cultivar is important for popularization among the growers. The breeding methodology for genetic improvement of fruit yield and its components depends upon the nature and magnitude of variability available for these traits. The estimation of genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense ($H^2$) and genetic advance (GA) is helpful in making selections effective for improving base population. Effectiveness of selection will increase if the nature of interrelationships among different characters is understood. Path analysis further unravels the cause of such associations by determining direct and indirect contributions. Although Giridharan and Jindal (1995) studied correlation and path analysis for some physiological parameters, but very little information with respect to these aspects is available in this crop. Therefore, the present investigation was conducted to estimate genetic parameters along with correlations and path coefficients among the fruit yield and its components in grapes.

## Material and Methods

The experimental material comprising 20 different cultivars *viz.*, Cardinal, Angur Early, Banqui Abyad, Khalili, Arkavati, Shadipur Local, Black Prince, Bharat Early, Madeliene Anguvine, Perlette, Arka Hans, Delight, Beauty Seedless, Rubi Red, Black Muscat, Tas-A-

*Author for Correspondence: E-mail: navjotgupta@pau.edu, brar164@hotmail.com, misgill@yahoo.com, nkarora@gmail.com

Ganesh, Arka Kanchan, Arka Shyam, Selection 7 and Lomanto were collected from different parts of India. All the cultivars were planted in randomized block design each with 3 replications at PAU, Regional Research Station, Bathinda, Punjab. The average rainfall at the experimental site was 400 mm, the annual maximum temperature was 31.5°C and annual minimum temperature was 16.9°C during fruiting season. The soil was sandy loam with pH (8.31), organic carbon (0.32%), electrical conductivity (0.24 dS/m), available N (212 kg/ ha), available P (21.5 kg/ha) and available K (357.0 kg/ ha). Three plants each, per replication of each cultivar, were grown at a spacing of 3 × 3 meters. Data were recorded on bunch length (cm), bunch width (cm), bunch weight (g), berry weight (g), berry length (mm), berry diameter (mm), total soluble solids (TSS %), acidity (%), bunch number and fruit yield (kg/vine) for nine years (2000-09). The genotypic and phenotypic coefficients of variation and heritability (in broad sense) were calculated after pooling of the data (Singh and Choudhary,1979) while genetic advances were estimated as per the procedure of Johnson *et al.* (1955). The path analysis was carried out following Dewey and Lu (1959).

## Results and Discussion

The analysis of variance showed significant differences among the cultivars for all the 10 traits (Table 1). The high estimates (>35%) of PCV and GCV for bunch weight, berry weight, bunch number and fruit yield indicated the presence of adequate genetic variation among the genotypes and suitability of these attributes for further improvement by selection (Table 2). High heritability estimates (>90%) coupled with high genetic advance percentage (>70%), for bunch weight, berry weight, bunch number and fruit yield confirmed that these traits are under the control of additive gene action and phenotypic selection for their improvement will be effective. Wei *et al.* (2002) and Kumar *et al.* (2002) also observed berry weight to be under strong additive genetic control. High heritability estimates for berry weight, bunch weight and bunch number were also reported by Wei *et al.* (2003). The estimates of PCV and GCV for bunch width and acidity percent were low in magnitude yet these were close to each other indicating little effect of environment in the inheritance of these traits.

The phenotypic and genotypic correlation coefficients between different characters are presented in Table 3. Fruit yield per vine showed significant positive association with bunch length (0.2976), bunch width (0.3238), bunch weight (0.2706) and bunch number (0.6348), while significant negative association with total soluble solids (–0.2851). These traits also showed high correlation with fruit yield per vine at genotypic level indicating little effect of environment on the expression of such traits. Hence, improving bunch length, bunch width, bunch weight and bunch number seemed to improve fruit yield per vine. Berry length, berry diameter and berry weight showed significant positive association with each other but significant negative association with bunch number. It indicated that improvement of berry length, berry diameter and berry weight will reduce bunch number. Significant negative association of berry length, berry diameter and berry weight with acidity percentage indicated that improvement of these traits through selection will also improve the quality of grapes by reducing acidity.

Path coefficient analysis revealed that bunch number made maximum direct contribution to fruit yield per vine followed by bunch weight, berry length and bunch width. Bunch length as well as bunch width contributed to fruit yield per vine indirectly via bunch weight. Berry length, berry diameter and berry weight also contributed to fruit yield per vine via bunch weight. In view of high

**Table 1. Pooled Analysis of variance of fruit yield and its components in grapes**

| Source | DF | Mean Square | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Fruit yield (kg/vine) | Bunch length (cm) | Bunch width (cm) | Bunch weight (g) | TSS (%) | Acidity (%) | Berry weight (g) | Berry length (mm) | Berry diameter (mm) | Bunch number |
| Environment | 8 | 601.92** | 15.95** | 18.05** | 80352.5** | 53.27** | 2.33** | 0.751 | 0.0695 | 0.0480 | 2865.4** |
| Block within Environment | 18 | 5.18 | 9.00** | 3.17 | 2314.2 | 36.23** | 0.015 | 0.694 | 0.3028** | 0.1595** | 53.199 |
| Genotype | 19 | 1101.03** | 113.57** | 76.99** | 318627.3** | 33.37** | 1.55** | 21.65** | 1.101** | 0.9754** | 16240.64** |
| Environment × Genotype | 152 | 112.88** | 11.03** | 4.68** | 21069.1** | 5.12 | 0.137** | 0.464 | 0.0317 | 0.0254 | 1268.21** |
| Pooled Error | 342 | 6.015 | 5.04 | 2.34 | 3095.5 | 5.16 | 0.02 | 0.166 | 0.0494 | 0.0576 | 88.2718 |

**Table 2. Genetic parameters for fruit yield and its components in grapes**

| Characters | Mean | PCV (%) | GCV (%) | Heritability (H2) | GA (%) |
|---|---|---|---|---|---|
| Bunch length (cm) | 16.82 | 13.22 | 11.81 | 79.81 | 21.74 |
| Bunch width (cm) | 10.81 | 16.43 | 15.88 | 93.44 | 31.63 |
| Bunch weight (g) | 274.25 | 41.97 | 40.67 | 93.93 | 81.20 |
| TSS (%) | 16.60 | 8.08 | 6.90 | 72.99 | 12.15 |
| Acidity (%) | 1.05 | 23.93 | 23.26 | 94.47 | 46.58 |
| Berry weight (g) | 2.47 | 35.46 | 35.77 | 96.13 | 70.22 |
| Berry length (mm) | 1.71 | 12.52 | 11.65 | 86.61 | 22.34 |
| Berry diameter (mm) | 1.55 | 13.12 | 11.90 | 82.29 | 22.24 |
| Bunch number | 51.34 | 49.34 | 49.01 | 98.65 | 99.27 |
| Fruit yield (kg/vine) | 12.96 | 48.88 | 48.31 | 97.68 | 98.35 |

**Table 3. Phenotypic ($r_p$) and genotypic ($r_g$) correlation coefficients of fruit yield and component characters in grapes**

| Characters | Bunch length (cm) | Bunch width (cm) | Bunch weight (g) | TSS (%) | Acidity (%) | Berry weight (g) | Berry length (mm) | Berry diameter (mm) | Bunch number | Fruit yield (kg/ vine) |
|---|---|---|---|---|---|---|---|---|---|---|
| Bunch length (cm) | 1.000 | | | | | | | | | |
| Bunch width (cm) | 0.7632** | | | | | | | | | |
| | 0.8898 | 1.000 | | | | | | | | |
| Bunch weight (g) | 0.7049** | 0.8660** | | | | | | | | |
| | 0.8415 | 0.9096 | 1.000 | | | | | | | |
| TSS (%) | 0.0152 | 0.1560 | 0.0330 | | | | | | | |
| | 0.1103 | 0.1875 | 0.0381 | 1.000 | | | | | | |
| Acidity (%) | -0.0793 | -0.1641 | -0.1589 | -0.1111 | | | | | | |
| | -0.0817 | -0.1609 | -0.1576 | -0.1328 | 1.000 | | | | | |
| Berry weight (g) | 0.3953** | 0.3766** | 0.4617** | -0.1902 | -0.4050** | | | | | |
| | 0.4108 | 0.3942 | 0.4791 | -0.2004 | -0.4120 | 1.000 | | | | |
| Berry length (mm) | 0.3670** | 0.4174** | 0.5112** | -0.0790 | -0.3452** | 0.7948** | | | | |
| | 0.3298 | 0.4578 | 0.5775 | -0.1103 | -0.3810 | 0.8650 | 1.000 | | | |
| Berry diameter (mm) | .4076** | 0.3184* | 0.4287** | -0.2936* | -0.3644** | 0.9191** | 0.6762** | | | |
| | 0.4372 | 0.4234 | 0.5032 | -0.2354 | -0.4047 | 1.0102 | 0.8248 | 1.000 | | |
| Bunch number | -0.2658* | -0.3690** | -0.4197** | -0.4718** | 0.2412 | -0.2774* | -0.4731** | -0.1999 | | |
| | -0.3004 | -0.3785 | -0.4383 | -0.5292 | 0.2580 | -0.2829 | -0.4947 | -0.2374 | 1.000 | |
| Fruit yield (kg/ vine ) | 0.2976* | 0.3238* | 0.2706* | -0.2851* | -0.0006 | -0.0285 | -0.0768 | 0.0066 | 0.6348** | |
| | 0.3312 | 0.3361 | 0.2865 | -0.3489 | -0.0124 | -0.0362 | -0.1068 | 0.0144 | 0.6630 | 1.000 |

* Significant at 5% level ; ** Significant at 1% level of significance

**Table 4. Path analysis coefficient of fruit yield versus component characters in grapes**

| Characters | Bunch length (cm) | Bunch width (cm) | Bunch weight (g) | TSS (%) | Acidity (%) | Berry weight (g) | Berry length (mm) | Berry diameter (mm) | Bunch number | PCC* with Fruit yield (kg/vine ) |
|---|---|---|---|---|---|---|---|---|---|---|
| Bunch length (cm) | 0.1346 | 0.1745 | 0.2794 | 0.0016 | 0.0134 | -0.1449 | 0.1109 | 0.009 | -0.281 | 0.2976 |
| Bunch width (cm) | 0.1027 | 0.2287 | 0.3433 | 0.0164 | 0.0277 | -0.1381 | 0.1262 | 0.0071 | -0.3901 | 0.3238 |
| Bunch weight (g) | 0.0949 | 0.198 | 0.3964 | 0.0035 | 0.0268 | -0.1693 | 0.1545 | 0.0095 | -0.4437 | 0.2706 |
| TSS (%) | 0.002 | 0.0357 | 0.0131 | 0.1049 | 0.0188 | 0.0697 | -0.0239 | -0.0065 | -0.4988 | -0.2851 |
| Acidity (%) | -0.0107 | -0.0375 | -0.063 | -0.0116 | -0.1689 | 0.1485 | -0.1043 | -0.0081 | 0.225 | -0.0006 |
| Berry weight (g) | 0.0532 | 0.0861 | 0.183 | -0.0199 | 0.0684 | -0.3666 | 0.2403 | 0.0204 | -0.2933 | -0.0285 |
| Berry length (mm) | 0.0494 | 0.0955 | 0.2026 | -0.0083 | 0.0583 | -0.2914 | 0.3023 | 0.015 | -0.5002 | -0.768 |
| Berry diameter (mm) | 0.0549 | 0.728 | 0.1699 | -0.0308 | 0.0615 | -0.337 | 0.2044 | 0.0222 | -0.2113 | 0.0066 |
| Bunch number | -0.0358 | -0.0844 | -0.1664 | -0.0495 | -0.0407 | 0.1017 | -0.143 | -0.0044 | 1.0572 | 0.6348 |

Bold figures are direct effects, *PCC stands for phenotypic correlation coefficient; Residual effect: 0.0850

indirect contribution of different traits through bunch weight, this trait will be most effective for selection of high-yielding cultivars of grapes. Although bunch number influenced fruit yield per vine, slightly negatively via different traits, yet in view of it's very high direct effect upon fruit yield per vine, selection for this trait can also be relied upon for improving fruit yield.

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# Trait-specific Amaranth Germplasm — Potentialities to Combat Climate Change

**Chithra Devi Pandey*, Anjali Kak, Sushil Pandey and Veena Gupta**
*Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India*

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Amaranth has great potential to combat climate change and malnutrition. It is receiving attention now-a-days because of its high nutritional value, rapid growth, adaptability to a wide range of climatic and soil conditions. It has traditionally been part of barter system in the Himalayan region. ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) has base collection of 5,804 accessions of amaranth representing 26 species. This vast genepool is available to the breeders, but due to large size of the collection and lack of detailed information on unique traits, there has been minimum use of germplasm in breeding programmes to develop new varieties and hybrids. Hence, genebank curators collated the trait-specific information from different sources to make an useful compilation for the breeders. A total of 623 accessions of amaranth representing different biotic and abiotic stress resistance (12), quality traits (106), agronomic traits (449), other traits (27), released varieties (27) and registered germplasm (2) are conserved in National Genebank (NGB). This compilation will enhance the utilization of diverse amaranth germplasm in future crop improvement programmes to develop climate-resilient varieties.

**Key Words: *Amaranthus* spp., Conservation, Germplasm, Trait-specific material, Utilization**

## Introduction

Amaranth belongs to the genus *Amaranthus* of the family Amaranthaceae. About 70 species have been reported in this crop (Sauer, 1967). The genus *Amaranthus* is unique in having species which are economically important and used for grain, leafy vegetable, fodder and ornamental purposes. *Amaranthus tricolor*, *A. dubius, A. lividus* (syn. *A. blitum*), are important leafy types (Peter *et al.*, 2011) and widely cultivated throughout India, especially during the summer and rainy seasons. Because of its low production cost, rich nutrition and availability at cheaper rate, it is often used by common people (Varalakshmi, 2004). The leaves are rich in dietary fibre, protein, vitamins and minerals (Shukla *et al*., 2003). Hence, *Amaranthus* species can help in alleviating under-nutrition and malnutrition, especially in developing countries (Rastogi and Shukla, 2013). It can contribute greatly to the nutritional well-being of rural and economically week people by providing the essential nutrients required for body growth and for prevention of diseases associated with nutritional deficiencies such as iron and vitamin A (Dua *et al*., 2009). The grain amaranth species are considered by many as the crop of the future because of the diversified purposes and superior nutritional quality of grain with high protein content in the range 13-18% and relatively high lysine content in comparison with common cereals (Janovska *et al*., 2012; Rastogi and Shukla, 2013). Amaranth shows a wide variation in morphological diversity both among and within certain species. Modern plant breeders are concerned about genetic diversity but farmers are most interested in morphological and agronomical variation (Mwase *et al*., 2014). Improving crops, therefore, requires diverse trait-specific germplasm and wild species for utilization in crop improvement programme to develop the climate-resilient varieties. The information about the base collection at National Genebank (NGB), ICAR-NBPGR, comprises 5,804 amaranth germplasm including 623 potential trait-specific accessions, will enhance the utilization of diverse germplasm including wild species in breeding programme to develop short duration, high yielding, bold seeded, non-shattering and non-lodging varieties particularly in the context of climate change.

## Materials and Methods

The main objective of this study was to collate the information about various traits present in the germplasm available in the genebank. To begin with a list of the germplasm available in NGB along with the passport information was taken and classified on the basis of their use into three categories *viz.* vegetable type, grain type and wild/weedy types. The information on the specific traits like dwarfness, early maturity, non-lodging, drought tolerant, resistance to pest and diseases, high leaf and grain yield, high protein and lysine content etc. were

*Author for Correspondence: E-mail: chitra@nbpgr.ernet.in

collated. The collated information was based on literature review of published sources like books, catalogues, research papers, ICAR-NBPGR annual reports and AICRP report of underutilized crops. A total of 5,300 amaranth germplasm was characterized and evaluated using the descriptor states developed by NBPGR (3,050 accessions) and Bioversity (2,250 accessions) from 1981 to 1990 at NBPGR, Regional Station, Phagli, Shimla, India, respectively (Joshi 1981, 1991).

## Results and Discussion

The genetic resources of amaranth have a wide spectrum of variability of both qualitative and quantitative nature. Availability information on conserved germplasm resources is key to its utilization. The entire collections of 5,804 accessions of amaranth germplasm were categorised based on passport information into grain type (4,569), vegetable type (442), wild/weedy relatives (90) that are conserved at -18$^{o}$C in NGB. The details of the species along with the number of accessions are presented in Table 1. The most promising genotypes in both indigenous and exotic germplasm for various biotic and abiotic stress resistances, variability in agronomic and quality characters have been identified and catalogued

**Table 1. Species-wise amaranth germplasm conserved in National Genebank, New Delhi, India (as on 30th June 2015)**

| S.No. | Common name | Botanical name | No. of accession |
|---|---|---|---|
| 1. | White pigweed | *Amaranthus albus* L. | 1 |
| 2. | Purple amaranth | *Amaranthus blitum* L. | 23 |
| 3. | Love lies-bleeding | *Amaranthus caudatus* L. | 224 |
| 4. | Pendant amaranth | *Amaranthus caudatus* var. *albiflorus* Moq. | 1 |
| 5. | Velvet flower | *Amaranthus caudatus* var. *atropurpurea* Roxb. | 1 |
| 6. | Crispleaf amaranth | *Amaranthus crispus* Terrac. | 1 |
| 7. | Red amaranth | *Amaranthus cruentus* L. | 147 |
| 8. | Spleen amaranth | *Amaranthus dubius* Mart. ex Thell. | 53 |
| 9. | Quilete | *Amaranthus edulis* Speg. | 2 |
| 10. | Fringed amaranth | *Amaranthus fimbriatus* S.Watson. | 1 |
| 11. | Smooth amaranth | *Amaranthus flavus* L. | 1 |
| 12. | Elephant head amaranth | *Amaranthus gangeticus* L. | 21 |
| 13. | Mediterranean amaranth | *Amaranthus graecizans* L. | 26 |
| 14. | Red amaranth | *Amaranthus hybridus* L. | 75 |
| 15. | Prince-of-Wales- feather | *Amaranthus hypochondriacus* L. | 4099 |
| 16. | Tumble pigweed | *Amaranthus leucocarpus* S. Watson. | 2 |
| 17. | Lividi amaranth | *Amaranthus oleraceus* L. | 23 |
| 18. | Palmer's amaranth | *Amaranthus palmeri* S.Watson. | 1 |
| 19. | Foxtail amaranth | *Amaranthus paniculatus* L. | 17 |
| 20. | Tropical amaranth | *Amaranthus polygonoides* L. | 4 |
| 21. | Powell amaranth | *Amaranthus powellii* S.Watson | 2 |
| 22. | Red-root amaranth | *Amaranthus retroflexus* L. | 4 |
| 23. | Prickly amaranth | *Amaranthus spinosus* L. | 27 |
| 24. | Chinese amaranth | *Amaranthus tristis* L. | 4 |
| 25. | Joseph's-coat | *Amaranthus tricolor* L. | 305 |
| 26. | Green amaranth | *Amaranthus viridis* L. | 36 |
| 27. | Amaranth | *Amaranthus* spp. | 703 |
| | | **Total** | **5804** |

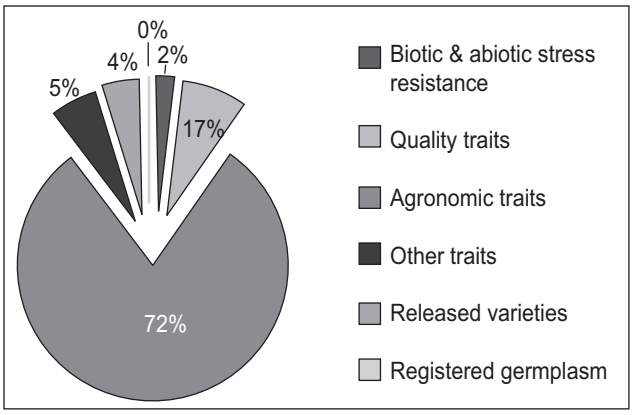


**Fig. 1. Status of trait-specific amaranth germplasm conserved in NGB**

by several workers (Ahuja *et al*., 1991; Joshi and Rana, 1991; *Varalakshmi,* 2004; Joshi *et al*., 2011). This trait-specific information was identified. About 623 accessions of potential germplasm are available in NGB, which will be of interest to the breeders. Promising accessions identified in different categories include agronomic traits (449), quality traits (106), sources against biotic and abiotic stress resistance (12), other traits (27), released cultivars (27) and registered genetic stock (2) (Fig.1). Genotypes resistance to various biotic and abiotic stresses constitutes merely 2%, whereas agronomic and quality traits constitute 72% and 17%, respectively, of the total trait-specific germplasm conserved in NGB and the details of unique traits are presented in Tables 2 and 3. Under the biotic stresses the main traits available in the NGB were root-knot nematode, leaf spot, leaf blight, steam borer and white rust which occur commonly in India. Trait-specific germplasm for abiotic stress such as drought tolerance (3 acc.) and suitable for arid zone (1 acc.) are also conserved in NGB. In addition, the germplasm for important quality traits such as high protein content from 11.0- 15.95 % (54 acc.), high oil content from 6.0-12.7% (46 acc.; Raiger *et al*., 2012), high lysine content >5.0-7.5 mg/100g (3 acc.) and other desirable traits such as non-shattering, non-lodging, suitable for inter-cropping, dual purpose and hard thrashability have been identified for use in breeding programmes to develop climate-resilient varieties.

**Table 2. Germplasm accessions identified for agronomic and other traits conserved in National Genebank, New Delhi, India**

| Traits | Trait-specific accessions identified | No. of accessions conserved |
|---|---|---|
| **Agronomic Traits** | | |
| Early maturity type (<110 days) | IC17947, IC26264, IC32156, IC35365, IC35404, IC35407, IC35416, IC38057, IC38069, IC38127, IC38133, IC38136, IC38269, IC38271, IC38280, IC38282, IC38327, IC38353, IC38422, IC38553, IC38658, IC42258, IC42264, IC258251, IC282307, IC303068 IC328965, IC322994, IC322997, IC333241, IC423408, IC444099, IC444159, IC536740, IC612197, EC157417, EC28889, EC321563,EC333744,C359409, EC359417, EC519550 | 42 |
| Early flowering (40-52 days) | IC38133 | 1 |
| Days to flowering (60-101 days) | EC519521, EC519533, EC519556 | 3 |
| Dwarf plant type (65-80 cm) | IC363768, IC363769, IC38541, IC38577, IC38598, IC398218, IC599589, EC169626, EC170304 | 9 |
| Plant height (>130 cm) | IC38269, IC38280, IC38658, IC42255-5, IC42290-17, IC95308, IC95314, IC95315, IC95320, IC255419, IC257794, IC257796, IC278914, IC317433, IC325880, IC341509, IC347566, IC363742, IC398213, IC398215, IC398233, IC398237, IC415262, IC415264, IC444183, IC444192, IC512322, IC526828, IC540812, IC540900, EC169642 | 31 |
| Number of branches > 15 | IC255986, IC257796, IC526828 | 3 |
| Leaf length >20cm | IC38340, IC95284, IC95320, IC415236, IC415272, IC415274, IC415297, IC421885, IC467886, IC467888, IC467894,IC467896, IC467908 | 13 |
| Leaf breadth >10cm | IC257793, IC526828, IC526831 | 3 |
| Inflorescence length (60-104 cm) | IC21926, IC21947, IC38052, IC38261, IC38553, IC95253, IC95308, IC363742, IC423400, IC423448, IC423468, EC157415, EC321563, EC359408 | 14 |
| Drooping type of panicles | IC255500, IC363742, IC381135, IC444173 | 4 |
| Spreading, robust and stem type | IC550326 (spreading), IC550330 (robust), IC395324 (stem type) | 3 |
| High leaf yielding lines 20-50 t/ha | IC257791, IC257794, IC296402, IC393730, IC469564, IC523791, IC523795, IC526828, IC550142, IC550145, IC550412, IC599591, IC612192, IC612193, IC612194 | 15 |
| 1000 seed wt (0.7 to > 1.0 gm) | IC21806, IC21938, IC21941, IC34749, IC38131, IC38185, IC38193, IC38250, IC38285, IC38313, IC38611, IC38665, IC282307, IC335807, IC415266, IC467897 | 16 |

Contd.

Table 2 Contd.

| Traits | Trait-specific accessions identified | No. of accessions conserved |
|---|---|---|
| High seed yield (40-100g/plant) | IC17923, IC17926, IC17936, IC17940, IC17947, IC17953, IC17956, IC21803-A, IC27790, IC35407, IC35467, IC35482, IC35501, IC35614, IC35624, IC35661, IC35696, IC37316, IC38047, IC38053, IC38066, IC38096, IC38123, IC38230, IC38243, IC38267, IC38269, IC38271, IC38280, IC38299, IC38327, IC38662, IC38663, IC38664, IC38665, IC42254, IC42254-2, IC42255-5, IC42258-1, IC42264, IC42290-17, IC42293, IC42293-15, IC42309, IC42316-1, IC42323, IC42332, IC42335, IC95383, IC95430, IC95516, IC95556, IC95588, IC95638, IC303068, IC321563, IC322996, IC325877, IC325880, IC326896, IC328897, IC333241, IC335807, IC341509, IC341565, IC359412, IC359413, IC359430, IC396973, IC415232, IC415250, IC415262, IC415264, IC423400, IC423448, IC436974, IC444190, IC467887, IC467892, IC467897, IC467912, IC469564, IC512322, IC547393, IC550142, IC550145, EC321563, EC322996, EC328875, EC359412, EC359413, EC359417, EC359430 | 93 |
| Bold seed (1000 seed wt > 1 gram) | IC17947, IC35415, IC38280, IC38282, IC38285, IC38269, IC38353, IC38600, IC38658, IC38661, IC38665, IC42258, IC42258-1, IC42264, IC43264, IC398214, IC406573, IC444146, IC444153, IC444159, IC444162, IC549660, EC321557, EC321563, EC359412, EC359417 | 26 |
| Early maturity, bold seed and high yielding | IC17947, IC38269, IC38280, IC38282, IC38353, IC38658, IC42258-11, IC42264, EC321563, EC359417 | 10 |
| Black seed | IC35488, IC35489, IC35490, IC35415, IC35645, IC38131, IC38661, IC255538, IC255554, IC25555, IC261949, IC261952, IC26197, IC278509, IC313269, IC319613, IC324045, IC324475, IC328951, IC331733, IC33863, IC341371, IC343034, IC343035, IC347983, IC347984, IC381062, IC385772, IC427411, IC427461 | 30 |
| Red/brown seed | IC16636, IC16637, IC35491, IC49887, IC49888, IC264820, IC264854, IC278232, IC278248, IC278510, IC316031, IC319612, IC321027, IC326899, IC356403, IC361327, IC362203, IC383571, IC383663, IC383594, IC396956, IC396963, IC412748, IC412833, IC423468, IC469601 | 26 |
| Cream/ white/ golden seed | IC16635, IC49618, IC255428, IC255446, IC255452, IC255453, IC255481, IC255482, IC255493, IC255512, IC255523, IC255555, IC255556, IC261957, IC261958, IC261961, IC261964, IC261965, IC261970, IC261980, IC261988, IC261992, IC262001, IC264805, IC278221, IC278285, IC278304, IC278315, IC278356, IC281427, IC281430, IC281434, IC281436, IC281440, IC281449, IC281455, IC281457, IC281461, IC281470, IC281474, IC281490, IC281744, IC281749, IC282307, IC282786, IC313253, IC316045, IC317455, IC319571, IC319816, IC319817, IC325587, IC326898, IC326901, IC326903, IC328559, IC328893, IC333211, IC335807, IC337330, IC337341, IC341364, IC355772, IC355777, IC355789, IC356393, IC356401, IC356407, IC361117, IC361129, IC361331, IC362201, IC362257, IC383578, IC383683, IC396949, IC396953, IC396955, IC396961, IC396970, IC396971, IC396972, IC396992, IC396997, IC398478, IC412770, IC415426, IC415439, IC415461, IC415591, IC415592, IC430340, IC444144, IC444148, IC444149, IC444152, IC444171, IC444176, IC444183, IC447625, IC526834, IC536740, IC612195 | 103 |
| Purple seed | IC255608, IC278305, IC317456, IC599590 | 4 |
| **Total** | | **449** |
| **Other traits** | | |
| Aneuploid | IC38261 | 1 |
| Highly branched with multiple inflorescence | IC0447624 | 1 |
| Non-lodging type | IC303068, IC35407, IC536740 | 3 |
| Non-shattering (moderately resistance) | IC35407 | 1 |
| Dual purpose | IC0545091, IC599589, IC599557 | 3 |
| Suitable for hills | IC35407, IC309876, IC42258-1, IC512322, IC549660 | 5 |
| Suitable for plains | IC282307, IC303068, IC335807, IC536740, IC586032 | 5 |
| Suitable for inter-cropping (potato and cotton) | IC321510, IC321511, IC333241, IC350249 | 4 |
| Hard threshability | IC5626, IC7934, IC38136 | 3 |
| Seed used to make white chapatti | IC362199 | 1 |
| **Total** | | **27** |

(Source: Joshi and Rana 1991; Gautam *et al*., 2000; Dhillon *et al*., 2001; Singh 2006; Dua *et al*., 2009; Joshi *et al*., 2011; NBPGR Annual Report (1987, 2005, 2010 and 2013)

**Table 3. Germplasm accessions identified for biotic, abiotic and quality traits conserved in National Genebank, New Delhi, India**

| Traits | Trait-specific accessions identified | No. of accessions conserved in NGB |
|---|---|---|
| **Biotic Stress** | | |
| Resistant to leaf spot | IC597082 | 1 |
| Resistant to leaf blight | IC512322, IC599586 | 2 |
| Moderately resistant to white rust | IC393729, IC395327, IC393730 | 3 |
| Resistant to root knot nematode | IC598178 | 1 |
| Resistant to stem borer | EC133839 | 1 |
| **Abiotic Stress** | | |
| Drought tolerant and widely adapted lines | IC42258-1, IC303068, IC335807 | 3 |
| Suitable to arid zone | IC586032 | 1 |
| **Total** | | **12** |
| **Quality Traits** | | |
| Oil percentage (6-12.7%) | IC35370, IC35415, IC35433, IC35482, IC35495, IC35496, IC35532, IC38109, IC38129, IC38156, IC38158, IC38192, IC38193, IC38196, IC38201, IC38256, IC38271, IC38281, IC38285 ,IC38289, IC38308, IC38310, IC38316, IC38340, IC38371, IC38375, IC38379, IC38380, IC38386, IC38408, IC38451, IC38456, IC38460, IC38480, IC38487, IC38496, IC38518, IC38522, IC38525, IC38555, IC38556, IC38561, IC42316, IC42328, IC120572, IC309876. | 46 |
| High protein content (11.7-15.95%) | IC16636, IC17926, IC35370, IC35482, IC35495, IC35496, IC35532, IC38129, IC38156, IC38158, IC38192, IC38193, IC38196, IC38201, IC38256, IC38271, IC38281, IC38285, IC38289, IC38308, IC38310, IC38316, IC38340, IC38371, IC38375, IC38379, IC38380, IC38386, IC38408, IC38451, IC38456, IC38460, IC38480, IC38487, IC38496, IC38518, IC38522, IC38525, IC38555, IC38556, IC38561, IC42302, IC42328, IC42258-1, IC120572, IC549660, IC599589, EC170317, EC289389, EC289412, IC309876, EC322032, EC328889, EC359442. | 54 |
| High lysine content (>5.0-7.5 mg/100g) | IC303068(5.23), IC586032 (5.8), IC599589(7.5) | 3 |
| Palmitic acid (15-21%) | IC35678 | 1 |
| Stearic acid (0.7-5.6%) | IC274446 | 1 |
| Linolic acid (41-52%) | IC274445 | 1 |
| **Total** | | **106** |

**Source:** Joshi and Rana, 1991; Gautam *et al*., 2000; Dhillon *et al*., 2001; Dua *et al*., 2009; Joshi *et al*., 2011; Raiger *et al*., 2012, NBPGR Annual Report, 1987, 2005, 2010 and 2013

Amaranth seeds varies from white, gold, brown, pink to black and have great potential for application in various agro-industries such as cosmetic (seed oil is rich in squalene: a cosmetic ingredient), pharmaceuticals (pharmaceutical formulations to reduce the drug dosage and the related side effects), natural dye manufactures (red pigment extracted from red/magenta/brown seed is used as a food dye) and cattle feed (black seeded genotypes). Because of high forage yields, high protein, low levels of oxalates and nitrates in amaranth, there is good scope for its utilization as a promising forage crop (Ahuja *et al*., 1991). In general, cream, white and golden colour seeds are used in culinary preparation. Popped grains are mixed with sugar syrup to prepare laddoo and porridge, which is consumed during fasting in India; it is also used for making chapatti/bread/biscuits, flakes and lysine rich baby foods (Joshi and Rana, 1991). The NGB holds 163 germplasm of *Amaranthus* species of which 103 accessions belong to cream/white/golden colour seeds, followed by 30 of black seed, 26 of red/brown seed and four of purple seed. Many of the identified germplasm are multiple traits and the accessions with more than one trait are repeated against each trait separately. The NGB holds 27 released varieties of *Amaranthus* species of which 14 belong to vegetable type with multi-cut, high leaf yield and suitable for different planting seasons, 12 are of grain type with high yield (12 to 23 q/ha), high protein (13 to 15.95%) and oil content (9.2 to 12%), and one dual purpose variety CO 4 (Table 4). Released varieties constitute 5% of the total conserved germplasm. Analysis of breeding methods of amaranth cultivars revealed that 85 % of them are the result of selection from local germplasm, 7.5% through pure line selection from exotic introduction and merely

**Table 4. Released varieties of *Amaranthus* species conserved in National Genebank, New Delhi, India**

| S.No | National Identity | Name of the variety | Taxonomic status | Year of release | Developing Institute/ University | Trait-specific information |
|---|---|---|---|---|---|---|
| 1. | IC599586 | CO-1 | *A. dubius* Mart. ex Thell. | 1968 | Tamil Nadu Agricultural University (TNAU) Coimbatore, Tamil Nadu, India | Suitable for late harvest, resistant to leaf blight, leaf yield 7.8 t/ha. |
| 2. | IC523790 | CO-2 | *A. tricolor* L. | 1979 | -do- | Suitable for early harvest, leaf-stem ratio 1.8, leaf yield 10.78 t/ha. |
| 3. | IC523791 | CO-3 | *A. tristis* L. | 1988 | -do- | Dwarf and clipping type, 10 clippings in 90 days, good taste and cooking quality, leaf yields 30.72 t/ha. |
| 4. | IC599589 | CO-4 | *A. hypochondriacus* L. | 1989 | -do- | Dual purpose crop, suitable for plains and hill regions of Tamil Nadu, seeds rich in protein (15.95%), lysine (7.5 mg/100g), phenylalanine (5 mg/100g), leucine (1.2 mg/100g) and isoleucine (1.8 mg/100g). |
| 5. | IC599590 | CO-5 | *A. tricolor* L. | 1998 | -do- | High leaf yielding 40 t/ha, suitable for entire Tamil Nadu, suitable for container cultivation. |
| 6. | IC523795 | Arun | *A. tricolor* L. | 1992 | Kerala Agricultural University (KAU), Vellanikkara, Thrissur, Kerala, India | Photo insensitive, leaves red, leaf yield 20 t/ ha. |
| 7. | IC598178 | Renusree | *A. tricolor* L. | 2006 | -do- | Purple stem with low anti-nutritional factors, leaf yield 15.5 t/ha. |
| 8. | IC561286 | Krishnasree | *A. tricolor* L. | 2006 | -do- | Red leaves with high nutritive value and low anti-nutritional factors, leaf yield (14.8 t/ha). |
| 9. | IC612197 | Konkan Durangi | *A. tricolor* L. | 2002 | Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Agricultural University, Dapoli, Ratnagiri Maharashtra, India | Early maturing (80-90 days), high yielding 220 q/ha. |
| 10. | IC612192 | Pusa Lal Chaulai | *A. tricolor* L. | 1993 | ICAR-Indian Agricultural Research Institute (IARI), Pusa, New Delhi, India | Suitable for growing in summer (45 t/ha) and *kharif* (40 t/ha). |
| 11. | IC612194 | Pusa Kiran | *A. tricolor* L. | 1993 | -do- | Suitable for Kharif sowing, broad ovate leaves, first harvest after 21–25 days of sowing, leaf yield 35 t/ha. |
| 12. | IC 612193 | Pusa Kirti | *A. tricolor* L. | 1991 | -do- | Suitable for commercial cultivation in summer, first picking after 30–35 days of sowing, leaf yield 50-55 t/ha. |
| 13. | IC393730 | Arka Arunima | *A. tricolor* L. | 2003 | ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru, Karnataka, India | Multicut variety, leaves broad and dark purple, first picking after 30 days and leaf yield 27 t/ha. |
| 14. | IC393729 | Arka Suguna | *A. tricolor* L. | 2003 | -do- | Multicut variety, 5-6 cuts in 90 days, moderately resistant to white rust, leaf yield 25-30 t/ha |
| 15. | IC555942 | Utkal Mayuri | *A. tricolor* L. | 2007 | Odisha University of Agriculture & Technology (OUAT) Bhubaneswar, Odisha, India | Suitable for summer and *kharif* season, prolonged harvest, good taste and cooking quality. |
| 16. | IC536740 | Kapilasa (BGA-2) | *A. hypochondriacus* L. | 2005 | -do- | Seed yield 13.5 q/ha, matures in 95 days, large inflorescence, non-lodging type and resistant to diseases and pests. |
| 17. | IC42258- 1 | Annapurna | *A. hypochondriacus* L. | 1984 | ICAR-National Bureau of Plant Genetic Resources, Regional Station, Phagli, Shimla, India | Seed yield 22.50 q/ha, high protein content (15%), drought tolerant and widely adapted. |

| S.No | National Identity | Name of the variety | Taxonomic status | Year of release | Developing Institute/ University | Trait-specific information |
|---|---|---|---|---|---|---|
| 18. | IC35407 | Durga | *A. hypochondriacus* L. | 2006 | -do- | Seed yield 21.0 q/ha, tall plants (170 cm), tolerant to lodging, moderately resistance to shattering. |
| 19. | IC335807 | Gujarat Amaranth-1 (GA 1) | *A. hypochondriacus* L. | 1991 | Sardarkrushinagar Dantiwada Agricultural University (SDAU), SK Nagar Banaskantha Gujarat, India | Seed yield 19.50 q/ha, matures in 100-110 days, semi-compact inflorescence. |
| 20. | IC282307 | Gujarat Amaranth-2 (GA 2) | *A. hypochondriacus* L. | 2000 | -do- | Seed yield 23q/ha, matures in 98 days, suitable for rabi season. |
| 21. | IC612195 | Gujarat Amaranth-3 (GA 3) | *A. hypochondriacus* L. | 2008 | -do- | Seed yield 12.58 q/ha, mature in 95-100 days, creamy white seeds; 1000-seed weight (0.80g). |
| 22. | IC303068 | Suvarna | *A. hypochondriacus* L. | 1992 | University of Agricultural Sciences (UAS), GKVK, Bangalore, India | Seed yield 16.0 q/ha, photo insensitive and grown throughout the year and early maturing type (80-90 days). |
| 23. | IC549660 | PRA 1 (Pant Rani Amaranth 8801) | *A. hypochondriacus* L. | 1997 | G.B. Pant University of Agriculture & Technology, Hill Campus Ranichauri, Tehri Garhwal, Uttrakhand, India | Seed yield 14.5 q/ha, bold creamish yellow seeds, rich in protein (13-14 %) and oil content (9.2 %). |
| 24. | IC309876 | PRA-2 (Pant Rani Amaranth-2) | *A. hypochondriacus* L. | 2000 | -do- | Seed yield 14.5 q/ha, rich in protein (14-15%) and oil content (12.0 %). |
| 25. | IC512322 | PRA-3 (Pant Rani Amaranth-3) | *A. hypochondriacus* L. | 2003 | -do- | Seed yield 16.5 q/ha, field tolerance to major pests and diseases including *Rhizoctonia* sp. |
| 26. | IC564887 | RMA- 4 (Rajasthan Mandor Amaranth 4) | *A. hypochondriacus* L. | 2008 | Agricultural Research Station, Rajasthan Agricultural University Mandor, Jodhpur, Rajasthan, India | Seed yield 13.90 q/ha, matures in 122 days and light green inflorescence. |
| 27. | IC586032 | RMA-7 (Rajasthan Mandor Amaranth 7) | *A. hypochondriacus* L. | 2008 | -do- | Seed yield 14.66 q/ha and highly productive under irrigated condition of arid zone. |

7.5% through hybridization. The most probable reason could be the out crossing nature of the crop (20-25%), which generates lot of variability in the germplasm leads to selection.

Indian Council of Agricultural Research (ICAR) has established a mechanism to register the trait-specific germplasm through ICAR-NBPGR in 1996 (Singh, 2006; Tyagi and Kak, 2012), to facilitate the flow of germplasm among the scientists working in crop improvement programme. Two accessions of *A. tricolor* are registered under this mechanism for the traits, thick stem type (Dantu Soppu; IC395324) and resistance to white rust (IC395327). These are also conserved in NGB for use in future breeding.

## Future Thrust

*Amaranthus* is a wide taxonomic group with large diversity of species showing a greater range of adaptation and also exhibits up to 25% of out-crossing in nature (Walton, 1968). These events can be exploited for genetic enhancement for nutritional characters and to achieve good combinations of gene complexes to develop composite or synthetic varieties. It is important to improve the traits such as dwarfness, early maturity, resistance to lodging, non-shattering and bold seeded genotypes through breeding programmes. Development of new varieties to combat climate change as well as nutritional (cheap, alternative rich source of protein and nutrient) requirement of ever increasing population should

be the target of future breeding programmes. NGB at ICAR-NBPGR conserves and distribute the potentially valuable germplasm to the farmers and breeders to popularise the same and their use in crop improvement programmes. Therefore, information available in this paper will facilitate the utilization of trait-specific germplasm conserved in the NGB by breeders in crop improvement programmes.

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# Genetic Variability and Correlation Analysis in Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] under Drought Stress

**Raju Lal Meena[1], JS Chauhan[2*], KH Singh[1] and SS Rathore[1]**
[1] *ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur-321303, Rajasthan, India*
[2*] *Indian Council of Agricultural Research, Krishi Bhawan, Dr. Rajendra Prasad Road, New Delhi-110001, India*

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Genetic variation study in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] revealed low phenotypic and genotypic variability for days to maturity and oil content but substantial for secondary branches/plant, biological yield/plant, seed yield/plant, plant height, primary branches/plant and siliquae on main shoot. The seed weight had high heritability with high genetic advance implying that additive gene effects were mainly responsible for the expression of the character. Seed yield/plant was positively and significantly correlated at both phenotypic and genotypic levels with days to maturity, plant height, primary branches/plant, secondary branches/plant, siliquae on main shoot and biological yield/plant. Selection for higher 1000-seed weight would bring forth positive correlated response in oil content owing to its positive genetic correlation with oil content. Indirect selection for high oil content through seed size might reduce siliquae on main shoot due to its negative genetic correlation of moderate magnitude with oil content. Positive association of days to maturity and plant height with seed yield is undesirable; therefore, efforts should be made to break this linkage by resorting to bi-parental mating to breed for varieties having earliness, short plant stature and high oil content in *Brassica juncea*.

**Key Words: *B. juncea*, Drought stress, Genetic advance, Genetic variability, Genotypic correlations, Indian mustard, Seed yield**

## Introduction

Rapeseed-mustard group of crops require low water (80-240 mm) and thus fits well in the rainfed cropping system, which accounts for 30% of the total cropped area in the country under these crops. Seed yield is a complex character and *per se* doesn't have major genes and largely influenced by components characters (Meena *et al*., 2006; Singh *et al*., 2006; Brar *et al*., 2007; Misra *et al*., 2007b). Yield improvement in Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is primarily dependent on nature and magnitude of genetic variability for component characters. The genetic variability coupled with heritability helps in the identification of the characters that offer scope for improvement through selection and predict the expected gain. Information on interrelationship among the yield components enables choosing appropriate selection criteria for yield improvement. Pleiotropic action of genes and/or linkage determines the inherent association between any two variables (Falconer, 1989). Studies on these aspects under drought stress is limited in Indian mustard (Mondal and Khajura, 2000; Tyagi and Chauhan, 2003). The present study was under taken to assess extent and nature of variability for seed yield and its components, their *inter se* associations to identify appropriate selection criteria for yield enhancement under drought stress in *B. juncea*.

## Materials and Methods

The materials for the present investigation comprised of 16 advanced breeding lines and 6 varieties of Indian mustard grown in a randomized complete block design with three replications under rainfed conditions during *rabi s*eason of 2007-08. There were 4 rows of 4 m length for each genotype in a block. The row spacing was 30 cm and plant spacing within a row was maintained at 10 cm by thinning. A fertilizer dose of 40:20:20 kg/ha ($N:P_2O_5:K_2O$) was applied at the time of sowing. Soil moisture content was recorded from the time of sowing till maturity at an interval of 15 days at 3 depths (15, 30 and 60 cm) using gravimetric method. The soil samples were dried in an oven at 75±2°C for at least 72 hrs till constant weight was achieved. The soil moisture content was expressed in percentage on wet basis. Days to maturity was recorded on plot basis. At the time of harvest, 10 random competitive plants were taken from the middle row to record plant height (cm), primary branches/plant (no.), secondary branches/plant (no.), main shoot length

*Author for Correspondence: E-mail: adgseedicar@gmail.com

(cm), siliquae on main shoot (no.), siliqua length (cm), seeds/siliqua (no.), 1000-seed weight (g) and seed yield/plant (g). Oil and protein content were recorded on a composite sample of 10 plants taken for recording seed yield using Near Infrared Reflectance Spectroscopy (Kumar *et al*., 2003).

The data were subjected to analysis of variance according to the procedure outlined by Panse and Sukhatme (1967). Phenotypic and genotypic coefficients of variation were calculated following the method of Burton (1952). Heritability in broad sense ($h^2_b$) and expected genetic advance at 5% selection intensity were calculated following the methods of Hanson (1963) and Johnson *et al.* (1955), respectively. The correlation coefficients at phenotypic ($r_{pxy}$) and genotypic ($r_{gxy}$) level among different characters were computed according to the methods suggested by Searle (1971).

## Results and Discussion

### *Soil Moisture Content*

There was steady and rapid decline in soil moisture content at all the three soil depths up to 65 days after sowing (DAS) coinciding with 50% flowering in majority of the genotypes. The soil moisture content at this time reached 4.6%, 5.6 % and 7.4% at 15, 30 and 60 cm, respectively. Thereafter, the moisture content stabilized and showed gradual decline. The reduction in soil moisture content from 65 DAS till the time of harvest was only 1.6% at 15 cm, 0.6% at 30 cm and 1.4% at 60 cm.

### *Analysis of Variance*

Analysis of variance revealed highly significant genotypic differences for days to maturity, plant height, and siliquae on main shoot, siliqua length, 1000-seed weight, seed yield/plant and oil content. The genotypic differences were significant for primary branches/plant, secondary branches/plant, seeds/siliqua and biological yield/plant (Table 1). Non-significant genotypic differences were recorded for main shoot length, harvest index, protein content and seed:husk ratio. Hence these characters were excluded from further discussion.

### *Range and Variability*

The oil content and secondary branches/plant, respectively, showed lowest and highest PCV and GCV (Table 2). The PCV >35%, 25-35% and < 25% were classified as high, moderate and low, respectively and GCV > 20%,10-20% and < 10% were categorized as high, moderate and low, respectively. The genotype BPR-542-6 was the earliest to mature (125 days) and BPR-549-9 being the latest maturing genotype (139.7 days). The PCV and GCV were low for days to maturity. The genotype RH-819 had the tallest plants whereas; Rohini showed the shortest plant stature among the genotypes. The PCV and GCV were 19.0% and 11.1%, respectively. Primary branches/plant ranged from 3.7 (BPR-542-6) to 5.7 (BPR-543-2) and showed low PCV and GCV (Table 2). The minimum (1.3) and the maximum secondary branches/plant (5.9) were recorded for the genotype BPR-542-6 and RCC-4, respectively. The PCV and GCV were the highest among

**Table 1. Analysis of variance for seed yield and other agro-morphological characters in Indian mustard under drought stress**

| Character/degree of freedom | Source of variation (Mean sum of squares) | | | SEM (±) | CD (5%) |
|---|---|---|---|---|---|
| | Replication | Genotype | Error | | |
| | 2 | 21 | 42 | | |
| Days to maturity | 35.64 | 108.96** | 13.14 | 2.05 | 5.97 |
| Plant height | 1837.81* | 1041.59** | 405.46 | 11.36 | 33.18 |
| Primary branches/plant | 0.53 | 0.60* | 0.32 | 0.32 | 0.93 |
| Secondary branches/plant | 5.37 | 5.00* | 2.30 | 0.86 | 2.50 |
| Siliquae on main shoot | 69.37* | 37.96** | 15.14 | 2.19 | 6.41 |
| Siliqua length | 0.13* | 0.15** | 0.03 | 0.10 | 0.30 |
| Seeds/siliqua | 1.91 | 1.36* | 0.64 | 0.46 | 1.32 |
| 1000-seed weight | 0.02 | 0.62** | 0.04 | 0.12 | 0.34 |
| Biological yield/plant | 214.36** | 84.12* | 40.47 | 3.59 | 10.48 |
| Seed yield/plant | 14.84* | 7.54** | 2.98 | 0.97 | 2.84 |
| Oil content | 0.03 | 0.91** | 0.35 | 0.34 | 0.98 |

*, **: Significant at 5% and 1% probability level, respectively.

**Table 2. Range, mean, phenotypic (PCV) and genotypic coefficient of variability (GCV), heritability and genetic advance for seed yield and other agro-morphological characters in Indian mustard under drought stress**

| Character | Range | Mean ± SEM | PCV (%) | GCV (%) | Heritability (%) | Genetic advance | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|
| Days to maturity | 125.0 -139.7 | 131.8 ± 2.1 | 5.1 | 4.3 | 70.9 | 980.0 | 7.4 |
| Plant height (cm) | 97.3 - 161.0 | 131.0 ± 11.6 | 19.0 | 11.1 | 34.3 | 1757.8 | 13.4 |
| Primary branches/plant (no.) | 3.7 - 5.7 | 4.4 ± 0.3 | 14.7 | 7.0 | 22.7 | 300.9 | 6.9 |
| Secondary branches/plant (no.) | 1.3 - 5.9 | 3.2 ± 0.9 | 55.8 | 29.6 | 28.1 | 103.5 | 32.3 |
| Siliquae on main shoot (no.) | 25.5 - 40.5 | 33.4 ± 2.2 | 14.3 | 8.2 | 33.5 | 328.6 | 9.8 |
| Siliqua length (cm) | 3.4 - 4.1 | 3.8 ± 0.1 | 7.0 | 5.2 | 54.7 | 30.8 | 7.9 |
| Seeds/siliqua (no) | 12.9 -15.9 | 13.9 ± 0.1 | 6.8 | 3.5 | 27.2 | 52.6 | 3.8 |
| 1000-seed weight (g) | 3.8 - 5.2 | 4.6 ± 0.1 | 10.6 | 9.6 | 82.0 | 82.1 | 17.9 |
| Biological yield/plant (g) | 9.9 - 29.2 | 18.9 ± 3.7 | 39.3 | 20.2 | 26.4 | 404.0 | 21.4 |
| Seed yield/plant (g) | 3.1 - 9.1 | 6.0 ± 1.0 | 35.6 | 20.7 | 33.8 | 147.8 | 24.8 |
| Oil content (%) | 42.4 - 43.9 | 43.1 ± 0.5 | 1.7 | 1.0 | 34.1 | 50.9 | 11.8 |

the characters studied. Siliquae on main shoot showed low phenotypic and genotypic variations. Rohini and BPR-538-12 had the lowest and the highest siliquae on main shoot, respectively. The GCV (3.5%) and PCV (6.8%) were the lowest for seeds/siliqua except for days to maturity and oil content. The genotype BPR-541-2 (12.9) and BPR-543-2 (15.9) had the minimum and maximum seeds/siliqua. The 1000-seed weight ranged from 3.8 (BPR-542-14)-5.2 g (BPR-549-2) with low phenotypic and genotypic variability.

The biological yield/plant had relatively high PCV and GCV. The genotype BPR-349-9 had the highest seed yield/plant (9.1g) whereas, the genotype BPR-542-6 showed the lowest (3.1g) with an overall mean of 6.0 ± 1.0 g. It had high phenotypic and genotypic variability (Table 2).The minimum (42.4%) and maximum (43.9%) oil content was recorded in the genotype BPR-538-12 and BPR-125-1, respectively and the character had the least variability. Seed yield, being a complex character and influenced by several quantitatively inherited characters, hence direct selection for seed yield is not usually very effective. Chauhan *et al.* (2000) also reported considerable variability for seed yield/plant, secondary branches/plant and siliquae on main shoot under rainfed conditions. Grafius (1964) suggested component(s) selection to improve seed yield. Appreciable variability was present for seed yield, secondary branches/plant, biological yield/plant, plant height, primary branches and siliquae on main shoot. Moderate to high variability available in the present materials could be quite useful for selection. The results of the present investigation concerning low variability for oil content and days to maturity were in agreement with the earlier reports (Chauhan *et al.*, 2000; Meena *et al.*, 2006). Therefore, these characters had limited scope of improvement through selection due to lack of enough variability in the experimental materials.

### *Heritability and Genetic Advance*

The heritability estimates ranged from 22.7% for primary branches/plant to 82.1% for 1000-seed weight. The expected genetic advance varied from 3.8% (seeds/siliqua) to 32.3% (secondary branches/plant). The heritability >70%, 50-70% and <50% were classified as high, moderate and low, respectively and the genetic advance was categorized as high (>20%), moderate (10-20 %) and low (<10%). Although days to maturity had high heritability but the genetic advance was low. Plant height exhibited low heritability accompanied by moderate genetic advance. The estimates for both heritability and genetic advance were low for primary branches/plant. Secondary branches/plant had low heritability with highest genetic advance (Table 2). Low heritability coupled with low genetic advance was recorded for siliquae on main shoot. Siliqua length had moderate heritability but low genetic advance. Both heritability and genetic advance were low for seeds/siliqua. The highest heritability for 1000-seed weight was associated with moderate genetic advance. High genetic advance was accompanied by low heritability for biological yield/plant and seed yield/plant. Oil content had low heritability as well as low genetic advance.

Success of selection in improving a character depends on both extent of variability and heritability estimate. The seed weight had high heritability and high genetic advance implying that additive gene effects were mainly

**Table 3. Phenotypic and genotypic correlation coefficients of seed yield and other agro-morphological characters in Indian mustard under drought stress**

| Character | PH | PB | SB | SMS | SL | SS | SW | BY | SY | OC |
|---|---|---|---|---|---|---|---|---|---|---|
| DM | 0.595** | 0.160 | 0.174 | 0.461* | 0.161 | -0.024 | 0. 307 | 0.538** | 0.539** | -0.059 |
| | **0.661** | **0.587** | **0.439** | **0.449** | **0.183** | **- 0.274** | **0. 354** | **0.863** | **0.816** | **-0. 313** |
| PH | | 0.336 | 0.386 | 0.841** | 0.263 | 0.052 | 0.184 | 0.795** | 0.751** | 0. 033 |
| | | **1. 347** | **1.054** | **0.894** | **0.041** | **-0.451** | **0.147** | **0.971** | **0.956** | **-0. 399** |
| PB | | | 0.631** | 0.374 | 0.113 | 0.268 | 0.050 | 0.533* | 0.588** | -0.194 |
| | | | **0.456** | **0.914** | **0.174** | **0.241** | **0.125** | **0.886** | **0.963** | **-0. 066** |
| SB | | | | 0.596** | 0.074 | 0.148 | 0.064 | 0.688** | 0.717** | -0.084 |
| | | | | **1.048** | **0.066** | **-0.127** | **-0.158** | **0.875** | **0.799** | **-0. 078** |
| SMS | | | | | 0.063 | 0.108 | 0.085 | 0.786** | 0.762** | -0.074 |
| | | | | | **-0.096** | **-0.672** | **-0.057** | **0.738** | **0.751** | **-0.455** |
| SL | | | | | | 0.216 | 0.386 | 0.269 | 0.240 | 0.059 |
| | | | | | | **0.313** | **0.594** | **0.351** | **0.274** | **- 0.339** |
| SS | | | | | | | 0.272 | 0.171 | 0.198 | -0.040 |
| | | | | | | | **0.294** | **-0.251** | **-0.132** | **-0. 285** |
| SW | | | | | | | | 0.238 | 0.226 | -0.353 |
| | | | | | | | | **0.256** | **0.228** | **0.562** |
| BY | | | | | | | | | 0.955** | -0.075 |
| | | | | | | | | | **0.998** | **- 0.348** |
| SY | | | | | | | | | | -0.123 |
| | | | | | | | | | | **-0.335** |

*, **: Significant at 5% and 1% probability level, respectively. Values in light and bold face are correlation coefficients at phenotypic and genotypic level, respectively. DM: Days to maturity; PH: Plant height; PB: Primary branches/plant ;SB: Secondary branches/plant; SMS: Siliquae on main shoot; SL: Siliqua length; SW: 1000-seed weight; BY: Biological yield/plant; SY: Seed yield/plant and OC: Oil content

responsible for the expression of these characters. Low heritability with low, moderate and high genetic advance or *vice versa* for days to maturity, plant height, primary branches/plant, secondary branches/plant, siliquae on main shoot, siliqua length, seeds/siliqua, biological yield/plant and oil content were indicative of predominant role of non-additive gene action in their inheritance and thus simple selection for improvement may not be effective. Moderate to high heritability and genetic advance for 1000-seed weight was also reported by Meena *et al.* (2006) whereas, Brar *et al.* (2007) observed high heritability coupled with low genetic advance.

### *Correlation Coefficients*

Genotypic correlations for seed yield and other characters were invariably higher than phenotypic correlations (Table 3). The high magnitude of genotypic correlation coefficients form sound base for their practical implications. The results of the present study are in agreement with earlier studies (Kumar *et al.,* 1999). Both correlations were in the same direction except for seeds/siliqua with plant height and siliqua length where genetic correlations were high and negative but phenotypic correlations were non-significant. Similarly, oil content had low/moderate negative genotypic correlations with plant height, siliquae on main shoot and seeds/siliqua but no correlation at phenotypic level. It also had positive correlation of moderate magnitude with biological yield at genotypic level.

### *Phenotypic Correlations*

Days to maturity and plant height were positively and significantly interrelated with each other. Biological yield/plant ($r_{pxy}$ = 0.538**) and siliquae on main shoot ($r_{pxy}$ = 0.461*) also had significant association with days to maturity. Positive and highly significant association of plant height with siliquae on main shoot and biological yield/plant was recorded. The relationship of primary branches/plant with secondary branches/plant and biological yield/plant was positive. However, the interrelationship of secondary branches/plant with siliquae on main shoot and biological yield/plant was positive and significant (Table 3). Positive and significant phenotypic correlation ($r_{pxy}$ = 0.786**) was also recorded between siliquae on main shoot and biological yield. Seed yield/plant was positively and significantly correlated with days to maturity, plant height, primary and secondary branches/plant, siliquae on main shoot and biological yield/plant (Table 3).

### *Genotypic Correlations*

The genotypic correlations were categorized as low (r < 0.400) moderate (r = 0.400-0.680) and high (r > 0.680). Seed yield/plant had high positive correlation with days to maturity, plant height, primary branches/plant, secondary branches/plant, siliquae on main shoot and biological yield/plant. The relationship between seed yield and oil content was negative (Table 3). Days to maturity and plant height were also correlated positively with each other, similarly days to maturity had high association with biological yield/plant and primary branches/plant. The association of days to maturity with other characters was positive and moderate except with oil content ($r_{gxy}$ = -0.313) and seeds/siliqua ($r_{gxy}$ = -0.274) where the correlations coefficient were negative. Plant height had high and positive correlation coefficients with siliquae on main shoot and biological yield/plant. The negative and moderate association of oil content and seeds/siliqua with plant height was also observed.

Primary branches and secondary branches/plant had high positive correlation with plant height, the correlation coefficient being 1.347 and 1.054, respectively. The relationship of primary branches/plant was positive and moderate with secondary branches/plant. The association of primary branches/plant with biological yield and siliquae on main shoot were positive and high (Table 3). A high and positive relationship of secondary branches/plant was also observed with siliquae on main shoot ($r_{gxy}$ = 1.048), biological yield/plant ($r_{gxy}$ = 0.875) and seed yield/plant ($r_{gxy}$ =0.799).The genetic correlation between siliquae on main shoot and biological yield/plant was high and positive whereas such correlation between oil content and siliquae on main shoot was negative and moderate ($r_{gxy}$ = -0.455). Siliqua length had positive association of low to moderate ($r_{gxy}$ = 0.274-0.594) strength with seeds/siliqua, 1000- seed weight, seed yield/plant and biological yield/plant but its association with oil content was negative and moderate ($r_{gxy}$ = -0.339). Seeds/siliqua had low and negative genetic correlation with oil content and biological yield/plant but low and positive association was observed with 1000-seed weight ($r_{gxy}$ = 0.294). Positive genetic correlation of moderate strength was recorded between 1000-seed weight and oil content. Further, 1000-seed weight had low positive association with biological yield/plant and seed yield/plant. Seed yield/plant was positively and significantly correlated at both phenotypic and genotypic levels with days to maturity, plant height, primary branches/plant, secondary branches/plant, siliquae on main shoot and biological yield/plant. Biological yield/plant showed positive and significant correlations with days to maturity, plant height, primary and secondary branches/plant and siliquae on main shoot. The results are in agreement with earlier reports (Kardam and Singh, 2005; Singh *et al*., 2006; Misra *et al*., 2007a; Patel *et al*., 2003). Singh *et al.* (1987) observed that oil content and seed weight were positively and significantly correlated. But all these studies were carried out under irrigated conditions.

The studies revealed that selection for higher 1000-seed weight would bring forth positive correlated response in oil content owing to their positive genetic correlations. Nevertheless, it might also result in reduction in siliquae on main shoot due to its negative genetic correlation of moderate magnitude with siliquae on main shoot, but this effect could be offset by selection for more branches/plant. Hence the number of siliquae/plant should be emphasized in selection programme rather than siliquae on main shoot. Considering the results of the present investigation it is concluded that donors with multiple determinants of seed yield like days to maturity, plant height, more primary and secondary branches/plant and high biological yield/plant should be used in the breeding programme for genetic enhancement of seed yield. However, a balance has to be struck between plant height, days to maturity and seed yield because of their positive associations suggesting that late maturing and very tall genotypes would have high seed yield while early maturity is a desirable character under drought stress. Therefore, efforts should be made to break these undesirable linkages by resorting to bi-parental mating.

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# Agri-biodiversity Maintained On-farm by Ethnic Groups in Peninsular India: Legacy of Landrace Sustainability in Cereals and Millets

**SR Pandravada[1*], N Sivaraj[1], R Jairam[1], N Sunil[1], SK Chakrabarty[1], R Eshwar Charan[2], P Ramesh[2] and IS Bisht[3]**

[1] *National Bureau of Plant Genetic Resources, Regional Station, Rajendranagar, Hyderabad-500030, Andhra Pradesh, India*

[2] *Acharya N.G.Ranga Agricultural University, Krishi Vigyana Kendra, Adilabad-504001, Andhra Pradesh, India*

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

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The on-farm sustainability of landrace diversity of cereal and millet genetic resources covering 10 crop species was analyzed for Adilabad, Andhra Pradesh, India. It was assessed based on 14 special agri-biodiversity surveys undertaken during 2010-12 for collection and salvaging the current spectrum of genetic diversity from the district. A total of 447 accessions belonging to landrace populations of cereals (172), millets (195) and small millets (80) could be collected during the missions which formed the source of the inventory documentation. In all, 88 named landraces, maximum represented by sorghum (45) and rice (18) could be collected. It was interesting to note that a number of landrace populations collected from the district during early nineties, 81 in rice, 43 in sorghum and three in wheat could not be recollected as these traditional varieties are no longer under cultivation. However, 16 landraces in sorghum and 12 in rice are under continuous patronage of the farming communities for livelihood reasons. A total of 48 new landraces: six in rice, 29 in sorghum, 10 in maize and three in wheat which were not collected earlier could be augmented due to intensive surveying in remote tribal pockets. The data documented is useful for proper planning and adopting appropriate strategies for crop genetic resources management at micro-level in the region and also devising a rational conservation plan, both *ex-situ* and on-farm.

**Key Words: Agri-biodiversity, Landraces, On-farm conservation, Sustainability**

Agri-diversity refers to inter and intra-specific variability in different crops that are used directly or indirectly for food, fodder, fibre, fuel and medicine. The role of agri-diversity is immense as elucidated by Thrupp (1997) which can "increase productivity, food security and economic returns, reduce the pressure of agriculture on fragile areas, forests, endangered species, make farming systems more stable, robust and sustainable, conserve soil and increase natural soil fertility and health, contribute to sustainable intensification, diversify products and income opportunities, reduce or spread risks to individuals and nations, help maximize effective use of resources and the environment, reduce dependency on external inputs, improve human nutrition and conserve ecosystem structure and stability of species diversity". The existing indigenous food production systems are under severe threat which has a bearing on local knowledge, culture and skills of tribal farmers resulting in fast erosion of landrace diversity. The degree of loss is largely extensive as more than 75% of diversity in crop genetic resources has been on the wane since 1900s. This can be attributed to farmers' abandoning their local landraces and traditional cultivars with genetically uniform and high-yielding varieties worldwide (FAO, 1999).

Adilabad is the fifth largest district in Andhra Pradesh State, India, which lies between 18° 40' and 19° 56' N latitudes and 77° 47' and 80° 00' E longitudes with a total geographical area of 16,128 sq.km which is quite a large area when compared to many of the small nations in Africa, Americas, Asia, Europe and Middle East. It is bounded by Yeotmal and Chandrapur districts in the North, Chandrapur in the East, Karimnagar and Nizamabad in the South and by Nanded district in the West. Adilabad is administratively divided into 52 mandals with 15 towns and 1,752 revenue villages and is also covered up to 44.8% area mostly by dry deciduous forests. About 65% of the district is inhabited by tribal groups to an extent of 17.8 % of the total population (second in the State of Andhra Pradesh) with Gond, Naikpod, Kolam (Primitive Tribal Group (PTG)), Pardhan, Koya, Manne, Andh, Thoti (PTG), Lambada and Yerukala, as the major groups. The tribal population is dominated by the *Gond* (52%), *Lambada*

*Author for Correspondence: E-mail: pandravadasr@yahoo.com

(22%), *Kolam* (8%) and others (*Naikpod, Koya, Andh, Manne, Pardhan* and *Porja*- 8%). The most important river that traverses the district is the Godavari with Penganga, Wardha, Pranahita, Kadem and Peddavaagu as the tributaries and the rivulets flowing through are Satnala, Swarna and Suddavaagu. The major crops of the district are rice, sorghum, cotton, pigeon pea, maize and soybean, etc. Very deep black cotton soils are predominant and also found are *chalkas*, red and sandy loams. The average annual rainfall ranges between 700 to 1,200 mm, mostly precipitated during the south-west monsoon. The minimum and maximum temperatures range between 5 to 52 °C (Anonymous, 2005 and Pandravada *et al*., 2012).

To arrest the alarming rate of depletion of local landraces, appropriate plant genetic resources (PGR) management strategies are to be adopted to mitigate the situation. The proper management strategy calls for inventorization of information from various sources including that of germplasm exploration and collection, conservation and documentation etc. In this regard, an attempt has been made to prepare the agri-biodiversity inventory, especially with respect to cereal and millet crops of tribal dominated Adilabad district of Andhra Pradesh, India based on extensive passport data generated during 14 biodiversity surveys undertaken in the district. It is hoped that the generated information would be highly useful for micro-level planning for sustainable PGR management, the results of which could be extrapolated to other parts of the country as well.

## Materials and Methods

A total of 14 agri-biodiversity surveys were undertaken during 2010-12 in 187 villages belonging to 52 mandals (District sub-units) of Adilabad district of Andhra Pradesh for collection, conservation, inventorization and documentation of agri-biodiversity in general and of cereals, millets and small millets in particular (Fig. 1). Under cereals, rice, wheat and maize, under millets sorghum and pearl millet and under small millets, Italian millet, little millet, proso millet, barnyard millet and kodo millet are the important crops under cultivation.

To conserve the prevailing genetic diversity in cereals, millets and small millets, population samples of germplasm were collected from tribal farmers' fields, threshing yards, farm stores and also augmented from the market. The overall collection tactics and logistics were taken into consideration as suggested by Astley (1991) and Bennett (1995). Garmin-12 model of Global Positioning System (GPS) was used to record the geographical coordinates of the collection sites.

The germplasm collections were properly cleaned, processed and packed in aluminium foil pouches for medium-term conservation in the MTS Module facility at the Station. An inventory of cereals, millets and small millets landrace diversity was prepared based on the germplasm collection missions organized and passport data recorded and the same is summarized in this paper.

## Results

During the 14 intensive collection missions organized in Adilabad, a total of 447 germplasm accessions belonging to cereals, millets and small millets could be sampled from tribal farmers' dwellings in 47 mandals (District sub-units). No landrace diversity could be recorded and collected under cereals and millets from the remaining five mandals (Dandepally, Laxmanchanda, Lokeshwar, Mandamarri and Tandur). Of the 10 crops belonging to cereals, millets and small millets, maximum crops could be collected from Sirpur (U) (9) mandal and maximum accessions from Kerameri (35) mandal. The ethnic groups associated with the origin, evolution, domestication and on-farm conservation of named landraces include, *Andh, Gond, Kolam, Koya, Lambada* and *Nayakpod*.

The tribal groups that contributed maximum to landraces are the Gond (59) and the Kolam (16). The landraces collected could be broadly categorized into two groups *viz.* named and unnamed landraces, characterized by distinct phenotypic traits which are under the patronage of ethnic groups. With respect to named landraces, maximum could be collected in sorghum (45) followed by rice (18) and no named landraces could be collected in crops pearl millet, barnyard millet, kodo millet and proso millet under the millets and small millets groups.

The inventory of landrace diversity augmented in all the three crop groups from the district is presented in Table 1. The distribution of diversity mandal-wise and crop-wise and landraces sampled under cereals, millets and small millets from the district is presented in Table 2. The diversity spectrum of collections made under cereals, millets and small millets crop groups is depicted in Fig. 2. The cereals contributed 38.5% of the total diversity assembled while the rest 61.5% was contributed by the millets and small millets. With respect to number of landraces, sorghum topped the list with

**Table 1. Inventory of cereals, millets and small millets diversity and named landraces collected from Adilabad, Andhra Pradesh**

| Crop group/ Crop | Diversity collected (No. of accessions) | Named Landraces collected (No.) | Landrace name |
|---|---|---|---|
| **Cereals** | | | |
| Rice | 66 | 18 | *Akasavai vadlu, Budamavanji, Chittimutyalu, Chittiporu, Dasara vadlu, Davaralvanji, Erra vadlu, Gowrani vadlu, Kakirekkala vadlu, Nalla vadlu, Pandadivanji, Pandrisadi, Pisodi vadlu, Polala vadlu, Puraval, Ragalvanji, Regadi vadlu, Tella vadlu* |
| Maize | 89 | 10 | *Chinna makka, Gangatriyulu, Gowrani makka, Gundu makka, Local makka, Pedda makka, Pelala makka, Popcorn makka, Ragal makka, Somaram makka* |
| Wheat | 17 | 3 | *Erra godhuma, Metta godhuma, Rabi godhuma* |
| **Millets** | | | |
| Sorghum | 188 | 45 | *Aragidi jonna, Badigi jonna, Boda jonna, Chikkati jonna, Chinna jonna, Chinnaboda jonna, Dambral, Darawat jonna, Deyam jonna, Dhane jowar, Erra jonna, Gadda jonna, Gundu jonna, Gunjidi jonna, Gunjidipedda jonna, Guvvi jonna, Jalleda jonna, Kathani jonna, Konkadala jonna, Leha jonna, Mudda jonna, Pachchaboda jonna, Pala jonna, Pandari jonna, Pandimutte jonna, Parasa jonna, Pasupu jonna, Pasupupachcha jonna, Pedda jonna, Pelala jonna, Potiki jonna, Purabodaka jonna, Pyru jonna, Rabi jonna, Sanna jonna, Sevata jonna, Sivira jonna, Talki jonna, Tekedari jonna, Tella jonna, Tellaboda jonna, Varagadi jonna, Vayunowka jonna, Vubiripatti jonna, Vullipitta jonna* |
| Pearl millet | 7 | – | – |
| **Small millets** | | | |
| Italian millet | 44 | 9 | *Amba korra, Chikto, Erra badi, Erra burakalu, Karri badi, Nalla badi, Nalla burakalu, Sivera korra, Tella burakalu* |
| Little millet | 12 | 3 | *Badhali, Erra sama, Ragal sama* |
| Barnyard millet | 20 | – | – |
| Proso millet | 2 | – | – |
| Kodo millet | 2 | – | – |
| **Total** | 447 | 88 | |

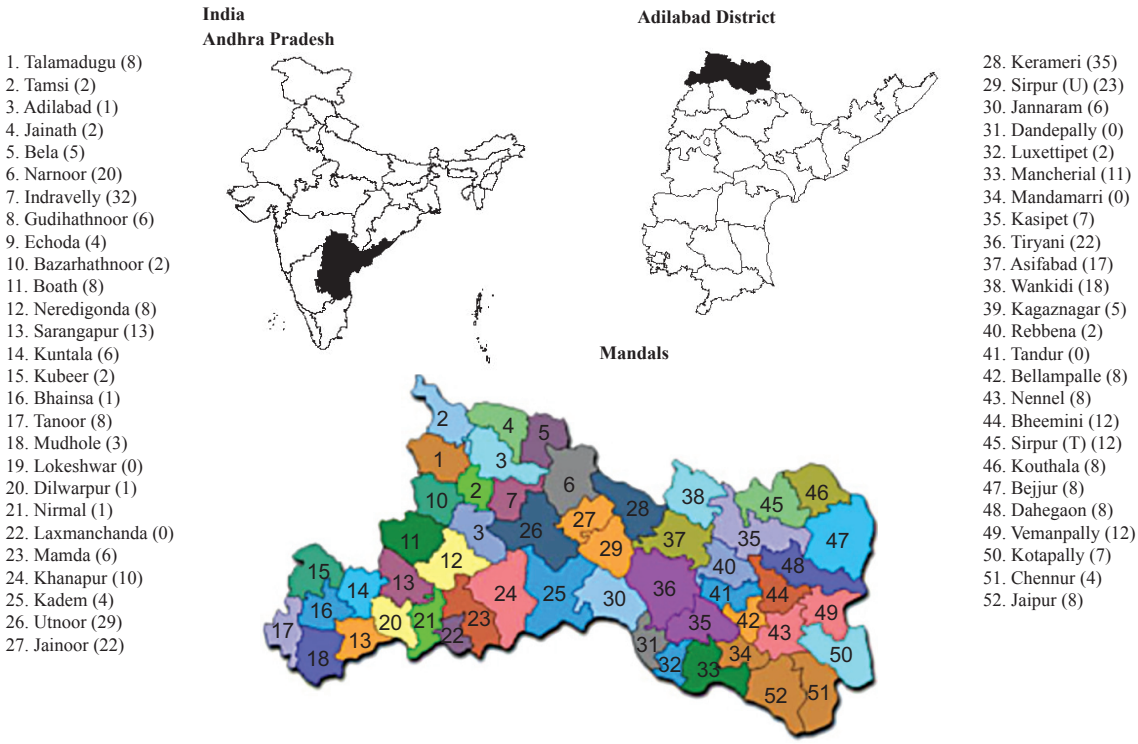


**Fig. 1. Map of Study Area (Adilabad district with 52 mandals)**

• *Values in parentheses indicate the numbers of germplasm accessions collected under cereals and millet from the respective Mandal*

**Table 2. Distribution of cereals, millets and small millets diversity (mandal wise and cropwise) in Adilabad, Andhra Pradesh**

| Mandal | Crop (No. of named landraces salvaged) | Total diversity collected (No. of accs.) |
|---|---|---|
| Adilabad | Maize (1) | 1 |
| Asifabad | Sorghum (7) | 17 |
| Bazarhathnoor | Rice (2) | 2 |
| Bejjur | Rice (1), Wheat (1), Maize (1), Sorghum (2) | 8 |
| Bela | Maize (1), Sorghum (1), Wheat (1) | 5 |
| Bellampalli | Rice (1), Maize (1), Sorghum (3) | 8 |
| Bhainsa | Rice (1) | 1 |
| Bheemini | Rice (2), Maize (1), Sorghum (6) | 13 |
| Boath | Maize (2), Sorghum (3) | 8 |
| Chennur | Rice (1), Maize (1), Sorghum (1) | 4 |
| Dahegaon | Rice (1), Maize (1), Sorghum (2) | 8 |
| Dilwarpur | Wheat (1) | 1 |
| Echoda | Rice (2), Sorghum (1) | 4 |
| Gudihathnoor | Rice (1), Sorghum (2), Wheat (1), Italian millet (1) | 6 |
| Indravelly | Rice (5), Maize (1), Sorghum (8), Italian millet (3) | 32 |
| Jainath | Rice (1), Sorghum (1) | 2 |
| Jainoor | Rice (4), Maize (2), Sorghum (7) | 22 |
| Jaipur | Maize (1), Sorghum (3) | 8 |
| Jannaram | Wheat (1), Maize (1), Sorghum (3) | 6 |
| Kadem | Rice (1), Maize (1) | 4 |
| Kagaznagar | Maize (1), Sorghum (1) | 5 |
| Kasipet | Maize (1), Sorghum (4) | 7 |
| Kerameri | Rice (2), Maize (2), Sorghum (8) | 35 |
| Khanapur | Wheat (2), Maize (3), Sorghum (4) | 10 |
| Kotapally | Maize (2), Sorghum (2) | 7 |
| Kouthala | Maize (1), Sorghum (2), Rice (1) | 8 |
| Kubeer | | 2 |
| Kuntala | Rice (1), Wheat (1), Sorghum (2), Little millet (1) | 6 |
| Luxettipet | Sorghum (1) | 2 |
| Mamada | Rice (2), Maize (1), Italian millet (1) | 6 |
| Mancherial | Maize (1), Sorghum (4) | 11 |
| Mudhole | Sorghum (2) | 3 |
| Neredigonda | Rice (2), Maize (2), Sorghum (1), Italian millet (2) | 8 |
| Narnoor | Rice (2), Maize (1), Sorghum (6), Italian millet (1) | 20 |
| Nennel | Maize (1), Sorghum (2) | 8 |
| Nirmal | | 1 |
| Rebbana | Maize (1), Sorghum (1) | 2 |
| Sarangapur | Rice (1), Maize (1), Sorghum (4) | 13 |
| Sirpur-T | Wheat (1), Maize (1), Sorghum (4) | 12 |
| Sirpur-U | Rice (3), Wheat (1), Sorghum (6), Italian millet (2) | 23 |
| Talamadugu | Rice (2), Maize (1), Sorghum (2) | 8 |
| Tamsi | Rice (1), Sorghum (1) | 2 |
| Tanoor | Sorghum (6) | 8 |
| Tiryani | Rice (2), Maize (2), Sorghum (9), Italian millet (1) | 21 |
| Utnoor | Rice (4), Maize (1), Sorghum (8), Italian millet (1) | 29 |
| Vemanpalle | Maize (3), Sorghum (6) | 12 |
| Wankhidi | Maize (1), Sorghum (4) | 18 |

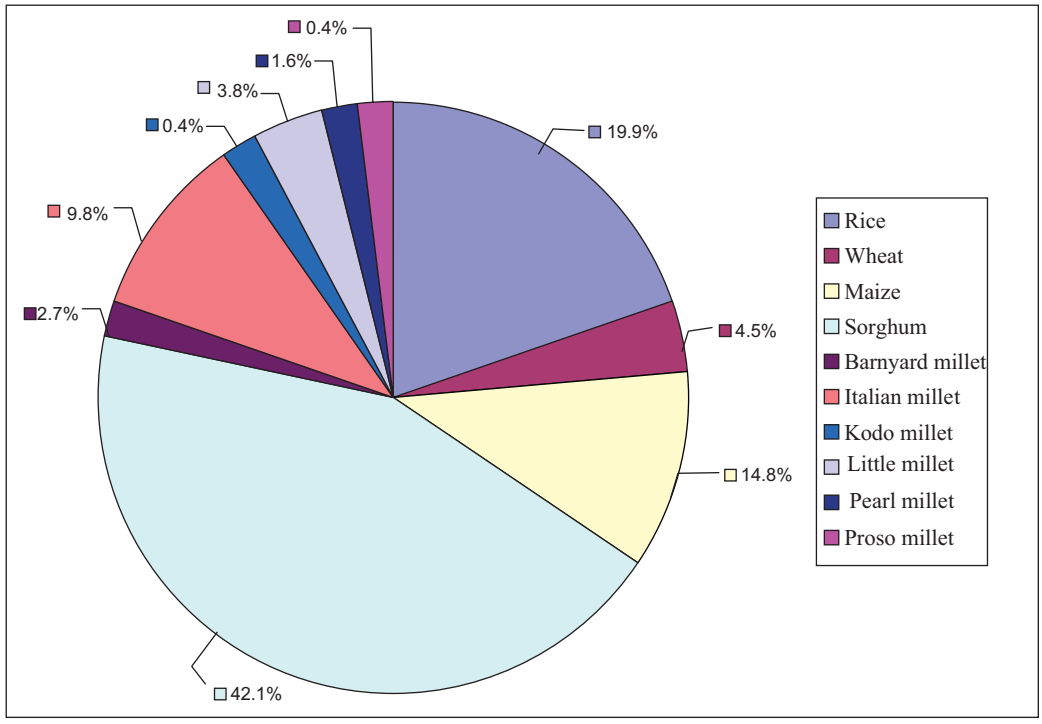


**Fig. 2. Diversity spectrum of collections made under cereals, millets and small millets from Adilabad, Andhra Pradesh**

**Table 3. Trends in on-farm sustainability of sorghum and rice landraces in Adilabad between 1988 and 2010-12 periods**

| Crop | Named landraces collected (No./Year(s)) | | Landraces collected in earlier missions salvaged during 2010-12 (No./Name) | Landraces could not be recollected (No.) | New landraces salvaged for the first time during 2010-12 (No.) |
|---|---|---|---|---|---|
| Sorghum | 59 (1988 & 1992) | 45 (2010-12) | 16<br>*Kharif* (Rainy season): *Gundu jonna, Leha jonna, Pandimutte jonna, Parasa jonna, Tekedari jonna*<br>*Rabi* (Post-rainy season): *Boda jonna, Chinnaboda jonna, Dhani jowar, Erra jonna, Mudda jonna, Pedda jonna, Pelala jonna, Pyru jonna, Rabi jonna, Tella jonna, Vayunowka jonna* | 43 | 29 |
| Rice | 93 (1993) | 18 (2010-12) | 12<br>Budamavanji, Davaralvanji, Erra vadlu, Gowrani vadlu, Kakirekkala vadlu, Nalla vadlu, Pandrisadi, Pisodi vadlu, Polala vadlu, Ragalvanji, Regadi vadlu, Tella vadlu | 81 | 6 |

(50.5%) followed by rice (20.6%) and maize (11.4%) among millets and cereals in the diversity share.

In Adilabad, significant landrace diversity was reported in cereals especially in rice (Pandravada and Sivaraj, 1996). In rice, maximum accessions (9) and maximum landraces (5) could be collected from Indravelly mandal. Most of the rice landrace contributors are Gonds. Variability was mainly observed for maturity duration (120 to 180 days), grain length (short to long), grain size (bold to slender), kernel colour (red/ white), husk color (shades of straw to black) and awn (absent/present) characters.

Of the 93 named rice landrace populations collected earlier during 1993 from the district by the authors (Pandravada and Sivaraj, 1996), only 12 are under continuous cultivation and maintained on-farm and all

**Table 4. Matrix ranking of sorghum landraces based on farmer selection criteria**

| Landrace | Farmers' perception (Rank*) | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Subsistence | Good initial establishment | Drought tolerance | Market value/ preference | Less bird damage | Fire wood | Earliness | Fodder value | Thatching value |
| Aragidi jonna | 14 | 1 | 19 | 22 | 10 | 2 | 17 | 18 | 19 |
| Badigi jonna | 18 | 18 | 4 | 44 | 24 | 28 | 33 | 25 | 4 |
| Boda jonna | 4 | 19 | 1 | 24 | 31 | 11 | 28 | 30 | 1 |
| Chikkati jonna | 26 | 20 | 43 | 15 | 3 | 17 | 41 | 32 | 43 |
| Chinna jonna | 27 | 21 | 28 | 4 | 42 | 29 | 34 | 19 | 27 |
| Chinnaboda jonna | 28 | 2 | 41 | 28 | 18 | 43 | 12 | 42 | 41 |
| Dambral | 29 | 22 | 36 | 16 | 32 | 36 | 35 | 20 | 36 |
| Darawat jonna | 15 | 3 | 3 | 41 | 2 | 37 | 36 | 38 | 3 |
| Deyam jonna | 30 | 23 | 29 | 43 | 43 | 9 | 27 | 34 | 29 |
| Dhane jowar | 31 | 32 | 20 | 21 | 27 | 26 | 10 | 5 | 20 |
| Erra jonna | 11 | 45 | 12 | 23 | 25 | 41 | 3 | 45 | 12 |
| Gadda jonna | 13 | 4 | 15 | 10 | 41 | 35 | 45 | 35 | 14 |
| Gundu jonna | 19 | 24 | 30 | 17 | 30 | 15 | 29 | 39 | 30 |
| Gunjidi jonna | 32 | 25 | 27 | 5 | 21 | 44 | 16 | 21 | 28 |
| Gunjidipedda jonna | 34 | 26 | 38 | 30 | 4 | 45 | 5 | 43 | 38 |
| Guvvi jonna | 35 | 5 | 21 | 20 | 11 | 12 | 40 | 22 | 22 |
| Jalleda jonna | 36 | 30 | 10 | 38 | 6 | 6 | 26 | 17 | 11 |
| Kathani jonna | 20 | 27 | 5 | 39 | 14 | 1 | 24 | 11 | 5 |
| Konkadala jonna | 12 | 28 | 9 | 11 | 22 | 27 | 42 | 33 | 9 |
| Leha jonna | 3 | 29 | 11 | 37 | 38 | 5 | 25 | 16 | 10 |
| Mudda jonna | 21 | 31 | 17 | 8 | 33 | 32 | 22 | 1 | 17 |
| Pachchaboda jonna | 22 | 33 | 8 | 12 | 34 | 7 | 19 | 24 | 8 |
| Palajonna | 37 | 42 | 44 | 26 | 17 | 20 | 14 | 41 | 45 |
| Pandari jonna | 6 | 34 | 42 | 27 | 7 | 42 | 1 | 27 | 42 |
| Pandimutte jonna | 38 | 6 | 2 | 40 | 1 | 3 | 43 | 12 | 2 |
| Parasa jonna | 23 | 7 | 26 | 6 | 35 | 18 | 30 | 2 | 26 |
| Pasupu jonna | 17 | 35 | 14 | 35 | 8 | 38 | 6 | 36 | 15 |
| Pasupupachcha jonna | 39 | 36 | 13 | 36 | 9 | 39 | 7 | 37 | 16 |
| Pedda jonna | 8 | 8 | 35 | 1 | 20 | 40 | 11 | 23 | 35 |
| Pelala jonna | 7 | 9 | 39 | 45 | 44 | 8 | 8 | 44 | 39 |
| Potiki jonna | 45 | 37 | 7 | 13 | 19 | 31 | 39 | 15 | 7 |
| Purabodaka jonna | 41 | 38 | 33 | 32 | 23 | 22 | 38 | 28 | 34 |
| Pyru jonna | 16 | 39 | 22 | 7 | 39 | 14 | 44 | 3 | 21 |
| Rabi jonna | 1 | 10 | 24 | 18 | 28 | 23 | 31 | 6 | 23 |
| Sanna jonna | 42 | 11 | 23 | 19 | 29 | 24 | 32 | 7 | 24 |
| Sevata jonna | 2 | 12 | 16 | 9 | 40 | 16 | 23 | 10 | 13 |
| Sivira jonna | 10 | 13 | 25 | 33 | 12 | 34 | 2 | 8 | 25 |
| Talki jonna | 43 | 14 | 31 | 3 | 36 | 30 | 15 | 4 | 31 |
| Tekedari jonna | 24 | 40 | 40 | 29 | 26 | 33 | 4 | 26 | 40 |
| Tella jonna | 5 | 41 | 45 | 25 | 16 | 19 | 13 | 40 | 44 |
| Tellaboda jonna | 25 | 15 | 18 | 34 | 15 | 4 | 18 | 9 | 18 |
| Varagadi jonna | 44 | 43 | 37 | 31 | 13 | 13 | 20 | 31 | 37 |
| Vayunowka jonna | 9 | 16 | 34 | 42 | 5 | 25 | 9 | 14 | 33 |
| Vubiripatti jonna | 33 | 44 | 32 | 2 | 45 | 10 | 37 | 13 | 32 |
| Vullipitta jonna | 40 | 17 | 6 | 14 | 37 | 21 | 21 | 29 | 6 |

**1- Most important; 45- Least important*

other 81 remaining landrace populations are replaced and no longer under cultivation. Rice landraces, *Budamavanji, Davaralvanji, Erra vadlu, Gowrani vadlu, Kakirekkala vadlu, Nalla vadlu, Pandrisadi, Pisodi vadlu, Polala vadlu, Ragalvanji, Regadi vadlu* and *Tella vadlu* are the ones under continuous cultivation since 1993. However, six new landraces (*Akasavai vadlu, Chittimutyalu, Chittiporu, Dasara vadlu, Pandadivanji* and *Puraval*) could be sampled for the first time during these biodiversity surveys which were not recorded and collected earlier (Table 3) due to intensive surveying in remote tribal pockets.

Interaction with the farmers yielded startling feed back with respect to sustained cultivation of these landraces the main premise being dependability under adverse situations in niche environments, the traits include good early plant vigour, good tillering ability, tall plant stature, earliness, reasonable panicle and grain length, good seed weight and assured yield levels. All these landraces, in addition to the above stated characters, also have good biomass suitable for straw for feeding the cattle in the backyards.

In maize, maximum accessions were collected from Kerameri (7) mandal and maximum landraces from Vemanpally (3) mandal. Of the 10 named landraces sampled, most of them were contributed by the Gond tribe and good diversity was observed mainly in plant, cob and grain characters. Not much diversity was observed in wheat landraces except for grain colour and size, and a total of three named landraces could be sampled which were not collected earlier.

Millets are small-seeded grasses that are hardy and grow well as rain-fed crops under marginal conditions of soil fertility and moisture in the surveyed district. A total of 188 accessions belonging to 45 named landraces, maintained by various tribal communities, were collected and documented in sorghum recording the highest named landrace diversity from the district. Maximum accessions were collected from Kerameri (17) mandal and maximum landraces from Tiryani mandal (9). High variability exists among the landraces for plant height, flowering, maturity, panicle size/ shape/ compactness, glume colour, glume covering, grain colour and grain size.

The landraces are a rich reservoir of diversity and valuable source for quality traits, resistance to diseases and pests and also to drought, high temperatures and other vagaries of climate change (Sivaraj *et al*., 2012). Of the cumulative 59 named sorghum landraces collected during 1988 (Pandravada and Gopal Reddy, 1988) and 1992 (Pandravada, 1992) from the district only 16 (*Kharif: Gundu jonna, Leha jonna, Pandimutte jonna, Parasa jonna, Tekedari jonna*; *Rabi*: *Boda jonna, Chinnaboda jonna, Dhani jowar, Erra jonna, Mudda jonna, Pedda jonna, Pelala jonna, Pyru jonna, Rabi jonna, Tella jonna, Vayunowka jonna*), mostly the *rabi* (winter season) cultivars could be salvaged from the present surveys and all other remaining populations eroded and are no longer cultivated and maintained on-farm (Table 3). However, 29 new landraces (*Aragidi jonna, Badigi jonna, Chikkati jonna, Chinna jonna, Dambral, Darawat jonna, Deyam jonna, Gadda jonna, Gunjidi jonna, Gunjidipedda jonna, Guvvi jonna, Jalleda jonna, Kathani jonna, Konkadala jonna, Mudda jonna, Pachchaboda jonna, Pala jonna, Pandari jonna, Pasupu jonna, Pasupupachcha jonna, Potiki jonna, Purabodaka jonna, Sanna jonna, Sevata jonna, Sivira jonna, Tellaboda jonna, Varagadi jonna, Vubiripatti jonna* and *Vullipitta jonna*) surfaced for the first time during the biodiversity surveys which were not recorded and collected earlier due to intensive combing of ethnic pockets.

The ranking of sorghum landraces of Adilabad based on utility perception by ethnic farmers which has a bearing on their on-farm sustainability is given in Table 4. Out of the nine utility traits listed, landrace *rabi jonna* was ranked number one for subsistence, *aragidi jonna* for good initial establishment, *boda jonna* for drought tolerance, *pedda jonna* for market value/ preference, *pandimutte jonna* for less bird damage, *kathani jonna* for fire wood, *pandari jonna* for earliness, *mudda jonna* for fodder value and *boda jonna* for thatching value. Among the landraces which were ranked as number one for different traits, *boda jonna, pandimutte jonna* and *pedda jonna* were in continuous cultivation since 1988 and incidentally *boda jonna* was ranked number one for two traits *i.e.* drought tolerance and thatching value. The desired traits from farmer perspective leading to continuous cultivation of landraces of sorghum include good initial plant vigour, medium tall plant habit, juicy stems, late maturity, medium grain size and semi-compact medium panicles, the characters of which are best suited for cultivation under *rabi* season under rainfed situations majority of landraces belong to.

In pearl millet even though local diversity exists, there are no endemic named landraces that could be collected.

In small millets endemic variability occurs especially in Italian millet and little millet and maximum accessions were collected from Utnoor (9) mandal. A total of nine named landraces in Italian millet and three in little millet could be sampled during the agri-biodiversity surveys undertaken in the district. Conspicuously, in barnyard millet, proso millet and kodo millet, no named landrace could be collected. Most of the small millet crops and their landraces are being replaced at an alarming rate and in due course of time they may become extinct.

**Discussion**

Maintenance of diversity for long term ecological balance and agricultural sustainability is primarily based on agro-climatic conditions, assured market and economic viability of farming. Under tremendous agricultural intensification pressures, the scope for on-farm conservation of different crops and their landrace diversity directly depends upon continuity of rituals/ customs/traditions/cultural practices and also their *sinequa-non* role in the livelihood/nutritional security of the ethnic groups only. Gradual decline in the cultivation of landraces on-farm resulting in genetic erosion in different parts of the world was reported by several workers. Hammer *et al*. (1996) reported the down trend in many crops in Albania and southern Italy, Peroni and Hanazaki (2002) and Willemen *et al*. (2007) in cassava in Brazil and Peru respectively, Gai *et al*. (2005) in soybean in China, Teklu and Hammer (2006) in tetraploid wheat and Mekbib (2008) in sorghum in Ethiopia.

Adilabad is a rich abode and a treasure trove for ethnic diversity in different cereal and millet crops which is a vibrant and indispensable component in the overall conservation strategies. However, bio-edaphic factors, population pressure and socio-economic policies especially the subsidized rice scheme transformed the hitherto subsistence farming being practiced by the tribal groups in to commercial farming looking for remuneration and profits in cultivation as they were getting rice at a very cheap rate for consumption. This has resulted in unforeseen changes in the cropping systems and replacement of traditional crops like sorghum, pearl millet and small millets with other profitable new crops (Bt cotton and soybean etc.) thereby losing the diversity in those crops (Pandravada *et al*., 2004).

The genetic erosion is more visible in case of rice with the replacement of 81 landraces (87.1%) with improved varieties having fine grains the cultivars of which people prefer for consumption due to changed food habits. However, in case of sorghum, the genetic erosion with the replacement of 43 landraces (72.9%) is comparatively low as the farmers grow the crop mostly during the *rabi* season as major staple for their own consumption, the quality of the landraces being much superior over improved varieties/ hybrids.

The inventory of landrace populations, as a case study of cereals and millets, of the tribal district of Adilabad, Andhra Pradesh raises several issues with regards to conservation *ex-situ* and management on-farm of crop landrace diversity. Large scale abandonment of traditional landraces calls for systematic combing of all diversity rich areas so that important diversity is collected and safely conserved *ex-situ* in gene banks before lost from production systems.

Further, as climate change is leading to the erosion of world's biological diversity, severe implications are predicted in agriculture and food supply notably in subsistence farming. As a consequence, a two-pronged strategy for mitigation and adaptation to climate change is advocated. Agro-biodiversity plays a key role in this and calls for a revision of the present conservation approaches. Instead of *ex-situ* conservation in gene banks a broader concept needs to be envisaged through which emphasis is on *in-situ* on-farm conservation complemented by gene banks. It has two-fold advantage, as the future needs are unknown, maximum genetic resources could be conserved at the lowest possible public cost and as the genetic resources get exposed to environmental changes, well adapted material gets evolved instead of being stored in a gene bank. In their study of rice landraces from Uttarakhand Himalayas, Kumar *et al*. (2010) reported greater number of alleles/ locus in on-farm conserved populations as compared to the ones under static management (Genebanks). However, climate change induced environmental stress may in fact go beyond the reach of adaptation and *in-situ* on-farm approach offers a great chance to shape a future worth living (Kotschi, 2006). On-farm conservation, however, cannot be made a system-wide approach in general but can be taken up as an approach at selected target sites.

All the above referred landraces are being conserved in the Medium Term Storage (MTS) facility at the ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), Regional Station, Hyderabad for posterity and present utilization of germplasm by breeders and

other researchers. Further, systematic characterization of landrace populations collected earlier and stored *ex-situ* in National Genebank at NBPGR, New Delhi and the present landraces being maintained on-farm needs to be investigated for loss of diversity over time and space at genetic (allele/genotype) level so that precise documentation of level of genetic diversity still maintained by farmers in traditional production systems could be assessed. The findings could also help optimize the number of populations of a particular named landrace to be collected and conserved *ex-situ* in gene banks, which is a capital intensive exercise. The research findings would also help suggest PGR researchers the need of periodic sampling of landrace populations as farmers deliberately introduce new diversity in production systems through informal seed exchange.

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SHORT COMMUNICATION

# Barley Lines with Higher Grain Beta Glucan Content Identified

**Dinesh Kumar*, RPS Verma, S Narwal, AS Kharub, R Malik, R Selvakumar, J Singh, V Kumar and Indu Sharma**

*ICAR-Indian Institute of Wheat and Barley Research (formerly DWR), Karnal-132001, Haryana, India*

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In recent years, there has been renewed interest in food barley due to it's health benefitting properties. Barley grain contains a polysaccharide, beta glucan, which has been shown to reduce blood cholesterol and glucose level. The varieties and some of the germplasm lines were screened for beta glucan content and promising lines were identified. Two lines namely BCU 554 and BK 306 had higher beta glucan and reasonably good protein content also.

**Key Words: Barley, Beta glucan, Bold grains, Protein content**

With the changing lifestyles and increasing urbanization, coronary heart disease, diabetes *etc*. are on the rise in India. One of the ways, suggested to control these diseases, is changes in the dietary habits. In the past few years, it has been shown that inclusion of nutraceuticals such as soluble dietary fibres can help in controlling the blood cholesterol and glucose levels besides providing benefits to gut health. Cereals, specifically, the barley and oats, possess higher amounts (3-7%) of one such dietary fibre called beta (β) glucan. The mixed linkage (1-3; 1-4) β-glucans have been shown to lower postprandial blood glucose and LDL cholesterol, and is recommended in many countries as health benefitting soluble fibre (Baik and Ullrich, 2008). With the identification of potential health benefits associated with barley grain due to the higher β-glucans, it will be appropriate to develop barley varieties and products meant for human food consumption. Flour from barley grains with higher β-glucans can be a part of regular *chapatti* in the form of multigrain *atta* to provide health benefits as part of a regular diet. Therefore, efforts are being made to identify barley lines with higher β-glucans for further use in barley improvement programme in the country.

In the initial stage, 75 varieties and around 250 germplasm lines/advance stage material from All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) trials screened for β-glucan concentration were grown at Directorate of Wheat Research, Karnal (29.68° N, 76.98° E), Haryana, India (Kumar *et al.*, 2012; Anonymous 2013). A total of five germplasm lines with higher β-glucan percentage were identified and grown along with seven varieties (as control) subsequently at seven locations (Karnal, Hisar and Ludhiana in North Western Plain Zone, Kanpur, Faizabad and Rewa in North Eastern Plain Zone, and in Bajaura in northern hill zone) during 2012-13 to confirm the trait. The β-glucan content was determined through an enzymatic method and Megazyme β-glucan estimation kit was used (Megazyme International, Ireland) following McCleary Enzymic Method for barley (McCleary and Codd, 1991). Crude protein content was predicted using NIR. The physical parameters like hectoliter weight, 1000 grain weight and bold grain percentage were determined as per standard procedures. There was one pooled sample from each location, which was treated as one replication, and data was analyzed using the statistical software *CropStat*.

It is clear from Table 1 that the lines BCU 554, DWR 30 and DWRUB 76 have higher β-glucan content (>6.0 % dwb) as compared to all the controls except BHS 352 and HBL 276. However the identified lines had higher 1000 grain weight (>45.0) and bold grain (>2.5 mm) percentage (>60%) as compared to the controls. Plump, uniform and round grains are preferred for milling and pearling purposes (Baik and Ullrich, 2008 and references therein).

There is renewed interest in the barley grain since last few years due to its health benefits and it is expected that in coming years, the consumption of food barley may increase. Therefore, the genotypes of barley

*Author for Correspondence: E-mail: dkbiochem69@gmail.com

**Table 1. Physico-chemical traits of promising barley germplasm lines**

| S.No. | Genotype | β-Glucan (% dwb) | Protein (% dwb) | 1000-grain wt (g) | Bold grain (>2.5 mm) (%) | Test wt (kg/hl) |
|---|---|---|---|---|---|---|
| 1 | BCU 554 | 7.1 | 13.4 | 50.9 | 74.6 | 62.2 |
| 2 | BK 306 | 6.0 | 15.1 | 53.3 | 95.6 | 58.1 |
| 3 | DWR 30 | 6.9 | 12.1 | 49.3 | 74.2 | 62.9 |
| 4 | DWRUB 76 | 6.6 | 11.8 | 50.1 | 88.8 | 59.6 |
| 5 | 20th I BON 3 | 6.2 | 12.6 | 46.7 | 67.7 | 63.2 |
| 6 | BHS 352 (c) | 6.5 | 12.8 | 29.7 | 14.2 | 70.5 |
| 7 | DWRUB 73 (c) | 5.8 | 13.0 | 49.5 | 74.8 | 60.9 |
| 8 | Dolma (c) | 5.5 | 13.5 | 33.8 | 12.5 | 69.0 |
| 9 | HBL 276 (c) | 6.0 | 14.0 | 29.4 | 20.7 | 67.5 |
| 10 | NB 2 (c) | 5.4 | 11.2 | 35.3 | 53.3 | 58.3 |
| 11 | NB 3 (c) | 5.3 | 11.1 | 37.1 | 47.0 | 59.3 |
| 12 | RD 2668 (c) | 5.7 | 11.9 | 40.5 | 62.2 | 61.6 |
| | SE | 0.2 | 0.4 | 1.9 | 4.7 | 1.0 |
| | LSD (5%) | 0.7 | 1.0 | 5.5 | 13.2 | 2.7 |

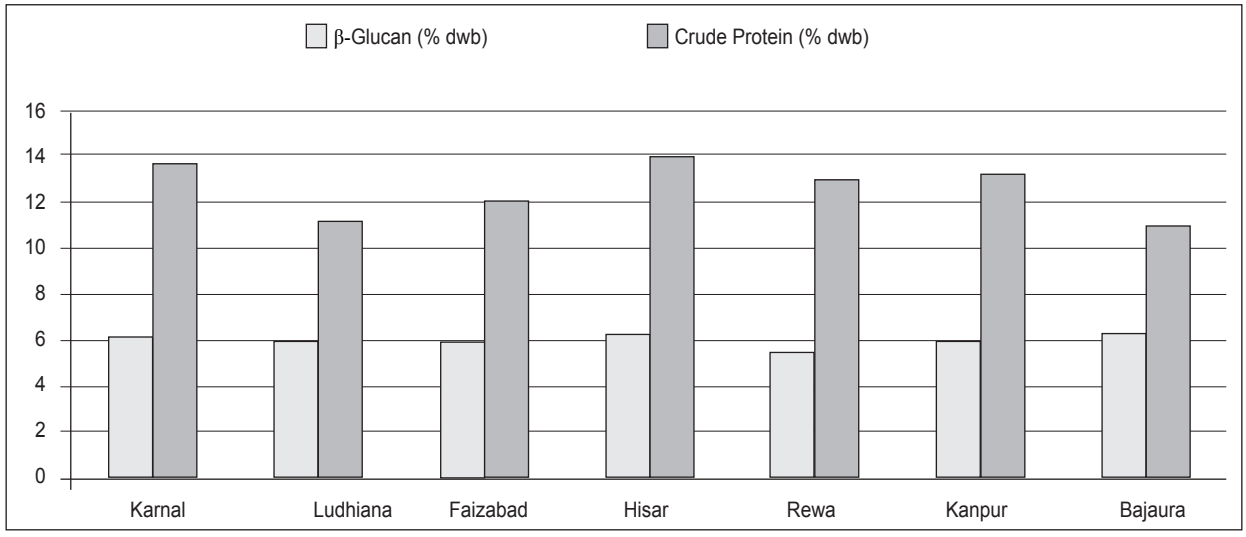


**Fig. 1. Mean grain β-glucan content and protein content of BK 306 at different locations**

were also screened for higher protein content without compromising the grain boldness. Germplasm line BK 306 was identified with higher protein content, higher bold grain percentage and reasonably good β-glucan percentage (6.0%), which is even higher or comparable with the naked barley cultivars developed in country (Fig. 1).

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SHORT COMMUNICATION

# Diversity for Stem Rust (*Puccinia graminis* f. sp. *tritici*) Resistance in Durum Wheat (*Triticum turgidum* ssp. *durum*) Germplasm

**AN Mishra*, VG Dubey, K Kaushal and SV Sai Prasad**
*ICAR-Indian Agricultural Research Institute, Regional Station, Indore-452001, Madhya Pradesh, India*

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Three hundred durum wheat genotypes showing field resistance to stem rust since 2003 under heavy inoculum pressure could be classified in to seven diverse resistance groups based on their seedling and adult-plant responses to two important stem rust pathotypes *viz.*, 40A (62G29), the most prevalent one, and 117-6 (37G19), the durum-specific one. Present information should be useful in providing guidelines for utilizing diverse resistance sources toward broadening of stem rust resistance base in durum improvement programmes.

**Key Words: Diversity for rust resistance, Durum wheat germplasm, Stem rust resistance**

India produces >90 million tons of wheat from an area of >25 million hectares, to which the contribution of durum wheat is about 5%. However, durum wheat has a special niche in Indian wheat economy for at least two reasons. Indian durum wheat is typically purchased by the private trade at a price premium, mainly for processing of high value products. In addition, durum wheat is preferred over bread wheat for several local food preparations. Durum wheat is mainly grown in the central and peninsular parts of India, where stem rust is one of the major disease problems of wheat crop. Cultivation of resistant varieties is the most effective, economic and eco-friendly method of disease management. Broadening of resistance base through utilization of diverse resistance sources is necessary for enhancing the durability of resistance in view of the continued evolution of the stem rust pathogen.

A total of 1105 durum wheat germplasm accessions including released varieties, advance generation lines, land races and indigenous as well as exotic genetic stocks were evaluated for field resistance to stem rust at IARI-RS, Indore during *rabi* 2002-03 under heavy inoculum pressure using mixtures of important stem rust pathotypes. In all, 300 genotypes showing adequate level of resistance (terminal rust severity up to 10S) to stem rust were selected and are being tested year-after-year for ascertaining the stability of resistance. They have been observed maintaining their stem rust resistance till date (authors' unpublished observations). An attempt was, therefore, made to gain an insight in to the extent of diversity among these genotypes through seedling and adult plant tests with two stem rust pathotypes 40A (62G29) and 117-6 (37G19). These pathotypes were chosen since the former is currently the most prevalent one (Anonymous, 2013), while the latter is one of the most virulent ones to durum wheat germplasm (Mishra *et al*., 2009) among the stem rust pathotypes occurring in India.

The avirulence/virulence characteristics of these pathotypes based on seedling tests (SC Bhardwaj, *personal communication*) are given below:

**40A (62G29) – P** *Sr7a*, *Sr13*, *Sr21*, *Sr22*, *Sr24*, *Sr25*, *Sr26*, *Sr27*, *Sr30*, *Sr31*, *Sr32*, *Sr33*, *Sr35*, *Sr36*, *Sr37*, *Sr38*, *Sr39*, *Sr40*, *Sr43*, *SrTmp* / **p** *Sr2*, *Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9a*, *Sr9b*, *Sr9d*, *Sr9e*, *Sr9f*, *Sr9g*, *Sr10*, *Sr11, Sr12, Sr14*, *Sr15*, *Sr16*, *Sr17*, *Sr18*, *Sr19*, *Sr20*, *Sr23*, *Sr28*, *Sr29*, *Sr 34*, *SrMcN*

**117-6 (37G19) – P** *Sr5, Sr8a, Sr8b, Sr9b, Sr22, Sr24, Sr25, Sr26, Sr27, Sr28, Sr30, Sr31, Sr32, Sr33, Sr35, Sr36, Sr37, SrTmp* / **p** *Sr2, Sr6, Sr7a, Sr7b, Sr9d*, *Sr9e, Sr9f, Sr9g, Sr10, Sr11, Sr12, Sr13, Sr14, Sr15, Sr16, Sr17, Sr19, Sr21, Sr23, Sr29, Sr34, SrMcN*

The seedling tests were conducted at 20-22$^{o}$C ± 2$^{o}$C using standard glasshouse procedures (Nayar *et al*., 1997). The seedlings tested for resistance were raised in 10 cm clay pots. Seedlings with primary leaf fully

**Author for Correspondence: E-mail: anmishra53@yahoo.co.in*

expanded and second leaf just emerged (generally 8-10 days old) were spray inoculated with aqueous suspension of uredospores of the individual test pathotypes, freshly collected from the actively sporulating pots of 'Agra Local' maintained in isolation in the glasshouse. Agra Local served as 'susceptible check'. Inoculated pots were incubated in moist chambers for 16-24 h, and were then transferred to glasshouse benches. Infection types (ITs) on the seedlings were recorded 12-15 days after inoculation on a 0-4 scale. The Infection Types (ITs) 3, $3^+$, 34 and 4 produced by a pathotype on a host line indicated susceptibility to that pathotype, whereas lower ITs ('0;' '1', '2' and 'X') indicated resistance (Nayar *et al*., 1997).

The adult palnt tests were conducted for two successive crop seasons during 2010-2012 in field nurseries isolated with paired border rows of maize. Around 50 seeds of each of the test lines were dibbled in 1.0 m long rows, planted 30 cm apart. Rust spreader rows consisting of mixtures of highly susceptible wheat varieties were planted after every 20 test rows, and all around the experimental plot. Beginning 55-60 days after sowing, the disease spreader rows were inoculated using hypodermic syringes and sprays with aqueous suspension of the uredospores of the test pathotypes, freshly collected from actively sporulating `Agra Local' pots maintained in isolation in the glasshouse. Disease scores were recorded combining the disease severity as per the modified Cobb's scale (Peterson *et al*., 1948), and the host response (Roelfs *et al*., 1992). Lines showing up to 10S reaction were classified as `resistant'.

Seven diverse groups for stem rust resistance were recognized among the test genotypes, based on their seedling and adult-plant responses to the two pathotypes, as listed below:

**Group I. Resistant to both the pathotypes in both the growth stages (seedlings and adult plants)** (No. of genotypes = 161)

AKDW 3347, AKDW 4256, B 101, B 206, B 212, B 414, B 662, Baxi dwarf, C 34, C 61, CIMB 1574, CIMB 1632, CIMB 1633, CIMB 1640, CIMB 1649, CIMB 1655, CPAN 1311, CPAN 6012, CPAN 6038, CPAN 6040, CPAN 6083, CPAN 6118, CPAN 6120, CPAN 6138, CPAN 6200, CPAN 6201, CPAN 6236, D 83, D 658, DBP 02-13, DD 276, DD 629, DD 703, DD 711, DD 2518, DR 140, DW 222, E 4282, ED 2398-A, Guji 'S', GW 1139, GW 1170, GW 1172, GW 1182, GW 1202, GW 1207, GW 1209, HD 363, HD 4672, HD 4685, HD 4703, HD 4708, HG 41, HG 42, HG 101, HG 113, HG 179, HG 195, HG 282, HG 320, HG 363, HG 378, HG 391, HG 402, HG 589, HG 764, HG 888, HG 1312, HI 8592, HI 8627, I 2334, I 2567, I 2577, I 2601, I 2644, I 2701, IDSN 47, IWP 5007, IWP 5050, IWP 5057, IWP 5061, IWP 5065, IWP 5070, Jairaj, JBL 89, JD 01-37, JD 01-46, JD 96-40, JD 98-2, MACS 2067, MACS 2846, MACS 3125, MACS 3425, MACS 3453, MACS 3493, MACS 3503, MACS 3507, MP 311, MPO 3-19, MPO 3-21, MPO 3-23, MPO 3-24, MPO 195, MPO 622, NI 8097, NIDW 9, NIDW 29, P 6046, PDSN 668, PDSN 671, PDSN 672, PDSN 689, PDSN 691, PDSN 692, PDSN 694, PDSN 702, PDSN 703, PDSN 704, PDSN 705, PDSN 707, PDSN 708, PDSN 709, PDSN 711, PDSN 713, PDSN 1025, PDSN 1026, PDSN 1027, PDSN 1036, PDSN 1074, PDSN 1083, PDSN 1084, PDSN 1085, PDSN 1086, PDSN 1087, PDSN 1088, PDSN 1089, PDSN 1090, PDSN 1091, PDSN 1092, Raj 6069, Raj 6516, Raj 6562, RD 773, RD 815, RD 893, RD 930, RKD 97, RS 749, S 21, Trinakria, UPD 45, VD 97-15, VD 2000-40, VD 2001-30, VD 2001-37, VD 2001-46, VD 2001-55, VDR 2001-2, VDR 2001-10, VDR 2002-2, and Yuk.

**Group II. Resistant to 40A in both the growth stages, but seedling susceptible and only adult plant resistant to 117-6** (No. of genotypes = 48)

AKDW 4258, AKDW 4339, Baxi 422, Bijapur 487-2, Castel Porziano, CIMB 1469, CIMB 1474, CIMB 1538, CIMB 1545, CIMB 1555, CIMB 1564, CIMB 1583, CIMB 1585, CIMB 1588, CIMB 1589, CIMB 1593, CIMB 1645, CIMB 1648, CIMB 1651, CPAN 6018, CPAN 6028, CPAN 6053, CPAN 6117, CPAN 6137, D 104, DBP 02-08, DD 653, DON 174, E 4291, HG 110, HG 418, HG 419, HG 434, HG 517, HG 590, I 2498, I 2595, IDSN 38, IWP 5013, IWP 5019, JD 01-14, Keerthi, Line 1172, MPO 3-20, MPO 615, NI 7444, RALLI-1, and WH 804.

**Group III. Resistant to 40A in both the growth stages, but susceptible to 117-6 in both the growth stages** (No. of genotypes = 49)

AKDW 4240, B 138, B 224, B 276, C 23, C 32, C 42, CPAN 6127, CPAN 6131, CPAN 6140, D 34, D 88, D 292, D 294, DD 279, DD 702, DR 155, HD 4562, HD 4696, HD 4707, HD 4709, HG 30, HG 43, HG 622,

HG 623, HG 677, HG 716, HI 171, HI 8498, HI 8591, HI 8634, IWP 5093, JD 01-12, JD 01-32, MACS 3061, MPO 414, P 7073, P 7100, PBW 34, PDW 289, RD 895, RD 932, VD 2001-06, VD 2001-14, VD 2001-15, VD 2001-17, VD 2001-20, VD 2001-35, and WG 7143.

**Group IV. Only adult-plant resistant, but seedling susceptible to 40A, and susceptible to 117-6 in both the growth stages** (No. of genotypes = 01)

Baxi 470-27

**Group V. Resistant to 117-6 in both the growth stages, but seedling susceptible and only adult plant resistant to 40A** (No. of genotypes = 13)

CIMB 1464, CIMB 1667, ED 155, ED 1096, Gulab 'S', HG 316, I 1221, I 1360, ID 1169, N 5749, NI 5779, NI 7121, and WH 213.

**Group VI. Resistant to 117-6 in both the growth stages, but susceptible to 40A in both the growth stages** (No. of genotypes = 01)

MPO 501

**Group VII. Adult-plant resistant, but seedling susceptible to both the pathotypes** (No. of genotypes = 27)

BD 72, Bijiga Red, CIMB 1537, CIMB 1550, CPAN 6019, CPAN 6132, E 1058, E 4303, E 7798, ED 2177, HI 162, HI 167, I 1142, I 1568, I 1805, I 7805, I 15171, I 15173, I 15177, I 15186, ID 1128, ID 1264, ID 1278, MPO 503, Saver Local 'S', Yal Forte, and Yuma.

The above listed 27 genotypes (Group VII) which showed seedling susceptibility, but adult-plant resistance to both the test pathotypes are of particular interest from the viewpoint that most examples of durable rust resistance are of adult-plant type. These genotypes need to be studied further for characterizing the resistance genes present in them. Only two genes for adult-plant resistance to stem rust *viz.*, the recessively inherited gene *Sr2* derived from *Triticum turgidum* var. *dicoccum* cv. Yaroslav Emmer (McIntosh *et al*., 1995), and the undesignated dominant gene present in durum cultivar 'Glossy Hugenot' (Hare, 1997) are known to be of tetraploid (AABB genomes) background origin (McIntosh *et al*., 2013).

Relatively little work has been done on the diversity for stem rust resistance in durum wheat germplasm based on multi-pathotype tests. At least 18 diverse groups for stem rust resistance were recognized among 71 durum genotypes based on their seedling reactions to 24 pathotypes (Mishra *et al*., 2011). In a recent study, 107 durum wheat genotypes could be classified in to eight diverse groups for stem rust resistance based on their seedling responses to five durum-virulent stem rust pathotypes (Mishra *et al*., 2015). However, the present study had a more focussed approach, as both seedling and adult-plant responses to two very important stem rust pathotypes including the most prevalent, and the most durum-virulent ones formed the basis of assessing diversity for resistance in durum genotypes with proven field resistance. Hence, the information communicated here should be useful in providing guidelines for utilizing diverse resistance sources toward broadening of stem rust resistance base in durum improvement programmes.

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SHORT COMMUNICATION

# Note on Occurrence of Fragrant False Garlic [*Nothoscordum gracile* (Aiton) Stearn] in India

**Anjula Pandey[1]*, KS Negi[2], K Pradheep[1] and Moolchand Singh[1]^**
[1] *Division of Plant Exploration and Germplasm Collection, ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India*
[2] *ICAR-National Bureau of Plant Genetic Resources Regional Station, Bhowali, Niglat-263132, Uttarakhand, India*
^ *Division of Plant Quarantine, ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India*

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Fragrant false garlic [*Nothoscordum gracile* (Aiton) Stearn] belonging to family Alliaceae is an ornamental species native to southern Mexico and western South America, and widely naturalized in many parts of the world. In this paper a note on occurrence of the species in parts of Himalaya, Nagaland and Punjab along with occasional use as ornamental was presented. Besides, note on botany, mode of propagation and weedy potential of the species in India using weed risk assessment technique is included.

**Key Words: Distribution, Fragrant false garlic, *Nothoscordum gracile*, Potential weed, Weed risk analysis**

Gardening industry is the largest importer of introduced plant species and also the dominant source of naturalised plants having weedy potential (Groves *et al.,* 2005). Fragrant false garlic or onion weed [taxonomically known as *Nothoscordum gracile* (Aiton) Stearn] is one such species native to southern Mexico and western South America, and widely naturalised in many parts of the world (Ravenna, 1991). This species belongs to the family Alliaceae, subfamily Allioideae and has resemblance to genus *Allium* but it lacks any onion or garlic odour when crushed. It is economically important as an ornamental species and introduced as a garden plant to different continents across the world; also reported for edible use. Due to extremely prolific and invasive behaviour it is difficult to eradicate and therefore poses high risk associated with its escape from gardens and naturalization. Among many introduced plant species under cultivation in home garden, the fragrant false garlic is reported to naturalise in parts of India. Since this species is not commonly known, the botany of the plant is discussed below:

*Nothoscordum gracile* (Aiton) Stearn [syn. *Allium gracile* Aiton (basionym), *A. fragrans* Vent., *A. inodorum* auct., *Nothoscordum fragrans* (Vent.) Kunth, *N. inodorum* auct.]: bulb ovoid, about 1.5 cm diameter, outer coats brown, bulblet over 50; leaf basal, 4-10, linear, flat, 25-30 × 0.4-1 cm, glabrous, sheathing at the base, die back from the tip before flower maturity; scape 1or 2, terete, semi-erect, 30-60 × 0.2-0.3 cm; umbel 10-15-flowered, loosely arranged, often asymmetrical, bract persistent, two, 1.2-2 × 0.5-0.8 cm, flower fragrant, bell-shaped, with greenish bases and reddish to brown mid veins on outer side of perianth, 8-15 mm long, tepal white, oblanceolate, apex obtuse, bases fused; anther dark brown, filament simple, adnate to tepals, 7-10 mm, style persistent in fruit, equalling stamens, stigma unlobed; capsule obovoid, 6-7 × 6-7 mm; seed 8-12 per locule, black, tear drop-shaped (one end pointed), 2-4 × 1-2 mm.

During study on genetic resources of *Allium* in India the first author came across an onion like plant growing in the experimental garden, ICAR-NBPGR, New Delhi. Critical study of the material for identity was undertaken using herbarium specimens housed in national herbaria – the Botanic Survey of India (BSI), Forest Research Institute (FRI), Dehradun and National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi. After confirmation of identification from

*Author for Correspondence: E-mail: anjuravinder@yahoo.com


**Fig. 1.** ***Nothoscordum gracile*** **(top: from left-right): uprooted plants of fragrant false garlic; seedlings arising from perennating bulblets; open flower; (bottom: from left-right): false bulb; seedlings; bulblets; seeds**

various national herbaria and digital images available with online herbaria the species was identified as *Nothoscordum gracile*.

Material was grown in experimental garden of ICAR-NBPGR, New Delhi and studied from seedling to maturity stage during the year 2013 to 2015. Observations were recorded at different growth stages for morphological characters and on mode of propagation. Information on distribution and use was primarily based on authors' field experience and herbarium study. Vouchers specimens (HS21510; HS18539; HS21669) and seed samples (IC383446; SS3043, SS3045) have been deposited in the National Herbarium of Cultivated Plants, NBPGR, New Delhi.

Original material was collected from Munshiyari in Uttarakhand (which in turn was brought from Arunachal Pradesh) and reported for edible use; it was earlier misidentified as *Allium clarkei* Hook.f. (see Negi *et al.*, 2006). The same was maintained in the field gene bank at Bhowali, Uttarakhand and voucher specimen was deposited at the NHCP, New Delhi. During explorations undertaken in parts of Uttarakhand, the second and third authors noted its cultivation for ornamental use in the backyard (2000-3500m). It was also observed under sporadic cultivation as ornamental in the kitchen garden in Mokokchung, Mokokchung district in Nagaland by the third author.

Mature plants (4-5 months old) of fragrant false garlic produced sweet scented flowers in December-March. The bulbs were deep-seated; bulblet developed a hard brown outer membrane at maturity (Fig.1). They could overwinter and sprout in the winter season. Seed shattered when plant was fully mature and dry. Plant responded well to propagation by both, seed or bulblets. An average fragrant false garlic plant produced over 75-110 seeds/inflorescence. Seeds were observed to show 80-90 per cent germination immediately after maturity but after six months the viability was reduced to less than 20 per cent (Dr J Radhamani, ICAR-NBPGR; *pers. com.*).

The bulblets easily get dislodged from the parent bulb when plants were manually uprooted. In nature, bulblets get separated from the parent plant and move along with soil clodes (spread through irrigation or by

contaminated agricultural produce) this process enables faster spread. Perennating bulblets emerged into new plants in growing season (November-December) (Fig.1). The seedlings generally escaped manual eradication due to their gross morphology resembling the common grasses. Repeated tillage helps in reducing the weedy growth.

Fragrant false garlic is an introduced species in India with poor documentation of its occurrence under cultivation. In earlier literature (Ambasta *et al*., 1986) there was no mention about occurrence of the genus as useful plant species or as weed from India. Fragrant false garlic was noted as a new record of occurrence in Patiala district, Punjab, India (Sharma, 1985); and also under naturalised condition in waste places in Punjab (Sharma, 1994). Many earlier reports on its use as a favourite material for cytological study indicated its probable introduction for experimental purpose (Sharma and Sarkar, 1957; Tandon and Kapoor, 1981). Study of floristic records using herbarium based study at Botanical Survey of India (BSI), Dehradun and Forest Research India (FRI), Dehradun confirmed its naturalization in parts of Punjab (Bhandari Gardens, Patiala; Model Town, Patiala and Punjab University, Chandigarh). However, exact time of introduction of this species in India is unknown.

Fragrant false garlic is a hardy bulbous perennial with potential to infest barren land, waste places and the abandoned areas. Globally it is reported as weed from many parts of the world as naturalized species in common habitats like roadsides, waste places, disturbed lands, landscaped areas, gardens, etc. (George, 1994; Groves *et al*., 2005).

In view of the above and earlier reports of its tendency to naturalise, this species was subjected to weed risk assessment to understand its weedy potential. During experimental study the species was found highly adaptable to wide range of habitats from hilly areas to plains; the plants showed quick plant growth, reproduction by seed and as well as by underground bulblets and high seed germination potential.

Weed risk assessment was done based on standard questionnaire (Singh *et al.,* 2013). This database is designed to provide information, including biological and ecological, on invasiveness mentioned in an international weed list, or are legislated against in a state or territory. *Nothoscordum gracile* was subjected to weed risk assessment system based on a question-based scoring containing 49 questions about its climatic preferences, biological attributes, reproduction and dispersal methods. The response to the questions generated a numerical score with positive correlation to the weediness (Annexure 1). The system generated a score of '14' for this species and therefore assessed it as an agricultural weed which revealed its potential as serious weed in agricultural land.

Information generated in the present study may add to our knowledge on occurrence of this species from various parts of India. Besides, weed risk assessment on this species will add its naturalization potential on escape from cultivation.

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## Annexure 1

### Weed Risk Assessment Questionnaire

Answer yes (y) or no (n), or don't know (leave blank or ?), unless otherwise indicated

| | | | | | |
|---|---|---|---|---|---|
| | | Botanical name: | *Nothoscordum gracile* | Outcome: | Reject |
| | | Common name: | Fragrant false garlic | Score: | 14 |
| | | Family name | Alliaceae | Your name:Dr. Mool Chand Singh | |
| | History/Biogeography | | | | |
| A | **1** | *Domestication/* | 1.01 | Is the species highly domesticated. If answer is 'no' go to question 2.01 | n |
| C | | *cultivation* | 1.02 | Has the species become naturalized where grown | y |
| C | | | 1.03 | Does the species have weedy races | |
| | **2** | *Climate and* | 2.01 | Species suited to Indian climates (0-low; 1-intermediate; 2-high) | 1 |
| | | *Distribution* | 2.02 | Quality of climate match data (0-low; 1-intermediate; 2-high) | 1 |
| C | | | 2.03 | Broad climate suitability | y |
| C | | | 2.04 | Native or naturalized in regions with extended dry periods | n |
| | | | 2.05 | Does the species have a history of repeated introductions outside its natural range | y |
| C | **3** | *Weed* | 3.01 | Naturalized beyond native range | y |
| E | | *elsewhere* | 3.02 | Garden/amenity/disturbance weed | y |
| A | | | 3.03 | Weed of agriculture/horticulture/forestry | y |
| E | | | 3.04 | Environmental weed | n |
| | | | 3.05 | Congeneric weed | |
| | | Biology/Ecology | | | |
| A | **4** | *Undesirable* | 4.01 | Produces spines, thorns or burrs | n |
| C | | *traits* | 4.02 | Allelopathic | n |
| C | | | 4.03 | Parasitic | n |
| A | | | 4.04 | Unpalatable to grazing animals | y |
| C | | | 4.05 | Toxic to animals | n |
| C | | | 4.06 | Host for recognised pests and pathogens | |
| C | | | 4.07 | Causes allergies or is otherwise toxic to humans | |
| E | | | 4.08 | Creates a fire hazard in natural ecosystems | n |
| E | | | 4.09 | Is a shade tolerant plant at some stage of its life cycle | n |
| E | | | 4.10 | Grows on infertile soils | n |
| E | | | 4.11 | Climbing or smothering growth habit | n |
| E | | | 4.12 | Forms dense thickets | n |
| E | **5** | *Plant type* | 5.01 | Aquatic | n |
| C | | | 5.02 | Grass | n |
| E | | | 5.03 | Nitrogen fixing woody plant | n |
| C | | | 5.04 | Geophyte | y |
| C | **6** | *Reproduction* | 6.01 | Evidence of substantial reproductive failure in native habitat | n |
| C | | | 6.02 | Produces viable seed | y |
| C | | | 6.03 | Hybridises naturally | |
| C | | | 6.04 | Self-fertilisation | n |
| C | | | 6.05 | Requires specialist pollinators | n |
| C | | | 6.06 | Reproduction by vegetative propagation | y |
| C | | | 6.07 | Minimum generative time (years) | 1 |
| A | **7** | *Dispersal* | 7.01 | Propagules likely to be dispersed unintentionally | y |

| | | | | | |
|---|---|---|---|---|---|
| C | | *mechanisms* | 7.02 | Propagules dispersed intentionally by people | n |
| A | | | 7.03 | Propagules likely to disperse as a produce contaminant | y |
| C | | | 7.04 | Propagules adapted to wind dispersal | n |
| E | | | 7.05 | Propagules have dormancy | |
| E | | | 7.06 | Propagules bird dispersed | |
| C | | | 7.07 | Propagules dispersed by other animals (externally) | |
| C | | | 7.08 | Propagules dispersed by other animals (internally) | |
| C | **8** | *Persistence* | 8.01 | Prolific seed production | y |
| A | | *attributes* | 8.02 | Evidence that a persistent propagule bank is formed (>1 yr) | |
| A | | | 8.03 | Well controlled by herbicides | y |
| C | | | 8.04 | Tolerates or benefits from mutilation, cultivation or fire | |
| E | | | 8.05 | Effective natural enemies present in India | |
| | A= agricultural, E = environmental, C= combined | | | | |

# Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXX$^{th}$ meeting held on September 4$^{th}$, 2014 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 18 germplasm lines out of 108 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. HI-8708 (IC0611303; INGR 14042), a Wheat (*Triticum turgidum* ssp.*durum*) Germplasm with Leaf Rust Resistance

**SV Saiprasad*, DK Verma, Divya Ambati, Kamini Kaushal, Prakasha TL, Jang Bahadur Singh, VG Dubey and AN Mishra**

*Indian Agricultural Research Institute (IARI) Regional Station, Indore-452001, Madhya Pradesh, India*

**(Email Id: sprasad98@yahoo.com)*

Leaf rust caused by *Puccinia triticina* is one of the most important diseases affecting durum wheat cultivation. Many Indian durums are susceptible to several leaf rust pathotypes particularly 12-5 and 104-2 (Mishra *et al.,* 2009). Central zone (CZ) is the migratory route of leaf rust urediospores (Nagarajan and Joshi, 1985) and rust inoculum built up on any susceptible variety in CZ could be a serious threat to later sown crop in the Indian wheat bowl, North Western Plains Zone. Hence, broadening of genetic base for resistance by developing the varieties with different leaf rust resistance genes is one of the most important strategies for leaf rust management. Hence, a leaf rust resistant durum wheat genetic stock was developed at Indian Agricultural Research Institute, Regional Station, Indore, MP by crossing agronomically superior and popular durum variety, HI 8498 with an advanced line HG 822 (both were developed at Indore station).

Durum wheat genotype, HI 8708 (HG 822/ HI 8498), was identified as resistant to leaf rust in multi-location testing *viz.,* Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2009 to 2012. It showed high levels of adult-plant resistance to most prevalent and virulent leaf rust pathotypes 77-5 and 104-2 of leaf rust (Table 1). It showed both seedling and adult plant resistance to all the leaf rust pathotypes tested (Table 2). It may be noted that most of the known examples of durable rust resistance in wheat are of adult-plant type.

Hence, this genotype can be used as potential resistance donor to breed varieties against prevalent and most virulent leaf rust pathotypes.

**Table 1. Field responses of HI 8708 to wheat Leaf rust**

| Year of testing | Trial | Mixed pathotypes | | | | APR to specific pathotypes | |
|---|---|---|---|---|---|---|---|
| | | South | | North | | 77-5 | 104-2 |
| | | HS | ACI | HS | ACI | Delhi | Delhi |
| 2008–09 | NIVT 5B | 10S | 2.1 | TR | 0.0 | - | - |
| 2009–10 | AVT I | 10MS | 2.1 | TMS | 0.2 | TR | 10R |
| 2010–11 | EPPSN | TR | 0.1 | TMR | 0.1 | - | - |
| 2011–12 | MDSN | TR | 0.1 | TR | 0.0 | - | - |

Source: AICW&BIP – Crop Protection report (2009-12)

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

**Table 2. Seedling responses of HI 8708 to individual pathotypes of wheat rusts (2009-10)**

| Leaf rust pathotypes | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11 | 12-2 | 12-3 | 12-5 | 12-7 | 12-9 | 77 | 77-1 | 77-2 | 77-5 | 77-7 | 77-8 | 77-10 | 77-11 | 77A-1 | 104-2 | 104-3 | 104-4 | 104B | 106 | 107-1 | 108-1 | 162-1 |
| R | R | R | R | R | - | R | R | R | R | R | R | R | - | R | R | - | - | MR | R | R | R | R |

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# 2. AHMM/BR-8 (IC0599709; INGR 14043), a Muskmelon (*Cucumis melo* L.) Germplasm with Monoecious Sex Form


**BR Choudhury*, SM Haldhar, SK Maheshwari, R Bhargava and SK Sharma**

*ICAR-Central Institute for Arid Horticulture, Beechwal, Bikaner-334006, Rajasthan, India*

*(Email: choudharybr71@gmail.com)*


Muskmelon (*Cucumis melo* L.) is an important cucurbitaceous crop grown as a 'Dessert Crop' throughout the warmer parts of world. Being cross pollinated crop it showed heterosis for earliness, fruit size, fruit weight, flesh thickness, total soluble solids, fruit flavour, transportability and fruit yield. Presently the main attention is being paid on the development of $F_1$ hybrids due to high yield, uniform fruit shape, size as well as consistently excellent quality. Muskmelon is predominantly andromonoecious in sex expression however, monoecious sex form is also found in natural populations (More *et al*., 1980). The cost of hybrid seed production is high due to emasculation in the available andromonoecious cultivars of muskmelon. The use of genetic male sterile lines also involves difficulties in identification and rouging of 50% male fertile plants and maintenance of male sterile plants which makes the hybrid seed production costly. Therefore, the breeders are interested in the development of female parent with monoecious sex expression to minimize the cost of hybrid production in muskmelon.

**Table 1. Salient characteristics of IC0599709**

| Character | Description |
|---|---|
| Sex form | Monoecious |
| Days taken to produce 50% female flower from sowing | 43.80-46.13 days |
| Days to first fruit harvest from sowing | 70.20-73.87 days |
| Fruit diameter | 11.32-12.76 cm |
| Flesh thickness | 3.43-4.00 cm |
| Width of seed cavity | 4.37-5.12 cm |
| Total soluble solids (TSS) | 10.8-11.3% |
| Flesh hardness | 478-570 g/cm$^2$ |
| Fruit weight | 0.8-1.10 kg |
| Number of fruits/plant | 3.47-4.27 |

Keeping in view, a monoecious line of muskmelon was identified and purified through inbreeding from the genetic stock collected from Sirohi district of Rajasthan (Choudhary, 2013). Single plant selection was exercised based on earliness, fruit size, flesh colour and TSS. Finally, the obtained population was tested for stability and observed stable monoecious sex form (Choudhary *et al.*, 2013). Plants of IC0599709 produced round fruits with salmon orange coloured flesh and develop full slip at ripening. The biochemical analysis has been done for total sugar (336.97 mg/g), tannin content (0.12 mg/g), phenol content (34.73 mg/g) and flavonoid content (1.05 mg/g) on dry weight basis (Haldhar *et al.*, 2013). Thus, the presence of stable monoecious sex form in IC0599709 could be utilized in $F_1$ hybrid production of muskmelon.

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## 3. Phoobsering-1258 (IC0610194; INGR 14044), a Tea (*Camellia sinensis* (L.) O. Kuntze) Hybrid with Thick Cuticle

*Department of Plant Physiology and Breeding, Tocklai Tea Research Institute, TRI, Jorhat-785008, Assam, India (Email:director@tocklai.net)*

P 1258 (*Camellia sinensis* L. var. P1258) is a China hybrid which was developed and released by Tocklai Tea Research Institute, Tea Research Association, in 1987 for cultivation in the hills of Darjeeling (Singh, 1989). The progeny selection method of plant breeding was applied to develop the hybrid.

**Morpho-agronomic characteristics:** The bush frame of the hybrid is compact and spreading. The leaf is ovate in shape. Apex of the leaf is acuminate and leaf base is obtuse in nature. The clone is high yielding but of average flavour.

**Associated characters and cultivation practices:** The clone is a drought tolerant and grows luxuriantly in lower elevation compared to high and mid elevations of Darjeeling hills (Barman, 2013). The clone is resistant to virulent diseases of tea especially in the hills of Darjeeling, the Blister Blight, possibly because of its thick cuticle in leaf (Debnath and Paul, 1994). It is fairly tolerant to red spider and other mites (Singh, 1989)

### References

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## 4. Phoobsering-1404 (IC0610195; INGR 14045), a Tea (*Camellia sinensis* (L.) O. Kuntze) Hybrid with Thickest Epidermal Cell Layer

*Department of Plant Physiology and Breeding, Tocklai Tea Research Institute, TRI, Jorhat-785008, Assam, India (Email:director@tocklai.net)*

Phoobsering-1404 (*Camellia sinensis* L. var. P1404)-Assam hybrid tea variety which was developed through progeny selection and released in 1985 by the Tocklai Tea Research Institute, Tea Research Association, for commercial cultivation in the hills of Darjeeling (Singh, 1985). It is interesting to note that it contains the thickest epidermal cell layer among all the Darjeeling clones released by the institute for commercial cultivation (Debnath and Paul, 1994).

**Morpho-agronomic characteristics:** The clone is early flusher and vigorous in growth with semi erect, medium size, light colour yellowish green leaf. The leaf is ovate in shape. Apex of the leaf is acuminate and downturned whereas leaf base is obtuse. The clone prefers the agro-climatic condition of lower elevation than high and mid elevations of Darjeeling hills.

**Associated characters and cultivation practices:** The rooting ability of the clone is high and resistance to drought. It is fairly tolerant to mites and blister blight disease (Singh, 1989).

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## 5. Rungali Rungliot-4/5 (IC0610203; INGR 14046), a Tea (*Camellia sinensis* (L.) O. Kuntze) Hybrid with Highest Number of Stomata/mm$^2$ area

*Department of Plant Physiology and Breeding, Tocklai Tea Research Institute, TRI, Jorhat-785008, Assam, India (Email:director@tocklai.net)*

Rungali Rungliot-4/5 (*Camellia sinensis* L. var. RR4/5) - A China hybrid tea variety. The variety was developed through progeny selection method. It was released in 1975 by the Tocklai Tea Research Institute, Tea Research Association for large scale commercial cultivation in the hills of Darjeeling (Sharma *et al*., 1975). Among all of the Darjeeling clones, RR4/5 contains the highest number of stomata in per unit leaf area (Debnath and Paul, 1994).

**Morpho-agronomic characteristics:** The leaves of the clone are semi-erect and dark green in colour. The leaf shape is lanceolate with acuminate leaf apex and attenuate leaf base (Barman, 2013). The young shoots have thick pubescence. The long and slender internodes of the growing shoots are the specific shoot morphology of the clone.

**Associated characters and cultivation practices:** The clone is drought tolerant but susceptible to all mites and fairly tolerant to blister blight (Singh, 1989). The clone grows well in low elevation of Darjeeling hills.

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## 6. Happy Valley-39 (IC0610207; INGR 14047), a Tea (*Camellia sinensis* (L.) O. Kuntze) Hybrid with Rose like Sweety Aroma Synthesises Highest Hexanal and t-2-Hexanal

*Department of Plant Physiology and Breeding, Tocklai Tea Research Institute, TRI, Jorhat-785008, Assam, India (Email:director@tocklai.net)*

Happy Valley-39 (*Camellia sinensis* L. var. HV-39) is a China hybrid which was developed and released by the Tocklai Tea Research Institute, Tea Research Association, in 1987 for cultivation in the hills of Darjeeling (Singh, 1989). The progeny selection method of plant breeding was applied to develop the variety. It synthesized the highest Hexanal and t-2-Hexanal among cultivars of Darjeeling hills and produces a attractive rose like sweet aroma (Bhuyan *et al*., 2012)

**Morpho-agronomic characteristics:** The bush frame of the variety is widely spreading and compact. The leaves are semi- erect, grayish dark green in colour. Shoot pubescence is very high. The leaf shape is lanceolate with acuminate leaf apex and attenuate leaf base. The flavour produced by this clone is above average.

**Associated characters and cultivation practices:** The clone has good rooting ability and can withstand at higher degree of soil moisture deficit. It has fairly resistant to red spider mites but susceptible to blister blight disease (Singh, 1989). The clone grows luxuriantly in lower elevation compared to high and mid elevations of Darjeeling hills.

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## 7. IIHR CA H13A (IC0610420; INGR14048), a China aster (*Callistephus chinensis* (L.) Nees.) Pure line with Early flowering and Higher Number and Weight of Flowers/Plant

**Rajiv Kumar[1*], T Manjunatha Rao[1] and T Janakiram[2]**

[1]*Division of Ornamental Crops, IIHR, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India*

[2]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi-110012, India*

[*]*(Email: rajiv@iihr.ernet.in)*

China aster [(*Callistephus chinensis* (L.) Nees] is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for its loose flowers, cut flower, landscape, floral decorations, making garlands and *venis*. The Pureline IIHR CA H13A is unique in early flowering, higher number and weight of flowers per plant. It is derived from the open pollinated seeds of Line No.173 through Individual Plant Selection developed at IIHR, Bengaluru, Karnataka (13$^{o}$ 58' N Latitude, 78$^{o}$E Longitude and 890 m above mean sea level) (IIHR Annual Report, 2013-14).

**Morpho-agronomic characteristics:** The plants are spreading type, medium in height. It is floriferous, flowers are pink (RHS 62.A) in colour, semi-double, 5.48 cm in diameter with 5-6 rows of ray florets. It produces more number of branches per plant and has extended blooming period.

**Table 1. Morpho-agronomic description of China aster Pureline IIHR CA H13A (pooled data of three years)**

| Characters | IIHR CA H13A |
|---|---|
| Plant height (cm) | 50.62 |
| Plant spread (cm) | 44.45 |
| Number of branches/plant | 16.30 |
| Days to flowering | 66.44 |
| Stalk length (cm) | 41.39 |
| Flower head diameter (cm) | 5.48 |
| Number of flowers/plant | 71.89 |
| Loose flower yield/plant (g) | 178.56 |
| Blooming period (days) | 16.11 |
| Shelf life (days) | 4.28 |
| Flower colour (RHS) | 62.A |
| Utility | Loose flower and bedding |

**Associated characters and cultivation practices:** It has field tolerance to lodging and does not require additional staking, and flowers have higher shelf life. It grows best in open and well drained loamy soil with soil pH 6-7. 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 flower production. Seeds are sown thinly on raised bed in rows across the length at 10-12 cm apart or in pro-trays with cocopeat as a substrate media. Thirty days seedlings should be transplanted at a spacing of 30 cm x 30 cm in four rows. Plants are pinched 35 to 40 days of transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra by marginal and small farmers (Rao *et al.*, 2012).

### References

IIHR Annual Report (2013-14) *Research Achievement*. The Director, IIHR, Bengaluru, p 44.

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## 8. IIHR CA J17 (IC0610421; INGR14049), a China aster (*Callistephus chinensis* (L.) Nees.) Pure Line with Early flowering, Higher Number and Weight of Flowers/Plant

**Rajiv Kumar[1*], T Manjunatha Rao[1] and T Janakiram[2]**

[1]*Division of Ornamental Crops, IIHR, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India*

[2]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi 110012, India*

[*]*(Email: rajiv@iihr.ernet.in)*

China aster [*Callistephus chinensis* (L.) Nees] is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for its loose flowers, cut flower,

landscape, floral decorations, making garlands and *venis*. The Pureline IIHR CA J 17 is unique in early flowering, higher number and weight of flowers per plant. It is derived from self seeds of Line No.15 through Individual Plant Selection at IIHR, Hessaraghatta Lake Post, Bengaluru-560 089, Karnataka (13$^{o}$ 58' N Latitude, 78$^{o}$E Longitude and 890 m above mean sea level) (IIHR Annual Report, 2013-14).

**Morpho-agronomic characteristics:** Plants are spreading type, medium in height. It is floriferous, flowers are white (RHS NN155.C) in colour, semi-double, 4.92 cm in diameter with 4 rows of ray florets. It produces more number of branches and flowers per plant. Flowers remain in blooms for about 18.44 days.

**Table 1. Morpho-agronomic description of China aster Pureline IIHR CA J17 (pooled data of three years)**

| Character | IIHR CA J 17 |
|---|---|
| Plant height (cm) | 47.21 |
| Plant spread (cm) | 46.92 |
| Number of branches/plant | 19.90 |
| Days to flowering | 69.40 |
| Stalk length (cm) | 45.20 |
| Flower head diameter (cm) | 4.92 |
| Number of flowers/plant | 84.34 |
| Loose flower yield/plant (g) | 222.62 |
| Blooming period (days) | 18.44 |
| Shelf life (days) | 3.55 |
| Flower colour (RHS) | NN155.C |
| Utility | Loose flower and bedding |

**Associated characters and cultivation practices:** It has field tolerance to lodging and does not require additional staking, and loose flowers have good shelf life. It grows best in open and well drained loamy soil with pH 6-7. 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 development of flowers. Seeds are sown thinly on raised bed in rows across the length at 10-12 cm apart or in pro-trays with cocopeat as a substrate media. Thirty days seedlings should be transplanted at a spacing of 30 cm × 30 cm in four rows. Plants are pinched 35 to 40 days of transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra by marginal and small farmers (Rao *et al.*, 2012).

## References

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# 9. IIHR-35 (IC0610422; INGR14050), a China aster (*Callistephus chinensis* (L.) Nees.) Pure Line with Violet (83.A) Flower Colour and Pompon Flower Type

**SS Negi[1], SPS Raghava[2], T Manjunatha Rao[3*], T Janakiram[4] and Rajiv Kumar[3]**

[1]*Central Institute for Subtropical Horticulture, Lucknow-227107, Uttar Pradesh, India*

[2]*AICRP on Floriculture, New Delhi-110012, India*

[3]*Division of Ornamental Crops, IIHR, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India*

[4]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi-110012, India*

[*]*(Email: tmrao@iihr.ernet.in)*

China aster [*Callistephus chinensis* (L.) Nees] is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for its loose flowers, cut flower, landscape, floral decorations, making garlands and venis. The flowers of pureline IIHR-35 have unique colour Violet (RHS 83.A) and pompon type. It is an advanced pedigree selection of the cross between 'Local Pink' × 'AST-2' developed at IIHR, Hessaraghatta Lake Post, Bengaluru-560 089, Karnataka (13$^{o}$58' N Latitude, 78$^{o}$E Longitude and 890 m above mean sea level) (IIHR Annual Report, 2013-14).

**Morpho-agronomic characteristics:** The plants are erect type, medium in height. It flowers 130 days after sowing. It produces Pompon type of flowers having 4-5 rows of ray florets with tubular disc of 4.5 cm diameter. On an average its flowers weigh 2 g each with stalk length of 19 cm.

**Associated characters and cultivation practices:** It produces high flower yield (113 g flowers/plant) and cut flowers have vase life of 8 days. It grows best in open and well drained loamy soil with pH 6-7. A temperature 20 to 30$^{o}$C during day and 15 to 17$^{o}$C during night

**Table 1. Morpho-agronomic description of China aster Pureline IIHR-35**

| Characters | IIHR-35 |
|---|---|
| Plant height (cm) | 57 |
| Stalk length (cm) | 19 |
| Flower diameter (cm) | 4.5 |
| Flower weight (g) | 2 |
| Number of flowers/plant | 70 |
| Flower yield/plant (g) | 113 |
| Days to flower | 130 |
| Vase life (days) | 8 |
| Flower type | Pompon |
| Flower colour (RHS) | Violet (83.A) |
| Utility | Garland, floral decoration and cut flower |

with relative humidity of 50-60% is most suitable for development of flowers. Seeds are sown thinly on raised bed in rows across the length at 10-12 cm apart or in pro-trays with cocopeat as a substrate media. Thirty days seedlings should be transplanted at a spacing of 30 cm × 30 cm in four rows. Plants are pinched 35 to 40 days of transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra by marginal and small farmers (Rao *et al.*, 2012).

## References

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# 10. IIHR-42 (IC0610423; INGR14051), a China aster (*Callistephus chinensis* (L.) Nees.) Pure Line with Creamy White Flower Colour and Powderpuff Flower Type. Resistant to Rootknot Nematode (*Meloidogyne incognita* race 1)

**T Manjunatha Rao[1*], SS Negi[2], SPS Raghava[3], T Janakiram[4] and Rajiv Kumar[1]**

[1]*Division of Ornamental Crops, IIHR, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India*

[2]*Central Institute for Subtropical Horticulture, Lucknow-227107, Uttar Pradesh, India*

[3]*AICRP on Floriculture, New Delhi-110012, India*

[4]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi-110012, India*

[*]*(Email: tmrao@iihr.ernet.in)*

China aster [*Callistephus chinensis* (L.) Nees] is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for its loose flowers, cut flower, landscape, floral decorations, making garlands and *venis*. The flowers of pureline IIHR-35 have unique colour Creamy white (RHS 4.B), Powderpuff type, and resistant to root knot nematode (*Meloidogyne incognita* race 1). It is an advanced pedigree selection of the cross between 'Local Pink' x 'AST-2' developed at IIHR, Hessaraghatta Lake Post, Bengaluru-560 089, Karnataka (13$^{o}$ 58' N Latitude, 78$^{o}$ E Longitude and 890 m above mean sea level) (IIHR Annual Report, 2013-14).

**Morpho-agronomic characteristics:** The plants are erect type, medium in height and flowers 124 days after sowing. On an average its flowers weigh 2.37 g each, having 24.68 cm of flower stalk.

**Associated characters and cultivation practices:** It produces 44 flowers per plant, yields 104 g loose flowers per plant and cut flowers have vase life of 9 days. It

**Table 1. Morpho-agronomic description of China aster Pureline IIHR-42**

| Characters | IIHR-42 |
|---|---|
| Plant height (cm) | 56.13 |
| Stalk length (cm) | 24.68 |
| Flower diameter (cm) | 5.76 |
| Flower weight (g) | 2.37 |
| Number of flowers/plant | 44.17 |
| Flower yield/plant (g) | 104.41 |
| Days to flower | 124.42 |
| Vase life (days) | 9.00 |
| Flower type | Powderpuff |
| Flower colour (RHS) | Creamy white (4.B) |
| Utility | Cut flower, floral decoration and garden display |

grows best in open and well drained loamy soil with soil pH 6-7. A temperature 20 to 30$^{o}$C during day and 15 to 17$^{o}$C during night with relative humidity of 50-60% is most suitable for development of flowers. Seeds are sown thinly on raised bed in rows across the length at 10-12 cm apart or in pro-trays with cocopeat as a substrate media. Thirty days seedlings should be transplanted at a spacing of 30 cm × 30 cm in four rows. Plants are

pinched 35 to 40 days of transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra by marginal and small farmers (Rao *et al.*, 2012).

## References

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# 11. P-16-1 x Eurovision (IC0611879; INGR 14052), an Early Blooming Gladiolus (*Gladiolus hybridus* Hort.) Germplasm which Flowers in 76-80 days after Planting and Florets Colour in Red Group

**T Janakiram[1*] and Kishan Swaroop[2]**

[1]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi-110012, India*

[2]*Division of Floriculture and Landscaping, Indian Agricultural Research Institute, New Delhi-110012, India*

[*]*(Email: tolety07@gmail.com)*

Gladiolus is one of the most important bulbous ornamentals for garden display, floral arrangements and cut flowers (Lepcha *et al.,* 2007). Multiplication of gladiolus is most important on large scale for availability of good quality germplasm/planting materials (Barman *et al.*, 2005). It is also essential to develop Indian hybrids/lines and evaluate them in comparision to the existing cultivars for their superior desirable characters (Archana *et al.,* 2007).

The fifteen gladiolus hybrids/lines along with check were evaluated for three years for earliness, higher multiplication and other unique characters. The germplasm was developed from the Melody Open (A selection among the open pollinated seedlings of the variety melody and another germplasm was a cross between P-16-1 x Eurovision. Initially this material was received at IARI, from secondary sources.

The two developed germplasms were evaluated in randomized block design with three replications. The evaluation revealed that among the 15 hybrids/lines, the most promising germplasm IC-14156 and IC14156 were identified as early to medium flowering and higher multiplier. The key morphological features of both the germplasm are provided here under:

It is early flowering (76-80 days after planting). Spikes are straight and long with good rachis length (48-59 cm) and close arrangement of florets on spike. Florets colour in red group (41 C, RHS colour chart) with dark stripes on inner two tepals (42 A, RHS colour chart) and red spots on outer throat which makes them more attractive. It produces straight and long spikes with more than 16 florets/spike. (Table. 1 a, b and c)

**Table 1. Performance of P-16-1 × Eurovision for growth and flowering (2011, 2012 and 2013)**

**a. Performance over parents during 2011**

| Character | P-16-1 × Eurovision | Parents | | C D at 5% |
|---|---|---|---|---|
| | | P-16-1 | Eurovision | |
| Plant height (cm) | 119.0 | 107.33 | 111.66 | 4.32 |
| Number of leaves | 6.33 | 7.33 | 6.33 | 0.33 |
| Number of shoots/corm | 2.00 | 1.66 | 2.00 | 0.29 |
| Days to flowering (days) | 80.00 | 83.00 | 85.33 | 1.87 |
| Spike length (cm) | 92.33 | 89.00 | 90.00 | 1.10 |
| Rachis length (cm) | 59.33 | 50.33 | 46.00 | 2.91 |
| Number of florets/spike | 17.00 | 13.33 | 13.00 | 2.19 |
| Floret diameter (cm) | 10.26 | 9.66 | 10.00 | 0.21 |
| Stem thickness (cm) | 1.88 | 1.75 | 1.82 | NS |
| Spike longevity (flowering days in field) | 33.33 | 25.00 | 30.00 | 2.33 |
| Number of corms/plant | 2.00 | 1.66 | 1.33 | 0.22 |
| Number of cormels/plant | 45.00 | 35.00 | 43.00 | 2.60 |
| Spike vase life in tap water (days) | 8.66 | 7.33 | 7.66 | NS |

**b. Performance over parents during 2012**

| Character | P-16-1 × Eurovision | Parents | | CD at 5% |
|---|---|---|---|---|
| | | P-16-1 | Eurovision | |
| Plant height (cm) | 117.66 | 110.33 | 115.67 | 1.65 |
| Number of leaves | 6.33 | 6.33 | 7.00 | NS |
| Number of shoots/corm | 2.33 | 1.99 | 2.00 | 0.23 |
| Days to flowering (days) | 76.00 | 81.00 | 78.00 | 1.61 |
| Spike length (cm) | 98.33 | 90.00 | 93.00 | 7.38 |
| Rachis length (cm) | 57.33 | 53.33 | 51.00 | 2.37 |
| Number of florets/spike | 15.66 | 14.33 | 14.00 | 0.17 |
| Floret diameter (cm) | 9.50 | 9.16 | 9.33 | NS |
| Stem thickness (cm) | 1.86 | 1.75 | 1.80 | NS |
| Spike longevity (flowering days in field) | 28.00 | 27.00 | 28.00 | NS |
| Number of corms/plant | 2.33 | 1.66 | 2.00 | 0.25 |
| Number of cormels/plant | 42.33 | 37.00 | 40.00 | 1.87 |
| Spike vase life in tap water (days) | 9.00 | 8.33 | 8.00 | NS |

**c. Performance over parents during 2013**

| Character | P-16-1 × Eurovision | Parents | | CD at 5% |
|---|---|---|---|---|
| | | P-16-1 | Eurovision | |
| Plant height (cm) | 112.66 | 109.33 | 111.67 | 0.33 |
| Number of leaves | 6.00 | 5.99 | 6.00 | NS |
| Number of shoots/corm | 2.66 | 1.99 | 2.00 | 0.07 |
| Days to flowering (days) | 78.00 | 82.00 | 79.00 | 1.33 |
| Spike length (cm) | 88.66 | 86.00 | 85.00 | 0.43 |
| Rachis length (cm) | 48.33 | 47.33 | 46.00 | 0.22 |
| Number of florets/spike | 16.66 | 14.33 | 14.00 | 0.99 |
| Floret diameter (cm) | 9.83 | 9.11 | 9.50 | NS |
| Stem thickness (cm) | 1.88 | 1.73 | 1.80 | 0.03 |
| Spike longevity (flowering days in field) | 29.00 | 24.00 | 27.00 | 0.32 |
| Number of corms/plant | 2.33 | 2.00 | 2.00 | 0.08 |
| Number of cormels/plant | 35.00 | 30.00 | 32.00 | 0.66 |
| Spike vase life in tap water(days) | 9.00 | 8.33 | 8.50 | NS |

## 12. Melody Open (IC0611878; INGR 14053), a Very Early Flowering (74 days after planting) Gladiolus (*Gladiolus hybridus* Hort.) Germplasm with Florets Colour in Red Group

**T Janakiram[1*] and Kishan Swaroop[2]**

[1]*ICAR, Horticultural Science Division, KAB-II, Pusa, New Delhi-110012, India*

[2]*Division of Floriculture and Landscaping, Indian Agricultural Research Institute, New Delhi-110012, India*

[*]*(Email: tolety07@gmail.com)*

**Melody Open:** This hybrid is very early and comes in flowering about 74 days. The outer florets are in red group (50C, RHS colour chart) and inner tepals (49B, RHS colour chart), with red spots on the centre of two tepals and white stripes on all tepals. Spikes are straight and long with good rachis length and close arrangement of florets on spikes. It has good spike length (more than 100 cm), rachis length more than 62.00 cm and number of florets/spike are 18.44. Further it is a higher multiplier and produces more than 2 corms and 42.55 cormels from each mother corm. (Table 2 a, b and c)

Both the germplasm/lines are recommended for NCR of Delhi and Northern plains of India.The soil pH 6-7 is recommended for the cultivation of gladiolus. At the time of planting, the soil should have sufficient moisture. The best time of planting in North Indian plains is first week of October. Healthy corms of 5-6 cm diameter should be selected. The quantity of corms depends on the planting distance, size of corms and method of planting. Generally 50-60 thousands corms/acre or 1.25-1.50 lakh corms/ hectare are to be planted at 45 cm in single row system and 60 cm in double row system keeping plant to plant

**Table 2. Performance of "Melody Open" for growth and flowering (2011, 2012 and 2013)**

**a. Performance over parents during 2011**

| Character | Melody Open | Parent variety ('Melody') | CD at 5% |
|---|---|---|---|
| Plant height (cm) | 122.00 | 98.33 | 4.66 |
| Number of leaves | 6.33 | 6.00 | 0.16 |
| Number of shoots/corm | 2.99 | 2.00 | 0.33 |
| Days to flowering (days) | 74.00 | 72.00 | 1.33 |
| Spike length (cm) | 104.00 | 70.66 | 5.66 |
| Rachis length (cm) | 62.00 | 42.66 | 3.33 |
| Number of florets/spike | 18.33 | 14.33 | 1.22 |
| Floret diameter (cm) | 10.00 | 8.50 | 1.13 |
| Stem thickness (cm) | 2.00 | 1.94 | NS |
| Spike longevity in field (day) | 39.00 | 32.00 | 1.99 |
| Number of corms/plant | 2.66 | 2.00 | 0.23 |
| Number of cormels/plant | 42.66 | 25.00 | 5.99 |

**b. Performance over parents during 2012**

| Character | Melody Open | Parent variety ('Melody') | CD at 5% |
|---|---|---|---|
| Plant height (cm) | 124.00 | 107.00 | 10.10 |
| Number of leaves | 6.33 | 6.33 | NS |
| Number of shoots/corm | 2.66 | 2.00 | 0.32 |
| Days to flowering (days) | 75.00 | 73.33 | 1.13 |
| Spike length (cm) | 114.00 | 88.33 | 7.11 |
| Rachis length (cm) | 64.86 | 49.33 | 6.22 |
| Number of florets/spike | 19.00 | 16.67 | 1.36 |
| Floret diameter (cm) | 11.10 | 8.66 | 0.99 |
| Stem thickness (cm) | 2.10 | 1.97 | NS |
| Spike longevity (Flowering in field days) | 41.00 | 33.00 | 3.66 |
| Number of corms/plant | 2.99 | 2.11 | 0.33 |
| Number of cormels/plant | 45.00 | 28.00 | 3.22 |

**c. Performance over parents during 2013**

| Character | Melody Open | Parent variety ('Melody') | CD at 5% |
|---|---|---|---|
| Plant height (cm) | 118.66 | 99.00 | 3.07 |
| Number of leaves | 6.66 | 6.33 | NS |
| Number of shoots/corm | 2.66 | 1.99 | 0.22 |
| Days to flowering (days) | 73.33 | 71.00 | 0.36 |
| Spike length (cm) | 103.00 | 73.66 | 3.46 |
| Rachis length (cm) | 65.00 | 45.00 | 2.29 |
| Number of florets/spike | 18.00 | 15.66 | 1.05 |
| Floret diameter (cm) | 10.95 | 8.44 | 1.06 |
| Stem thickness (cm) | 2.11 | 1.89 | NS |
| Spike longevity (Flowering in field days) | 40.00 | 31.00 | 4.11 |
| Number of corms/plant | 3.00 | 2.33 | 0.31 |
| Number of cormels/plant | 40.00 | 27.00 | 6.33 |

distance at 15 cm. Planting depth may be kept as 5-8 cm in soil. The corms after planting should be covered at least 4 cm by adjoining soil. Well rotten F.Y.M. @ 300 quintal/ha should be added in the soil at the time of field preparation. Chemical fertilizers application depend upon the fertility of the field, however, according to a general recommendation it is applied as 80-120 kg N, 80-100 kg P and 100 kg K/ha.

There are two major disease, *Fusarium* wilt which causes geotropic bending of plants and yellowing, and finally corm rotting. Another disease *Botrytis* which infects during cold, windy and humid weather, but can be controlled by weekly spraying with Dithane M-45 @ 0.2 % spraying. Gladiolus is attacked by insects and mites and sometimes aphids, termite, thrips etc. also attack in gladiolus which can be controlled by spraying of Malathion @0.2 % or Nuvan 0.2 %. For local market, when first floret is open and for distant markets when bottom florets showing colour should be harvested by leaving 4 leaves intact on the plants. Spikes should be packed in corrugated sheet in bundles of dozen each, which stand well at the atmospheric temperature for short distances and overnight journey.The number of corms would be doubled (one plant produces two corms), hence about 1, 20,000 spikes/acre will be produced.

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# 13. Sel-5 (IC0610820; INGR 14054), a Makhana (*Euryale ferox* Salisb.) Germplasm with White flowers


**Lokendra Kumar**

*ICAR Research Complex for Eastern Region, Research Centre for Makhana, Darbhanga-800014, Bihar, India (Email: dr.lokendrakumar@yahoo.com)*


Makhana *(Euryale ferox* Salisb), also known as Gorgon nut or Fox nut, is a prickly water plant with gigantic floating leaves (Das and Patnayak, 2003). In lowland areas of eastern India (north Bihar and parts of Assam, West Bengal and Orissa), makhana is grown as an important cash crop for its popped seeds.

**Table 1. Descriptor and descriptor state of Sel-5 (IC0 610820, INGR14054) line of makhana (average over 4 years)**

| Descriptor | Descriptor state |
|---|---|
| Days to seedling emergence | 31.2 |
| Seedling vigor | High |
| Leaf shape | Orbicular |
| Leaf diameter | 127.3 cm |
| Flower size | Small |
| Flower colour | White |
| Days to 50% flowering | 126 days |
| Fruit shape | Spheroid |
| Fruit colour | Brown |
| Status of fruit prickles | Very dense |
| Size of fruit prickles | 1.3 cm |
| Fruit diameter | 5.5 cm |
| Number of seeds/fruit | 68.5 |
| Number of fruits/plant | 14.2 |
| Seed yield /fruit | 40.3 g |
| Seed yield /plant | 547.9 g |
| Seed colour | Black |
| Seed shape | Spherical |
| 100-seed weight | 66.8 g |
| Seed diameter | 6.6 mm |

**Morpho-agronomic characteristics:** Purple is the characteristic color of flowers in makhana (Kumar *et al*., 2011). Contrary to purple flowers, this line possesses white flowers. In addition to white flowers, it is unique due to high number of fruits/plant. Fruits are brown in colour and covered with dense prickles.

**Traits of interest:** It can be used to study the inheritance pattern of flower color in makhana. Further, it can be utilized in breeding programmes for incorporating the trait of high number of fruits/plant


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# 14. Korgut (IC0599689; INGR 14055), a Rice (*Oryza sativa* L.) Germplasm Tolerant (SES score 3) to Salinity Stress (EC=12 dS/m) at Seedling Stage


**Manohara KK[1*], Krishnendu Chattopadhyay[2], Bishnu Charan Marndi[2], Onkar Nath Singh[2] and Narendra Pratap Singh[1]**

[1]*ICAR Research Complex for Goa, ELA, Old Goa-403402, Goa, India*

[2]*Crop Improvement Division, ICAR-Central Rice Research Institute,Cuttack-753006, Odisha, India*

[*]*(Email: manohar.gpb@gmail.com)*


Korgut, a traditional rice landrace from the State of Goa, was collected during *kharif* 2010 in farmers' field at Chorao Island of North Goa District (Manohara and Singh, 2013). It is being conserved and maintained at

ICAR Research Complex for Goa. Phenotyping for salt stress tolerance at seedling stage under hydroponics culture with EC = 12 dS/m was conducted at CRRI, Cuttack in *kharif* 2012 and repeated in *kharif* 2013. It showed tolerance (SES score 3) to salinity stress at seedling stage. Its tolerance was associated with low ratio of $Na^+$-$K^+$ (0.18) in shoot as compared to susceptible check IR29 (0.68) (CRRI Annual report 2011-12; Nath *et al.,* 2013; NICRA, 2012).

**Morpho-agronomic characteristics:** Based on the data recorded during *kharif* 2012 & 2013, the mean values of different agro-morphological and yield and its components are given in Table 1.

**Associated characters and cultivation practices:** Korgut is cultivated during *kharif* season between June to October month. It shows an additional trait of early seedling vigour which aids in establishment under the stress situation. Farmers' cultivate this rice accession by direct sowing with limited use of chemical inputs. Hence, the packed rice of this landrace fetches premium price in the market. Apart from this, the accession has various other uses such as suitability for parboiled rice; for ganji preparation; and has a property of slow digestion upon consumption. This germplasm can be used as a genetic stock for future breeding programmes aiming at development of high yielding salt tolerant rice varieties for coastal saline soils.

**Table 1. Agro morphological description of the rice germplasm Korgut**

| Characteristics | Description |
|---|---|
| Basal leaf sheath colour | Green |
| Early plant vigour | Intermediate |
| Days to 50% flowering | 92 |
| Days to maturity | 123 |
| Plant height (cm) | 145 |
| Leaf length (cm) | 49.03 |
| Leaf width (cm) | 1.26 |
| No. of tillers/plant | 7-8 |
| Panicle type | Semi erect |
| Panicle length (cm) | 29.80 |
| Panicle exertion | Mostly exerted |
| Awning | Fully awned |
| Apiculi colour | Brown |
| Stigma colour | White |
| 100 grain weight (g) | 3.26 |
| Decorticated grain length (mm) | 6.19 |
| Decorticated grain width (mm) | 2.56 |
| L/B ratio | 2.54 |
| Hull colour | Brown |
| Grain yield (t/ha) | 1.5 - 2.0 |

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# 15. IC0144901 (IC0144901; INGR 14056), a Black gram (*Vigna mungo* (L.) Hepper.) Germplasm Resistant to Mungbean Yellow Mosaic Virus (MYMV)

**NK Gautam*, Manas Kumar Bag, TV Prasad, Sushil Pandey, Anirban Roy, Neeta Singh, Babu Ram and M Dutta**

*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*

**(Email nkgautam@nbpgr.ernet.in, nkgautam54@gmail.com)*

Yellow mosaic disease (YMD) is a major constraint in improving the productivity of a variety of leguminous crops including blackgram. In order to identity potential sources of resistance that could serve as valuable genetic resource for future disease resistance breeding programme a part from national collection of blackgram germplasm was screened against mungbean yellow mosaic virus (MYMV) and IC-144901 a collection from Kanpur, Uttar Pradesh, India, was identified as highly resistant germplasm. Field experiments were conducted at NBPGR experimental farm, New Delhi (geographical co-ordinates 28°64' N, 77°15' E). Two popular blackgram cultivars namely Barabanki Local (highly susceptible) and T-9 (high yielder) were included as checks. The response of 344 blackgram germplasm accessions against the MYMV virus was examined based on incidence and

severity of the symptoms under field conditions with natural disease pressure and the response was different among the accessions during three cropping seasons (*Kharif* 2010-2012). Germplasm accessions indicating resistance response during three consecutive years under natural disease pressure were subjected to further screening through artificial inoculation using viruliferous whiteflies. Those germplasm accessions which showed resistance response after whitefly inoculation were further tested for validation of the resistance through agro inoculation with the infectious cloned DNA-A and DNA-B components of a New Delhi isolate of MYMV. Yield attributing traits of selected accessions were also recorded along with susceptible (Barabanki local) and agronomic checks (T-9) and on this basis IC144901 germplasm was observed as an erect, short (25cm), early maturing (70 days), medium grain yielding (8.5 to 10g/plant) having medium seed size (100 seed weight 4.3g). The germplasm accession can be used in YMD resistant breeding programme or can be released directly for cultivation after verifying its adaptation to various regions and accepting quality traits.

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# 16. DOGR-1203-DR (IC0598327; INGR 14057), an Onion (*Allium cepa* L.) Germplasm with Very Early Maturity (harvested within 90 days after transplanting during *rabi*) and 100% Uniform Neck-fall

**Amar Jeet Gupta*, Vijay Mahajan and Jai Gopal**

*ICAR- Directorate of Onion and Garlic Research, Rajgurunagar-410505, Pune, Maharashtra, India*

**(Email: ajgupta@dogr.res.in; guptaaj75@yahoo.co.in)*

The onion varieties developed by different organizations in the country, generally mature in 120-140 days after transplanting in *rabi* season. There is no common onion variety of early maturity in India for *rabi* season. There is need to develop early maturing varieties of onion. The work in this direction led to development of an early maturing elite line DOGR-1203-DR. This has been registered with NBPGR, New Delhi.

The genotype DOGR-1203-DR was developed through mass selection in germplasm collected from Rukatpur, Sukhsagar and Murshidabad (WB). It is better than parental population in respect of uniformity, earliness and yield parameters. It matures in 85-90 days after transplanting and is thus 30-50 days earlier than other onion varieties grown in India (DOGR 2010, 2012 & 2013; AINRPOG 2014). Further, this genotype has dark red bulbs which are in demand. Most of the varieties in cultivation during *rabi* have light red bulbs.

**Morpho-agronomic characteristics:** Plants are erect of 40-50 cm height with 8-10 leaves/plant. Foliage is dark green, waxy and has no cranking. Bulb diameter is 4.0-4.5 cm; height 3.5-4.0 cm and neck thickness 0.4-0.6 cm. Bulbs are very shiny dark red and oval in shape tapering towards neck. These are symmetrical with single axis non-splitting type and have exerted root disc. Bulb skin has strong adherence, rings are medium, purplish with strong firmness of flesh.

It was evaluated along with onion germplasm maintained at DOGR during *rabi* 2010-11, 2011-12 and 2012-13 at Rajgurunagar (Table 1). Complete and uniform neck-fall was observed in this at 85-90 days after transplanting (DOGR 2010 & 2012) (Fig.1). Its average yield is 20-22 t/ha and total soluble solids is 11-12$^0$B. Storability of bulbs is very good. It can be stored up to 5-6 months (DOGR 2011). No crop establishment is observed during *kharif* due to early sets formation in the nursery.

**Table 1. Earliness and neck-fall performance of DOGR-1203-DR and checks**

| Entry | Days to 75% neck fall after transplanting | | | | Days to harvest after transplanting | | | | Percentage of neck-fall at time of harvesting | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | *Rabi* 2010-11 | *Rabi* 2011-12 | *Rabi* 2012-13 | Mean | *Rabi* 2010-11 | *Rabi* 2011-12 | *Rabi* 2012-13 | Mean | *Rabi* 2010-11 | *Rabi* 2011-12 | *Rabi* 2012-13 | Mean |
| DOGR-1203-DR(Dark Red, oval bulbs) | 80.00 | 84.00 | 77.00 | 80.33 | 92.00 | 96.00 | 84.00 | 90.66 | 100.00 | 100.00 | 100.00 | 100.00 |
| Agrifound Light Red (C) (Light Red, globe bulbs) | 119.00 | 122.00 | 117.00 | 119.33 | 119.00 | 126.00 | 118.00 | 121.00 | 70.00 | 75.00 | 73.00 | 72.66 |
| Bhima Kiran (C)(Light Red, globe bulbs) | 108.00 | 121.00 | 113.00 | 114.00 | 111.00 | 125.00 | 116.00 | 117.33 | 76.00 | 74.00 | 75.00 | 75.00 |

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# 17. CNH CB 211 (IC0597397; INGR 14058), a Cotton (*Gossypium hirsutum*) Germplasm with Cluster Boll Bearing Habit, Deeply Palmate Leaf Lobe


**Punit Mohan[1*], Vinita Gotmare[1], BR Rode[1], KR Kranthi[1], M Saravanan[1] and Anjali Kak[2]**

[1]*Central Institute for Cotton Research, post Bag No-2, Shankar Nagar, Nagpur-440010, Maharashtra, India*

[2]*National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi 110112, India*

[*]*(Email: punitmohan@gmail.com)*


CNH CB-211(*Gossypium hirsutum*) is having unique feature cluster boll bearing habit and coupled with deeply palmate leaf lobed developed single boll progeny selection.

**Morpho-taxonomical characters :** Leaf – deeply palmate and lanceolate; bracteoles-3 broad, heart shaped, persistant and anterior portion serrated, gossypol glands present on abaxial and adaxial surfaces; calyx-cup shaped, five lobed, gossypol glands distributed in linear fashion; corolla-five petals, imbricate, yellow, petal blotch absent and gossypol glands distributed randomly; ovary-superior and composed of 3-4 united carpels; bolls/capsules-oval and moderately tapering apex and developed in the form of clusters. Economic features and fibre quality traits are presented in Table 1. The developed genetic stock could ideally serve as a resourceful donor for cluster boll bearing trait, which can serve as an essential component of a breeding programme.

**Table 1. Economic features and fibre quality traits of IC 0597397; INGR 14058**

| | |
|---|---|
| Average seed cotton yield/plant (g) | 54.9 |
| Average boll weight (g) | 4.2 |
| Ginning outturn (%) | 32.0 |
| Seed index (g) | 9.0 |
| Lint index (g) | 4.2 |
| Staple length (mm) | 27.1 |
| Uniformity ratio (%) | 51.0 |
| Micronaire (µg/inch) | 3.3 |
| Fibre bundle strength (g/tex) | 19.2 |
| Fibre elongation (%) | 4.8 |

# 18. CNH CB 212 (IC0597398; INGR 14059), a Cotton (*Gossypium hirsutum*) Germplasm with Cluster Boll Bearing Habit, Zero Monopodia and Compact Habit

**Punit Mohan[1*], Vinita Gotmare[1], BR Rode[1], KR Kranthi[1], M Saravanan[1] and Anjali Kak[2]**

[1]*Central Institute for Cotton Research, post Bag No-2, Shankar Nagar, Nagpur-440010, Maharashtra, India*

[2]*National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110112, India*

[*]*(Email: punitmohan@gmail.com)*

CNH CB-212 is a cluster boll bearing genetic stock developed through single boll progeny selection and differs from CNH CB-212 in the features *viz.,* presence of unique distinct morpho-marker traits *viz.,* normal palmate leaf lobed, shorter monopodia coupled with short internodal length and forms a compact plant stature. Economic features and fibre traits are presented in Table 1. This genetic stock developed for compactness can serve as an essential component in a breeding programme.

**Table 1. Economic features and fibre quality traits of IC0597398; INGR 14059**

| | |
|---|---|
| Average seed cotton yield/plant (g) | 65.3 |
| Average boll weight (g) | 4.0 |
| Ginning outturn (%) | 29.5 |
| Seed index (g) | 9.2 |
| Lint index (g) | 3.8 |
| Staple length (mm) | 27.4 |
| Uniformity ratio (%) | 48.0 |
| Micronaire (µg/inch) | 3.0 |
| Fibre bundle strength (g/tex) | 21.7 |
| Fibre elongation (%) | 4.6 |

# Referees for Volume 28 (1, 2 & 3), 2015

The Editors gratefully acknowledge the help rendered by following referees in reviewing the manuscripts published during 2015.

**Babu Naresh**
Principal Scientist (Horticulture)
Central Institute for Women in Agriculture
Bhubaneswar-751 003, Odisha

**Bhadana VP**
Senior Scientist
ICAR-Indian Institute of Rice Research
Rajendranagar, Hyderabad, Telengana

**Bhardawaj Rakesh**
Senior Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Chandra Ramesh**
Professor & Head
Department of Plant Pathology
Banaras Hindu University
Varanasi-221 005, Uttar Pradesh

**Chaturvedi Sushil K**
Head
ICAR-Indian Institute of Pulse Research
Kalyanpur Kanpur-208 024, Uttar Pradesh

**Chaudhary Babita**
Senior Scientist
Sunhemp Research Station
Pratapgarh-230 001, Uttar Pradesh

**Dubey A K**
Principal Scientist
Division of Fruits and Horticultural Technology
Indian Agricultural Research Institute,
Pusa Campus, New Delhi-110 012

**Dinesh MR**
Principal Scientist & Head
Division of Fruit Crops
ICAR-Indian Institute of Horticultural Research (IIHR)
Bengaluru-560 089, Karnataka

**Dubey SC**
Principal Scientist & Head
Division of Plant Quarantine
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Gangopadhyay KK**
Principal Scientist
ICAR- National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Gopala Krishnan S**
Senior Scientist
Indian Agricultural Research Institute
Pusa Campus, New Delhi-110 012

**Gupta Amar Jeet**
Senior Scientist
Directorate of Onion and Garlic Research
Rajgurunagar-410 505, Maharashtra

**Jayabose C**
Senior Scientist
ICAR-Central Plantation Crops Research Institute
Kasaragod-671 124, Kerala

**Karibasappa GS**
Principal Scientist
National Research Centre for Grapes
Pune-442 307, Maharashtra

**Khar Anil**
Principal Scientist
Indian Agricultural Research Institute
Pusa Campus, New Delhi-110 012

**Kochhar Sudhir**
Block C, Sector 18, Rohini
New Delhi-110 089

**Kumar Sundeep**
Senior Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Lal G**
Principal Scientist
National Research Centre on Seed Spices
Ajmer-305 006, Rajasthan

**Mary Sheela**
Scientist
ICAR- National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Mishra AK**
Officer-In-Charge
ICAR- NBPGR Regional Station,
Shillong-793 103, Meghalaya

**Mitra Jiban**
Principal Scientist
ICAR-Central Research Institute for Jute and Allied Fibres
Kolkata-700 120, West Bengal

**Naimuddin**
Senior Scientist
Division of Plant Pathology
ICAR-Indian Institute of Pulses Research
Kanpur-208 024, Uttar Pradesh

**Negi KS**
Principal Scientist
ICAR-NBPGR Regional Station
Bhowali-263 132 Uttarakhand

**Pandey Arun Kumar**
Professor
University of Delhi
New Delhi-110 007

**Rana RS**
D-43, Indraprastha Apartments
Sector 14, Rohini, New Delhi-110 025

**Singh Rakesh**
Principal Scientist
ICAR- National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Sthapit Bhuwon**
Regional Project Coordinator
Bioversity International
93.4 Dharahara Marg, Fulbari, Ward #11
Pokhara, Nepal

**Yadav Rashmi**
Senior Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Vasimalla Celia Chalam**
Principal Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Tyagi Vandana**
Principal Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Pandey Anjula**
Principal Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110 012

**Shukla Anil Kumar**
Head
Regional Research Station
Central Arid Zone Research Institute
Pali-Marwar-306 401, Rajasthan

# GUIDELINES TO AUTHORS

## GENERAL

The Indian Journal of Plant Genetic Resources (IJPGR) is the official publication of the Indian Society of Plant Genetic Resources. For publication in the journal, the authors must be a member of the Society. IJPGR publishes full-length papers or short communications of original scientific research in the field of plant genetic resources. Review articles (with prior consent or invitation only) summarizing the existing state of knowledge in topics related to plant genetic resources will also be published.

Contributions should be as concise as possible. The maximum length of the review article, full-length papers and short communications is usually restricted to 12, 6, 3 printed pages including illustrations and tables, respectively.

## ORGANIZATION OF THE MANUSCRIPT

### Full-length papers

**Title Page:** The title page of the manuscript should be the first page and should include the title, names and addresses of the authors, abstract and keywords.

**Title:** Keep the title brief, specific and informative and amendable to indexing. It should be typed in running text with first letter of word as capital and latin names in italics.

**Name and Address:** The name of authors and the address of the institution where the work was carried out should be mentioned below the title. Present address of correspondence, if different, should be given as footnote indicating by asterisk (*) the author to whom the correspondence and reprint requests are to be made. E-mail addresses should also be indicated, if any.

**Abstract:** The abstract should clearly state the rationale, objectives, methods, and important conclusions of the study. It should not exceed 150 words.

**Key Words:** The abstract should be followed by not more than five key words indicating the contents of the paper and useful for abstracting purposes.

**Main Text:** The main text of the paper should start from the second page which should contain the title of the paper followed by the text divided into following main headings which are to be typed in running text and flushed with the margin: Introduction, Materials and Methods, Results, Discussion, Acknowledgements, References. Wherever appropriate, results and discussion can be combined and acknowledgements be omitted.

**Introduction** should be brief and limited to the statement of the problem and aim of the experiment.

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**Results and Discussion** should be clear to readers in different disciplines. Units of measurement should be SI.

**Tables** should be typed on separate sheets, each with a heading stating its contents clearly and concisely. Numerical data and calculations should be thoroughly checked.

**Figures** of only good quality that are essential to a clear understanding of the paper shall be accepted. Legends to the illustrations should be typed on separate paper. Information in the legend should not be repeated in the text and similarly, the same data should not be represented in both graph and table form. All figures, whether photographs, maps, graphs or line drawings should be numbered consecutively. Illustration number and title of the article with authors' name should be given at the back of the plates in soft pencil.

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**Acknowledgements** should mention only guidance or assistance received in real terms, and financial grant provided by an agency. Acknowledgements for inspiration, typing etc., need not be mentioned.

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1. Bisht IS, RK Mahajan, TR Loknathan and RC Agarwal (1998) Diversity in Indian sesame collection and stratification of germplasm accessions in different diversity groups. *Genet. Resour. Crop Evol.* **45**: 325-335.
2. Withers LA and F Engelmann (1998) In vitro conservation of plant genetic resources. In: A Altman (ed.) *Agricultural Biotechnology*. Marcell Dekker Inc., New York, pp 57-58.
3. WOI (1985) *The Wealth of India - Raw Materials. A Dictionary of Indian Raw Materials and Industrial Products - Raw Material* Vol 1: A (Revised). Publications and Information Directorate, Council of Scientific and Industrial Research, New Delhi, 513 p.
4. Engels, JMM and V Ramanatha Rao (eds) (1988) *Regeneration of seed crop and their wild relatives*. Proceedings of a Consultation Meeting, 4-7 December 1995. ICRISAT, Hyderabad, India and IPGRI, Rome, Italy, 167 p.

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