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# CONTENTS

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# Improved Sorghum Restorers for Diverse Uses

**C Aruna*, S. Audilakshmi and JV Patil**
*ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad-500030, Telangana, India*

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Sorghum (*Sorghum bicolor* (L.) Moench) is an important dry land crop which is being used for food, feed, fodder and fuel in the semi-arid tropics of the world. Heterosis breeding is an important component in the yield improvement of sorghum. In an effort to improve the parental lines for yield and quality, a number of restorers were developed for diverse uses using different germplasm lines and genetic stocks at Directorate of Sorghum Research, Hyderabad. Sixty such restorers were evaluated for their grain, fodder and sweet sorghum traits over three years (2008-2010) and restorers promising for different traits over C 43 and the specific checks for sweet and forage sorghum were identified. DSRR84 was the most promising restorer for grain yield, fodder yield and sweet sorghum traits. DSRR79, DSRR456 and DSRR460 were promising for grain and fodder yields. The identified restorers can be used in the breeding programs aimed at development of sorghum hybrids for different target traits.

**Key Words: Brix, Forage, IVDMD, Panicle components, Protein, Sweet sorghum**

## Introduction

Sorghum ranks fifth in area among the cereals after maize, rice, wheat, and barley, on a global scale. It provides food, feed, fodder and fuel to millions of poor farm families and their livestock in the arid and semi-arid tropical regions of the world. In India, demand for sorghum is increasing as sorghum is being utilized in industries, especially as poultry feed (Reddy *et al*., 2005b). It is also being used for production of potable ethanol, syrup, starch and cellulose and other industrial products. Another important use of sorghum is its suitability as a forage crop. The demand for forage sorghum is increasing because the recent efforts towards increasing milk and meat production put an immense pressure for increasing quantities of green and dry fodder. Under the semi-arid situations, sorghum is the major supplier of fodder, and its role becomes important during the lean period of winter and summer months. Sweet sorghum has shown potential as a raw material for fuel-grade ethanol production due to its rapid growth rate, greater water-use efficiency, limited fertilizer requirement, high total value, and wide adaptability (Reddy *et al*., 2005a; Blummel *et al*., 2009). The higher cost of cultivation of sugarcane, highly sensitive molasses prices, and ultimately instabilities in the price of ethanol have created ground to search for an alternative source for ethanol production (Prasad *et al*., 2007).

Through the efforts of sorghum breeders in India, the grain yield levels have increased by more than 50% compared to early sixties (Audilakshmi *et al*., 2003), but of late in India and in the world, the potential yield levels of sorghum are stagnating. Thus, there is an urgent need for use of new diverse parental lines for improving the grain yield levels. Since sorghum is an often cross pollinated crop, heterosis breeding is an important component of sorghum improvement. In general, hybrids are known to produce higher grain and biomass yields, besides being early than the pure line varieties (Reddy *et al*., 2005). Many traits associated with higher grain and biomass yields and quality such as plant height, stem girth, brix and stalk yield are governed by non-additive gene action (Sankarapandian *et al*., 2003; Audilakshmi *et al*., 2010) implying that heterosis breeding will help in developing sorghum hybrids with high yields. Since the requirement of parental lines for different uses of sorghum are different, there is a need for developing sorghum parental lines which suit to different end uses.

Keeping this in view the genetic base of restorers was diversified using diverse germplasm lines from world collection at Directorate of Sorghum Research (DSR). Sixty such restorers were evaluated for their performance for high grain yield, fodder yield and quality. This article aims at identifying improved sorghum restorers that are suitable for different end uses.

**Author for Correspondence: Email- aruna@sorghum.res.in*

## Materials and Methods

A total of 60 restorers were evaluated in RCBD with three replications during rainy season of three years (2008-2010) at DSR, Hyderabad. These were the outcome of an intensive breeding program to improve restorers, where a number of crosses were made by involving germplasm lines from world collection, improved genetic stocks from AICSIP and the elite lines. The germplasm lines that are involved in the promising lines in this study are listed in Table 1. All these restorers were confirmed for their restoration ability. Each entry was planted in two rows of 4 m length with 0.6m spacing between the rows. C43, a restorer of the high yielding kharif sorghum hybrids, CSH 16 and CSH 25 were used as check for comparison. Recommended agronomic practices were followed throughout the crop season. Data on traits related to grain yield, fodder yield and sweet sorghum were recorded on 10 individual plants in all the genotypes in each replication during all the three years.

**Table 1. Germplasm lines involved in the development of promising restorers in the study**

| S No. | Restorer | Germplasm lines involved |
|---|---|---|
| 1 | DSRR81 | SR 532-1-16, CO22 |
| 2 | DSRR84 | IS 23521, IS 3675, IS 3541 |
| 3 | DSRR86 | CO25, MR 836 |
| 4 | DSRR116 | IS 23549, IS 3675, IS 3541, IS 12622, IS 3612, E 35-1 |
| 5 | DSRR306 | IS 3675, IS 3541, IS 23549, CO 18, CO 27 |
| 6 | DSRR307 | SAR 1, IS 3675, IS 3541, IS 23549 |
| 7 | DSRR315 | IS 12622, IS 3612, E 35-1, IS 3687, Aispuri, IS 1151, IS 2947, TNS 30 |
| 8 | DSRR316 | SC 108, IS 2947, IS 3687, IS 1151 |
| 9 | DSRR318 | SB 1085, NSV 13 |
| 10 | DSRR327 | IS 3977, IS 23549, IS 3675, IS 3541 |
| 11 | DSRR329 | IS 23549, IS 3675, IS 3541, IS 12622, IS 3612, E 35-1 |
| 12 | DSRR431 | IS 3691, E 36-1, IS 2947, IS 3687 |
| 13 | DSRR434 | IS 18522, MR 836, IS 3675, IS 3541 |
| 14 | DSRR435 | IS 23521, IS 12622, IS 3612, E 35-1, IS 3687, Aispuri, IS 2947 |
| 15 | DSRR439 | SB 1066, IS 18522 |
| 16 | DSRR443 | IS 23521, IS 12622, IS 3612, E 35-1 |
| 17 | DSRR446 | IS 23549, SAR 1, IS 3675, IS 3541 |
| 18 | DSRR449 | GM 15373, NSV 13 |
| 19 | DSRR456 | IS 3675, IS 3541, IS 23549, CO 18, CO 27 |
| 20 | DSRR458 | IS 12622, IS 3612, E 35-1, IS 3687, Aispuri, IS 2947, IS 3443 |
| 21 | DSRR460 | GMRP 13, NSV 13 |

### *Observations on yield related traits*

Days to 50% flowering was recorded as the number of days required from planting for 50% of the plants in a plot to reach mid-anthesis. Plant height was recorded as the height of the plant from the ground to the tip of the plant at maturity. For estimating the green fodder yield, ten plants were cut at the bottom and the whole plant weight was taken after removing the panicle. For estimating the cane yield, the leaves were removed from the plant and weight of the cane was taken. The panicles were harvested at maturity to record data on grain yield traits like panicle weight, panicle length, number of primary branches, seed yield per plant and 100 seed weight.

### *Observation on quality attributes*

Brix, a measure of the soluble solids, is a widely used approximation for sugar content. The brix values were recorded with hand refractometer at maturity from the juice of stalk of ten plants and their average was taken. For estimating the fodder quality, samples were drawn from whole plants that were harvested for collecting fodder yield, and analysis was done to estimate crude protein percent and *in vitro* dry matter digestibility (IVDMD) in the fodder. For estimation of protein percentage, the total nitrogen of each sample was determined by the Modified Micro-Kjeldahl Method (Jackson, 1973). IVDMD (*In-vitro* Dry Matter Digestibility) was determined by following the technique developed by Mechrej and Orskov (1977).

### *Statistical analysis*

Data of individual locations and pooled over locations were subjected to analysis of variance (ANOVA) using Genstat 12$^{th}$ edition.

## Results and Discussion

The meteorological data during the experimental period of three years is given in Table 2. The results of analysis of variance showed significant differences among the genotypes for all the traits studied except for IVDMD indicating availability of variation among the genotypes studied. The genotype × environment interactions (GEI) were significant for all the traits except for panicle length, crude protein and IVDMD (Tables 3). The significant GEI showed that the genotype performance was influenced by the environment. Although the genotypes showed considerable variation in magnitude in the three environments, none of the lines showed high performance

**Table 2. Meteorological data during the crop period for three years (2008-2010)**

| Month and Year | Temperature | | Relative humidity % | | Rainfall (mm) | Rainy days |
|---|---|---|---|---|---|---|
| | Minimum | Maximum | I | II | | |
| 2008 | | | | | | |
| June | 34.5 | 25.0 | 73 | 45 | 66.7 | 6 |
| July | 32.3 | 24.4 | 79 | 58 | 83.7 | 8 |
| August | 29.3 | 23.1 | 89 | 70 | 172.5 | 15 |
| September | 30.1 | 22.4 | 91 | 71 | 204.6 | 7 |
| 2009 | | | | | | |
| June | 36.3 | 24.8 | 72 | 41 | 82.0 | 5 |
| July | 32.0 | 23.4 | 80 | 57 | 54.0 | 4 |
| August | 31.2 | 23.3 | 81 | 64 | 203.7 | 9 |
| September | 31.4 | 22.2 | 90 | 64 | 165.5 | 9 |
| 2010 | | | | | | |
| June | 35.2 | 24.7 | 82 | 60 | 113.7 | 6 |
| July | 29.4 | 22.5 | 89 | 77 | 278.9 | 16 |
| August | 30.3 | 22.6 | 91 | 75 | 203.1 | 13 |
| September | 29.6 | 22.2 | 89 | 71 | 243.8 | 13 |

in one environment and very poor performance in other environment. This indicates that the environmental effects did not override the genotype performance.

The mean values of grain yield, fodder yield and cane yield were found to be less during the third year which could be due to retardation of initial plant growth because of high rainfall (Table 2). Promising genotypes for grain yield, sweet sorghum and fodder yield are given in the Tables 4, 5 and 6.

### *Promising restorers for grain yield traits*

The grain yield of the genotypes evaluated ranged from 26.8 to 88.3g per plant. DSRR84 was the highest grain yielder with significantly higher grain yield compared to the check, C43, whileDSRR458, DSRR456, DSRR306 and DSRR460 yielded statistically on par with the check. Even though yield per se is important, individual yield components play an important role in improving grain yield through component breeding where the genotypes will be improved for yield components through pyramiding of the genes responsible for different yield components such as number of primary branches, number of secondary branches, number of grains/panicle, panicle length, width and weight etc (Aruna and Audilakshmi, 2008 and Aruna *et al*., 2010). In this study, number of primary branches ranged from 41 to 76, the highest number being in DSRR306, followed by DSRR81, DSRR456, DSRR315 and DSRR435. The panicle length varied from 16.9 to 29.5 cm. DSRR446 had the longest panicles, followed by DSRR307, DSRR327, DSRR456 and DSRR316. For panicle weight, DSRR458 was the best genotype followed by DSRR84, DSRR456, DSRR306 and DSRR78. The line, DSRR84 had bolder seed compared to the check, C43. The days to 50% flowering varied from 59 to 85 days. DSRR320 was the earliest to flower. Among the promising lines, DSRR316 and DSRR435 were early (65 days) to flower compared to the check, C43.

DSRR84 with high grain yield, more panicle weight and bolder grain was the best line, followed by DSRR456 with good grain yield, more number of primary branches, and longer and heavier panicles. DSRR306 was another promising line for grain yield with more number of primary branches, heavier panicles with more 100 grain weight.

### *Promising restorers for sweet sorghum*

The cane yield of the test entries varied from 119.7 to 299.4gm/ plant. The highest cane yield was observed in DSRR318 followed by DSRR449, DSRR306, DSRR329, DSRR86 and DSRR443, all showing more than 30% superiority in cane yield over C43. High brix values were also observed in DSRR431, DSRR329, DSRR443,

**Table 3. ANOVA for different traits in sorghum during three years (2008-2010)**

| Source of variation | df | Mean sum of squares | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Primary Branches | Panicle length | Panicle weight | Plant height | Grain yield | Fodder Yield | Brix | Crude protein | Cane yield | IVDMD |
| Replication | 2 | 138.4 | 97.7 | 5607.8 | 3036.5 | 3966.9 | 442105 | 40.72 | 0.37 | 1930 | 9.80 |
| Genotype(G) | 59 | 513.2** | 65.3** | 1782** | 6414** | 1175.5** | 12603** | 43.9** | 2.85* | 35344** | 9.76 |
| Year(Y) | 2 | 2147** | 1570** | 125352** | 759.6* | 57945.5** | 431863** | 440.7** | 422.1** | 964746** | 453.3** |
| GxY | 113 | 112.6** | 10.2 | 769.3** | 744.1** | 576.5** | 373307** | 17.7** | 2.31 | 8166** | 7.99 |
| Error | 344 | 51.6 | 11.9 | 329.5 | 217.4 | 238.8 | 164064 | 4.93 | 1.91 | 2489 | 7.44 |

*- significant at p≤ 0.05, **-significant at p≤ 0.01

**Table 4. Promising sorghum restorers for grain yield traits during three years (2008 to 2010)**

| Restorer | No. of Primary branches | | | | Panicle length (cm) | | | | Panicle weight (g) | | | | Grain yield (g/pl) | | | | Plant height (cm) | DF | 100 grain wt(g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | | | |
| **Promising restorers for grain yield and panicle weight** | | | | | | | | | | | | | | | | | | | |
| DSRR84 | 56.3 | 46.1 | 43.4 | 48.60 | 24.4 | 25.87 | 17.2 | 22.50 | 136.5 | 139 | 71.1 | 115.6 | 110.3 | 98 | 56.7 | 88.33 | 189 | 75 | 3.52 |
| DSRR458 | 57.3 | 53.8 | 55.3 | 55.49 | 28.7 | 29.47 | 24.2 | 27.46 | 142.3 | 120 | 90.2 | 117.4 | 100.3 | 85 | 64.67 | 83.33 | 195 | 71 | 2.67 |
| DSRR456 | 73.4 | 70.5 | 68.3 | 70.75 | 29.9 | 29.67 | 24.3 | 27.99 | 129.3 | 103 | 94.7 | 109.1 | 95 | 78.3 | 63.3 | 78.87 | 203 | 75 | 2.98 |
| DSRR306 | 84.5 | 82.3 | 61.4 | 76.09 | 26.5 | 27.47 | 21.9 | 25.29 | 122.5 | 113.7 | 87.33 | 107.8 | 93.67 | 88.3 | 49 | 77.00 | 194 | 73 | 3.06 |
| DSRR460 | 64.1 | 57.2 | 47.6 | 56.31 | 28.1 | 28.8 | 21.7 | 26.19 | 117 | 115 | 76 | 102.7 | 83.3 | 98.7 | 42.4 | 74.8 | 187 | 72 | 2.78 |
| **Promising restorers for primary branch number** | | | | | | | | | | | | | | | | | | | |
| DSRR81 | 72.1 | 72.2 | 70 | 71.44 | 27.2 | 28 | 23.6 | 26.26 | 116.7 | 98.33 | 69.67 | 94.89 | 74.33 | 69 | 56.67 | 66.67 | 200 | 74 | 2.65 |
| DSRR315 | 70.6 | 68.7 | 71.5 | 70.27 | 27.1 | 28.27 | 21.6 | 25.63 | 109.3 | 93.67 | 87 | 96.67 | 92.33 | 69 | 44.67 | 68.67 | 187 | 74 | 2.75 |
| DSRR435 | 78.5 | 59.1 | 69 | 68.87 | 28.6 | 26.47 | 24.1 | 26.39 | 113 | 95.33 | 63.67 | 90.67 | 82.33 | 68 | 45 | 65.11 | 163 | 65 | 2.64 |
| **Promising restorers for panicle length** | | | | | | | | | | | | | | | | | | | |
| DSRR446 | 56.1 | 57.9 | 59.9 | 57.96 | 31.1 | 30.07 | 27.4 | 29.53 | 105.8 | 85.67 | 81 | 90.82 | 63.67 | 67 | 64.67 | 65.11 | 168 | 67 | 3.13 |
| DSRR307 | 62.5 | 65.5 | 62.1 | 63.38 | 31 | 28.87 | 27.7 | 29.18 | 118.2 | 82 | 83.7 | 94.63 | 96.67 | 61 | 60.33 | 72.67 | 169 | 73 | 3.19 |
| DSRR327 | 61.9 | 61.6 | 66.5 | 63.35 | 29.7 | 31.2 | 26.4 | 29.12 | 93.7 | 69 | 51.7 | 71.47 | 70.67 | 52.9 | 36.37 | 53.32 | 166 | 72 | 3.04 |
| DSRR316 | 62.5 | 59.4 | 53.3 | 58.39 | 28.9 | 30.62 | 23.7 | 27.73 | 101.7 | 82.2 | 70 | 84.63 | 79.7 | 60 | 44.3 | 61.33 | 159 | 65 | 3.01 |
| C43-Check | 51.2 | 48.3 | 45.7 | 48.41 | 22.6 | 26.33 | 19 | 22.65 | 112 | 82 | 57 | 83.67 | 75.67 | 65.9 | 41 | 60.85 | 160 | 74 | 3.45 |
| Mean | 61.5 | 56.7 | 54.6 | 57.6 | 26.4 | 26.32 | 21.1 | 24.61 | 111.8 | 87.6 | 58.2 | 85.9 | 76.5 | 65.8 | 40.93 | 61.1 | 176 | 73 | 2.93 |
| l.s.d(5%) | 9.5 | 14 | 12 | 6.66 | 5.99 | 4.64 | 4.32 | 3.2 | 30.5 | 26.0 | 22.3 | 29.15 | 17.0 | 23.9 | 24.7 | 24.82 | 23.7 | 2.9 | 0.37 |
| CV (%) | 9.5 | 15 | 21 | 12.5 | 18.1 | 10.9 | 12.7 | 14 | 20 | 22.1 | 20.8 | 21 | 13.8 | 22 | 21 | 25.3 | 8.4 | 4.8 | 7.76 |

DF- Days to flower

**Table 5. Promising sorghum restorers for sweet sorghum traits during three years (2008 to 2010)**

| S. No. | Restorer | Brix | | | | Cane yield (g/pl) | | | | Plant height (cm) | DF |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | | |
| Promising restorers for brix | | | | | | | | | | | |
| 1 | DSRR431 | 16.8 | 16.9 | 19.53 | 17.74 | 316.7 | 254.67 | 200 | 257.11 | 173.03 | 72 |
| 2 | DSRR329 | 18.07 | 14.38 | 18.67 | 17.04 | 364 | 318.67 | 185.3 | 289.33 | 170.40 | 71 |
| 3 | DSRR443 | 18.07 | 12.6 | 19.8 | 16.82 | 381 | 303.67 | 155.3 | 280.00 | 169.07 | 69 |
| 4 | DSRR84 | 16.87 | 15.53 | 17.4 | 16.60 | 300.3 | 292.67 | 154 | 248.99 | 188.77 | 75 |
| 5 | DSRR86 | 16.93 | 15.43 | 17.07 | 16.48 | 386.7 | 312 | 141.3 | 280.00 | 176.73 | 74 |
| 6 | DSRR116 | 16.87 | 17.52 | 15 | 16.46 | 252 | 303.33 | 180.7 | 245.33 | 160.90 | 73 |
| **Promising restorers for cane yield** | | | | | | | | | | | |
| 7 | DSRR318 | 6.07 | 9.9 | 11.8 | 9.26 | 336.7 | 320.33 | 241.3 | 299.44 | 171.20 | 69 |
| 8 | DSRR449 | 12.33 | 12.68 | 14.27 | 13.09 | 469 | 278 | 132.7 | 293.22 | 159.27 | 68 |
| 9 | DSRR306 | 11.73 | 11.58 | 12.87 | 12.06 | 400.7 | 288.67 | 183.3 | 290.89 | 193.53 | 73 |
| 10 | DSRR434 | 15.6 | 16.23 | 14.2 | 15.34 | 319.7 | 256 | 212.7 | 262.79 | 200.27 | 70 |
| 11 | DSRR439 | 11.4 | 10.02 | 9.4 | 10.27 | 341.3 | 280 | 124 | 248.43 | 177.77 | 68 |
| 12 | C43-Check | 10.67 | 11.87 | 13.87 | 12.14 | 257.7 | 231.33 | 157.3 | 215.44 | 159.93 | 74 |
| 13 | RSSV 9-Sweet sorghum check | 18.17 | 15.98 | 15.53 | 16.56 | 458.3 | 518.0 | 379.3 | 451.9 | 304.07 | 85 |
| | l.s.d.(5%) | 3.57 | 3.35 | 3.77 | 3.56 | 97.4 | 61.7 | 77.0 | 80.09 | 23.7 | 2.9 |
| | CV (%) | 17.9 | 16.9 | 15.8 | 16.9 | 20.1 | 15.0 | 29.7 | 20.9 | 8.4 | 4.8 |

DF- Days to flower

DSRR84, DSRR86 and DSRR116, and all these lines had brix value on par with the sweet sorghum check, RSSV9. DSRR329 and DSRR86 were observed to be promising with high cane yield and brix values.

### *Promising restorers for fodder yield and quality*

Thirteen restorers had given higher fodder yield compared to C43. DSRR431 was the highest yielder with 38% increase in fodder yield over C43. The lines, DSRR79, DSRR449, DSRR443 and DSRR456 had given more than 20% increase in fodder yield over C43. DSRR431 and DSRR79 recorded green fodder yield similar to the forage sorghum check, HC 308. Genotypes with sweet stem as indicated by higher brix values, are more palatable to the animals (Blummel *et al*., 2009). High brix value of 17.7 was observed in DSRR431, while it was 12 in C43. The crude protein varied from 4.53 to 7.14% in the genotypes studied. DSRR328 had highest crude protein (7.1%) followed by DSRR112, DSRR116, DSRR310 and DSRR460, all of which showed higher protein percentage compared to C43 (5.56%). For IVDMD, the variation was between 47.6 to 53.1%. IVDMD was highest in DSRR431 (53.1%) followed by DSRR442, DSRR451, DSRR84 and DSRR307, all of which recorded more than 51% IVDMD, while it was 49.8% in C43.

Among the restorers tested, DSRR431 with high fodder yield, sweet stem and high digestibility and protein was the best line. It was found to perform better than the forage sorghum check, HC 308 for fodder yield, brix and IVDMD. Selection of parental lines with superiority in different agronomic traits would help in realizing higher heterosis (Wang *et al*., 2013).

In conclusion, we could develop improved sorghum restorers by utilizing different germplasm lines. These can be used for developing hybrids for different end uses. DSRR84 was promising for grain yield, fodder quality and sweet sorghum traits. DSRR79, DSRR456 and DSRR460 were promising for grain and fodder yields. DSRR306 and DSRR318 for grain yield and sweet sorghum traits, and DSRR431, DSRR449, DSRR306, DSRR329 and DSRR116 were promising for fodder yield and sweet sorghum traits. These restorers can be used in the sorghum breeding program aimed at development of

**Table 6. Promising sorghum restorers for fodder yield and quality traits during 3 years (2008-2010)**

| S.No. | Restorer | Green fodder yield (kg/5 pl) | | | | Brix (%) | | | | Crude protein (%) | | | | IVDMD (%) | | | | Plant height (cm) | DF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | 2008 | 2009 | 2010 | Mean | | |
| **Promising restorers for fodder yield** | | | | | | | | | | | | | | | | | | | |
| 1 | DSRR431 | 3020 | 1927 | 2100 | 2349.0 | 16.8 | 14.9 | 21.5 | 17.74 | 7.29 | 6.79 | 3.6 | 5.89 | 51.92 | 54.24 | 53.13 | 53.10 | 173 | 72 |
| 2 | DSRR79 | 3623 | 2100 | 1233 | 2318.7 | 8.67 | 15.6 | 14.5 | 12.93 | 5.32 | 6.7 | 4.12 | 5.38 | 49.58 | 53.82 | 51.67 | 51.69 | 191 | 72 |
| 3 | DSRR449 | 3190 | 1800 | 1733 | 2241.0 | 12.33 | 9.68 | 17.3 | 13.09 | 7.02 | 6.58 | 4.41 | 6.00 | 48.88 | 52.63 | 51.9 | 51.14 | 165 | 68 |
| 4 | DSRR443 | 2775 | 2280 | 1433 | 2162.7 | 18.07 | 12.6 | 19.8 | 16.82 | 7.95 | 6.28 | 3.64 | 5.96 | 49.54 | 52.2 | 50.68 | 50.81 | 169 | 69 |
| 5 | DSRR456 | 2852 | 1947 | 1667 | 2155.3 | 9.07 | 9.9 | 14.2 | 11.06 | 6.48 | 6.49 | 4.72 | 5.90 | 51.34 | 50.76 | 49.81 | 50.64 | 203 | 75 |
| **Promising restorers for crude protein percent** | | | | | | | | | | | | | | | | | | | |
| 6 | DSRR328 | 2200 | 1237 | 867 | 1434.7 | 7.87 | 8.4 | 15.3 | 10.51 | 9.9 | 7.37 | 4.16 | 7.14 | 46.34 | 51.32 | 50.41 | 49.36 | 150 | 69 |
| 7 | DSRR112 | 1392 | 1333 | 680 | 1135.0 | 13.6 | 11.6 | 15.6 | 13.60 | 8.99 | 6.6 | 5.61 | 7.07 | 46.29 | 54.38 | 51.19 | 50.62 | 165 | 68 |
| 8 | DSRR116 | 2372 | 2270 | 1333 | 1991.7 | 16.87 | 17.52 | 15 | 16.46 | 7.9 | 7.61 | 4.28 | 6.60 | 51.06 | 54.25 | 50.25 | 51.85 | 161 | 73 |
| 9 | DSRR310 | 1590 | 1320 | 1367 | 1425.7 | 12.83 | 11.27 | 7.47 | 10.52 | 8 | 7.59 | 3.91 | 6.50 | 50.69 | 52.77 | 45.97 | 49.81 | 144 | 68 |
| 10 | DSRR460 | 2780 | 2143 | 933 | 1952.0 | 11.4 | 12.6 | 13.7 | 12.56 | 7.07 | 8.26 | 3.51 | 6.28 | 49.09 | 54.24 | 49.77 | 51.03 | 187 | 72 |
| **Promising restorers for digestibility (IVDMD)** | | | | | | | | | | | | | | | | | | | |
| 11 | DSRR442 | 2305 | 1357 | 1267 | 1643.0 | 17.8 | 12.53 | 15.7 | 15.35 | 7.58 | 6.6 | 3.7 | 5.96 | 52.72 | 53.4 | 52.19 | 52.77 | 179 | 67 |
| 12 | DSRR451 | 1533 | 1473 | 733 | 1246.3 | 11.97 | 14.67 | 14.9 | 13.84 | 6.33 | 6.92 | 3.88 | 5.71 | 52.07 | 53.23 | 51.93 | 52.41 | 148 | 74 |
| 13 | DSRR84 | 2943 | 2320 | 1067 | 2110.0 | 16.87 | 15.53 | 17.4 | 16.60 | 6.22 | 6.83 | 3.72 | 5.59 | 51.61 | 52.41 | 52.38 | 52.13 | 189 | 75 |
| 14 | DSRR307 | 1810 | 1583 | 1433 | 1608.7 | 11.13 | 12.77 | 16.5 | 13.46 | 5.33 | 6.13 | 5.73 | 5.73 | 50.51 | 53.64 | 52.07 | 52.07 | 169 | 73 |
| 15 | C43-Check | 2260 | 1540 | 1300 | 1700.0 | 8.67 | 11.87 | 15.9 | 12.14 | 6.5 | 5.22 | 4.97 | 5.56 | 48.79 | 52.55 | 48.2 | 49.85 | 160 | 74 |
| 16 | HC 308-fodder check | 2322 | 2010 | 2633 | 2322 | 13.75 | 10.77 | 16.7 | 13.75 | 5.9 | 6.68 | 5.12 | 5.90 | 50.41 | 50.67 | 51.91 | 51.00 | 279 | 84 |
| | l.s.d(5%) | 685 | 580 | 572 | 650.3 | 3.57 | 3.35 | 3.77 | 3.56 | 2.68 | 1.70 | 2.06 | 2.22 | 5.94 | 2.29 | 4.01 | 4.38 | 23.7 | 2.9 |
| | CV (%) | 18.5 | 21.0 | 26.3 | 22.7 | 17.9 | 16.9 | 15.8 | 16.9 | 25.3 | 15.8 | 21.6 | 24 | 5.94 | 2.29 | 4.01 | 5.4 | 8.4 | 4.8 |

DF- Days to flower

sorghum hybrids for grain, fodder and sweet sorghum improvement.

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# Field Screening of Sesame Accessions against Leaf Roller and Capsule Borer (*Antigastra catalaunalis* Dup.)

**MK Mishra[1]*, SR Tahkur[1], MP Gupta[1] and Yogranjan[2]**
[1]*All India Coordinated Research Project on Oilseeds (Sesame & Niger), JNKVV, Jabalpur-482004, Madhya Pradesh, India*
[2]*Department of Biotechnology, College of Agriculture, JNKVV, Tikamgarh-472001, Madhya Pradesh, India*

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One hundred accessions of sesame with susceptible (TC-25) and resistant check (SI-250) were screened under natural conditions during two consecutive seasons of 2013 and 2014 to identify sources of resistance against leaf roller and capsule borer (*Antigastra catalaunalis* Dup.) at AICRP (Sesame) centre of College of Agriculture, JNKVV, Tikamgarh (M.P.). The accessions were categorized based on 0 to 9 scoring methodology. In pooled analysis, flower damage ranged from 1.0 to 65.0 against 42.6 and 8.5% on susceptible and resistant checks, respectively, while capsules damage ranged from 0.25 to 15.0% against 9.0 and 2.0% on susceptible and resistant checks, respectively. In pooled analysis none of the accessions were found free from infestation of *A. catalaunalis*. Based on the cumulative scoring, thirteen accessions namely IS-355, IS-413-A, RJS-56-A, IS-58-2-A, NIC-16401-A, OLT-44, IS-425-C, SI-2670, SP-1162-B, IS-178-C, IC-14160-1, ES-110-C and resistant check SI-250 (RC) were rated as resistant. These could be a possible source of resistant and used in breeding programmes to develop resistant varieties.

**Key Words: Sesame, *Antigastra catalaunalis* (Dup.), Screening, Accession**

## Introduction

Sesame (*Sesamum indicum* L.) is an ancient oilseed crop also known in India as til, ellu, beniseed, simsim and is a rich source of edible oil. In India, it is grown on 1.82 million ha with a total production of 0.68 million tonnes. The crop has very poor productivity of 376 kg/ha as compared to the world average productivity of 558 kg/ha (FAOSTAT, 2012). In India, sesame is cultivated in Rajasthan, Maharashtra, Gujarat, Madhya Pradesh, Andhra Pradesh, Karnataka, Uttar Pradesh, West Bengal, Odisha, Punjab and Tamil Nadu (Sankar Narayanan and Nadarajan, 2005). Damage due to insect pests is one of the major factors causing low productivity. The crop is attacked by 29 species of insect pests in different stages of its growth (Biswas *et al*., 2001). Among these, leaf roller/capsule borer (*Antigastra catalaunalis* Dup.) is one of the major pests of sesame. It damages the crop during vegetative, flowering and maturity stages of growth. Larvae feed on the tender shoots of the host plants; roll the leaves and make nest by webbing of the leaves together, whereas at flowering stage it feeds on the flowers and at capsule stage it bores into the capsules. It causes economic loss to an extent of 43.1% (Gupta *et al.,* 2002). Chemical insecticides are widely used for the management of this pest but it is not environment friendly. Development of resistant variety is a cheap, viable and environment friendly approach to overcome this problem. Considering this, evaluation studies of the sesame accessions to identify the resistant line against *A. catalaunalis* were carried out.

## Materials and Methods

One hundred accessions of sesame with susceptible (TC-25) and resistant check (SI-250) were screened under natural conditions against *A. catalaunalis* at AICRP (Sesame) centre of College of Agriculture, JNKVV, Tikamgarh (M.P.). Sesame accessions were provided by the Project Coordinating unit AICRP (Sesame & Niger), Jabalpur (M.P.). The experiment was conducted during two consecutive seasons of 2013 and 2014. The accession lines were sown in the first fortnight of July during each season with recommended agronomic practices except plant protection. Two rows of each accession were grown in 5 m row length with spacing of 45 cm between rows and 10 cm between plants. Two lines of susceptible checks (TC-25) were grown across the periphery of accessions lines as well as after every ten accession lines to create favorable environment for *A. catalaunalis* infestation. Observations on damage caused by *A. catalaunalis* were recorded at flowering (45 DAS) and capsule stage (70 DAS) on ten randomly

**Author for Correspondence: Email- manishpbg@gmail.com*

selected plants of each genotype. The per cent damage was calculated according to the equation.

$$\text{Per cent damage (Flower or capsule)} = \frac{\text{Number of damaged flowers or capsules)}}{\text{Total number of flowers or capsules}} \times 100$$

Per cent flower and capsule damage of two seasons were pooled. Range of damage per cent of each reaction was taken according to AICRP on Sesame and Niger (Anonymous, 2014) presented in Table 1. According to reaction, first the accessions were categorized 0-9 score chart formulated by Sridhar and Gopalan (2002), but with modification of range of per cent of damage. According to cumulative score, allotted a grade and resistant rating of each accession.

## Results and Discussion

In the first year of field screening of accessions, flowers damage were ranged from 2.7 to 85.0% against 56.0 and 12.0% on susceptible and resistant checks, respectively. In the second year of field screening, it ranged from 0.0 to 73.3% against 29.2 and 4.9% on susceptible and resistant checks, respectively. Pooled analysis of flowers damage ranged from 1.0 to 65.0 against 42.6 and 8.5% on susceptible and resistant checks, respectively. Our results are in parallel with those of Shrivastava *et al.* (2002), who reported flower damage by *A. catalaunalis* up to 75.0%.

Capsules damage varied from 0.0 to 17.2% against 10.6 and 3.1% on susceptible and resistant checks, respectively, during the first year of field screening, while it was varied from 0.0 to 12.5% against 7.3 and 0.8% on susceptible and resistant checks, respectively during second year of field screening. Pooled analysis of capsule damage ranged from 0.25 to 15.0% against 9.0 and 2.0% on susceptible and resistant checks, respectively. In pooled analysis none of the accessions were found free from infestation of *A. catalaunalis*. Parallel finding was also reported by Gupta (2004) and Kumar *et al.* (2010). In the present study, flowers and capsules were damaged maximally in almost all the accessions of first year of field screening; it was directly related to the incidence of *A. catalaunalis*. Comparable finding was also reported by Balaji and Selvanarayanan (2009).

Based on the cumulative scoring of accessions, thirteen accessions namely IS-355, IS-413-A, RJS-56-A, IS-58-2-A, NIC-16401-A, OLT-44, IS-425-C, SI-2670, SP-1162-B, IS-178-C, IC-14160-1, ES-110-C and resistant check SI-250 (RC) were rated resistant, 46, 40 and 3 accessions were rated moderately resistant, moderately susceptible and susceptible, respectively (Table 2). Results of field screening revealed that most of the accessions were rated moderately resistant and moderately susceptible, while none of the accessions were found highly susceptible. Gupta (2004), Balaji and Selvanarayanan (2009) also reported that none of the accessions were found highly susceptible. It is concluded, that the accessions IS-355, IS-413-A, RJS-56-A, IS-58-2-A, NIC-16401-A, OLT-44, IS-425-C,

**Table 1. Scoring and grading methodology of sesame accessions for resistant against *A. catalaunalis***

| Per cent damage | | Score | Cumulative score | Grade | Degree of resistance |
|---|---|---|---|---|---|
| Flower | Capsule | | | | |
| Up to 10 | Up to 5 | **1** | 0-1 | 1 | Resistant (R) |
| 11-20 | 6-10 | 3 | 1.1 – 3 | 3 | Moderately resistant (MR) |
| 21-30 | 11-15 | 5 | 3.1-5 | 5 | Moderately susceptible (MS) |
| 31-50 | 16-25 | 7 | 5.1-7 | 7 | Susceptible (S) |
| Above 50 | Above 25 | 9 | 7.1-9 | 9 | Highly susceptible (HS) |

**Table 2. Number of accessions under different category**

| Degree of resistance | Number of accessions | Name of accessions |
|---|---|---|
| Resistant (R) | 13 | IS-355,IS-413-A, RJS-56-A, IS-58-2-A, NIC-16401-A, OLT-44, IS-425-C, SI-2670, SP-1162-B, IS-178-C, IC-14160-1, ES-110-C, SI-250 (RC) |
| Moderately resistant (MR) | 46 | GSM-22, EC-310421, NIC-8526, SI-2973, NIC-8984, KMR-77-1, S-0429-A, GRT-00115-A, SI-1665, OLT-61-A, IS-353-A, NIC-17335-A, IS-280-A, IS-296-A, IS-607-A, NIC-16095-A, DSK-1-A, S-0062-A, SI-1016, IS-481, IS-52, IS-552, IS-56-1, IS-8480-B, IS-607-1-84,ES-35-B,ES-72-C-B, SI-7818-B,SI-2182-B ,NIC-10645,SI-953-B,IC-204962,EC-303417,IS-152,IS-1804-A ,SI-1074-1, NIC-16124-A ,EC-303454-A, NIC-16114-A, IC-204139, IC-43177-A , SI-3279-1, S-0185, IC-205649,NIC-9627, IC-14146-C |
| Moderately susceptible (MS) | 40 | IC-14093, SI-2116, GRT-83135, MT-6725, NIC-16328, NIC-16275, GRT-83125, NAL/28/27/31/4, IS-52359-A, SI-3178-1, SI-318, NIC-16236, IS-722, ES-165-B, SI-255-1, IS-104, RJS-738-1-84, IS-319-1, IS-3100, IS-1848, SI-1667-2, IS-17-1, ES-234-1-84, NIC-8252, SI-788, S-0025-1, IS-250, IS-615, KMR-71, ES-127-B, NIC-16237, ES-3196, SI-75, IS-74, SP-3267,RME-111, NIC-8224-A, SI-3315-16, SI-1188-1, TC-25 (SC) |
| Susceptible (S) | 3 | IS-65, NIC-16227-A, IC-1025-A |

SI-2670, SP-1162-B, IS-178-C, IC-14160-1, ES-110-C and SI-250 could be a possible source of resistant and it could be used in breeding programme to develop resistant varieties.

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# Non-destructive Method of Seed Vigour Testing of Traditional Rice (*Oryza sativa* L.) Varieties Conserved in Genebank under Medium-term Storage Conditions

**AD Sharma, Reshma Shaheen, Aradhana Mishra, Kalyani Srinivasan and RK Tyagi**
*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India*

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Plant genetic resources are commonly conserved in the form of seeds in genebanks for their present and future use in crop improvement programmes. It is commonly understood that the loss in vigour, precedes loss in viability during storage. However, vigour tests cannot be conducted routinely for a large number of varieties processed for conservation and monitoring seed quality in genebanks. Hence, rapid and non-destructive tests will be immensely useful to provide additional information during monitoring of seed samples. The seeds of 31 traditional varieties of rice, conserved in medium-term storage (MTS) module (4°C and 35% relative humidity) at ICAR-National Bureau of Plant Genetic Resources, New Delhi, for past 10 years, were used to assess the seed quality by recording the germination percentage, mean germination time, seedling length and vigour index I, electrical conductivity, potassium ($K^+$) and sodium ($Na^+$) ion concentration in leachates. Results of the study clearly confirmed the fact that $K^+$, $Na^+$ ion concentrations in leachate and $K^+/Na^+$ ratio can be used as reliable and non-destructive method of vigour tests for assessing the quality of rice seeds. Several varieties with similar high percentage of initial germination deteriorated drastically leading to highly variable germination percentages after 10 years in MTS, indicating genotype-specificity.

**Key Words: Genotype, Germination, Leachate, Paddy, Potassium, Sodium, Vigour**

## Introduction

Seed vigour testing is becoming increasingly important for ranking of various kinds of seed lots in terms of physiological potential. To ascertain the quality of seeds for long-term storage in genebanks, germination tests are carried out periodically. It is commonly understood that loss in vigour precedes loss in viability during storage. Seed vigour testing is thus assigned high importance as a measure of seed quality. Being time consuming and labour intensive, vigour tests cannot be routinely conducted for the large number of accessions. Hence, rapid and non-destructive vigour tests will be immensely useful to provide additional information during monitoring of seed samples. The leakage intensity during imbibition of soybean and Chinese cabbage seeds revealed a strong relation between $K^+/Na^+$ ratio and germination and the evaluation of specific ion ratio $K^+/Na^+$ test yields more consistent results than electrical conductivity (Cheng *et al*., 2005). When the seeds are soaked for a definite period in distilled water, low vigour seeds leak out larger quantity of inorganic ions into the seed steep medium, which can be quantified using flame photometry. Potassium ($K^+$) ion leakage has been used as an indicator of cell membrane integrity which, in turn, is related to seed vigour (Mc Kersie and Stinson, 1980; Webes and Karseen, 1990; Dias *et al.,* 1997).

The present study was envisaged to (i) evaluate the relationship between $K^+$ and $Na^+$ in the seed leachate with the physiological parameters of seeds of thirty one traditional varieties of rice conserved for 10 years under medium-term storage (MTS) conditions in the National Genebank at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi and (ii) to study the correlations behaviour on seed quality traits under MTS conditions.

## Material and Methods

### *Seed Material*

Seeds of 31 traditional varieties of rice were procured from Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, in 2004 and stored in MTS module (4°C and 35% relative humidity) at ICAR-NBPGR, New Delhi. In 2014, *i.e*., after 10 years, the seeds of the 31 varieties were retrieved from MTS to monitor the seed viability, seedling vigour and to study the pattern of changes in the EC, leakage of $K^+$ and $Na^+$ ions into the seed leachate.

**Author for Correspondence: E-mail: axma.sharma@icar.gov.in, reshmaisrar@yahoo.com, aradhanamishra82@gmail.com, kalyani.srinivasan@icar.gov.in, rishi.tyagi@icar.gov.in*

### *Germination Test and Mean Germination Time*

Fifty seeds of each variety, replicated four times, were placed evenly on top (TP method) two layers of filter papers (Axiva Sichem Biotech, India) saturated with double distilled water. Seeds were allowed to germinate in a seed germinator (Sanco, India) in dark at 30°C. The seeds with at least 2 mm long radicle were considered as germinated and final germination percentage was counted on the 7$^{th}$ day of sowing the seeds (ISTA, 1985). Similarly, for recording mean germination time (MGT), 50 seeds of each variety, in four replications, were placed randomly and the germinated seeds were counted after every 24 h until no further germination was observed; MGT was calculated by using the formula of Ellis and Roberts (1981), as given below:

Mean germination time = $\Sigma nd/\Sigma n$

Where, n = number of seeds germinated on day d, and

d = number of days counted from the beginning of germination test.

### *Seedling Length and Vigour Index I*

Batches of 10 seeds of each variety in four replications were sown between moist germination/towel papers and allowed to germinate at 30°C in dark for 10 days in a seed germinator (Sanco, India). The sum of mean length (cm) of root and shoot, measured on a linear scale was calculated as seedling length (Srinivasan and Saxena, 2007). The product of germination percentage and seedling vigour was tabulated for the estimation of Vigour index I (Abdul-Baki and Anderson, 1973).

Vigour Index I = Seedling length (cm) × Germination percentage

### *Electrical Conductivity Test and Assay of Ion Concentration in Leachate*

A total of 25 seeds of each variety, replicated four times, were soaked in 25 ml double distilled water for 24 h at 30°C in dark. The seed leachate conductivity (µsi/cm/gfw of seed) was estimated using a digital conductivity meter (Control Dynamics) after calibration with a solution of 0.01 M KCl (Mathews and Bradnock, 1968).

$K^+$ and $Na^+$ ion concentrations in the seed leachate were measured using a flame-photometer (Jenway, U.K.) after calibration with 10 ppm solution of KCl and NaCl, respectively. The ratio of $K^+$ and $Na^+$ was calculated on the basis of the concentration of $K^+$ and $Na^+$ (µg/g seeds) in the seed leachate.

### *Data Analyses*

Collected data were statistically analysed by using SPSS software (version 16.0) and treatment means were compared by applying Duncan's multiple range test (DMRT) at 5% probability.

The data recorded as percentage were transformed to the respective angular (arcsine) values before subjecting them to statistical analyses.

## Results and Discussion

The initial germination (before storage in October, 2004) ranged from 85 to 99%, whereas final germination (after 10 years of storage in September, 2014) in MTS was recorded between 5.33 to 98%. For all the parameters tested, wide ranges of values were observed in 10-year-old conserved rice varieties. The range of mean germination time (1.44-5.66 days), seedling length (7.68-47.84 cm), vigour index I(53.26-4304.10), electrical conductivity (49.48-112.82 µsi/cm/gfw of seed)), $K^+$ in the seed leachate (55.68-129.18 µg/g seeds), $Na^+$ (2.45-11.62 µg/g seeds) and the ratio of $K^+$/ $Na^+$ (5.70-30.72) were recorded in 31 traditional varieties of rice germplasm (Table 1).

The details of data on seed vigour parameters, EC, $K^+$, $Na^+$ and $K^+/Na^+$ ratio are presented in Table 2. Genotypic effects were recorded on almost all the parameters tested. Out of 31 rice varieties tested, 12 varieties showed ≥ 85% germination after 10 years of storage in MTS; 5 varieties showed ≥ 50% and remaining showed < 50% germination. In general, the varieties showing higher seed germination

**Table 1. Range of seed quality parameters of traditional varieties of rice conserved for 10 years under medium-term storage conditions**

| Seed quality parameter | Minimum (Mean) | Maximum (Mean) |
|---|---|---|
| Initial germination (%) - 2004 | 85.00 (67.19) | 99.00 (85.34) |
| Final germination (%) - 2014 | 5.33 (13.16) | 98.00 (83.41) |
| Mean germination time (days) | 1.44 | 5.66 |
| Seedling length (cm) | 0.68 | 47.84 |
| Vigour index-I | 53.26 | 4304.10 |
| Electrical conductivity (µsi/cm/gfw) | 49.48 | 112.82 |
| Potassium ion (µg/g seeds) | 55.68 | 129.18 |
| Sodium ion (µg/g seeds) | 2.45 | 11.62 |
| Ratio ($K^+/Na^+$) | 5.70 | 30.72 |

Values in parentheses are arc sine transformed values for germination percentage

maintained higher vigour and vigour index also. Seed longevity is a quantitative trait controlled by several genes scattered throughout the genome and influenced largely by environmental conditions (Kochanek *et al.,* 2010). Niedzielski *et al.* (2009) also observed that wheat, secale and triticale seed lots with high initial germination percentages revealed widely varying longevities. In the present study, several varieties where the initial germination was very high (96-99%), final viability declined to various levels indicating that genotype plays a very important role in controlling viability and also that vigour assessment is essential to differentiate the performance potential of various genotypes. Lower EC values of electrical conductivity were recorded in seeds with high germination percentage; however, no consistent linear trend was observed in relation to linear decrease in seed germination values. Most of the varieties that showed higher germination (≥ 85%) exhibited relatively low ratio of $K^+/Na^+$ ions, except Bhudkud, Khuddi and Ratna.

It is also evident from Table 3 that germination exhibited a significantly positive correlation with seedling length (r =0.860), Vigour index I(r = 0.934) and $Na^+$ ion (r = 0.681), but significantly negative correlation with mean germination time (r = -0.724 and the ratio of $K^+/Na^+$(r = -0.763). Seedling length was recorded to be significantly and positively correlated with Vigour index I (r = 0.957) and $Na^+$ ion (r = 0.656), but negatively correlated with the $K^+$ ion (r = -0.367) and the ratio of $K^+/Na^+$ (r = -0.791).

The electrical conductivity recorded highly positive correlation with $K^+$ ion (r = 0.841) and $Na^+$ ion (r = 0.296). The $K^+$ ion content in the leachate registered a significant positive correlation with $K^+/Na^+$ ratio (r =0.460), while $Na^+$ ion showed a highly significant negative correlation with $K^+/Na^+$ ratio (r = -0.829). Loss of cell membrane integrity is considered to be one of the primary and early events of the ageing process in seed (Mc Donald, 1999; Mathew and Powell, 2006). Consequently, seeds with low vigour exhibit higher degree of loss of their cellular constituents such as inorganic ions. Present results, however, show that $K^+$ ions are leached maximum by imbibing seeds. Such cation leakage has been used as an indicator of cell membrane integrity in cotton (Woods Stock *et al.,* 1985), radish, cabbage and broccoli (Min, 1995), maize (Miguel and Marcos Filho, 2002) and soybean (Cheng *et al.,* 2005). Also, it has been observed that the leakage of individual cation was significantly correlated ($K^+$ ion negatively and $Na^+$ ion positively) with seedling length along with $K^+/Na^+$ ratio. Cheng *et al.* (2005) demonstrated a strong relation between $K^+/Na^+$ ratio in the imbibition medium and germinability of seeds of soybean and Chinese cabbage. Since these ions are physiologically important, $K^+/Na^+$ ratio in soaking water could be more consistent and considered as a better indicator of vigour level than the EC of the seeds (Woodstock, 1985; Dias *et al*., 1997; Cheng *et al*., 2005). Highly vigorous seed lots often leak more charged particles into the imbibing medium initially, but the ions are later absorbed back leading to higher EC initially, followed by a gradual decrease, however, when the integrity of the membrane decreases due to disorganization and disintegration process during ageing, the ability of the membrane to reabsorb the ions also consequently decreases. Similarly, it has been postulated by Cheng *et al*. (2005) that poor membrane integrity in partially or completely aged seeds disables ion pumping mechanism, thus preventing the $Na^+$ ion from being pumped out into the soaking medium, thereby resulting in low amount of $Na^+$ in the soaking medium. Thus, when cells leak out more $K^+$ and less $Na^+$ through the cell membrane, a higher $K^+/Na^+$ ratio is obtained in seeds with lower membrane integrity.

Our results corroborate the findings of Cheng *et al.* (2005), who reported inconsistency between electrolyte leachate conductivity and vigour levels in Chinese cabbage seeds while observing highly consistent relationship between $K^+/Na^+$ ratio and vigour levels. Wang *et al.* (2003) also reported that the higher seed vigour was correlated with lower concentration of $K^+$ and $Ca^{2+}$ in leachate from *Ulmus pumila* and *Brassica perkensis* seeds.

It is a general opinion that the seeds with low initial germination undergo accelerated deterioration (Mead and Gray, 1999). Poor correlation between initial germination and longevity of a seed lot is a well acknowledged fact. In the present study also, several varieties with similar high percentage of initial germination have undergone deterioration at differential rates, leading to highly variable final germination percentages.

On the basis of above results, it can be inferred that $K^+$ ion leakage and $K^+/Na^+$ ratio are more sensitive measures for assessing the physiological potential, rather than EC measurement in rice seeds. It can be used as a non-destructive method for monitoring the seed quality of rice germplasm conserved in genebanks. As many

**Table 2. Seed quality of traditional varieties of rice stored for 10 years under medium-term storage conditions**

| S. No. | Traditional varieties | Accession No. | Initial germination (%) in 2004 | Final germination (%) in 2014 | MGT (days) | Seedling length (cm) | Vigour index I (Seedling length × germination percentage ) | Electrical conductivity (µsi/cm/gfw) | $K^+$ (µg/g seeds) | $Na^+$ (µg/g seeds) | Ratio ($K^+$/ $Na^+$) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Bawara Haruna | IC-133156 | 99.00 (85.34$^{a}$) | 98.00(83.41)$^{a}$ | 1.44$^{n}$ | 40.28$^{bc}$ | 3940.6$^{abc}$ | 63.83$^{efgh}$ | 76.23$^{hijkl}$ | 9.20$^{abcd}$ | 9.00$^{ghi}$ |
| 2 | Nokhi | IC-135521 | 99.00 (85.34$^{a}$) | 98.00(83.41)$^{a}$ | 1.75$^{lmn}$ | 41.82$^{abc}$ | 4095.2$^{ab}$ | 61.63$^{efgh}$ | 61.47$^{mn}$ | 7.15$^{cdefg}$ | 8.71$^{ghi}$ |
| 3 | Kera Khan | IC-134580 | 93.00 (74.65$^{bc}$) | 94.00(75.92)$^{ab}$ | 1.91$^{klmn}$ | 36.98$^{bcd}$ | 3485.8$^{de}$ | 61.15$^{efgh}$ | 60.88$^{mn}$ | 6.90$^{cdefgh}$ | 9.22$^{ghi}$ |
| 4 | Khuraban | IC- 134752 | 99.00 (85.34$^{a}$) | 94.66(76.80)$^{ab}$ | 1.68$^{lmn}$ | 37.53$^{bc}$ | 3553.7$^{cde}$ | 69.15$^{cdefg}$ | 72.31$^{ijklm}$ | 9.54$^{abc}$ | 7.58$^{hi}$ |
| 5 | Kansari | IC-134447 | 96.00 (78.49$^{b}$) | 93.33(75.17)$^{ab}$ | 1.83$^{lmn}$ | 35.69$^{cd}$ | 3323.6$^{e}$ | 67.85$^{cdefg}$ | 63.76$^{lmn}$ | 11.62$^{a}$ | 5.70$^{i}$ |
| 6 | Khuddi | IC-134642 | 99.00 (85.34$^{a}$) | 93.00(74.82)$^{ab}$ | 1.55$^{mn}$ | 35.23$^{cd}$ | 3274.4$^{e}$ | 76.01$^{bcde}$ | 94.27$^{cde}$ | 6.50$^{defghi}$ | 14.88$^{fgh}$ |
| 7 | Chipda | IC-133610 | 99.00 (85.34$^{a}$) | 90.00(72.04)$^{ab}$ | 2.59$^{hijklm}$ | 47.84$^{a}$ | 4304.1$^{a}$ | 49.48$^{h}$ | 55.68$^{n}$ | 5.79$^{efghij}$ | 9.60$^{ghi}$ |
| 8 | Pandari Luchai | IC- 135117 | 92.00 (73.56$^{cd}$) | 89.33(70.98)$^{ab}$ | 1.96$^{klmn}$ | 43.15$^{ab}$ | 3854.7$^{bcd}$ | 63.63$^{efgh}$ | 76.57$^{ghijkl}$ | 8.50$^{bcde}$ | 9.06$^{ghi}$ |
| 9 | Bhata Khuji | IC- 134669 | 99.00 (85.34$^{a}$) | 88.00(69.88)$^{b}$ | 1.92$^{klmn}$ | 41.40$^{bc}$ | 3649.1$^{cde}$ | 75.17$^{bcde}$ | 80.72$^{fghij}$ | 10.16$^{ab}$ | 7.93$^{hi}$ |
| 10 | Ratna | IC- 135624 | 96.00 (78.49$^{b}$) | 88.00(69.88)$^{b}$ | 2.67$^{ghijkl}$ | 28.85$^{ef}$ | 2531.0$^{f}$ | 85.47$^{b}$ | 114.81$^{b}$ | 4.46$^{ghijk}$ | 25.88$^{abcd}$ |
| 11 | Bhudkud | IC-133267 | 99.00 (85.34$^{a}$) | 86.00(68.03)$^{bc}$ | 2.08$^{jklmn}$ | 26.75$^{efg}$ | 2298.3$^{f}$ | 112.82$^{a}$ | 129.18$^{b}$ | 11.56$^{a}$ | 14.93$^{fgh}$ |
| 12 | Gurmatiya | IC-134030 | 99.00 (85.34$^{a}$) | 85.66(68.26)$^{bc}$ | 1.76$^{lmn}$ | 40.46$^{bc}$ | 3477.6$^{de}$ | 57.06$^{gh}$ | 60.29$^{mn}$ | 7.31$^{cdefg}$ | 8.27$^{ghi}$ |
| 13 | Mararin Buta | IC-133353 | 99.00 (85.34$^{a}$) | 78.66(62.48)$^{c}$ | 1.91$^{klmn}$ | 30.80$^{de}$ | 2421.1$^{f}$ | 65.08$^{defg}$ | 81.31$^{efghij}$ | 5.13$^{fghijk}$ | 15.89$^{efg}$ |
| 14 | Kosam Khuta | IC-134713 | 92.00 (73.56$^{cd}$) | 66.66(54.83)$^{d}$ | 2.91$^{fghijk}$ | 26.50$^{efg}$ | 1760.0$^{g}$ | 64.40$^{efg}$ | 80.13$^{fghij}$ | 7.53$^{bcdef}$ | 10.67$^{ghi}$ |
| 15 | Lako Kunwar | IC- 134891 | 96.00 (78.49$^{b}$) | 62.66(52.32)$^{de}$ | 2.39$^{ijklmn}$ | 27.50$^{ef}$ | 1717.2$^{g}$ | 83.71$^{b}$ | 89.45$^{cdefgh}$ | 4.61$^{ghijk}$ | 19.34$^{def}$ |
| 16 | Lal Koram | IC- 134805 | 96.00(78.49$^{b}$) | 57.33(49.20)$^{ef}$ | 3.73$^{def}$ | 12.34$^{jkl}$ | 707.20$^{hij}$ | 56.76$^{gh}$ | 68.91$^{jklm}$ | 3.24$^{jk}$ | 22.08$^{bcdef}$ |
| 17 | Newari | IC-135447 | 85.00 (67.19$^{ef}$) | 50.66(45.36)$^{fg}$ | 3.52$^{efgh}$ | 15.68$^{ijk}$ | 792.97$^{hij}$ | 59.68$^{fgh}$ | 77.81$^{fghijk}$ | 3.05$^{jk}$ | 26.03$^{abcde}$ |
| 18 | Ramker | IC- 135869 | 96.00 (78.49$^{b}$) | 50.66(45.36)$^{fg}$ | 3.77$^{def}$ | 17.71$^{hij}$ | 896.46$^{hi}$ | 81.26$^{bc}$ | 113.87$^{b}$ | 3.72$^{ijk}$ | 30.65$^{a}$ |
| 19 | Londi | IC- 134882 | 99.00 (85.34$^{a}$) | 45.33(42.29)$^{gh}$ | 4.80$^{abc}$ | 22.25$^{fghi}$ | 990.20$^{h}$ | 61.14$^{efgh}$ | 82.61$^{efghi}$ | 3.36$^{jk}$ | 24.58$^{abcd}$ |
| 20 | Chhoti Lal | IC-134913 | 92.00 (73.56$^{cd}$) | 42.66(40.76)$^{ghi}$ | 3.32$^{efghi}$ | 17.91$^{hij}$ | 762.78$^{hij}$ | 65.91$^{defg}$ | 85.74$^{defgh}$ | 3.09$^{jk}$ | 27.71$^{abc}$ |
| 21 | Koliyari | IC- 134780 | 99.00 (85.34$^{a}$) | 37.33(37.64)$^{hij}$ | 4.91$^{abc}$ | 20.30$^{ghi}$ | 765.26$^{hij}$ | 54.54$^{gh}$ | 68.21$^{jklmn}$ | 3.27$^{jk}$ | 21.00$^{cdef}$ |
| 22 | Luchai | IC- 135027 | 96.00 (78.49$^{b}$) | 37.33(37.56)$^{hij}$ | 2.89$^{fghijk}$ | 23.30$^{fgh}$ | 874.89$^{hi}$ | 55.22$^{gh}$ | 66.18$^{klmn}$ | 2.85$^{jk}$ | 23.19$^{abcde}$ |
| 23 | Karhani | IC-134516 | 96.00(78.49$^{b}$) | 34.66(36.00)$^{ij}$ | 3.98$^{cde}$ | 9.21$^{kl}$ | 322.00$^{ijk}$ | 65.45$^{defg}$ | 77.09$^{ghijk}$ | 3.13$^{jk}$ | 25.89$^{abcd}$ |
| 24 | Longa | IC-134983 | 96.00(78.49$^{b}$) | 33.33(35.13)$^{j}$ | 4.54$^{bcd}$ | 13.17$^{jkl}$ | 449.53$^{ijk}$ | 67.61$^{cdefg}$ | 84.76$^{efghi}$ | 3.54$^{jk}$ | 23.95$^{abcd}$ |
| 25 | No:22 | IC- 135543 | 88.33 (70.02$^{de}$) | 30.66(33.21)$^{j}$ | 3.10$^{efghij}$ | 23.29$^{fgh}$ | 682.60$^{hij}$ | 61.11$^{efgh}$ | 87.22$^{cdefgh}$ | 3.04$^{jk}$ | 29.17$^{ab}$ |
| 26 | Lodiyar | IC-134966 | 99.00 (85.34$^{a}$) | 18.66(25.37)$^{k}$ | 3.70$^{defg}$ | 19.88$^{hi}$ | 350.00$^{ijk}$ | 79.28$^{bcd}$ | 98.54$^{cd}$ | 3.61$^{jk}$ | 27.47$^{abc}$ |
| 27 | Safed Ludka | IC-135170 | 91.00 (72.53$^{cd}$) | 16.00(23.46)$^{k}$ | 3.53$^{efgh}$ | 9.30$^{kl}$ | 149.73$^{k}$ | 68.48$^{cdefg}$ | 90.62$^{cdef}$ | 4.23$^{hijk}$ | 21.72$^{bcdef}$ |
| 28 | Nirguni | IC- 135507 | 99.00 (85.34$^{a}$) | 12.00(20.08)$^{kl}$ | 2.20$^{jklmn}$ | 11.03$^{kl}$ | 152.40$^{k}$ | 59.08$^{fgh}$ | 68.92$^{jklm}$ | 2.45$^{k}$ | 30.72$^{a}$ |
| 29 | Lodiyari | IC- 134967 | 99.00 (85.34$^{a}$) | 10.66(18.98)$^{kl}$ | 3.34$^{efghi}$ | 7.68$^{kl}$ | 82.20$^{k}$ | 83.95$^{b}$ | 112.27$^{b}$ | 4.49$^{ghijk}$ | 25.20$^{abcd}$ |
| 30 | Lohandi | IC-134975 | 96.00 (78.49$^{b}$) | 10.66(18.45)$^{kl}$ | 5.17$^{ab}$ | 10.26$^{kl}$ | 113.22$^{k}$ | 73.75$^{bcdef}$ | 99.77c | 3.58$^{jk}$ | 27.91$^{abc}$ |
| 31 | Nunga | IC- 135550 | 99.00 (85.34$^{a}$) | 5.33(13.16)$^{l}$ | 5.66$^{a}$ | 10.05$^{kl}$ | 53.26$^{k}$ | 67.64$^{cdefg}$ | 89.77$^{cdefg}$ | 3.35$^{jk}$ | 27.30$^{abc}$ |

Values in parentheses are arc sine transformed values for germination percentage given in column 4 and 5

**Table 3. Coefficient of correlation (r) between physiological and biochemical parameters of traditional varieties of rice**

| | Germination (%) | Mean germination time (days) | Seedling length (cm) | Vigour index I | Electrical conductivity (µsi/cm/gfw) | $K^+$ ion (µg/g seeds) | $Na^+$ ion (µg/g seeds) | Ratio ($K^+$/$Na^+$) |
|---|---|---|---|---|---|---|---|---|
| Germination (%) | 1 | –0.724** | 0.860** | 0.934** | 0.029 | –0.250* | 0.681** | –0.763** |
| Mean germination time (days) | | 1 | –0.684** | –0.728** | –0.061 | 0.191 | –0.538** | 0.566** |
| Seedling vigour (cm) | | | 1 | 0.957** | –0.089 | –0.367** | 0.656** | –0.791** |
| Vigour index | | | | 1 | –0.044 | –0.343** | 0.713** | –0.822** |
| Electrical conductivity (µsi/cm/gfw) | | | | | 1 | 0.841** | 0.296** | 0.115 |
| Potassium ion (µg/g seeds) | | | | | | 1 | –0.088 | 0.460** |
| Sodium ion (µg/g seeds) | | | | | | | 1 | –0.829** |
| Ratio ($K^+$/$Na^+$) | | | | | | | | 1 |

** Correlation is significant at the 0.01 level
* Correlation is significant at the 0.05 level

as 12 varieties were found to be good storers for up to 10 years, maintaining full complement of seed viability and vigour as per international genebank standards.

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# Maximum Entropy (Maxent) Approach to Sorghum Landraces Distribution Modelling

**N Sivaraj[1], M Elangovan[2], V Kamala[1], SR Pandravada[1], P Pranusha[1] and SK Chakrabarty[1]**
[1]*ICAR-National Bureau of Plant Genetic Resources, Regional Station, Hyderabad-500030, Telangana, India*
[2]*ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad-500030, Telangana, India*

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Maximum entropy method (Maxent) for modelling of selected sorghum landraces (*Errajonna, Kondajonna, Pachchajonna* and *Tellajonna*) geographic distributions with presence-only data from Khammam district of Telangana state, India for future climate was attempted. Variability occurs among the models generated for specific landraces. Specific potential districts in Telangana state were identified for further cultivation and *on-farm* conservation of sorghum landraces in the light of climate change regime.

**Key Words: DIVA-GIS, Maxent, Niche modelling, Sorghum**

## Introduction

Sorghum is the fifth most important cereal crop and is the dietary staple of more than 500 million people in 30 countries. It is grown on 40 million ha in 105 countries of Africa, Asia, Oceania and the Americas. Sorghum [*Sorghum bicolor* (L.) Moench] landraces have been cultivated in parts of Khammam district of Telangana state by the tribal communities since ancient times providing nutritional security. Early introduction of *Sorghum* into India from African region has a profound effect on the genetic variability available in the country, and India thus becoming a secondary centre of diversity. Landraces of sorghum from this centre of diversity harbour genes for resistance to diseases, insect pest and other abiotic stresses *viz*. drought and high temperature. They also act as sources of traits to improve food, animal feed and nutritional security among the tribal population in this region. However, sorghum landrace diversity is under severe threat due to the loss of habitats, industrial activities and large-scale adoption of cash crops. As sorghum is the staple crop of many tribal communities of this region, the genetic diversity needs to be collected and conserved for ensuring food security. These landraces are rich sources of novel genes that may be utilized for enhancing quality, resistance to biotic and abiotic stresses. This variability and genetic diversity needs to be collected and conserved. With the changing cropping pattern and farmers' preference and the ensuing climate change, these characters are at the verge of extinction. Hence, it is imperative to develop suitable strategies for the conservation of sorghum landraces both *ex-situ* and *in-situ*. In the present study, an attempt has been made for the niche modelling of sorghum landraces of Khammam district of Telangana state, India in the light of climate change using MaxEnt method.

## Characteristics of the Study Area

The study zone includes the Khammam district of Telangana state, India. It occupies an area of approximately 16,029 square kilometres (Geographical coordinates: 17.2500$^{o}$N and 81.1500$^{o}$E). Summer season is hot and the temperatures can rise rapidly during the day. Monsoon season brings certain amount of rainfall and the temperatures gradually reduce during this period. After the onset of the monsoon day temperatures are much lower and as the winter approaches they reduce further. Summer season commence in March and lasts till the end of May. During this time day temperatures are high and can reach 50°C to 55°C. Humidity is low as it is not located near the ocean. Conditions are generally dry during this period and the day temperatures range from a minimum of 40°C and can rise up to a maximum of 45°C to 50°C. Monsoon season brings much needed relief from the heat. Monsoon seasons are from the months of June to September. Temperatures average around 30°C during this period. The place gets rain from the South West Monsoon. Some amount of rainfall can be experienced in October as well. Winter season is from December to February. January is usually the coldest part

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

of the year. Temperatures range around 28 °C to 34 °C during this time. The annual average rainfall is 900-1150 mm mostly from the south west monsoon. Red soils are predominant in the district which includes chalkas, red sandy and deep red loamy. Very deep black cotton soils are also seen in some parts of the district. Khammam district is endowed with agro-climatic and soil conditions in which a wide range of agri-horticulture crops like paddy, sorghum, cotton, mango, banana, cashew, coconut, oil palm, cocoa, pepper etc. are grown.

The Khammam district has a tribal population of 5,58,958 which is about 13.29% of the total tribal population of the Telangana state. *Koyas, Guttikoyas, Konda Reddis, Lambadas* are the major tribal groups of this region cultivating sorghum landraces. Tribal women belonging to the above groups are responsible to conserve the sorghum germplasm for growing in the next season and their contribution is more in farm activities apart from their routine household activities.

## Materials and Methods

MaxEnt software version 3.3.3k downloaded from www.cs.princeton.edu/~schapire/maxent was used for sorghum landraces habitat modelling. Maximum entropy (Maxent) is a niche modelling method that has been developed involving species distribution information based only on known presences and is a general-purpose method for making predictions or inferences from incomplete information. Using 27 selected sorghum landraces evidence points (Table 1) which were collected during two exploration missions jointly organised by the ICAR-National Bureau of Plant Genetic Resources (NBPGR) and Directorate of Sorghum Research (DSR), MaxEnt runs were performed for each of the sorghum landraces (*Errajonna, Kondajonna, Pachchajonna* and *Tellajonna*). The sorghum landrace evidence points (27) were recorded using Global Positioning System (Garmin GPS-12). WorldClim (WC) database (http://www.worldclim.org) was used for the study and it provides interpolated global climate surfaces using latitude, longitude, and elevation as independent variables and represents long-term (1950–2000) monthly means of maximum, minimum, mean temperatures and total rainfall. For future climates (2020), we used the Global circulation model outputs from the Intergovernmental Panel on Climate Change, Fourth Assessment Report (Solomon *et al*., 2007). Default settings were used in Maxent so that the complexity of the model varied depending upon the number of data points used for model fitting. The *ASCI* file generated by the maxent run for each of the sorghum landraces was imported to grid file using DIVA-GIS software version 7.5 (Hijmans *et al*., 2012). The grid layer generated for each run was overlayed on India shapefile using DIVA-GIS and analysed.

**Table 1. Evidence points of *Sorghum* landraces sourced from Khammam district, Telangana state, India for Maxent modelling**

| Accession identity | Vernacular name | Longitude (East) | Latitude (North) | Altitude (feet) |
|---|---|---|---|---|
| IC0283753 | *Errajonna* | 80.9105 | 17.7210 | 428 |
| IC0347580 | *Errajonna* | 81.5100 | 17.7417 | 400 |
| IC0596013 | *Errajonna* | 80.9000 | 17.6667 | 435 |
| IC0596016 | *Errajonna* | 80.5500 | 18.4833 | 311 |
| IC0596017 | *Errajonna* | 80.4000 | 18.5500 | 315 |
| IC0596011 | *Kondajonna* | 81.3833 | 17.7500 | 432 |
| IC0306486 | *Kondajonna* | 81.3833 | 17.5833 | 320 |
| IC0596021 | *Kondajonna* | 81.4000 | 17.6000 | 310 |
| IC0596015 | *Kondajonna* | 80.5900 | 18.2890 | 287 |
| IC0596009 | *Kondajonna* | 80.3667 | 18.6000 | 315 |
| IC0596018 | *Kondajonna* | 80.9105 | 17.7210 | 428 |
| IC0347592 | *Kondajonna* | 81.0400 | 17.7133 | 207 |
| IC0596014 | *Kondajonna* | 81.2467 | 17.6845 | 311 |
| IC0596008 | *Pachchajonna* | 81.1500 | 17.7333 | 445 |
| IC0596010 | *Pachchajonna* | 81.0333 | 17.7000 | 447 |
| IC0596026 | *Pachchajonna* | 81.0667 | 17.7333 | 432 |
| IC0596029 | *Pachchajonna* | 81.2667 | 17.5833 | 310 |
| IC0596012 | *Pachchajonna* | 80.9000 | 17.6667 | 435 |
| IC0596020 | *Pachchajonna* | 81.2267 | 17.6033 | 307 |
| IC0596021 | *Pachchajonna* | 82.2267 | 18.6033 | 307 |
| IC0596022 | *Pachchajonna* | 81.1500 | 17.7333 | 326 |
| IC0249063 | *Tellajonna* | 81.3717 | 17.7533 | 214 |
| IC0347590 | *Tellajonna* | 80.6717 | 18.1983 | 222 |
| IC0347585 | *Tellajonna* | 81.5033 | 17.7483 | 500 |
| IC0347591 | *Tellajonna* | 80.4233 | 18.5417 | 307 |
| IC0347588 | *Tellajonna* | 81.0400 | 17.7117 | 206 |
| IC0249067 | *Tellajonna* | 81.0200 | 17.3167 | 700 |

## Results and Discussion

The important landraces in sorghum germplasm studied include *Errajonna, Kondajonna, Pachchajonna* and *Tellajonna*. The panicles are compact, loose or semi-compact. The seed colour varied from shades of white/yellow/red and the seed size ranging from medium-bold to bold (Fig. 1). Characteristics of the sorghum landraces selected for niche modelling are presented in Table 2.

Maxent model for *Errajonna* generated for future climate (2020) is presented in Fig. 2. Warmer colours show areas with better predicted conditions. The graph represented in Fig. 2 shows the omission rate

**Table 2. Characteristics of selected landraces of Sorghum occurring in Khammam district, Telangana State, India**

| Characters/Landraces | Errajonna | Kondajonna | Pachchajonna | Tellajonna |
|---|---|---|---|---|
| Race | Durra-bicolor | Guinea-caudatum | Durra-bicolor | Guinea-caudatum |
| Plant height (cm) | 155-250 | 160-390 | 230-440 | 240-330 |
| Plant pigmentation | Pigmented | Pigmented | Pigmented | Pigmented |
| Basal tillers number | 2 | 2 | 2 | 2 |
| Midrib colour | White | White | White | White |
| Days to flowering | 68-106 | 92-143 | 62-118 | 69-128 |
| Panicle length (cm) | 26 | 16 | 16 | 16 |
| Panicle width (cm) | 12 | 7 | 7.5 | 11 |
| Panicle compactness and shape | Semi-compact elliptic | Semi-compact elliptic | Semi-loose stiff branches | Semi-compact elliptic |
| Glume colour | Purple | Straw | Straw | Straw |
| Glume covering | Grain fully covered | 1/4th grain covered | 3/4th grain covered | ½ grain covered |
| Seed colour | Reddish brown | White | Yellow | White |
| Seed lustre | Lustrous | Lustrous | Lustrous | Lustrous |
| Seed size (mm) | 3 | 2.5 | 3 | 2.8 |
| 100 Seed weight (g) | 2.9 | 2.8 | 2.8 | 2.75 |

and predicted area as a function of the cumulative threshold. The omission rate is calculated both on the training presence records, and (if test data are used) on the test records. The omission rate should be close to the predicted omission, because of the definition of the cumulative threshold.The image uses colours to indicate predicted probability that conditions are suitable, with red indicating high probability (0.77 to 1.0) of suitable conditions for the Errajonna, green indicating conditions typical of those where the species is found and lighter shades of green indicating low predicted probability of suitable conditions. Adilabad, Karimanagar and Nalgonda districts of Telangana state are the potential regions for introducing and cultivating the *Errajonna* landrace and for planning *in-situ on-farm* conservation sites in the light of climate change scenario.

MaxEnt models for *Kondajonna*, *Pachchajonna* and *Tellajonna* and respective omission and predicted areas are provided in Figs. 3-5. The highest probability (0.7 to 1.0) of distribution of these landraces is represented by red colour. Of all the landraces, *Pachchajonna* may be affected due to climate change. Most of the high probable areas of distribution for *Pachchajonna* shifted to coastal region of Andhra Pradesh state. Highest probable areas of distribution of sorghum landraces in the light of climate change as indicated in the present study is as follows: *Tellajonna*>*Errajonna*>*Kondajonna*> *Pachchajonna* respectively.

The probability distribution of selected sorghum landraces is the sum of each weighted variable divided by a scaling constant to ensure that the probability value ranges from 0 to 1. The information available about the target distribution of sorghum landraces often presents itself as a set of real-valued variables, called 'features', and the constraints are that the expected value of each feature should match its empirical average (Phillips *et al*., 2006). The program starts with a uniform probability distribution and works in cycles adjusting the probabilities to maximum entropy. It iteratively alters one weight at a time to maximize the likelihood of reaching the optimum probability distribution. Maxent is considered as the most accurate model performing extremely well in predicting

**A. *Errajonna*** **B. *Kondajonna*** **C. *Pachchajonna*** **D. *Tellajonna***

**Fig. 1. Select landraces of sorghum from Khammam district, Telangana State, India**

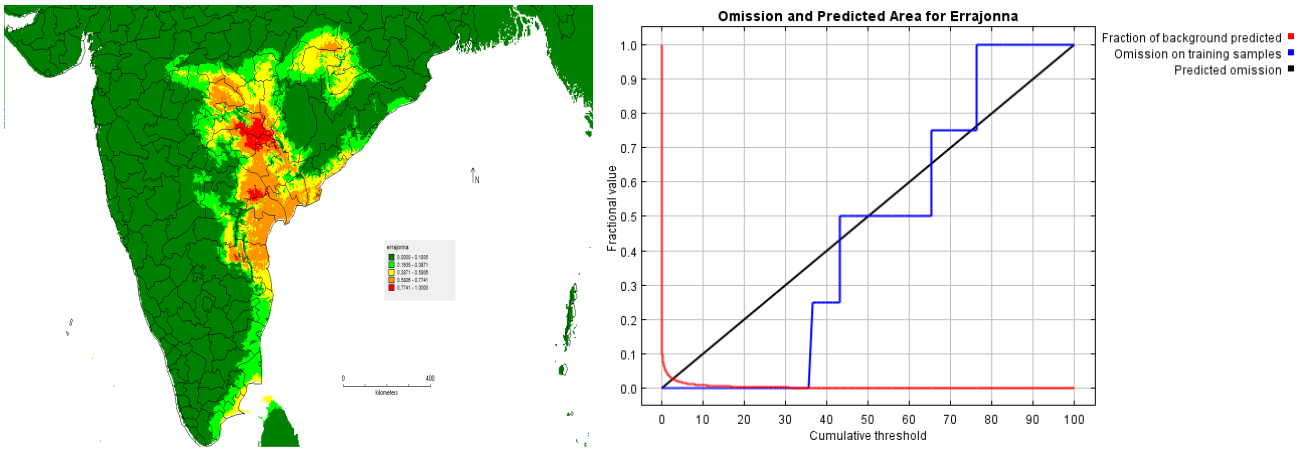


**Fig. 2. MaxEnt model for *Errajonna* sorghum landrace and plot showing predicted area**

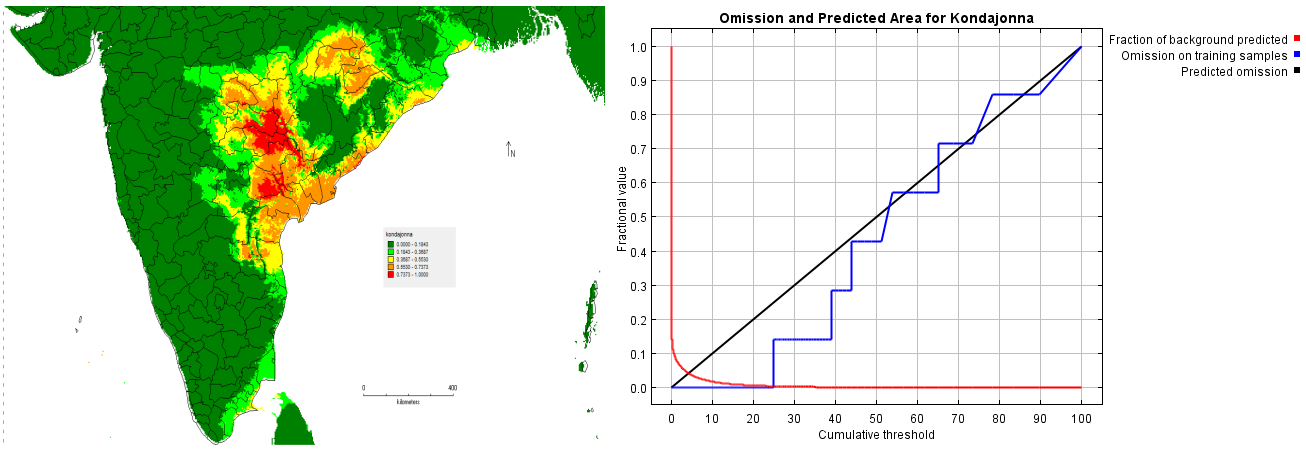


**Fig. 3. MaxEnt model for *Kondajonna* sorghum landrace and plot showing predicted area**

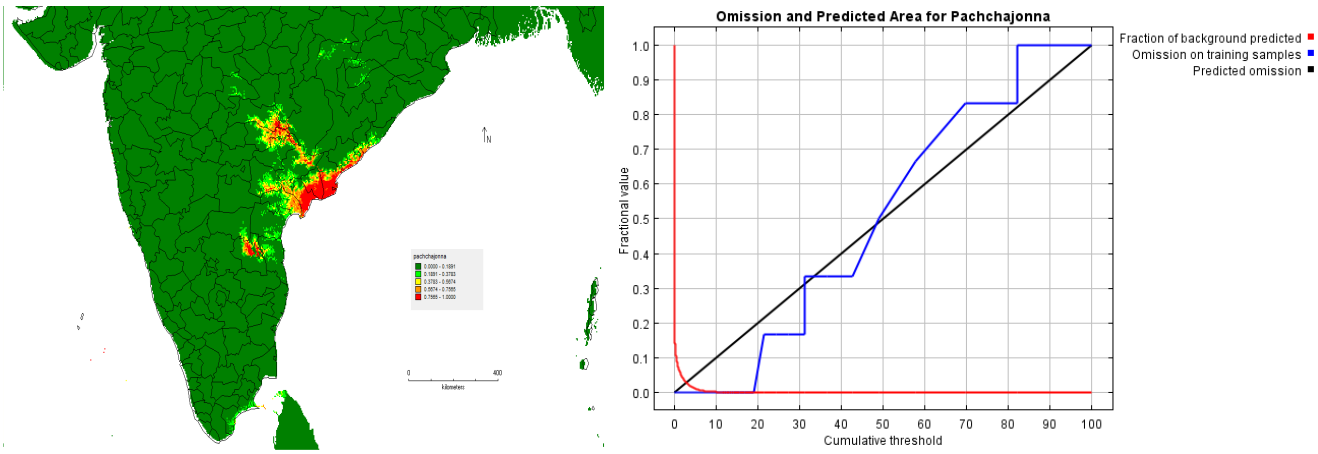


**Fig. 4. MaxEnt model for *Pachchajonna* sorghum and plot showing predicted area**

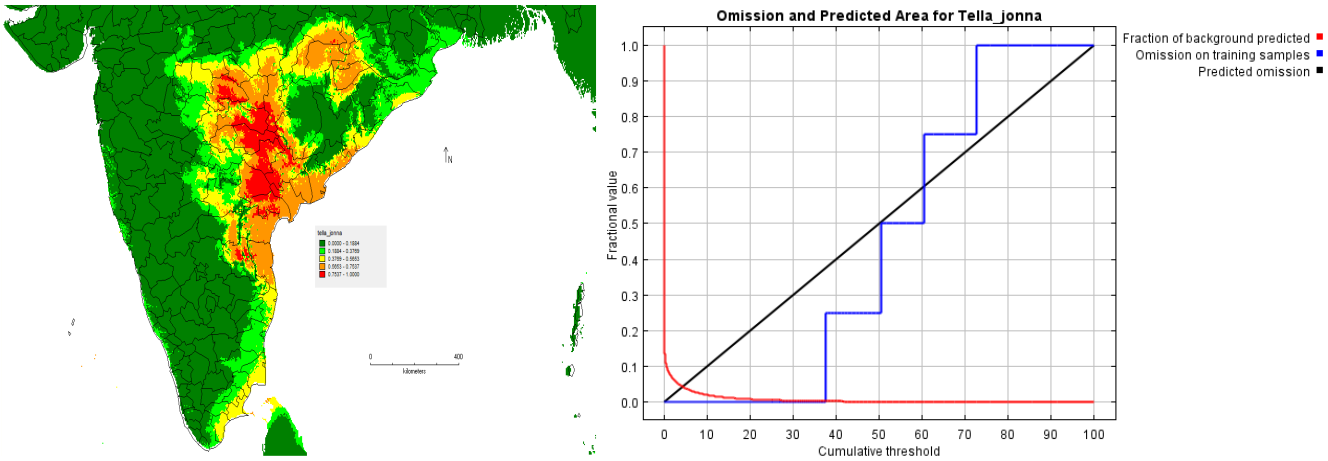


**Fig. 5. MaxEnt model for *Tellajonna* sorghum and plot showing predicted area**

occurrences in relation to other common approaches (Elith *et al*., 2006; Hijmans and Graham, 2006; Graham and Hijmans, 2006), especially with incomplete information. Predictive modelling of sorghum landraces geographic distributions based on the environmental conditions of sites of known presence establishes an important technique in analytical biology, with applications in conservation and reserve planning, ecology, evolution, epidemiology, invasive-species management and other fields (Corsi *et al*., 1999; Peterson and Shaw, 2003; Peterson *et al*., 1999; Scott *et al*., 2002; Welk *et al*., 2002; Yom-Tov and Kadmon, 1998). The MaxEnt modelling approach can be used in its present form for many applications with presence-only datasets, and merits further research and development (Eitzinger *et al*., 2013). Maxent has been successfully used by many researchers earlier to predict distributions such as stony corals (Tittensor *et al*., 2009); macrofungi (Wollan *et al*., 2008); seaweeds (Verbruggen *et al*., 2009); forests (Carnaval and Moritz, 2008), rare plants (Williams *et al*., 2009) and many other species (Elith *et al*., 2006).

The availability of detailed environmental databases, composed with cheap and efficient computer technology, has driven a rapid increase in predictive modelling of species environmental requirements and geographic distributions. The potential impact of climate changes on agricultural crop production varies spatially and depends on crop specific biophysical constraints (Eitzinger *et al*., 2013). Due to population expansion worldwide, the demand for food sources would increase in the changed climate regime. Because of sorghum's extensive adaptation would prove vital in meeting the food security of the people, use of MaxEnt method is highly warranted in preserving the important sorghum landraces.

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# Variability in Grain Quality Characters of Local Winter (*Sali*) Rice of Assam, India

**Khanin Pathak[1], Sunayana Rathi[1], Harendra Verma[2], Ramendra Nath Sarma[2] and Samindra Baishya[1]**
[1]*Department of Biochemistry & Agricultural Chemistry, Assam Agricultural University, Jorhat-785013, Assam, India*
[2]*Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat-785013, Assam, India*

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The study on rice germplasm showed considerable genetic variation in different quality characters analyzed. The grain length varied from 5.10 to 8.03 mm, grain width from 2.00 to 3.17 mm, cooked grain length from 7.40 to 12.37 mm, cooked grain width from 3.30 to 7.17 mm, grain elongation ratio from 1.29 to 2.02 and grain widening ratio from 1.37 to 3.32. On dry weight basis, moisture contents of genotypes ranged from 8.33 to 10.74 per cent, amylose from 0.05 to 29.6 per cent, starch from 70.37 to 82.83 per cent, GC from 53 to 100.03 mm, GT from 2 to 7, crude fat content from 2.64 to 3.76 per cent, crude protein content 8.10 to 10.32 and lysine content from 2.71 to 3.39 (g/100 g of protein). UPGMA based cluster analysis revealed the existence of two major clusters (A and B) with additional sub clusters within each major cluster in *indica* rice genotypes under study for grain quality data. The difference between GCV and PCV was less for all characters except GT, which indicate greater correspondence between phenotype and genotype and less environmental influence and greater role of genetic factors on expression of grain quality traits. Based on above results amylose content trait would be highly effective to be used in breeding programmes for improving cooking and eating quality.

**Key Words: Amylose content, Gel consistency, Gelatinization temperature, Genetic variability, Grain quality, Local winter/*Sali* rice**

## Introduction

After grain yield, grain quality is the major determinant for fetching higher price in the market. With the increase in demand for better grain quality in the economically developed and developing countries, quality has become important breeding objective in rice breeding programme in all countries. Quality improvement is also gaining prominence as unattractive grain character and unsatisfactory cooking quality hampers the acceptance and spread of high yielding variety. Rice quality is determined by some subjective and objective criteria based on the physical appearance of the milled rice, the cooking properties and the presence and absence of aroma of the rice. Generally, consumer preference is based on appearance, milling and cooking processes, grain shape and size.

Assam including North-East India, is traditionally a rice growing area and in which rice plays a significant role in economic and the socio-cultural life of the people of the region. *Sali* or winter rice (June/July-Nov/December) is dominant crop of the State covering 17 lakh hectares (71 percent of rice area) and contributing 73 percent of the total rice production (Anonymous, 2014). Based on grain quality parameters farmers traditionally classify *Sali* rice as normal *Sali* (*Sali* with coarse grain, *Lahi* with medium grain), *Joha* (scented), *Chakua* (semi glutinous) and *Bora* (glutinous). Farmers have been growing a large numbers of *Sali* traditional rice germplasms since long back for their livelihood without much information about the quality of the germplasm. The breeding efforts in Assam are mainly directed towards yield without focusing on grain quality parameters of the traditionally grown rice varieties of *Sali* season. A clear understanding of genetic base, through the characterization of local landraces for grain quality is essential to use them in a breeding programme. The information regarding those aspects in case of *sali* landraces are scanty and sporadic. Therefore, the present experiment was conducted to evaluate nature and intensity of variability in terms of grain quality of winter/*sali* landraces from Assam.

## Materials and Methods

The experiment was conducted with 100 local winter/Sali rice genotypes including Ranjit (as check) a popular high yielding variety, collected from Regional Agricultural

*Author for Correspondence: Email- khanin_bio@yahoo.in

Research Station, Assam Agricultural University, Jorhat, Assam, India. After harvest, samples were cleaned thoroughly using winnower to remove the chaff and other foreign matter and dried to 12-14% moisture content. Brown rice samples were used for analysis and three samples were drawn from same seed lot and treated as replication. Moisture content was determined by following the methods of AOAC (1970). The genotypes were characterized for grain length (mm), grain width (mm), cooked grain length (mm), grain elongation ratio after cooking, cooked grain width (mm), grain widening ratio after cooking following standard procedures (Shouichi *et al.,* 1976; Juliano and Perez, 1984). Similarly, alkali spreading value (Little *et al.,* 1958), gel consistency (Cagampang *et al.,* 1973), starch content (Chopra and Konwar, 1976), amylose content (Juliano, 1971), crude fat content (AOAC, 1970), crude protein content (Scales and Harrison, 1920) and lysine content (Mertz *et al.,* 1965) were also determined. The data generated from three replications were analyzed using analysis of variance (ANOVA) and the genetic parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad-sense ($h^2$), and genetic advance as percent of mean (genetic gain) were worked out as suggested by Johanson *et al.* (1955). Correlation coefficients were calculated according to Al-Jibouri *et al.* (1958). For clustering, data were analyzed using the software package, NTSYS-pc Version 2.1 (Rohlf, 2000).

**Table 1. Analysis of variance for grain quality characters in Sali/ winter rice from Assam, India**

| Characteristics | Sources of variation | | |
|---|---|---|---|
| | Replication | Genotype | Error |
| df | 2 | 99 | 198 |
| Moisture | 0.00224 | 1.017** | 0.0086 |
| Grain length | 0.2916 | 1.067** | 0.0391 |
| Grain width | 0.03183 | 0.408** | 0.0169 |
| Cooked grain length | 0.41314 | 3.517** | 0.0496 |
| Cooked grain width | 0.1747 | 1.803** | 0.0182 |
| Grain elongation ratio | 0.00971 | 0.072** | 0.0042 |
| Grain widening ratio | 0.00048 | 0.353** | 0.0181 |
| Amylose content | 0.00218 | 226.4** | 0.0055 |
| Amylopectin content | 0.02936 | 228** | 0.0194 |
| Starch content | 0.03387 | 18.51** | 0.0003 |
| GC | 0.04843 | 375.9** | 0.0056 |
| GT | 38.6533 | 6.719** | 1.7106 |
| Fat | 0.02707 | 0.212** | 0.0005 |
| Protein | 0.03368 | 0.876** | 0.0037 |
| Lysine (g/100 g protein) | 0.00781 | 0.066** | 0.0031 |

Df: Degrees of freedom; ** Significant at 1% level. Data for grain quality characteristics are mean sum of square.

## Results and Discussion

The analysis of variance revealed significant variation among genotypes for all the characters studied (Table 1), indicating plentiful genetic variation in the genotypes under investigation. Selection of parents is an important criterion for the successful breeding programme. Sometimes the *per se* performance of genotypes are used for choosing parents. The *per* se performance of genotypes for different quality traits under investigation are shown in Table 2. Genetic improvement and success

**Table 2. Estimates of genetic parameters for grain quality characteristics in Sali /winter rice from Assam, India**

| | Maximum | Minimum | Mean±SE | PCV (%) | GCV(%) | Heritabilty in broad sense | Genetic advance (5%) |
|---|---|---|---|---|---|---|---|
| Moisture (%) | 10.74 | 7.29 | 9.3248±0.05 | 6.30 | 6.22 | 0.9752 | 12.65 |
| Grain length (mm) | 8.03 | 5.10 | 6.356±0.11 | 9.72 | 9.21 | 0.8977 | 17.98 |
| Grain width (mm) | 3.17 | 2.00 | 2.490±0.08 | 15.40 | 14.50 | 0.8854 | 28.11 |
| Cooked grain length (mm) | 12.37 | 7.40 | 10.3283+0.13 | 10.60 | 10.41 | 0.9589 | 20.99 |
| Cooked grain width (mm) | 7.17 | 3.30 | 5.223±0.08 | 15.00 | 14.77 | 0.9704 | 29.97 |
| Grain elongation ratio | 2.02 | 1.29 | 1.6315±0.04 | 10.00 | 9.21 | 0.8428 | 17.42 |
| Grain widening ratio | 3.32 | 1.37 | 2.1268±0.08 | 16.90 | 15.70 | 0.8605 | 30.00 |
| Amylose content (%) | 29.63 | 0.05 | 5.3997±0.04 | 161.00 | 160.86 | 0.9999 | 331.37 |
| Amylopectin (%) | 99.96 | 70.37 | 94.5986±0.08 | 9.22 | 9.22 | 0.9997 | 18.98 |
| Starch (%) | 82.83 | 70.37 | 76.7985±0.01 | 3.23 | 3.23 | 1.0000 | 6.66 |
| GC (mm) | 100.00 | 53.00 | 93.3948±0.04 | 12.00 | 11.99 | 1.0000 | 24.69 |
| Alkali spreading value | 8.00 | 1.33 | 5.8733±0.76 | 31.30 | 21.99 | 0.4939 | 1.87 |
| Fat (%) | 3.76 | 2.64 | 3.1306±0.01 | 8.51 | 8.47 | 0.9927 | 17.39 |
| Protein (%) | 10.43 | 8.07 | 9.3091±0.03 | 5.83 | 5.79 | 0.9876 | 11.86 |
| Lysine (g/100gProtein) | 3.39 | 2.65 | 2.9601±0.03 | 5.24 | 4.90 | 0.8731 | 9.42 |

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation.

of breeding programmes mainly depend on magnitude of genetic variation and extent of heritability for desirable characters in the germplasm, therefore conservation of variability has immense potential in breeding programmes for future generations. Rice grain shape preference varies among consumer group and regions and even in same region preference varies based on its end use. For instance, long and slender grain varieties are preferred by consumers in the United States and Western Europe and in most Asian countries or areas, including China, India, Pakistan, and Thailand; in contrast, consumers in Japan, South Korea, and Sri Lanka prefer short bold grain cultivars (Unnevehar *et al.,* 1992; Juliano and Villareal, 1993; Wan *et al.,* 2006) and in southern part of india medium/short slender type of grains are preferred (Viratmath *et al*, 2010) and in north eastern part of India short bold and medium slender grain cultivars with intermediate amylose content, soft GC and intermediate GT are preferred. In the present study, kernel length varied from 5.10 mm (Misiri Bora) to 8.03 mm (Pakhori Bora) and grain width ranged from 2.00 mm (Kmj Bora-16) to 3.17 mm (Silatika Bora, Sontuki). Kernel length with L/B ratio determines the grain shape. Very short grain and short grain rice class with L/B ratio were classified as short bold and medium slender. 18 genotypes were short bold, seven ecotypes classified as medium slender genotypes. Two genotypes were long slender (Ronga Bora-2 and Rupohi Bora-2) and 55 genotypes were long bold, 16 genotypes were long slender in grain shape with waxy type amylose content (1-2%), soft GC and high GT. Two genotypes Kmj Bora-56 and Pakhori Bora were extra long with very high (28.40%) and low (0.3%) amylose content respectively with soft GC and intermediate GT. In the present study, three short bold cultivars (Kmj Bora-8, Tangun Bora-2 and Til Kochu Bora) with preferred intermediate amylose content, soft gel consistency and intermediate gelatinization temperature were identified; and one medium slender genotypes Kmj Bora-90 was waxy type with soft GC and intermediate GT, these genotypes can be used in breeding programmes to develop short bold and medium slender with desirable or preferred eating and cooking quality rice. The length wise elongation upon cooking increase in girth is considered most desirable in high quality rice. During cooking rice grains absorb water and increase in length, breadth and volume (Sood, 1978). In the present study, cooked grain length varied from 7.40 (Kmj Bora-8) to 12.37 mm (Pakhori Bora). Cooked grain width ranged from 3.30 mm (Kola Bora-4) to 7.17 (Kmj Bora-61). Elongation ratio is an important parameter for cooked rice. Rathi *et al.* (2010) reported that cooked grain length varied from 6.5 mm to 10 mm and cooked grain width varied from 3 mm to 5 mm in *Ahu* rice of Assam, which is slightly less than present study due to difference in cultivars studied. If rice elongates length wise, it gives finer appearance and if it expands girth wise, it gives coarse look. Rice with high cooked grain length with finer appearance are preferred. In the present study, the linear elongation ratio varied from 1.29 mm (Kola Ampakhi) to 2.02 mm (Kmj Bora-61) while breadth wise elongation ratio ranged from 1.37 (Til Bora-1) to 3.32 (Kmj Bora-61). Srivastava and Jaiswal (2013) reported that elongation ratio in short grain aromatic cultivars varied from 1.36 to 1.70 with breadth wise expansion ratio of 1.12 to 1.54 and in basmati genotypes length wise elongation ratio varied from 1.70 to 1.91 while the breadth wise expansion ratio of 1.25 to 1.61 and non-aromatic types showed linear elongation ratio from 1.27 to 1.52 and breadth wise elongation ratio of 1.30 to 1.54. The grain elongation ratio varied from 1.0 to 1.6 while grain widening ratio was varied from 1 to 2.5 in upland rice of Assam (Rathi *et al.,* 2010), which is less than present study.

Amylose content is the major determinant of rice eating and cooking quality (Kumar and Khush, 1986; Juiano, 1993). The amylose content determines the stickyness, fluffyness, cohesiveness and tenderness or hardiness of the cooked rice. The varieties with intermediate amylose content (20-25%) are most preferred because they become fluffy, soft, moist and tender after cooking. The result of the present investigation revealed that altogether 78 of the genotypes could be grouped in to waxy (glutinous) category due to very low amylose rice (0-12% amylose) as per Juliano *et al.* (1981). Eleven genotypes could be considered as low amylose rice (12-20% amylose), another six as intermediate amylose rice (20-25% amylose) and the remaining four glutinous rice genotypes as the high amylose rice (>25% amylose). On the other hand, Allahgholipour *et al.* (2006) considered rice with 0-8% amylose as waxy or glutinous rice. In this context, about seventy four of the genotypes under study could be considered as glutinous. The amylose contents in some rice of Assam were recorded to vary from 0.95 to 1.25 per cent (Kandali *et al.,* 1995), from 0.679 to 1.892 per cent (Bahar, 2000) and from 0.92-1.19 per cent of starch (Bhagabati, 2000) and accordingly

classed them as glutinous rice. Even a higher range of amylose contents (0.136-11.4%) for some glutinous rice of Assam was reported by Bhattacharjee (2006). A special class of rice locally known as *Chokuwa* rice (soft rice), indigenous to Assam needs no cooking and can be consumed after simply soaking in cold to lukewarm water. This rice is characterized by its semi glutinous character with amylose content ranging from 12 to 17 per cent (Barkakaty, 1975). Amylose contents in three of the *Chokuwa* rice varieties were reported to range between 15.02-16.95 per cent (Bhagabati, 2000). Nine of the glutinous rice genotypes used in the study, namely, Kola Ampakhi, Kmj Bora-10, Kmj Bora-80, Kmj Bora-90, Lothow Bora, Mon Bora-2, Nashinggeti Bora, Rupohi Bora-2 and Tuloxee Bora were found to have amylose contents in the range of 8.2-16.63 per cent, thus can be considered as *chokuwa* rice. Such variation in amylose contents among the genotypes facilitate the breeder to select genotypes in breeding programme in developing rice varieties with desired amylose level.

In present investigation, out of 99 local genotypes, 73 genotypes were found to have low GT (55–68°C, ASV: 5-7) and 22 genotypes showed intermediate GT (69-74°C, ASV: 3-5). The intermediate ASV indicated the medium disintegration and classified as intermediate GT which highly desirable for quality grain (Bansal *et al.,* 2006). Vanaja *et al.* (2003) also revealed that high-amylose rice varieties absorb more water, have low gelatinization temperature and produce more cooked material. Park *et al.* (2007) postulated that the crystalline regions of non-waxy (high amylose) rice starch restricted the hydration of amorphous regions whereas waxy (high amylopectin) rice starch consisted mostly of crystalline regions and thus could begin gelatinization at a lower temperature. Singh and Singh (2006) found the alkali spreading value between 2.5 to 7.0 with low variation in some of the scented varieties of rice. Out of 100 *ahu* rice genotypes of Assam, 97 genotypes showed low GT range (55–68ºC) with ASV 5.0-7.0 (Rathi *et al.,* 2010). The findings of the present study are, thus well comparable with these reports. In the present investigation, the range of fat content of 99 rice genotypes was 2.64-3.76 per cent and the values were found close to the findings of many earlier workers. Juliano (1977) recorded lipid content from 2.4 to 3.9 per cent in brown rice, 17.5-21.7 per cent in bran and 0.3 to 0.6 per cent in polished rice. The lipid content in glutinous rice of Assam was reported to vary from 2.22 to 3.62 per cent (Dutta and Baruah, 1978). Bhagabati (2000) recorded a little lower range of 3.34 to 3.51 per cent crude fat in glutinous rice varieties of Assam. The range of crude protein content in the rice genotypes including Ranjit was varying from 8.1 to 10.32 per cent. Juliano *et al.* (1964) reported the average protein content of brown rice in the range of 7.32 to 13.46 per cent for *indica* varieties. Kandali and Borah (1992) reported that the grain crude protein in 19 local rice varieties of Assam varied between 8.4 to 14.0 per cent on dry weight basis. The crude protein content of three glutinous rice varieties of Assam was found to vary from 9.96 to 10.39 per cent (Kandali *et al.,* 1995). Bhagabati (2000) revealed the crude protein content of nine different Assam rice varieties from 9.23 to 11.29 per cent. Thus the present findings conform to all these earlier reports. Lysine content of rice genotypes ranged from 2.71 to 3.39 g/100g protein and the value was comparable to the findings of Pathak (2008). However, the lysine content in rice genotypes used in the study was found to be lower than the reported values by Sekhar *et al.* (1982) and Begum *et al.* (1993). A wide variation in lysine content (1.73 to 7.13 g/16 g N) in milled rice grains of some Indian rice land races was reported by Banerjee *et al.* (2011). The average lysine contents in the rice land races were recorded as 4.62 g/16 g N which was much higher than the present findings. They observed that variation for lysine content was higher than that of protein content. These results indicated the existence of wide genetic variability for eating and nutritional quality parameters in among the genotypes studied. The variation in the lysine content of rice grains may primarily be due to genotype differences, genetic makeup of the genotypes, climatic condition, nutrient status of soil as well as the analytical methods used (Baishya *et al* 2010).

Various variability parameters studied are presented in the Table 2. The difference between GCV and PCV was less for all characters except GT, which indicate greater correspondence between phenotype and genotype, and less environmental influence and greater role of genetic factors on expression of grain quality traits. Similar results were obtained by Rathi *et al.* (2010) and Subbaiah *et al.* (2011). Among the grain quality parameters very high GCV and PCV was recorded for amylose content which indicate enormous variability for amylose content in the present study material and vast scope for region specific improvement of amylose content. However protein content and lysine content showed low PCV and GCV estimates, indicated limited scope for

selection within the experimental materials. Babu *et al.* (2012) and Shejul *et al.* (2013) reported low PCV and GCV with low genetic advance for protein content; Rathi *et al.* (2010) and Arulselvi *et al.* (2007) reported high heritability with low genetic advance for starch content, which supports the present findings. High heritability with low genetic advance indicates that these characters were predominantly governed by non-additive gene action (dominance and epistasis). Vaneja *et al.* (2006) reported low GCV and PCV with high broad sense heritability and for grain length and kernel elongation ratio. Ogunbayo *et al.* (2014) reported similar finding for grain length. However, broad sense heritability includes both additive and non additive effects. Heritability estimates along with genetic advance is more reliable in selection of individuals than heritability estimate alone (Johanson *et al.,* 1955). High heritability coupled with high genetic advance as per cent of mean was recorded for amylose content, which indicates preponderance of additive gene action and can be improved through simple selection. High heritability with moderate genetic advance recorded for grain widening ratio. Low heritability along with moderate genetic advance was recorded for gelatinization temperature. High heritability with low genetic advance was recorded for starch content, gel consistency, grain length, grain elongation ratio, amylopectin, grain width, cooked grain length, cooked grain width, fat (%), protein (%) and lysine content (%).Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.,* 1955). The high heritability estimates along with low genetic advance indicates that non-additive type of gene action and genotype-environment interaction plays a significant role in the expression of the traits. Thus the characters showing high heritability along with moderate or low genetic advance could be improved by intermating the superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

In the present study, genotypic and phenotypic correlation coefficients were studied for grain quality characteristics are presented in Table 3. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the major role of genetic factors for association (Pandey *et al*, 2012; Ehdaie *et al*, 1989; Ullah *et al*, 2012). Amylose content is negatively correlated with alkali spreading value (ASV), a measure of the time required for cooking. ASV is inversely proportional to GT. This indicate that rice varieties with high amylose content have high gelatinization temperature, amylose tends to act as a restraint to gelatinization because it diffuses out of the granules during swelling, making up the continuous phase (network) outside the granule (Hermansson and Svegmark, 1996). The GT affects the degree of cooking of rice because of the cooking gradient from the surface to the core of the grain. In the present study most of the genotypes possess low GT and GT correlates directly with cooking time, i.e. low GT favours fuel conservation, provided eating quality is not adversely affected. Park *et al.* (2007) postulated that the crystalline regions of non-waxy (high amylose) rice starch restricted the hydration of amorphous regions whereas waxy (high amylopectin) rice starch consisted mostly of crystalline regions and thus could begin gelatinization at a lower temperature. Generally gel consistency is negatively related with amylose content. Gel consistency decide either rice remain soft (gel consistency->than 60 mm gel length) or medium (gel consistency-41-60 mm gel length) or hard (gel consisteny-<than 40 mm gel length) after cooking. Odenigbo *et al.* (2013) reported negative correlation between amylose content and GC, but in present study there was no correlation observed between amylose content and GC. The negative correlation between grain elongation and amylose content was observed, which indicates that cultivars that elongate more during cooking would likely have a decreased content of amylose. This finding is similar with the finding of Oka *et al.* (2012). The negative correlation between amylose content and cooked grain width and grain widening ratio indicate that cultivars with low amylose content swell more and would have more grain widening ratio. Grain elongation showed positive correlation with GT, indicates that cooked grain elongation increases with increase in gelatinization temperature but high gelatinization temperature elongates less during cooking than low and intermediate gelatinizing rice. Therefore, here GT showed positive correlation with grain elongation. This finding was similar with the findings of Perez *et al.* (1987). Amylose content showed negative correlation with grain width and grain widening ratio, thus it is not possible to breed for low amylose content variety with fine grain. Amylopectin showed positive correlation with starch content, which is in conformity with the findings of Rathi *et al.* (2010) and Chakraborty *et al.* (2009), who reported positive correlations of starch content with amylopectin content. GT was negatively correlated with fat. The lysine content

**Table 3. Genotypic (above diagonal) and phenotypic (below diagonal) coefficients of correlation between grain quality characteristics in Sali/winter rice from Assam, India**

| | MC | GL | GW | CGL | CGW | GLR | GWR | AC | AmC | SC | GC | ASV | FC | PC | LC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MC | 1 | 0.0637 | 0.0111 | 0.019 | 0.0923 | -0.0219 | 0.0942 | 0.0964 | -0.0942 | -0.1029 | -0.1499 | -0.098 | -0.0144 | 0.0500 | 0.1231 |
| GL | 0.0219 | 1 | -0.2774** | 0.5596** | -0.0739 | -0.3365** | 0.1598 | -0.0328 | 0.0334 | 0.046 | -0.1085 | -0.0267 | 0.1745 | 0.0602 | -0.0806 |
| GW | 0.0021 | -0.0546 | 1 | -0.2203* | 0.4404** | 0.0331 | -0.4928** | -0.0461 | 0.0476 | -0.0141 | 0.1373 | 0.0031 | 0.0305 | -0.2217** | 0.1616 |
| CGL | 0.0113 | 0.3455** | -0.0866 | 1 | 0.3648** | 0.5881** | 0.5585** | -0.7291** | 0.7293** | 0.4947** | -0.2094* | 0.5474** | 0.1125 | -0.0092 | 0.0815 |
| CGW | 0.0393 | -0.0316 | 0.1225 | 0.3029** | 1 | 0.4915** | 0.5573** | -0.4871** | 0.4899** | 0.3285** | -0.066 | 0.3768** | 0.0254 | -0.1287 | 0.1629 |
| GLR | -0.002 | -0.0407 | 0.0006 | 0.1039 | 0.0566 | 1 | 0.4705** | -0.7861** | 0.786** | 0.5098** | -0.1413 | 0.6434** | -0.0281 | -0.062 | 0.1741 |
| GWR | 0.0177 | 0.0283 | -0.0745 | 0.2018* | 0.1517 | 0.0246 | 1 | -0.4325** | 0.4341** | 0.3197** | -0.1905 | 0.3609** | 0.002 | 0.0674 | 0.0098 |
| AC | 0.4867** | -0.1679 | -0.1455 | -0.809** | -0.5638** | -0.8262** | -0.539** | 1 | -1 | -0.6323** | 0.1567 | -0.8091** | 0.0149 | 0.1000 | -0.1725 |
| AmC | -0.4774** | 0.1723 | 0.1492 | 0.836** | 0.5295** | 0.8296** | 0.625** | 0.7255** | 1 | 0.6326** | -0.1576 | 0.8085** | -0.0168 | -0.1000 | 0.1724 |
| SC | -0.1481 | 0.0669 | -0.0127 | 0.4212** | 0.6296** | 0.1904 | 0.2653** | -0.6434** | 0.701** | 1 | 0.0284 | 0.3908** | 0.1361 | 0.1127 | 0.0420 |
| GC | -0.9713** | -0.711** | 0.5543** | -0.5208** | -0.5702** | -0.2378* | -0.7115** | 0.1592** | -0.1532** | 0.7887** | 1 | -0.2335* | 0.0951 | -0.1593 | 0.1239 |
| ASV | -0.076 | -0.0489 | -0.0082 | 0.7368** | 0.3962** | 0.1285 | 0.1672 | -0.975** | 0.9053** | 0.3544** | -0.3809** | 1 | -0.2046* | -0.1072 | 0.1874 |
| FC | -0.0024 | 0.027 | 0.0029 | 0.0317 | 0.0048 | -0.0011 | -0.0001 | 0.0347 | -0.0387 | 0.0897 | 0.2823* | -0.0704 | 1 | 0.0504 | -0.1061 |
| PC | 0.0158 | 0.0191 | -0.0427 | -0.0064 | -0.0538 | -0.0052 | 0.0117 | 0.468** | -0.4688** | 0.1511 | -0.9614** | -0.0752 | 0.0074 | 1 | -0.7274** |
| LC | 0.0107 | -0.0078 | 0.0086 | 0.0132 | 0.0187 | 0.0041 | 0.0009 | -0.217* | 0.2181* | 0.0151 | 0.2011* | 0.0364 | -0.0042 | -0.0569 | 1 |

MC: Moisture content; GL: Grain length, GW: Grain width; CGL: cooked grain length; CGW: cooked grain width; GLR: grain elongation ratio after cooking; GWR: Grain widening ratio; AC: Amylose content; Amc: Amylopectin content, SC: Starch content; GC: Gel consistency; ASV: Alkali spreading value; FC: Fat content; PC: Protein content; LC: Lysine content.
* and **, Significant at 5% and 1% probability levels, respectively.

of the rice genotypes was found to be negatively correlated ($r$= -0.750) to the protein contents. Juliano *et al.* (1973) observed a negative correlation between the lysine content of protein and protein content of brown and milled rice only in samples with protein below 10 per cent. As protein content increased water-soluble nitrogen also increased as a percentage of brown rice. Lasztity (1996) reported that a negative correlation between protein and lysine content. He explained the negative correlation by the fact that increase in protein content is highest in the starchy endosperm and lower in the germ and aleurone layer. This suggests that the increased biosynthesis of the protein mainly produces storage proteins. Above discussion revealed that rice grain quality index can be improved by decreasing the breadth of the grain. The desired characters showing significant positive correlation can be improved with simple selection for one trait, while the desirable characters showing significant negative correlation compromise has to be done in deciding the extent of loss of one traits over other during selection.

### *Diversity Analysis*

UPGMA Cluster analysis revealed the existence of two major clusters (A and B) with additional sub clusters within each major cluster in *indica* rice genotypes under study for grain quality data (Fig. 1). The cluster A comprised of short bold (8 genotypes), long bold (12 genotypes), basmati type (5 genotypes) with one medium slender and one long slender genotype and extra long slender. The cluster B comprised of short bold (12 genotypes), long bold (42 genotypes), basmati type (12 genotypes) with four medium slender and one extra long slender genotype. Average amylose content (AC) (23.50 %), grain length (8.0 mm), grain width (2.89 mm), cooked grain length (11.10), cooked grain width (4.83 mm), grain widening ratio (1.94) and fat percentage (3.35 %) of sub cluster A2 was greater than sub cluster A1 which have average amylose content 17.68 %, grain length 6.18 mm, grain width 2.48 mm, cooked grain length 8.86 mm, cooked grain width 4.56 mm, grain widening ratio 1.86 and fat percentage 3.10 %. A1 sub cluster was characterized by non waxy type amylose content; soft gel consistency, high protein percentage and majority of genotypes have medium type grain length. A2 sub cluster was characterized by very long grain type, intermediate GT, soft GC and low lysine content. B1 sub cluster comprised of three genotypes, these genotypes were characterized by waxy type genotypes, broad type grain width, high lysine, fat, moisture content and low protein content. B2 sub cluster comprised of 68 genotypes, these genotypes were characterized by waxy type amylose content, high GT, high cooked grain width, high grain widening ratio, high starch content and low moisture content.

Rice varietal improvement for grain quality is directed towards improving traits associated with consumer acceptance, nutritional quality and post harvest processing. All characters showed high broad sense heritability estimates except GT, which suggest that selection based on phenotypic performance, would be effective in improvement of these traits. Based on above discussion amylose content trait would be highly effective to be used in breeding programmes for improving cooking and eating quality. These local genotypes must not be left out, since they form a rich resource for incorporation into breeding programmes.

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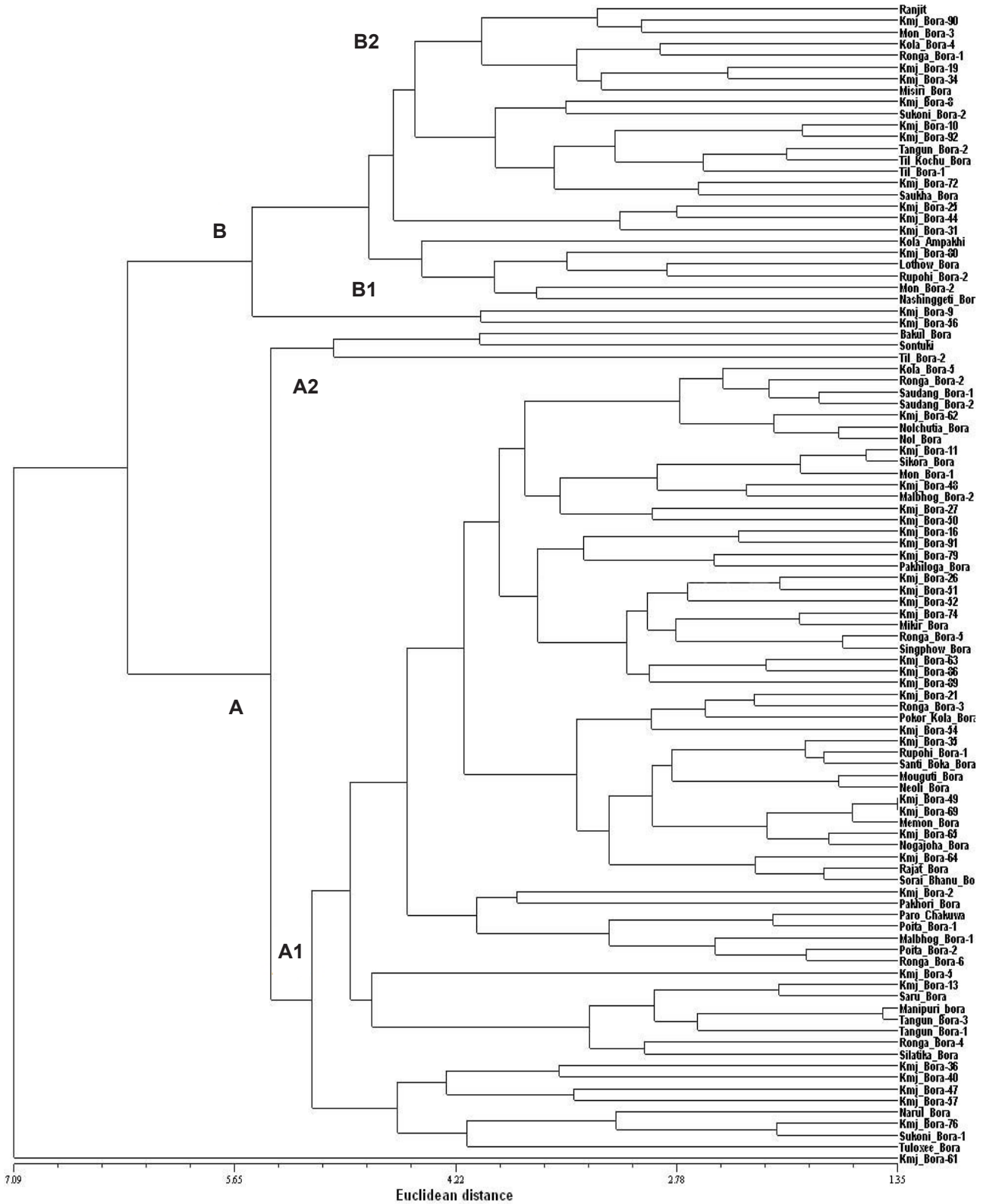


**Fig. 1. UPGMA cluster analysis based on grain quality characteristics of local winter (Sali) rice of Assam, India.**

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# Methodology for Collecting and Preparing Herbarium Specimen of *Allium*

**Anjula Pandey, K Pradheep and Rita Gupta**
*ICAR-National Bureau of Plant Genetic Resources, New Delhi 110 012, India*

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Taxa belonging to the genus *Allium* are bulbous or rhizomatous with hollow or flat leaves and small delicate flowers, therefore preparing an ideal herbarium specimen is difficult. Quite often some of the characters are not well preserved while processing for herbarium specimen; occasionally they are misunderstood for characters therefore defeat the very purpose of their use as source for taxonomic study. In this paper the authors have made an attempt to provide methodology on collection and preparation of herbarium specimens of different species of *Allium*. Information provided herein is primarily based on the authors' field experience and experimental and herbarium study on the genus in the Indian context. Most significant observations to be recorded in field during collecting include characters of root and bulb/rhizome, leaf, scape and flower. The paper also includes modified procedures for 'difficult to preserve herbarium specimens' with special notes on plant odour, flower colour and leaf colour. This can be broadly applied to taxa belonging to other bulbous groups with appropriate modification. Illustrations provided in this paper depict the representative types to facilitate better understanding by the readers.

*Allium* is among the largest monocotyledonous genera comprising of more than 800 species (Fritsch *et al*., 2010; Fritsch and Abbasi, 2013). Many economically important crops such as garlic, onion, leek, shallot, bunching onion, chives and Chinese chives, giant onion, and ball-head onion are cultivated as vegetables, spices, condiments and ornamentals (Fritsch and Friesen, 2002). The genus *Allium* shows remarkable variation in vegetative characters [underground storage organs–bulbs, rhizomes, swollen/ fleshy roots; leaf-size, shape, anatomy (section), sheath/ lamina ratio], mode of propagation (seed, bulb, rhizome, bulbils), floral characters (morphology of spathe, pattern of opening of flowers, tepal size and shape, stamen length and colour) and seed characters (size, shape, and ultra-structure of seed coat). Variation also occurs in growth form (annual to perennial habit) and winter dormancy, biochemical composition, chromosomes and ploidy levels.

In India the genus is represented by about 35-40 species that occur in temperate and alpine region of Himalaya (Polunin and Stainton, 1984; Pandey *et al*., 2008) including major cultivated species such as onion and garlic. Alpine-subtemperate region (2500-4500m) of the western Himalaya with about 25 taxa is the zone of rich species diversity (Gohil, 1992; Pandey *et al*., 2008). Assessment of species distribution *vis-a-vis* germplasm collected and conserved under genetic resource programme has shown thrust in this direction (Negi and Pant, 1992; Pandey *et al*., 2005b; Pandey *et al*., 2008; Khosa *et al*., 2014; Pandey *et al*., 2014). Hitherto unexplored areas are the potential regions for new variability as well as of probable new taxa.

Some of the important characteristics for identification of different species of *Allium* are bulb or rhizome (shape, outer tunic/membrane), leaf (succulent, flat, fistular, keeled), and inflorescence (inflorescence shape, flower colour, perianth shape and length) and presence of bulbils (Fig. 1; Appendix 1). Additionally some ultra-structures of stamen (teeth on inner ones) and orientation of ovarian crests are important for species identification in the genus (Wheeler *et al*., 2013).

Among vegetative characters used for taxonomic identification the bulb coat characters are of importance for delineation of taxa. Species with cellular-reticulate bulb coats, with considerable variation in the patterns of cells on the inner surface of the outer bulb coat are particularly important for identifying species. Outer bulb coat with an open-celled "mesh" tunic has lesser moisture retaining properties as compared to that of the closed-cell coat that acts as effective barrier to moisture (Rola, 2014).

Well preserved and documented herbarium resources are of high value for taxonomic research globally besides their use in molecular study (Rogers and Bendich, 1985). Heavy dependency on herbarium

*Author for Correspondence: Email- anjula.pandey@icar.gov.in

material on the genus, lack of access to study material in field, and different period of availability of vegetative and reproductive stages has lead to difficulty in taxonomic and revisionary studies in this genus (Friesen *et al*., 2006).

Bulbous taxa are categorized as group "difficult to collect and process as herbarium specimen" for a plant collector (Pandey *et al*., 2013). Many characteristics of systematic value in the genus *Allium* (root morphology, bulb coat colour, leaves if hollow or flat, keeled beneath, inflorescence– globose, spherical or hemispherical, scape solid or hollow, shape and colour of perianth segment, and stamen characters) are lost while drying, hence difficult to represent in the herbarium specimen. This paper provides a comprehensive methodology to facilitate collecting and processing of herbarium specimens and recording of essential data pertaining to species delineation.

The present study is an outcome of work done under project on "Genetic Resources and Systematic study of Alliaceae in India–*Allium*" at the ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Data were collected while germplasm collection trips undertaken during 2009-14 and observations noted during experimental study carried out at NBPGR, New Delhi using standard IPGRI passport (http://www.ecpgr.cgiar.org/fileadmin/bioversity/publications/pdfs/728_Descriptors_for_*Allium*__*Allium*_spp._.pdf). Additionally, herbarium based study using 700 specimens at NBPGR herbarium (NHCP), BSI (BSD), FRI (DD) and NBRI (LWG) were used apart from online virtual herbaria (K, P, E, PE, GAT). For validation of characters selected e-resources in major herbaria (www.efloras.org/florataxon.aspx?flora_id=2&taxon_id=101086;,http://www.efloras.org/florataxon.aspx?flora_id=5&taxon_id=101086;http://www.efloras.org/florataxon.aspx?flora_id=1&taxon_id=101086, USDA Plant Database, http://linnean-online.org/view/collection/linnean=5Fherbarium/*Allium*.html) were also used. Herbarium techniques for collecting and drying were used as per the standard procedures (Jain and Rao, 1977) with modifications for processing of leaves and bulbs. Methodology was validated by the authors while collecting in fields and processing of material at the National Herbarium of Cultivated Plant (NHCP), New Delhi.

Herbarium specimen prepared of a material only at vegetative or reproductive stage is inadequate and therefore of less value for use in systematic study. For a cultivated or wild species one should take as many observations as possible at various growth stages in the field during collection and while processing and grow out in experimental study. The collector needs to go during early growth period (in December-January) for vegetative material and for flowering specimen (in May-June when bulb mature). It demands visiting the same area at least two times or else hunt for early and late sown plants. It is recommended that collected material should be pressed fresh (especially flowers) in the field or collected in polythene bag (closed with rubber band) during collection. Standard digging instrument, blotters, plant press, camera, hand lens, bottles (with 10 per cent FAA) were used following methods given by Jain and Rao (1977).

Specimens of cultivars show variation in morphology of mature bulb coat, colour, size of bulb, shape, pungency, etc. and therefore representation of distinct type is suggested. The specimen with detailed notes on specific features, hand drawn line diagrams of bulb shape on the herbarium sheet and photographs with close up of parts can be put on sheet along with magnification range. Additionally wet collections can be made to depict variation in bulb characters especially the shape, size, etc., although colour is lost during preservation. The bulb coat can be separately collected and preserved for a longer period without deterioration. Among the reproductive characters, the flower and seeds being small are difficult for study in field; perianth is fragile and loses colour and shape and study of internal structures therefore is difficult. If herbarium specimen is collected for molecular study, mounted specimen should not be treated with any chemical protectants other than deep freezing treatments; it should have label clearly demarcating the purpose of study (Wheeler *et al*., 2013).

Given below are some specific observations to be recorded while collecting in the field and preparing herbarium specimens:

### *Habitat*

Notes on habitat conditions for different species of *Allium* (wild, semi-domesticated or cultivation), collected from farmer's field, kitchen garden or experimental conditions; record data on frequency of occurrence (abundant, frequent, rare, occasional, etc.), associated species, soil type (rocky, saline, sandy), colour and texture, topography, etc., are essentially needed for wild plants. Data on latitude, longitude and other geographic parameters can be recorded using GPS; this can help in


**Fig. 1. Illustrations showing characters to be noted for different parts of *Allium:* (top row) fleshy roots; fasciculate roots; bulb with fibrous coat; (middle row) bulb with membranous coat; freshly harvested bulb with normal roots and triquetrous leaves; (bottom row) hollow leaves shown by insertion of strip on cut end; inflorescence showing exerted anthers.**

locating the species at similar location elsewhere in the area of exploration.

### Habit

It is often difficult to collect a complete specimen with fully mature bulb and leaves and floral parts together for preparing into a herbarium specimen; in many cases bulb may be fully mature but leaves, scape or inflorescence withered away. The freshly dug out specimen with immature bulb does not really represent the actual shape of the particular species. Fresh harvest of *Allium* sold in the market may only represent part of species (leaves of *A. tuberosum, A. hookeri*) and young bulb with leaves (*A. cepa, A. chinense, A. ampeloprasum*). In such cases one should try to represent different stages of plant at vegetative growth (bulb, leaf, etc.) and reproductive stages (scape, inflorescence, flower).

### Bulb

Tunicated bulb formed from basal leaves is a well demarcating character that helps delimiting *Allium* from many bulbous taxa (*Amaryllis, Drimia* called wild onion in many regions of India). Notes/observations on bulb (single or in cluster, cylindrical, bulb shape, size, level of development, membrane character–outer and inner coat colour, texture, etc.) are important in identifying different taxa of *Allium*. Collector should ensure that intact bulb is collected, or if peeling off collect the sample of membrane in paper pouch. Notes on bulb colour at harvest/maturity are to be recorded; in an immature bulb the coat colour often an unstable character and can mislead in the identification of species. Take observations of the inner wall of outer coat making peel mount and examining it for cell shapes under 10X magnification.

Presence of underground bulbils is an additional character that delimits taxa. Bulbs in single or in cluster, size and shape of the bulb, and leaf characters can distinguish species even at vegetative stage (*A. chinense* vs. *A. cepa* var. *cepa*, *A. cepa* var. *aggregatum* and *A. proliferum*). *A. chinense* has cylindrical-long necked bulbs, triquetrous leaves and white membrane whereas in others the leaves are fistular (round/elliptical in section, bulb not cylindrical with short neck, membrane white or shades of brown, violet, lilac).

Usefulness of bulblets/bulbils to serve as taxonomic identity especially when detached from the mother plant is questionable. Bulblets (cloves) of garlic (*A. sativum*) and *A. ampeloprasum* (great headed garlic) can be distinguished on the basis of size and texture of bulb coat; the former with thin membranous flat leaves but latter has thick, leathery and keeled leaves. Underground/aerial bulbils are always thick walled, smaller than the normal bulblets. Underground bulbils are located below the bulblets or may be with stoloniferous roots. Aerial bulbils are smaller than the underground bulbils, borne in the scape/floral heads. While collecting the position, size and shape (morphological structure) of the bulbils must be carefully noted. In case of doubt grow out tests are essential.

### Rhizome

Presence of a developed rhizome, its position–horizontal or vertical is characters associated with subgenus and section. Subg. *Amerallium*, rarely produce a notable rhizome; subg. *Anguinum* and *Melanocrommyum* consist of small rhizomes and no bulb whereas subg. *Butomissa, Rhizirideum, Allium, Cepa, Reticulatobulbosa* and *Polyprason* have both rhizome and bulbs (reduced, modified or condensed state). Well developed rhizome is generally deep-seated and collector should use digging tools to take out carefully. Presence of thick rhizomes in a dried specimen can only be seen if specimen is dug properly and processed (*A. tuberosum*). Condensed rhizome in garlic and onion can be visible through the vertical section of bulb. Fibrous coat on bulb/rhizome needs special observations for colour and texture.

### Root

Root structure is very important character at infrageneric level identification. Fleshy root character associated with subg. *Bromatorrhiza- A. hookeri, A. fasciculatum* and *A. macranthum* is distinct feature to delineate species. Fleshy roots generally dry or shrink on processing and may be noted or sketched on herbarium label; photo of freshly dug out sample can serve the purpose.

### Leaf

Number of leaves, shape (triquetrous, round/channeled, flat, keeled) can be examined in fresh material. Longitudinal/transverse section of leaf can delimit *A. cepa, A. cepa* var. *aggregatum, A. fistulosum* and *A. proliferum.* Keeled nature of leaf can distinguish *A. ampeloprasum* at pre-flowering stage from *A. sativum.* Colour of leaf, shape of the leaf tip, leaf orientation with respect to vertical axis, density of leaves, texture-membranous or thick, leaf length with respect to scape are important characters to identify taxa. The two species,

*A. auriculatum* (subg. *Cyathophora* sect. *Coleoblastus*) and *A. przewalskianum* (subg. *Rhizirideum*) co-occur on dry slopes, ravines and rocky crevices are difficult to distinguish in routinely preserved herbarium specimens as fistular leaf and perianth characters of the latter species, as a distinguishing trait from the former species are lost during processing.

### *Inflorescence*

Shape of the inflorescence- globose, compact; spreading pattern, opening of flower (regular, irregular, centrifugal), number of flower opened at a time, scape length (longer or shorter than leaves), shape (cylindrical-tapering), hollow or solid (at maturity), shape of flower, can be noted at any stage of collection to drying of herbarium. In pressed condition the inflorescence of *A. cepa* var. *cepa* and *A. cepa* var. *aggregatum* are difficult to distinguish; others like *A. semenovii* and *A. macranthum* can be quickly identified with distinct inflorescence.

### *Flower*

Macroscopic characters as colour, streak on the perianth, orientation of perianth in open flower, perianth shape, and stamen length with respect to perianth and orientation; shape of the basal part of inner filament, orientation, presence or absence of teeth and its shape can distinguish closely related taxa. *A. ramosum* and closely related *A. tuberosum* differ in flower characters, the former has pink mid line on the dorsal side of perianth. Orientation of perianth and stamen in an open flower is lost during drying so need to be recorded in field data book. Notes on flowering time (day hours) vs. stage of flower (early-late), pollinators' specificity should be noted. Among the insect pollinators *Aphis dorsata* the common honey bee, and *A. cerana* and *A. mellifera* are the most frequent visitors to *Allium cepa* and *A. schoenoprasum* whereas the common fly prefers to visit *A. ampeloprasum* (Kumar and Gupta 1993). A note on these should be recorded.

### *Seed*

Seeds are very small and not readily observed in the field for detailed micro-characters; however an outline and overall shape (angular, round, broader) can be noted with help of hand lens. Seeds shape round (*A. victorialis*), sickle shaped (*A. carolinianum*), tear shaped (*Nothoscodum gracile*), etc. can be drawn on the field note book.

### *Odour*

Onion or garlic type odour on crushing can be noted when sample is harvested and recorded on label. For example *A. tuberosum* and *A. schoenoprasum* have mild onion flavour whereas *A. ampeloprasum* has garlic odour.

### *Photographs and Other Material*

Plants at different stages of growth, inflorescence at different angles, flower when fully open (close-up view), perianth and anther orientation need to be photographed. Additionally, the dried parts (flowers, stamens, leaves may be collected) and information on important features and ethnobotanical data should be recorded in herbarium specimen label.

## Synopsis of Specific Notes

### *Field Observation*

- **Habitat/ecological aspects:** record habitat details using standard IPGRI passport (http://www.ecpgr.cgiar.org/fileadmin/bioversity/publications/pdfs/728_Descriptors_for_*Allium__Allium*_spp._.pdf) with niche-specific information, distinct habitat (locality latitude, longitude using GPS), altitude, soil type, moisture, atmospheric temperature, topography (slope condition -steep/shallow; rocky, crevices, cliffs), exposure/sun exposure and if endemic. Note-sympatric allopatric species; habitat condition, co-associated species, etc.
- **Life form:** perennials/annuals, perennating organs–bulb/rhizome, leaf, scape visible at the time of visit.
- **Co-associates:** associated plants in field.
- **Texture and colour of plant parts:** flower colour (use colour chart), glaucous, texture, shininess; outer coat if membranous, coriaceous or fibrous, if fibrous loosely or finely knitted, colour of coat on harvest, roots fleshy, leaf thick, thin, erect or pendent, bulb shape, size, colour, inflorescence as seen fresh (flower opening pattern, spathe valves in fresh; compact/spreading, shape seen as 3-d in fresh but 2-d in press are lost in drying process).
- **Stage at which observations recorded (bulb and leaf):** prepare herbarium specimen of vegetative/reproductive plant over various growth stages; variation can be noted at early stage (1 month, 2 month), fully mature plant (at flowering). Plants at

seedling stage do not show leaf and bulb characters at two month old stage. They may show the hollow or flat type of leaves. Determine the standard stage for taxa at which the collection is to be done. Bulbils if present should be represented with mother plant.

- **Flower characters:** pattern of opening of flowers, perianth orientation-horizontal or erect, filaments longer/shorter than perianth, striations on the dorsal side of perianth, colour and length of stamen, etc. to be noted in fresh. Opened flower can be dried with care and mounted in cotton strip/kept in pouch. Field/hand held microscope can be used for micro characters.
- **Phenology:** early/late flowering, length of flowering time, pollinator specificity, if any.
- **Extreme variants:** variants with respect to good taxonomic characters within population (field and herbarium based study); variation range in a species with high ecological amplitude (*A. carolinianum*).
- **Illustrations:** drawings/cross sections of parts, leaves/scape (hollow or solid), sketches/line diagrams to show details.
- **Supplementary information:** photographs of field/ population; close up of the leaf, bulb, flower, anthers; etymology, local use, ethnobotanical information/ local name, etc. may help in identification.
- **Equipments:** humidity recording equipment, relative humidity meter, soil PH meter, GIS (location data recording).

**Herbarium Preparation**

While making herbarium specimen, one needs to depict:

- **Tall plant:** to be bent into parts/small parts: cultivated (*e.g. A. ampeloprasum, A. cepa*) groups with bigger upper, lower leaf surfaces, bending long scape; basal, middle and tip parts of leaf portion (in case of long leaf).
- **Bulb:** expose the bulb membrane showing outer and inner coat characters; bulb in full or section (poured with salt/disinfectant on the cut), vertical section to show arrangement of basal leaves. Membrane from completely dry or mature bulb can be preserved during processing of herbarium specimen (collect and dry it separately in pouch).
- **Leaf:** cross section, leaf insert (cut/oblique) with coloured stick/strip to show the hollowness; longitudinal section of leaf from bottom- tip to show the entire length wise and also same for scape. To depict the character of density in leaf, trim some leaves (only in dense condition) leaving only 5-6 cm basal part.
- **Pseudostem:** length (size); arrangement of leaves to be noted; one should try to alter orientation/ arrangement of leaf.
- **Inflorescence:** take measurements of diameter and draw line diagrams to depict the shape of the inflorescence; spathe is generally well preserved, yet splitting can be noted or drawn. Similarly the pattern of flower opening (centripetal/centrifugal vs. irregular) are sometimes hidden in pressed state so may be depicted pictorially or with photograph. Compact vs. loose arrangement of flowers in inflorescence is difficult after pressing, so data to be recorded in label or notes.
- **Flower:** colour of flower, perianth shape, perianth orientation in fully wide open flower are the characteristics for differentiation but generally lost while drying. Anthers exerted or included, stamen colour, orientation of anthers, micro-characteristics of stamen (base of filament, toothed or not), ovary shape are to be examined using the microscope. Take a flower and wide open and dry in a small piece of blotter after opening/slitting it wide to show all parts clearly. Some of the fully mature flowers, buds can be separately dried and put in the pouch for later study (detaching plant part to be studied, soak in 5-10 percent salt water in ambient temperature for 8-10 hours, spread on mounting glass and put under dissection microscope). Put dried flowers, scape, capsule in a pouch; draw diagram of individual flower.
- **Illustration:** prepare on-spot/free hand drawing to show the unique part (anther, fibrous nature of membrane; photos in close view from top of flower, longitudinal view of inflorescence to show anther viz. tepals ratio (anthers included or peeping out).
- **Treatments:** the bulb may continue to grow while in plant press; apply artificial heat, alcohol or formalin to kill the tissue (bulb/rhizome). Fleshy parts can be dried slowly through blotters/corrugated sheets. However, standard methods used for fleshy material

can be used with modification (Jain and Rao, 1977). The authors have found significant use of salt powder to facilitate fast drying and no fungal/microbial growth on tissue.

- **Extra material:** complementary parts-use paper pouch to put roots, bulbils, underground bulbils or left over parts with herbarium specimen. One flower to be split open longitudinally and pressed with corolla spread out to show androecium and gynoecium; corolla to be pressed separately in tissue paper on tepals/non- absorbent tissue paper; large parts/fleshy or those with complex flowers in wet preservation in alcohol/formaldehyde (4 per cent); apply even pressure on leaves and flowers to prevent sticking. To depict the variation in bulb characters of a cultivar one can use wet preservation method.
- Completely processed specimen can be mounted as per standard herbarium procedures (Jain and Rao, 1977). Mounting and stitching with thread vs. glue application depends on discretion of user. If the herbarium material is to be used later for some study (biosystematics, chemotaxonomy, or molecular work) one should avoid sticking with glue or any adhesive.

The NHCP has mandate to build-up herbarium collections of crops/crop cultivars and its wild relatives. Herbarium resources available with these details are of much value for preparing key to identification based on leaf, bulb and seed characters. Standardized methodology given here on the genus *Allium* may be used for collection and processing of material as herbarium useful for plant genetic resource related studies.

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## Appendix 1

### Significant features to be noted for infra-generic categories

| S. No. | Infra-generic category (subgenus)/species | Plant parts/characters |
|---|---|---|
| 1 | **Amerallium** | |
| | *A. hookeri, A. macranthum, A. fasciculatum* | Root shape and fleshy character; bulb outer coat, leaf shape |
| 2 | **Anguinum** | |
| | *A. victorialis, A. pratii* | Rhizome shape/size, leaf shape and width, vein characters |
| 3 | **Butomissa** | |
| | *A. tuberosum, A. oreoprasum, A. ramosum, A. gilgiticum* | Rhizome, bulb shape/size, outer and inner coat colour, texture, leaf in section; flower- perianth shape, colour of the dorsal mid-line on perianth |
| 4 | ***Allium*** | |
| | *A. sativum, A. ampeloprasum, A. griffithianum* | Bulb shape, number, coat texture; presence of bulblets; leaf shape, density; presence of aerial bulbils |
| 5 | **Cepa** | |
| | *A. atrosanguineum, A. semenovii; A. cepa, A. fistulosum; A .longistylum; A. schoenoprasum; A. chinense* | Rhizome size; bulb shape, bulb coat characters; leaf fistular |
| 6 | **Polyprason** | |
| | *A. stracheyi, A. roylei, A. consanguineum, A. carolinianum* | Bulb shape, single/clustered, rhizome size, if produced into a neck; leaf shape, texture (leathery); tunic outer colour, texture- fibrous, coriaceous, brown |
| 7 | **Cyathophora** | |
| | *A. auriculatum* | Bulb shape, coat colour, texture; leaf shape, leaf in cross section, scape size, erectness/orientation |
| 8 | **Melanocrommyum** | |
| | *A. atropurpureum, A. chitralicum, A. loratum* | Flowers if showy, nectaries located in the lower half of the ovaries; excretion through spur or rather than short tube; excretory tubes bent downwards. |
| 9 | **Reticulatobulbosa** | |
| | *A. humile, A. schrenkii, A. lineare, A. sikkimense, A. tenuicaule* | Bulb shape, number, tunic colour, texture; leaf length, flat, spathe-valve number, perianth colour, filament length, scape length, ovary apex orientation |
| 10 | **Rhizirideum** | |
| | *A. przewalskianum* | Bulb shape, tunic character, leaf length, if channelled, tepal: filament length |

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# Evaluation of Indigenous and Exotic Mango Germplasm for Resistance to Hopper, *Idioscopus nitidulus* (Walker) and Thrips, *Scirtothrips dorsalis* Hood

**JK Bana*, PD Ghoghari, GB Kalaria, SP Saxena and NI Shah**
*Agriculture Experimental Station, Navsari Agricultural University, Paria, Gujarat-396145, India*

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Studies were carried during 2008-09 to 2014-15 to evaluate the indigenous and exotic mango germplasm against hopper, *Idioscopus nitidulus* and thrips, *Scirtothrips dorsalis*. A total of 39 indigenous and exotic mango accessions were screened against these pests and results showed that none of germplasm was found highly resistant against these pests under field conditions. Bombai was found resistant against hoppers and seven accessions *viz.,* T×V, Bombai, CISHM-1 (Ambica), Mahmud Vikarabad, Vellai Kolumban, Mankurad and Ratna were found resistant to inflorescence thrips.

**Key Words: Germplasm, Hopper, *Mangifera indica*, Resistant, Susceptibility**

## Introduction

Mango, *Mangifera indica* L. (Anacardiaceae) is one of the choicest fruit crops of tropical as well as subtropical region of India and is known as "king of fruits" (Vasugi *et al.,* 2012) for its delicious taste, attractive color, savoring flavour and high nutritive value [being rich in vitamins A and C, mineral and fiber content] (Lakshminarayana, 1980). It is cultivated in 2516 thousand hectares with a total production of 18 million tonnes, contributing to 34.90% of the total world mango production (Indian Horticulture database, 2014). More than 400 insect-pest species have been recorded on mango in different parts of the world. Of these, 188 species have been reported in India (Tandon and Verghese 1985). Mango hoppers and thrips are recorded as major pests in the mango ecosystem. Different species of mango hoppers *i.e. Amritodus atkinsoni* (Lethierry), *Idioscopus clypealis* (Lethierry) and *I. nitidulus* (Walker) are serious pests at flowering to fruiting stages (Babu *et al.,* 2002; Patil *et al.,* 1988; Sushil kumar *et al.,* 2005 and Gundappa *et al.,* 2014) and cause significant yield losses in the fields (Gangolly *et al.,* 1957, Wadhi and Batra, 1964 and Rahman and Kuldeep, 2007). Other than hoppers, foliage thrips, *Rhipiphorothrips cruentatus* Hood and inflorescence thrips, *Scirtothrips dorsalis* Hood are also serious pests at new flush, flowering and fruiting stages of mango. Out of these, *I. nitidulus* and *S. dorsalis* are major dominant species and can cause significant damage at flowering stage of the crop. Both nymphs and adults of hoppers aggregate on the underside of leaves, puncture and suck the sap of young leaves and inflorescence (Das *et al*., 1969). Hoppers also excrete honey dew resulting in growth of sooty mould on dorsal surface of leaves, inflorescence, branches and rachis of the fruits. Which further interferes with the photosynthetic activity of the plant, ultimately resulting in non-setting of flowers, dropping of immature fruits and reducing the yield. Similarly, nymph and adult thrips also suck the sap from the young leaves, tender shoots, inflorescence and fruits of the mango which result in silvery shine with upward curling of the leaf edges, stunted growth, discoloration of buds and panicles resulting in malformation and bronzing of the fruit surface with feeding scars on fruits leading to pre-mature fruit drop (Higgins, 1992; Pena *et al*., 2002, Sanap and Nawale, 1987, Grove *et al.,* 2000 and Nault *et al.,* 2003).

For control of these pests, several insecticides have been recommended in the past (Kaushik *et al.,* 2014; Singh *et al.,* 2010; Samanta *et al.*, 2009 and Sushil kumar *et al*., 2005). But, repeated and extreme use of insecticides to control mango hopper and thrips has led to development of resistance and resurgence; besides, leaving excessive residue on edible fruits (Sushil Kumar *et al.,* 2005 and Singh, 2008). So, resistant sources of mango germplasm is one of the best tools in pest management. Hence, in the present study, indigenous and exotic mango accessions were screened to find out their susceptibility to mango hoppers and thrips.

**Author for Correspondence: Email- jugalbana@gmail.com*

## Materials and Methods

The experiment was conducted at Agriculture Experimental Station (All India Coordinated Research Project (AICRP) on Fruits Centre), Navsari Agricultural University, Paria (22º26' N and 72º58' E with an altitude of 10 meters above sea level) on 8-10 years old different indigenous and exotic mango trees. A total of 39 mango accessions were screened against hopper and thrips incidence over seven consecutive years *i.e.,* 2008-09 to 2014-15. Each accession was replicated twice and maintained at a distance of 8m x 8m (from plant to plant and row to row). The germplasm blocks were kept free from pesticide application during the study period. Population of hoppers, *Idioscopus nitidulus* and thrips, *Scirtothrips dorsalis* (both nymph and adult stages) were counted visually on tagged 10 twigs or panicles/tree at standing height during peak flowering period twice at 15 day interval and thrips population were recorded by tapping the inflorescence on a simple white paper (NICRA team of mango pest surveillance, 2011, Patel *et al.,* 2013 and Sushil Kumar *et al.,* 2005). The arbitrary rating scale (0-5) used to grade the hopper and thrips population was; free (0 hoppers or thrips /panicle), highly resistant (0.1-1.0 hoppers or thrips /panicle), resistant (1.0-2.0 hoppers or thrips/panicle), moderately susceptible (2.0- 3.0 hoppers or thrips/panicle), susceptible (3.0- 4.0 hoppers or thrips/ panicle) and highly susceptible (>4 hoppers or thrips/ panicle) (Anonymous, 2009).

## Results and Discussion

The mango germplasm differed greatly in terms of susceptibility to mango hopper and thrips (Table 2). None of the genotypes were found free or highly resistant against these pests. The mean hopper population varied from 1.86 to 14.71 hoppers/twig or panicle (Table 1). Lowest hopper population was recorded in Bombai (1.86 hoppers/twig or panicle) and categorized as resistant germplasm. Whereas, Himsagar (2.40 hoppers/twig or panicle), Shebar (2.53hoppers/twig or panicle) and Mankurad (2.81 hoppers/twig or panicle) were observed moderately susceptible against mango hopper. Keitt was found to be highly susceptible to mango hopper (14.71 hoppers/twig or panicle) followed by Maya (13.15 hoppers/twig or panicle), Mahmood Vikarabad (12.59 hoppers/twig or panicle) and Vellai Kolumban (11.20 hoppers/twig or panicle). Thus, on the basis of overall susceptibility index, one accession was found resistant, three accessions were found moderately susceptible, five as susceptible and 30 were found to be highly susceptible to mango hopper.

Against thrips, lowest population was recorded in Mahmooda Vikarabad (1.09 thrips/twig or panicle) followed by CISHM-1 (Ambica) (1.32 per twig or panicle), Bombai (1.44/twig or panicle), T×V (1.61 / twig or panicle), Mankurad (1.76/twig or panicle), Vellai Kolumban (1.77/twig or panicle), Ratna (1.79/twig or panicle) and Kent (1.84 /twig or panicle). Whereas, maximum thrips population was recorded in Mallika (6.19 /twig or panicle) followed by Chandram (5.56/ twig or panicle) and Bappakai (5.41/twig or panicle). Based on susceptibility index eight accessions were found resistant to thrips, 14 accessions were categorized moderately susceptible [*viz.,* Gulabkhas, Hybrid-13-3, Shebar, Apple, Fernandin, Lilly, Maya, Muvandan, Ajod Sindurio, Kensington, Arka Anmol, Himsagar, Karel (Rewa) and Goa manchur] and seven mango accessions were found highly susceptible (Gajiria, Malviabhog, Keitt, Mallika, Hybrid-10, Chandram and Bappakai). The results of the present investigation are in conformity with Reddy and Dinesh (2005) who evaluated ten exotic mango germplasm on the basis of four susceptibility groups [*viz.,* least susceptible (0-2 hoppers/panicle), moderately susceptible (2-6), susceptible (>6-10) and highly susceptible (>10)] and found that Kensington and Ostin were susceptible and Sensation was recorded moderately susceptible against *I. nitidulus*. Devi Thangam *et al.,* 2013 screened 392 mango accessions against *I. nitidulus* on the basis of 0-3 grading scale and found that Himsagar, Sensation, Goa Mankurad, Ratna and Keitt moderately susceptible to hopper.

Viraktamath *et al.* (1996) studied the varietal influences against mango hopper and reported that maximum hopper population was recorded in Neeleshan followed by Neeluddin, Mallika and Rumani. Singh and Singh (2007) screened 23 cultivars of mango and reported that none of the cultivars showed immune reaction, though two cultivars, *viz.,* Bangalora and Amebela were rated as resistant and five *viz.,* Gillas, Gulabkhas, Chandra Karan, Mallika and Gourjeet as tolerant to the hoppers. Eleven cultivars *viz.,* Safeda Lucknow, Bombay Green, Totapuri, Deshi, Himsagar, Shukul, Langra, Kakori, Barahmasi, Banarsi Langra, SB Chausa and Sundraza were rated as susceptible and five *viz.,* Dashehari, Nisar pasand, Zardalu, Ratul and Neelum as highly susceptible against mango hopper in field conditions.

**Table 1. Screening of indigenous and exotic mango germplasm against hopper, *Idioscopus nitidulus* and thrips, *Scirtothrips dorsalis* under field condition from 2008-09 to 2014-15**

| S. No. | Germplasm | Hopper population/ twig or panicle | | | | | | | | Thrips population/ twig or panicle | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 2008-09 | 2009-10 | 2010-11 | 2011-12 | 2012-13 | 2013-14 | 2014-15 | Mean | 2008-09 | 2009-10 | 2010-11 | 2011-12 | 2012-13 | **2013-14** | **2014-15** | **Mean** |
| 1 | Gajiria | 2.75 | 4.00 | 8.30 | 7.00 | 8.00 | 10.60 | 9.60 | 7.18 | 2.30 | 8.05 | 4.10 | 2.70 | 2.50 | 6.00 | 2.50 | 4.02 |
| 2 | Ostin | 6.90 | 4.60 | 4.90 | 1.90 | 1.50 | 1.50 | 1.85 | 3.31 | 2.50 | 1.00 | 1.60 | 7.00 | 7.50 | 1.70 | 1.45 | 3.25 |
| 3 | Palmer | 3.30 | 11.50 | 11.20 | 4.00 | 4.00 | 9.40 | 6.70 | 7.16 | 3.90 | 2.50 | 2.20 | 4.40 | 4.50 | 4.90 | 4.15 | 3.79 |
| 4 | Lilly | 4.25 | 9.15 | 10.90 | 2.90 | 2.50 | 3.40 | 4.00 | 5.30 | 2.95 | 2.15 | 3.90 | 1.70 | 1.50 | 3.00 | 2.20 | 2.49 |
| 5 | Maya | 14.55 | 18.10 | 20.40 | 3.50 | 3.50 | 18.80 | 13.20 | 13.15 | 4.15 | 2.00 | 1.90 | 2.20 | 2.00 | 1.90 | 3.05 | 2.46 |
| 6 | Malviyabhog | 5.55 | 17.35 | 17.50 | 2.90 | 3.00 | 3.30 | 14.45 | 9.15 | 2.95 | 6.30 | 8.00 | 3.60 | 3.50 | 3.90 | 4.15 | 4.63 |
| 7 | Muvandan | 18.50 | 10.10 | 9.20 | 3.80 | 3.50 | 17.60 | 13.95 | 10.95 | 1.50 | 2.45 | 2.80 | 2.50 | 2.50 | 3.20 | 2.60 | 2.51 |
| 8 | Ajod Sindurio | 2.20 | 9.70 | 7.80 | 6.40 | 6.00 | 14.50 | 4.20 | 7.26 | 1.20 | 4.00 | 5.00 | 1.60 | 1.50 | 4.10 | 2.55 | 2.85 |
| 9 | Kensington | 2.70 | 17.25 | 14.80 | 3.30 | 3.00 | 10.40 | 12.45 | 9.13 | 1.55 | 1.90 | 2.20 | 2.80 | 2.50 | 1.50 | 1.90 | 2.05 |
| 10 | Keitt | 1.20 | 15.40 | 23.30 | 10.00 | 10.50 | 23.60 | 18.95 | 14.71 | 1.50 | 2.90 | 2.70 | 8.30 | 8.50 | 5.80 | 3.15 | 4.69 |
| 11 | Madhukrupa | 3.55 | 10.95 | 8.20 | 1.80 | 2.00 | 3.20 | 7.35 | 5.29 | 2.00 | 5.00 | 1.00 | 1.60 | 1.50 | 5.00 | 5.50 | 3.09 |
| 12 | Kent | 19.90 | 2.95 | 5.00 | 5.80 | 5.50 | 10.30 | 12.35 | 8.83 | 2.70 | 1.70 | 2.50 | 1.90 | 2.00 | 1.40 | 0.70 | 1.84 |
| 13 | Arka Neelkiran | 13.40 | 12.15 | 12.60 | 5.20 | 5.00 | 11.30 | 9.75 | 9.91 | 3.05 | 2.95 | 3.60 | 3.30 | 3.00 | 4.00 | 4.10 | 3.43 |
| 14 | Arka Anmol | 18.40 | 8.05 | 18.30 | 3.90 | 3.50 | 12.10 | 8.60 | 10.41 | 2.80 | 2.85 | 5.90 | 0.90 | 1.00 | 0.60 | 0.90 | 2.14 |
| 15 | T × V* | 5.80 | 13.00 | 9.00 | 2.00 | 2.00 | 3.80 | 4.40 | 5.71 | 2.05 | 2.65 | 2.60 | 0.60 | 0.50 | 1.70 | 1.20 | 1.61 |
| 16 | Sensation | 3.65 | 6.30 | 5.10 | 5.80 | 5.50 | 10.00 | 11.00 | 6.76 | 1.45 | 1.20 | 1.80 | 4.00 | 4.00 | 4.90 | 4.75 | 3.16 |
| 17 | Himsagar | 3.00 | 3.05 | 2.10 | 1.20 | 1.50 | 2.80 | 3.15 | 2.40 | 3.05 | 2.65 | 2.60 | 2.80 | 2.50 | 2.10 | 1.55 | 2.46 |
| 18 | Bombai | 2.40 | 3.15 | 2.20 | 1.20 | 1.00 | 1.90 | 1.20 | 1.86 | 2.35 | 0.95 | 0.70 | 1.70 | 3.00 | 0.80 | 0.55 | 1.44 |
| 19 | Karel (Rewa) | 5.80 | 3.95 | 11.90 | 6.80 | 6.50 | 5.80 | 7.30 | 6.86 | 4.05 | 1.10 | 3.10 | 3.20 | 1.50 | 1.40 | 2.70 | 2.44 |
| 20 | CISHM-1 (Ambica) | 13.10 | 14.05 | 4.60 | 4.00 | 4.00 | 14.40 | 12.35 | 9.50 | 2.15 | 0.65 | 1.30 | 1.80 | 1.50 | 1.40 | 0.45 | 1.32 |
| 21 | Mahmood Vikarabad | 16.80 | 16.30 | 18.20 | 6.90 | 8.50 | 12.40 | 9.05 | 12.59 | 2.00 | 1.05 | 0.90 | 0.90 | 1.00 | 0.70 | 1.05 | 1.09 |
| 22 | Kishanbhog | 12.05 | 2.45 | 17.00 | 2.00 | 2.00 | 2.50 | 9.30 | 6.76 | 1.85 | 3.30 | 3.90 | 5.00 | 5.00 | 3.90 | 2.95 | 3.70 |
| 23 | Vellai Kolumban | 3.95 | 2.95 | 6.10 | 13.70 | 14.50 | 21.50 | 15.70 | 11.20 | 3.00 | 0.70 | 1.70 | 2.10 | 2.00 | 1.50 | 1.40 | 1.77 |
| 24 | Mankurad | 2.85 | 5.85 | 1.80 | 2.20 | 2.00 | 2.80 | 2.15 | 2.81 | 2.60 | 1.50 | 2.10 | 1.50 | 1.50 | 1.30 | 1.85 | 1.76 |
| 25 | Goa manchur | 2.90 | 7.80 | 6.80 | 3.00 | 3.00 | 3.80 | 5.80 | 4.73 | 2.10 | 2.65 | 3.90 | 3.50 | 3.50 | 2.70 | 2.30 | 2.95 |
| 26 | Kokan Ruchi | 3.85 | 13.25 | 2.90 | 6.10 | 6.00 | 11.60 | 13.40 | 8.16 | 2.65 | 3.30 | 3.40 | 3.40 | 3.50 | 3.00 | 2.95 | 3.17 |
| 27 | Hybrid -10 | 16.30 | 10.95 | 1.80 | 2.10 | 2.00 | 3.60 | 11.25 | 6.86 | 3.95 | 3.80 | 4.90 | 5.30 | 5.50 | 4.00 | 3.95 | 4.49 |
| 28 | Pusa Arunima | 4.60 | 12.95 | 6.90 | 2.80 | 3.00 | 2.10 | 2.90 | 5.04 | 2.20 | 4.30 | 3.50 | 3.00 | 3.00 | 2.70 | 2.65 | 3.05 |
| 29 | Gulab Khas | 2.05 | 11.60 | 6.00 | 1.40 | 1.50 | 1.30 | 2.50 | 3.76 | 2.15 | 3.60 | 3.00 | 3.00 | 3.00 | 2.60 | 1.85 | 2.74 |
| 30 | Ratna | 3.95 | 22.45 | 13.10 | 3.40 | 3.50 | 19.00 | 15.05 | 11.49 | 1.45 | 2.30 | 1.70 | 2.00 | 2.00 | 1.50 | 1.60 | 1.79 |
| 31 | Zardalu | 3.40 | 2.15 | 16.60 | 1.10 | 1.00 | 1.80 | 1.10 | 3.88 | 2.00 | 2.40 | 2.80 | 3.90 | 4.00 | 4.00 | 3.95 | 3.29 |
| 32 | Mallika | 1.95 | 13.10 | 5.40 | 2.70 | 2.50 | 2.50 | 2.35 | 4.36 | 2.30 | 5.80 | 7.80 | 8.00 | 8.00 | 5.70 | 5.70 | 6.19 |
| 33 | Hadgood Seedling | 2.40 | 5.00 | 1.60 | 4.20 | 4.50 | 11.80 | 14.40 | 6.27 | 2.90 | 3.00 | 3.90 | 3.90 | 4.00 | 3.30 | 2.80 | 3.40 |
| 34 | Hybrid -13-3 | 7.00 | 2.20 | 3.70 | 1.80 | 1.50 | 3.30 | 6.90 | 3.77 | 1.70 | 2.40 | 1.30 | 2.20 | 4.00 | 2.00 | 2.40 | 2.29 |
| 35 | Shebar | 5.85 | 2.85 | 1.00 | 2.00 | 2.00 | 1.50 | 3.65 | 2.69 | 1.50 | 2.05 | 2.10 | 2.00 | 4.00 | 1.20 | 1.30 | 2.02 |
| 36 | Chandram | 7.35 | 5.80 | 13.00 | 6.00 | 6.00 | 13.70 | 9.35 | 8.74 | 1.90 | 4.95 | 7.10 | 6.10 | 6.50 | 5.70 | 6.70 | 5.56 |
| 37 | Apple | 6.65 | 4.00 | 15.60 | 3.90 | 4.00 | 16.50 | 14.10 | 9.25 | 2.40 | 1.90 | 2.00 | 2.70 | 2.50 | 2.40 | 1.90 | 2.26 |
| 38 | Bappakai | 3.75 | 3.60 | 7.00 | 2.50 | 2.50 | 2.90 | 2.80 | 3.58 | 2.35 | 6.95 | 7.90 | 6.00 | 6.00 | 4.90 | 3.80 | 5.41 |
| 39 | Fernandin | 2.75 | 2.60 | 6.00 | 4.90 | 5.00 | 11.30 | 10.60 | 6.16 | 2.80 | 2.40 | 3.10 | 2.80 | 2.50 | 2.50 | 2.50 | 2.66 |

T×V* (cross between Totapuri and Vanraj)

**Table 2. Susceptibility ratings of mango germplasm against hopper and thrips during 2008-09 to 2014-15**

| Susceptibility category | Pest population/ twig or panicle | Hopper | | Thrips | |
|---|---|---|---|---|---|
| | | Accession | No. of entries | Accession | No. of entries |
| Free/Escape | 0 | Nil | 00 | Nil | 00 |
| Highly resistant | 0.1-1.0 | Nil | 00 | Nil | 00 |
| Resistant | 1.0-2.0 | Bombai | 01 | Kent, T×V, Bombai, CISHM-1 (Ambica), Mahmud Vikarabad, Vellai Kolumban, Mankurad and Ratna | 08 |
| Moderately susceptible | 2.0-3.0 | Himsagar, Mankurad and Shebar | 03 | Gulabkhas, Hybrid-13-3, Shebar, Apple, Fernandin, Lily, Maya, Muvandan, Ajod Sindurio, Kensington, Arka Anmol, Himsagar, Karel (Rewa) and Goa manchur | 14 |
| Susceptible | 3.0-4.0 | Ostin, Gulabkhas, Zardalu, Hybrid -13-3 and Bappakai | 05 | Madhukrupa, Sensation, Kishanbhog, Ostin, Palmer, Arka Neelkiran, Kokan Ruchi, Arunima, Zardalu, and Hadgood seedling | 10 |
| Highly susceptible | > 4.0 | Madhukrupa, Malviabhog, Lily, Hybrid -10, Goa manchur, T×V, Arunima, Kishanbhog, Mallika, Gajiria, Palmer, Maya, Muvandan, Ajod Sindurio, Kensington, Keitt, Kent, Arka Neelkiran, Arka Anmol, Sensation,CISHM-1 (Ambica), Karel (Rewa), Mahmood Vikarabad, Vellai Kolumban, Kokan Ruchi, Ratna, Hadgood seedling, Chandram, Fernandin and Apple | 30 | Gajiria, Malviabhog, Keitt, Mallika, Hybrid-10, Chandram and Bappakai | 07 |

On the basis of present studies, it is concluded that mango accession, Bombai can be one of the resistant sources against mango hopper and accessions *viz.,* T×V, Bombai, CISHM-1 (Ambica), Mahmud Vikarabad, Vellai Kolumban, Mankurad and Ratna could be used as resistance sources for thrips in future breeding programmes.

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# Genetic Variability for Morphological Traits in Released Varieties of Barley (*Hordeum vulgare* L.) under Partially Reclaimed Saline-Sodic Soil

**Arun Kumar[3]*, Baudh Bharti[4], Jaydev Kumar[2], Anurag Tripathi[3], NC Gahtyari[3], JP Jaiswal[3] and SR Vishwakarma[1]**

[1]*Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture & Technology, Faizabad-224229, Uttar Pradesh, India*

[2]*Department of Genetics & Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur-208002, Uttar Pradesh, India*

[3]*Department of Genetics & Plant Breeding, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India*

[4]*Department of Genetics & Plant Breeding, Maharana Pratap University of Agriculture & Technology, Udaipur-313001, Rajasthan, India*

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Morphological traits of barley showed differences among varieties released for different uses and climatic zones. Understanding these morphological variations is an important part for development of crop models for different purposes, and to know the plant worth. Narrow and waxy leaves are good indication for tolerant to abiotic stresses like drought, salinity, alkalinity and rainfed situation. Sixty four released varieties of barley were grown under partially reclaimed saline- sodic soil, under irrigated conditions during *rabi* 2010-11 showing wide spectrum of variation for various characters. The characters studied for morphological variation were – growth habit, morphology of leaf, presence of anthocyanin pigmentation, spikelet arrangement, presence of awn, tip sterility, waxiness on leaf, seed colour and seed shape. The characters studied for yield were namely plant height, days to maturity, fertile tillers/plant, length of main spike, grains per main spike, 1000-grains weight, grain yield per plant. The data on seven yield traits used for estimation of mean, range and least significant differences. Based on this study eight varieties selected were – RD-2552, HBL-276, RD-2592, PL-419, Kedar, PL-751, JB-58, K-508 produced higher grain yield plant$^{-1}$.

**Key Words: Barley (*Hordeum vulgare* L.), Genetic Variability, Morphological characters, Partially reclaimed soil**

## Introduction

Barley (*Hordeum vulgare* L.) is an annual cereal crop, which belongs to the tribe Triticeae of family Poaceae (Harlan, 1976; Martin *et al.,* 2006). It has persisted as a major cereal crop through many centuries and it is the world's fourth important cereal crop after wheat, maize and rice (Martin *et al.,* 2006). Barley has a long history of cultivation in Ethiopia and it is reported to have coincided with the beginning of plow culture (Zemede, 2000). It is popular hunger breaker or relief crop during season of food shortage in some parts of the country (Baye and Berhane, 2006). It is a diploid (2n= 2x= 14), largely self fertilizing species with a large genome (Bennett and Smith, 1976). During centuries, early domestication and local knowledge have generated through diverse local barley used mainly for feed and lowly for food (Vavilov, 1951). Morphological characters have been used to evaluate distinctness, uniformity and stability, and to establish the description of a genotype. This method is thought to be often influenced by environmental conditions (Russel *et al.,* 1997) as well as being labour intensive. Assessment of the extent of genetic variability within cultivated crop has important consequences in plant breeding and conservation of genetic resources (Petersen *et al.*. 1994). The objectives of this study were to assess the extent of morphological variation in released barley varieties in order to classify them into relatively homogenous groups and to identify the major traits contributing to the overall genetic diversity.

## Materials and Methods

The experimental material comprised of sixty four released varieties of barley collected from Directorate of Wheat Research, Karnal, Haryana were grown under partially reclaimed saline- sodic soil (pH 8.6-8.9, EC = 4-4.2 dSm$^{-1}$, ESP = > 15). These varieties were evaluated in a Simple Lattice Design with two replications. Each plot consisted of three rows, each of three meter long with

**Author for Correspondence: E-mail:* arungangwar0581@gmail.com

spacing of 23 cm. The plants within a row were spaced approximately 10 cm apart. The eight contiguous plots collectively constituted one tier. Thus there were eight tiers each of eight plots in a replication. The varieties were allocated randomly in each replication. The data for morphological variation were recorded on growth habit, morphology of leaf, presence of anthocyanin pigmentation, spikelet arrangement, presence of awn, tip sterility, waxiness on leaf, seed colour and seed shape, and five randomly selected plants used for data on 7 quantitative traits namely, plant height (cm), days to maturity, number of fertile tillers$^{-1}$, length of main spike (cm), grains per main spike, 1000-grain weight (g), grain yield plant$^{-1}$ (g). The present investigation was conducted during *rabi* 2010-11 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture & Technology, Narendra Nagar, Kumarganj, Faizabad Uttar Pradesh, situated between 26°47' N latitude, 82°12' E longitude and at an altitude of 113 m above the mean sea level. The climate of district Faizabad is semi-arid with hot summer and cold winter. Nearly 80 per cent of total rainfall is received during the monsoon with a few showers in the winter. The recommended cultural practices were adopted to grow varieties.

## Result and Discussion

The results of the analysis of variance for Simple Lattice Design in respect of 7 characters are presented in (Table 1). The variation due to replication was highly significant for plant height, days to maturity, fertile tillers per plant, and length of main spike, grains per main spike, 1000-grain weight, and grain yield per plant. The variation due to treatment were found to be highly significant for plant height, days to maturity, length of main spike, grains per main spike, and significant for grain yield per plant, but non-significant for remaining two characters *viz.* fertile tillers per plant, 1000-grain weight. The mean performance for adjusted mean, range and least significant difference of 64 genotypes for 7 characters are presented in table 2. The general mean for plant height was 66.18 cm. The lowest value was recorded in case of BH-393 (52.46 cm) and highest value for RD-2035 (89.44 cm). Sixteen varieties were significantly shorter in plant stature than the general mean. Top eight significant groups for plant height were Alfa-93, Gitanjali, Manjula, RD-2503, JB-58, DWRUB-52, K-508, and DL-88. The days to maturity ranged from 110.98 (BG-101) to 119.05 days (RD-2552) with general mean of 115.27 days. Out of 64 varieties twenty two varieties matured significantly earlier than the general mean in which eight varieties namely BG-101, Bilara-2, BH-169, Vijay, K-508, Dolma, BH-75, and PL-419, matured earlier. Fertile tillers per plant ranged from 3.47 (BH-902) to 5.50 tillers per plant (HBL-276) with general mean of 4.375 tillers per plant. Among sixty four varieties, forty-six varieties showed significantly greater tillers per plant than the general mean in which top eight varieties order of merit were HBL-276, Lakhan, RD-2508, K-508, DL-88, PL-172, BHS-380, and Sonu. The general mean for length of main spike was 7.89 cm. The lowest value was recorded in case of PL-426 (5.39 cm) and highest value for Jagrity (8.89 cm). Thirty-seven varieties showed significantly longer spike length than general mean. Top eight varieties for longer spike length in order of merit were Jagrity, BHS-46, DL-88, UPB-1008, Alfa-93, RD-2552, K-141, and RD-2624.The lowest and highest values for grains per spikes were recorded for Clipper (29.34) and RD-2552 (39.18) respectively.

**Table 1. Analysis of variance of Simple Lattice Design for 7 characters in released varieties of barley**

| S. No. | Character | Source of variation | | |
|---|---|---|---|---|
| | | Replication | Treatments | Error |
| | Degree of freedom (d. f.) | 1.00 | 63.00 | 63.00 |
| 1 | Plant height (cm) | 214.78** | 113.01** | 2.46 |
| 2 | Days to maturity | 76.57** | 6.09** | 0.74 |
| 3 | No. of fertile tillers per plant | 13.78** | 0.52 | 0.93 |
| 4 | Length of main spike (cm) | 15.46** | 0.80** | 0.30 |
| 5 | No. of grains per main spike | 250.32** | 10.75** | 5.00 |
| 6 | 1000-grain weight (g) | 298.62** | 6.02 | 4.70 |
| 7 | Grain yield per plant (g) | 21.73** | 0.99* | 0.64 |

* Significant at 5 % probability level,
** Significant at 1 % probability level.

**Table 2. Adjusted means, range and least significant differences for 7 characters in released varieties of barley**

| S. No. | Varieties | Plant height (cm) | Days to maturity | No. of fertile tillers/plant | Length of main spike (cm) | No. of grains/ Main spike | 1000 grain weight (g) | Grain yield/ plant (cm) |
|---|---|---|---|---|---|---|---|---|
| 1 | Clipper | 53.39 | 116.01 | 4.52 | 7.19 | 29.34 | 38.53 | 6.20 |
| 2 | Jyoti | 64.12 | 115.99 | 4.50 | 7.48 | 31.50 | 36.59 | 6.09 |
| 3 | Amber | 63.41 | 115.01 | 3.51 | 8.22 | 33.39 | 36.63 | 6.13 |
| 4 | RS-6 | 55.52 | 115.02 | 4.51 | 7.78 | 31.64 | 36.56 | 6.79 |
| 5 | Ratna | 52.92 | 113.95 | 4.47 | 6.89 | 31.80 | 34.78 | 6.17 |
| 6 | RDB-1 | 55.37 | 115.98 | 3.50 | 6.90 | 32.02 | 36.62 | 5.85 |
| 7 | Vijay | 54.93 | 112.48 | 3.49 | 6.25 | 31.93 | 36.82 | 7.16 |
| 8 | Himani | 63.45 | 115.02 | 4.00 | 7.27 | 30.59 | 35.47 | 6.40 |
| 9 | Dolma | 58.28 | 113.00 | 4.52 | 7.50 | 32.55 | 35.18 | 6.81 |
| 10 | BG-101 | 59.96 | 110.98 | 4.50 | 8.09 | 33.71 | 39.01 | 6.21 |
| 11 | Azad | 55.40 | 113.99 | 4.51 | 7.18 | 34.09 | 38.28 | 7.09 |
| 12 | PL-56 | 57.06 | 116.01 | 3.51 | 7.49 | 31.84 | 38.41 | 6.60 |
| 13 | RD-31 | 71.51 | 115.44 | 4.47 | 8.40 | 34.00 | 41.16 | 7.64 |
| 14 | Bilara-2 | 62.61 | 111.97 | 3.50 | 7.06 | 31.73 | 37.33 | 6.43 |
| 15 | Kedar | 73.17 | 115.97 | 4.49 | 8.51 | 36.14 | 40.07 | 8.11 |
| 16 | Sonu | 77.14 | 115.01 | 5.00 | 8.08 | 34.30 | 40.46 | 7.17 |
| 17 | K-141 | 76.12 | 114.00 | 4.02 | 8.77 | 37.21 | 40.01 | 7.16 |
| 18 | Lakhan | 68.76 | 115.98 | 5.50 | 8.11 | 34.86 | 38.58 | 7.08 |
| 19 | Jagrity | 71.80 | 116.99 | 4.51 | 8.89 | 38.25 | 41.67 | 7.79 |
| 20 | BH-75 | 68.85 | 113.01 | 3.51 | 8.06 | 34.50 | 37.53 | 6.72 |
| 21 | BHS-46 | 77.00 | 113.94 | 4.47 | 8.87 | 36.66 | 40.07 | 7.36 |
| 22 | PL-172 | 68.81 | 115.47 | 5.00 | 8.12 | 32.89 | 39.66 | 7.18 |
| 23 | VLB-1 | 69.56 | 115.97 | 4.49 | 8.03 | 34.30 | 36.52 | 6.88 |
| 24 | RD-2052 | 60.43 | 114.01 | 4.00 | 7.84 | 31.45 | 38.94 | 6.51 |
| 25 | Manjula | 66.01 | 115.03 | 3.52 | 8.73 | 36.48 | 38.36 | 7.54 |
| 26 | BH-169 | 62.10 | 112.01 | 4.50 | 7.97 | 34.14 | 38.03 | 6.91 |
| 27 | Karan-16 | 59.68 | 114.53 | 4.01 | 7.35 | 30.52 | 35.79 | 6.39 |
| 28 | Gitanjali | 66.04 | 116.04 | 4.51 | 8.07 | 34.77 | 40.44 | 7.78 |
| 29 | RD-2035 | 89.44 | 114.47 | 4.97 | 8.08 | 36.93 | 39.66 | 7.45 |
| 30 | HBL-316 | 52.90 | 114.00 | 4.50 | 7.38 | 33.66 | 37.88 | 6.76 |
| 31 | Alfa-93 | 66.10 | 115.00 | 4.99 | 8.78 | 38.07 | 38.26 | 7.09 |
| 32 | PL-419 | 77.37 | 113.04 | 4.50 | 7.75 | 34.73 | 37.04 | 8.15 |
| 33 | PL-426 | 67.18 | 116.03 | 4.53 | 5.39 | 33.39 | 34.51 | 5.64 |
| 34 | BCU-73 | 67.77 | 116.51 | 4.52 | 7.83 | 31.55 | 40.30 | 7.83 |
| 35 | RD-2503 | 65.16 | 115.02 | 4.02 | 7.97 | 29.43 | 38.80 | 7.41 |
| 36 | RD-2508 | 75.67 | 115.03 | 5.03 | 7.18 | 30.68 | 38.10 | 6.82 |
| 37 | K-409 | 73.11 | 116.47 | 4.49 | 7.89 | 31.84 | 37.89 | 7.84 |
| 38 | K-508 | 64.42 | 112.99 | 5.02 | 7.84 | 35.57 | 40.95 | 7.96 |
| 39 | K-551 | 74.52 | 116.49 | 4.01 | 7.90 | 36.98 | 38.63 | 6.88 |
| 40 | K-560 | 73.55 | 114.03 | 4.52 | 7.66 | 33.14 | 39.61 | 7.03 |
| 41 | DL-88 | 64.17 | 116.04 | 5.02 | 8.84 | 36.02 | 37.22 | 7.17 |
| 42 | RD-2552 | 71.91 | 117.02 | 4.50 | 8.78 | 39.18 | 39.89 | 8.52 |
| 43 | HBL-276 | 70.60 | 115.53 | 5.51 | 8.67 | 33.07 | 40.37 | 8.35 |
| 44 | NB-1 | 63.16 | 115.05 | 3.51 | 7.83 | 34.32 | 38.01 | 6.29 |
| 45 | NB-2 | 68.96 | 115.98 | 3.97 | 8.14 | 33.98 | 37.78 | 6.63 |
| 46 | K-603 | 54.41 | 113.51 | 4.50 | 7.80 | 32.21 | 35.77 | 6.33 |
| 47 | BH-393 | 52.46 | 116.51 | 4.49 | 7.90 | 30.11 | 35.67 | 5.72 |
| 48 | NB-3 | 60.84 | 113.05 | 4.00 | 7.02 | 33.77 | 37.15 | 6.16 |
| 49 | DWR-28 | 70.29 | 115.04 | 4.50 | 8.20 | 33.39 | 37.47 | 7.07 |
| 50 | RD-2624 | 68.33 | 117.52 | 4.48 | 8.74 | 38.05 | 36.38 | 5.87 |

| S. No. | Varieties | Plant height (cm) | Days to maturity | No. of fertile tillers/plant | Length of main spike (cm) | No. of grains/ main spike | 1000 grain weight (g) | Grain yield/ plant (cm) |
|---|---|---|---|---|---|---|---|---|
| 51 | BHS-352 | 76.66 | 115.53 | 4.99 | 8.07 | 35.93 | 37.14 | 6.99 |
| 52 | RD-2592 | 76.32 | 119.05 | 4.49 | 8.69 | 32.18 | 39.83 | 8.17 |
| 53 | NDB-1173 | 75.37 | 117.48 | 4.46 | 8.35 | 30.34 | 38.45 | 6.42 |
| 54 | JB-58 | 64.88 | 114.51 | 4.99 | 7.30 | 31.07 | 35.82 | 8.06 |
| 55 | VLB-56 | 66.18 | 117.51 | 4.48 | 7.50 | 31.98 | 36.60 | 7.00 |
| 56 | RD-2660 | 64.05 | 113.05 | 3.98 | 7.97 | 30.64 | 36.09 | 6.33 |
| 57 | DWRUB-52 | 64.59 | 115.49 | 5.02 | 7.54 | 32.66 | 36.21 | 7.50 |
| 58 | RD-2668 | 66.83 | 115.97 | 4.00 | 7.58 | 30.82 | 35.05 | 6.29 |
| 59 | PL-751 | 62.57 | 114.48 | 4.50 | 8.12 | 33.71 | 35.85 | 8.10 |
| 60 | RD-2715 | 62.98 | 118.99 | 3.51 | 8.03 | 32.95 | 38.99 | 6.39 |
| 61 | BH-902 | 60.22 | 116.92 | 3.47 | 8.29 | 35.12 | 36.85 | 7.06 |
| 62 | BHS-380 | 69.28 | 118.45 | 5.00 | 8.19 | 35.34 | 37.75 | 6.84 |
| 63 | DWR-73 | 69.48 | 118.95 | 3.99 | 8.15 | 36.25 | 40.16 | 6.39 |
| 64 | UPB-1008 | 70.46 | 117.99 | 4.50 | 8.81 | 37.91 | 38.42 | 7.84 |
| Lowest | | 52.46 | 52.46 | 110.98 | 3.47 | 5.39 | 29.34 | 34.51 |
| Highest | | 89.44 | 89.44 | 119.05 | 5.51 | 8.89 | 39.18 | 41.67 |
| Mean value | | 66.181 | 66.18 | 115.27 | 4.38 | 7.89 | 33.65 | 37.94 |
| LSD1 5% | | 3.034 | 3.03 | 1.74 | 1.95 | 1.09 | 4.33 | 4.32 |
| LSD2 5% | | 3.100 | 3.10 | 1.73 | 1.95 | 1.10 | 4.42 | 4.35 |
| LSD3 5% | | 3.086 | 3.09 | 1.73 | 1.95 | 1.10 | 4.40 | 4.35 |

The general mean for grains per spike was 33.64. Out of 64 varieties, thirty one varieties exhibited significantly greater number of grains per spike as compared to general mean. The eight promising varieties for greater number of grains per spike identified on the basis of merit were RD-2552, Jagrity, Alfa-93, RD-2624, UPB-1008, K-141, K-551, and RD-2035.The general mean for 1000-seed weight was 37.93g and varied from 34.51g (PL-426) to 41.67g (Jagrity). Among 64 varieties, thirty two varieties showed significantly greater 1000-seed weight than the general mean, in which eight varieties had higher 1000 seed weight. These were Jagrity, RD-31, K-508, Sonu, Gitanjali, HBL-276, BCU-73, and DWR-73.The general mean calculated for grain yield per plant was 6.97g. It ranged from 5.63g (PL-426) to 8.52g (RD-2552). Twenty varieties showed significantly higher grain yield per plant than the general mean. Eight varieties most promising for grain yield identified on the basis of merit were RD-2552, HBL-276, RD-2592, PL-419, Kedar, PL-751, JB-58, and K-508.

Nine morphological characters were recorded for morphological variation in released varieties (Fig. 1) of barley, the details are:

***Growth Habit (erect/prostrate):*** The erect group had higher plant yield than prostrate which indicate to be attributable mainly to the significantly larger grain size of this group. The erect group was also significantly earlier and taller than the prostrate group. The erect type bended at an angle of $30^{o}$ are supposed to accumulate more photosynthate during photosynthesis. Chlorophyll content and its kind differ in erect and prostrate type which is researchable.

***Morphology of Leaf (narrow/medium/broad):*** Broad leaved plants had more green biomass, more chlorophyll content indicating suitable for green forage i.e., dual purpose. On the other hand plants having narrow leaves become tolerant to abiotic stresses like drought, salinity, alkalinity and rainfed situation.

***Presence of Anthocyanin Pigmentation (root/auricle):*** Anthocyanin pigment is an indication of presence of malt in barley. The barley varieties having anthocyanin pigment on awn/tip of the ear, were categorised in two groups malty or non-malty barley. Anthocyanin pigment is associated with photosynthetic activity.

***Spikelet Arrangement (dense/lax):*** An arrangement of spikelet expresses their ability to enhance productivity in crop. Denser and bolder grain add per unit increase in grain yield. Denser arrangement of spikelet provides less opportunity to reside the spore of serious disease.

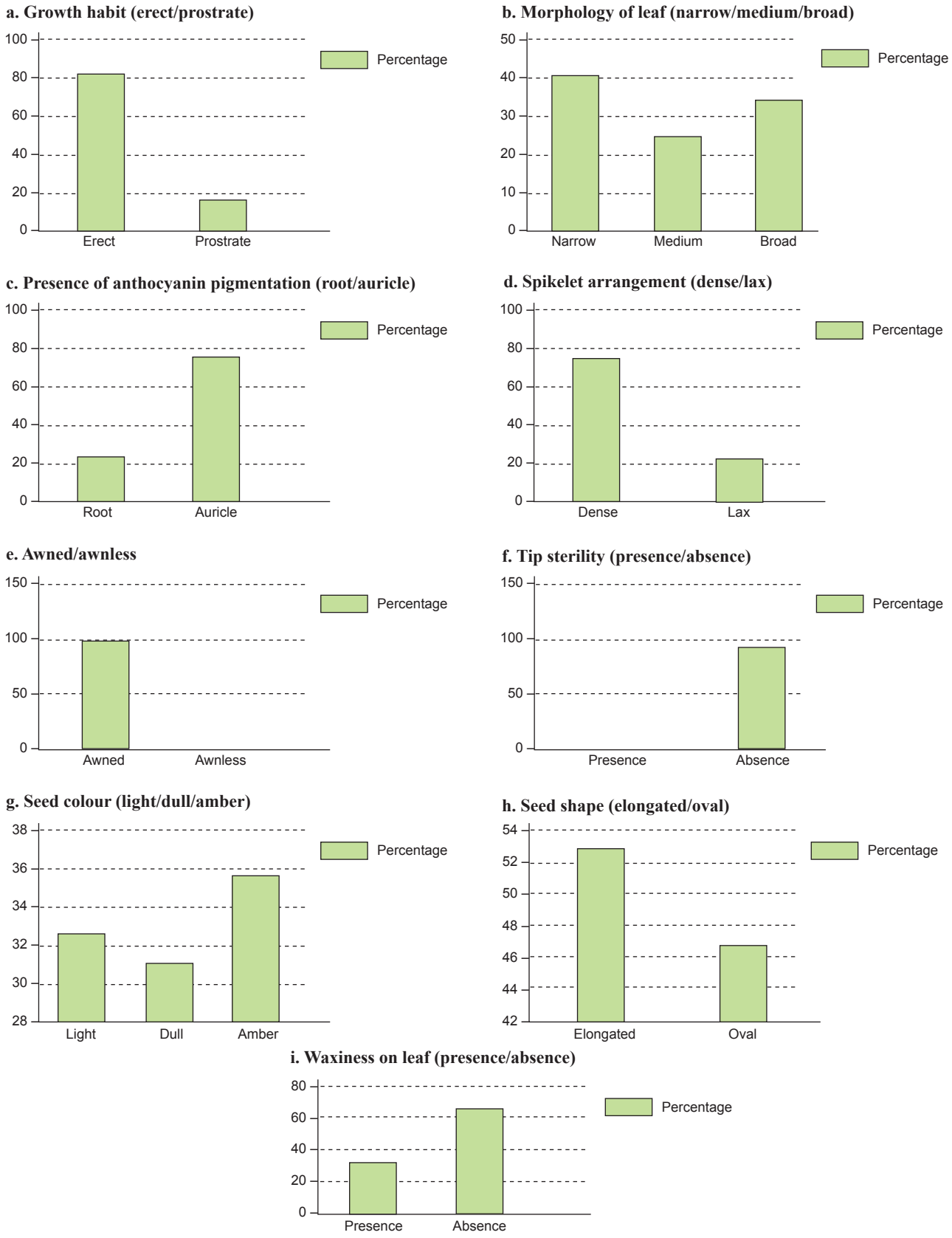


**Fig. 1: Morphological characters for variation in traits (a-i)**

***Awned/ Awnless:*** Awned trait is a specification hulled form of barley. It assists in scarring of birds thus facilitates non damaging the crop yield. Awned trait is indirectly influenced the photosynthetic activity/formation of chlorophyll.

***Tip Sterility (presence/absence):*** Tip sterility had raised variety to variety reflection and crop to crop. This trait had negative effect on yield. This trait, in general appears under abiotic stress condition e.g., problematic soil. For this trait arises due to physiological irregularities/ nutrient deficiency.

***Seed Colour (light yellow/dull/amber):*** Seed colour is a quality trait which attracts the preference of consumers, processors or grower. Most appealing seed colour is amber (in case of cereals) and light yellow in other. Dull-ness downs the rate of grain as much as purchase is concerned.

***Seed Shape (elongated/oval):*** Seed shape varied crop to crop and variety to variety. In general oval type grains are much preferred by the people in cereals. Elongated or oblong grain is a special trait in barley which differentiates it from other cereals.

***Waxiness on Leaf (presence/absence):*** Waxiness on leaf is a peculiar trait in cereal. Waxiness having genotype may be well suited for rainfed/drought/salt affected condition because waxiness restricts evaporation as well as transpiration in plant. Waxiness also reflects beta glucon particularly in barley which regulates deposition of cholesterol level in the body.

The erect group (82.81%) had higher plant yield and also significantly earlier and taller than the prostrate group (17.18%). Broad leaves (34.37%) plants revealed more green biomass as a consequence more chlorophyll content indicating suitable for green forage, whereas narrow leaves (40.62%) revealed tolerant to abiotic stresses like drought, and rainfed situation, medium leaves plants (25%) performed intermediate. Some of the varieties had anthocyanin pigmentation on root (23.43%) and some on auricle (76.56%), Anthocyanin pigment is an indication of presence of malt in barley, on the basis presence of anthocyanin pigmentation varieties we can categories in two group malty or non malty barley. Anthocyanin pigment is associated with photosynthetic activity. Anthocyanins play key roles in many plant physiological processes; for example, they form photoprotective screens in vegetative tissue, act as visual attractors to aid pollination and seed dispersal, and function as antimicrobial agents and feeding deterrents in the defense response, Winkel-Shirley (2001). Anthocyanin accumulation in vegetative organs has a relationship to stress resistance in plants; biosynthetic pathway of anthocyanin is well described in plants in *Arabidopsis* and other plants, including *Antirrhinum majus* and *Petunia hybrida*.

Spikelet arrangement expresses their ability to enhance productivity in crop, denser (76.56%) arrangement of spikelet provides less opportunity to reside the spore of serious disease, while lax (23.43%) spikelet avoid these. Awned (100%) trait is indirectly influenced the photosynthetic activity/ formation of chlorophyll content, contributed 80-90% of total spike photosynthesis. Some varieties have fertile tip (96.87 %), while some are sterile (3.12%), tip sterility had negative on yield, physiological irregularities. Seed colour is the quality trait which attracts the preference of consumer processors and grower, most appealing seed colour is amber (35.93%) and light yellow (32.81%) while, dull colour (31.25%) downs the rate of grain. Seed shape varied crop to crop and variety to variety. In general oval type (46.87%) grains are much preferred by the people in cereals, elongated (53.12%) grain is a special trait in barley which differentiates it from other cereals. Waxiness on leaf is a peculiar trait in cereals; waxiness restricts evaporation as well as transpiration in plant. Some varieties exhibited waxiness (32.81%), rest of varieties lack this trait. Presence of substantial variation in the barley varieties indicated possibility of selection in these traits.

The structure of morphological variation in barley varieties strongly influenced by the environmental factors so that the degree of variation of characters differs with regions and altitudes from where the accessions collected. In studies of spring barley (*Hordeum vulgare* L.) awned isolines had higher yield, seed weight and seed plumpness than awnless isolines (Quaset *et al*., 1965; Schaller *et al.,* 1972). Full and half-awned lines of Atlas barley produce more grain than quarter-awned and awnless lines. Computations of Schaller *et al.* (1972) showed that the awns of a full awned Atlas type contributed 19.3Va of the total grain yield. Kjack and Witters (1974) used the same lines as those of the Schaller *et al.* (1972).

Based on this study eight varieties were selected namely RD-2552, HBL-276, RD-2592, PL-419, Kedar, PL-751, JB-58 and K-508 produced higher grain yield plant$^{-1}$ and showed high to very high mean performance

for several other yield component also. These varieties can be used in barley improvement programme and will be helpful in breaking the yield plateau.

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# Genetic Variability and Diversity Pattern for Agromorphological Traits in Indian Mustard Germplasm

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

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Genetic diversity studies were carried out on 302 indigenous accessions of Indian mustard [*Brassica juncea* (L.) Czern & Coss] for variability assessment and identification of trait-specific germplasm. The Indian mustard germplasm was evaluated for eight important morpho-agronomic traits. Geographic information system (GIS), principal component and cluster analysis were carried out to analyse major clusters. Four principal components were identified explaining more than 74% of total variation. Three promising germplasm accessions (IC342781, IC570320 and IC426354) identified with maximum number of seeds per siliqua (>18.0 seeds) were collected from districts Patna (Bihar) and Adilabad (Andhra Pradesh). Similarly, three promising accessions (IC426398, IC521376 and IC395557) were identified with high oil content (>40%) from districts Nizamabad (Andhra Pradesh), Godda (Jharkhand) and Gorakhpur (Uttar Pradesh) respectively. The cluster analysis grouped mainly in two major clusters I and II and further sub-divided into a and b sub-groups. In cluster I sub-group b which indicates a close relationship between traits - the days to mean flowering and days to mean maturity while the plant height was grouped individually. In cluster II, number of primary branches and number of seeds/siliqua showed close relationship with oil content as compared to other traits. GIS based grid maps using Shannon-Weaver diversity index (0-4.0) were generated for showing high variability areas (light red/dark red grids) in different agro-ecological regions of India. The results indicated that Indian mustard germplasm collected by NBPGR from different parts of India has broad genetic base. Thus, promising genotypes identified for various economically important morpho-agronomic traits can be utilized to develop improved varieties of Indian mustard.

**Key Words: Genetic diversity, GIS tools, Indian mustard, Trait-specific germplasm, Variability assessment**

## Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] commonly known as raya, rai or laha, is the second most important oilseed crop of India. It is cultivated over seven million hectares, primarily in the north-western states of India, either as a sole or as inter-crop under irrigated or rain-fed conditions (Mahto and Haider, 2012). In India, a great diversity exists in *B. juncea* for plant type, seed size, siliqua length, oil content and maturity period (Rana and Singh, 1992; Misra, 2012; Semwal *et al*., 2013). The crop is moderately tolerant to acidic soils, thrives well under cold and drought conditions (Singh, 1997; Duhoon and Koppar, 1998; Singh and Sharma, 2007). Indian mustard is a potential oilseed crop to meet the challenges that may arise due to climate change and can play an important role to enhance the production and productivity (Kumar *et al*., 2004; Singh and Sharma, 2007). The low productivity can considerably be increased through the use of diverse donor genotypes for various qualitative and quantitative traits.

So far studies pertaining to geo-referencing and diversity distribution pattern have been conducted in only a few crops namely jatropha (Sunil *et al*., 2009), black gram (Abraham *et al*., 2010) and rapeseed-mustard (Semwal *et al*., 2013). Attempt has been made to analyse variability in different germplasm accessions of *B. juncea* collected from diverse agro-ecological regions (western Himalaya, north-western plains, gangetic and eastern plains, central India, north-eastern hill region and peninsular region) of India. Promising/trait-specific germplasm have been identified and relationship among yield related traits has been studied. Geo-referenced maps as well as grid based diversity indices maps using GIS tools have been developed to represent areas of high variability.

## Materials and Methods

A total of 302 accessions of Indian mustard germplasm were collected from over 261 collection sites in 83 districts of 19 states of India. Geo-coordinates of the

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

collection sites were used for spatial distribution pattern of Indian mustard in the present study (Fig. 1). These accessions were grown at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi along with five check varieties *viz*. Laxmi, Pusa Jai Kisan, Rajat, RH-30 and Varuna during two crop seasons (2009-10 and 2010-11) in a plot of two rows of 3 m row length in Augmented Block Design (ABD), maintaining 30 and 10 to 15 cm row to row and plant to plant spacing respectively to record observations. Five random plants of each accession were selected at appropriate growth stages and observations were recorded on eight important morpho-agronomic traits (plant height, siliqua length, number of seeds per siliqua, number of siliquae on main fruiting branch, days to mean maturity, days to mean flowering and oil content). Near infra-red (NIR) method was used to analyse the oil content (%).

Mean and coefficient of variation (CV) were computed using standard statistical methods (Gomez and Gomez, 1984). The principal component analysis (PCA) was done on the correlation matrix of transformed data (Rao, 1964). Studies on cluster analysis were done on the basis of correlation coefficient and similarity matrices following Ward's methods (Ward, 1963; Kaufman and Rousseeuw, 1990). In order to know the spatial distribution and diversity assessment, DIVA-GIS tool was used for point to grid analysis (Hijmans *et al*., 2000). DIVA-GIS was run for each trait separately to assess the geographical distribution of diversity in different states of the country. Diversity indices values were mapped using Shannon-Weaver method (Shannon and Weaver, 1963).

## Results and Discussion

### *Characterization and Evaluation of Indian Mustard*

302 accessions of Indian mustard showed wide genetic variability in collected germplasm. Maximum number of germplasm accessions of Indian mustard used for evaluation were from Uttar Pradesh (97) followed by Andhra Pradesh (62), Himachal Pradesh (38), Jharkhand (42) and Bihar (31).

Quantitative characters of Indian mustard germplasm showed wide variation for majority of the morpho-agronomic traits (Table 1). Data indicated maximum variation for number of primary branches followed by number of seeds per siliqua and oil content (%). Three accessions (IC342781, IC570320 and IC426354) were found to have more than 19 seeds/siliqua. There was a good variation for oil content and yield related characters such as number of seeds per siliqua, siliqua length and days to mean maturity. Five promising accessions (IC426398, IC521376, IC395557, IC342772 and IC312500) had more than 40% oil content. High variation for number of siliquae on main fruiting branch indicated the potential of the germplasm accessions for the development of high yielding varieties to fulfil the demand of oil in the country.

### *Promising Donor Genotypes Identified*

Based on characterization and evaluation of Indian mustard, promising accessions for various agro-morphological traits have been identified. The details of important traits and promising accessions have been presented in Table 2. Maximum promising accessions

**Table 1. Statistical values of important quantitative traits in Indian mustard (*B. juncea*) germplasm**

| Traits | Min. | Max. | Mean | CV (%) Phenotypic | Mean values of check varieties | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | Pusa Jai Kisan (1) | Rajat (2) | RH-30 (3) | Varuna (4) | Laxmi (5) |
| Plant height (cm) | 116.7 | 275.4 | 202.1 | 13.7 | 204.3 | 212.1 | 185.7 | 212.6 | 218.4 |
| No. of primary branches | 4.4 | 16.8 | 7.9 | 24.1 | 7.8 | 7.2 | 6.9 | 7.87 | 8.1 |
| No. of siliquae on main fruiting branch | 14.7 | 71.2 | 48.4 | 20.6 | 49.3 | 48.9 | 49.2 | 45.7 | 53.5 |
| Siliqua length (cm) | 1.5 | 5.3 | 3.8 | 15.6 | 4.1 | 3.8 | 3.9 | 3.7 | 3.7 |
| No. of seeds per siliqua | 6.0 | 25.1 | 13.5 | 15.0 | 13.5 | 13.1 | 13.2 | 12.8 | 12.4 |
| Days to mean flowering | 35.0 | 110.0 | 59.0 | 23.2 | 53.0 | 50.0 | 50.0 | 48.0 | 50.0 |
| Days to mean maturity | 139.0 | 168.0 | 155.0 | 3.1 | 155.0 | 154.0 | 152.0 | 154.0 | 155.0 |
| Oil content (%) | 24.1 | 41.0 | 33.2 | 11.8 | 36.8 | 34.2 | 35.8 | 35.7 | 35.6 |

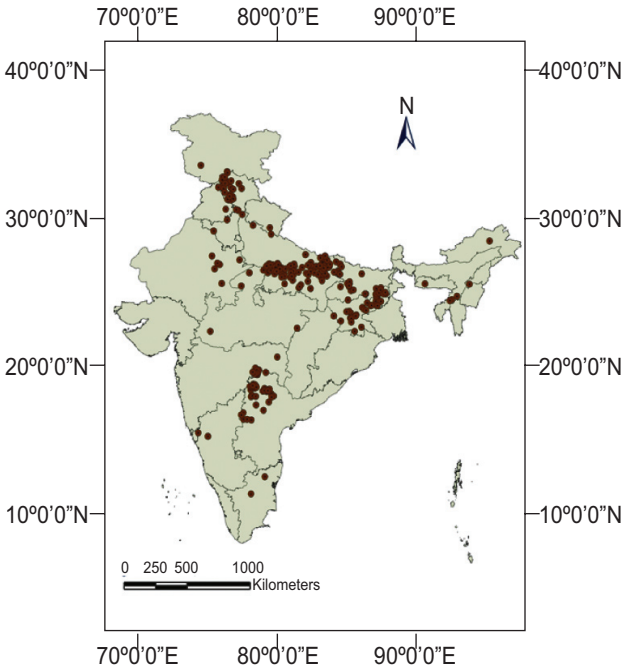


**Fig. 1. Geographic distribution of collection sites of Indian mustard (*B. juncea*) germplasm**

related to eight important morpho-agronomic traits of Indian mustard germplasm were identified from Uttar Pradesh, Jharkhand, Bihar and Himachal Pradesh. Trait like plant height (dwarf nature) is desirable because plants scape lodge at maturity. Promising accessions for dwarf types were identified from Andhra Pradesh and Uttar Pradesh. It is concluded that three regions viz. western Himalaya, gangetic plains and eastern India are complimentary sites for collection of promising germplasm of Indian mustard. More number of primary branches (> 15) per plant, higher number of siliquae on main fruiting branch (> 50), long siliqua length (> 5.0cm) and high number of seeds per siliqua (> 18.0) are important yield contributing traits. Promising/trait-specific germplasm identified for various economically useful traits, could be used as donor genotypes in the Indian mustard improvement programme.

### *Principal Component and Cluster Analysis*

The identification of a principal component was based on the correlation coefficient between different agronomic characters, their Eigen values of the principal components. Interrelationships among traits have been presented in Figure 2 and Table 3. Principal component analysis revealed that four principal components explained more than 74% of total morphological variation (Fig. 2). Out of the four indigenous collections shown in Fig. 2, only IC310757 was observed as promising accession collected from Morena (Madhya Pradesh). Correlation coefficients between oil content, siliqua length, number of seeds per siliqua and other morphological traits are useful in selection of desirable plant type in designing crop improvement programme. The plant height was positively and significantly correlated ($r$ = 0.51) with days to mean maturity while days to mean flowering was also positively and significantly correlated ($r$ = 0.70) with days to mean maturity.

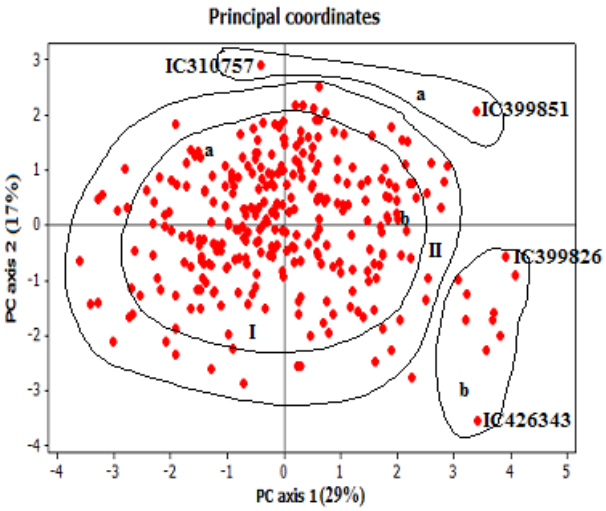


**Fig. 2. Principal coordinates highlighting grouping of 302 accessions of Indian mustard**

Based on correlation coefficient and similarity matrices, dendrograms, Principal Coordinates were depicted in Figure 2. These values indicated a very good fit of the data to the clustering pattern. The cluster analysis grouped mainly in two major clusters I and II and further sub-divided into a and b sub-groups. In cluster II sub-group b which indicates a close relationship between traits - days to mean flowering and days to mean maturity while the plant height was grouped individually. In cluster I, number of primary branches and number of seeds/siliqua showed close relationship with oil content as compared to other traits.

The germplasm evaluated showed a large amount of divergence for characters considering the absolute range. Diversity analysis among accessions of *B. juncea* provided information on distinctness, similarities and overlap based on different morpho-agronomic traits, which corresponds firmly to their genetic status and contribution to the phenotype and environment.

**Table 2. Promising donor genotypes identified for different traits in Indian mustard (*B. juncea*) germplasm**

| S.No. | Characters/Traits | Promising accessions (values) | State (Source of collection) |
|---|---|---|---|
| 1 | Dwarf plant height (cm) (< 134 cm) | IC426400 (116.7) | Andhra Pradesh |
| | | IC385680 (121.0) | Uttar Pradesh |
| | | IC395583 (130.4) | Uttar Pradesh |
| | | IC426381 (131.0) | Andhra Pradesh |
| | | IC570310 (133.4) | Andhra Pradesh |
| 2 | Number of primary branches (> 15) | IC520756 (16.8) | Jharkhand |
| | | IC426343 (16.7) | Andhra Pradesh |
| | | IC520752 (15.7) | Jharkhand |
| | | IC447547 (15.2) | Himachal Pradesh |
| 3 | Number of siliquae on main fruiting branch (> 65) | IC248997 (71.2) | Bihar |
| | | IC397901 (70.2) | Himachal Pradesh |
| | | IC426299 (69.8) | Andhra Pradesh |
| | | IC312514 (68.2) | Uttar Pradesh |
| | | IC520754 (67.0) | Jharkhand |
| 4 | Long siliqua length (cm) (> 5.0cm) | IC310757 (5.4) | Madhya Pradesh |
| | | IC355371 (5.3) | Uttar Pradesh |
| | | IC520769 (5.2) | Jharkhand |
| | | IC538744 (5.2) | Himachal Pradesh |
| | | IC264133 (5.1) | Rajasthan |
| 5 | High number of seeds per siliqua (> 18.0) | IC342781 (25.1) | Bihar |
| | | IC570320 (19.6) | Andhra Pradesh |
| | | IC426354 (19.4) | Andhra Pradesh |
| | | IC385700 (18.4) | Uttar Pradesh |
| | | IC426319 (18.0) | Andhra Pradesh |
| 6 | Early mean flowering (< 40 days) | IC331819 (35) | Chhattisgarh |
| | | IC385782 (37) | Jharkhand |
| | | IC398759 (38) | Bihar |
| | | IC398763 (39) | Bihar |
| | | IC426383 (39) | Andhra Pradesh |
| 7 | Early mean maturity (< 142 days) | IC406349 (139) | Jharkhand |
| | | IC426376 (139) | Andhra Pradesh |
| | | IC426354 (140) | Andhra Pradesh |
| | | IC426322 (141) | Andhra Pradesh |
| | | IC426372 (141) | Andhra Pradesh |
| 8 | High oil content (%) (> 40%) | IC426398 (41.0) | Andhra Pradesh |
| | | IC521376 (40.7) | Jharkhand |
| | | IC395557 (40.5) | Uttar Pradesh |
| | | IC342772 (40.3) | Jharkhand |
| | | IC312500 (40.0) | Uttar Pradesh |

**Table 3. Analysis of phenotypic correlation coefficient in different morpho-agronomic traits in Indian mustard (*B. juncea*)**

| PLH | NPB | SFB | SLL | | NSS | DMF | DMM | OIC |
|---|---|---|---|---|---|---|---|---|
| PLH | 1.000 | | | | | | | |
| NPB | 0.290 | 1.000 | | | | | | |
| SFB | 0.149 | -0.040 | 1.000 | | | | | |
| SLL | 0.186 | -0.158 | 0.110 | 1.000 | | | | |
| NSS | -0.061 | 0.112 | -0.089 | 0.190 | 1.000 | | | |
| DMF | 0.412 | 0.281 | -0.144 | 0.002 | -0.138 | 1.000 | | |
| DMM | 0.516* | 0.129 | -0.056 | 0.230 | -0.211 | 0.702* | 1.000 | |
| OIC | 0.071 | -0.024 | -0.171 | -0.038 | 0.034 | 0.087 | 0.134 | 1.000 |

**PLH**= plant height (cm), **NPB**=number of primary branches, **OIC**=oil content (%), **NSFB**=number of siliquae on main fruiting branch, **SLL**=siliqua length (cm), **NSS**=number of seeds/siliqua, **DMF**=days to mean flowering, **DMM**=days to mean maturity, * significant values.

### *Diversity Analysis Studies of Indian Mustard using GIS Tools*

GIS based grid maps were generated using Shannon-Weaver diversity index for plant height (cm), number of primary branches, oil content (%) and number of seeds per siliqua under different agro-ecological regions of the India. In the map, red/dark red colour of the grid indicated high variability observed in *B. juncea* germplasm accessions for different morpho-agronomic traits (Fig. 3). Geo-referenced grid maps were used to identify oil content and the diversity pattern (0.5 - 3.0), in different states of India (Fig. 3).

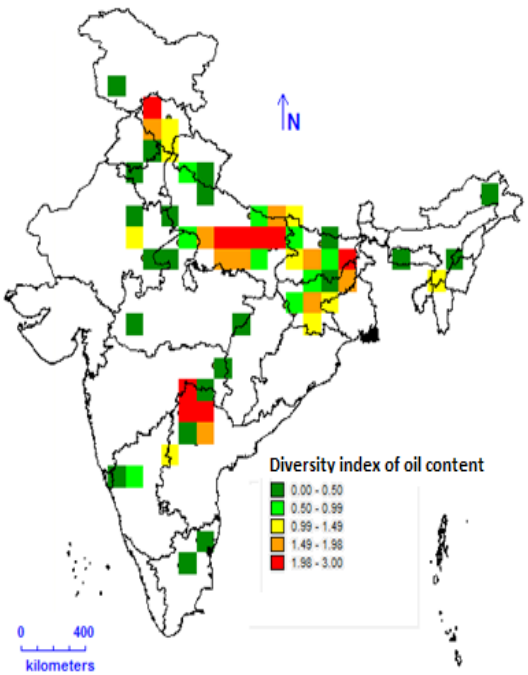


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**Fig. 3. High diversity areas (red grids) for important morpho-agronomic traits of Indian mustard *(B. juncea)***

Variability studies play a very important role in crop improvement programme. In view of climate change resulting in the loss of biodiversity, there is a need to analyse the existing collections, identifying promising accessions and collect as much variability as possible before it is eroded (Upadhyaya *et al*., 2012). National Bureau of Plant Genetic Resources in collaboration with crop-based institutes of Indian Council of Agricultural Research (ICAR) and State Agricultural Universities (SAUs) has collected *B. juncea* germplasm (302 accessions) mainly from northern, north-western and peninsular states of India and evaluated during crop seasons of 2009-10 and 2010-11. Of these, 40 accessions were identified as promising genotypes for different economic traits.

The present study indicated wide range of variability for plant height, number of primary branches per plant, oil content (%) and number of seeds per siliqua. There was a good variation for oil content and yield contributing traits such as number of seeds per siliqua and siliqua length. Jindal and Labana (1985) presented information on the genetic components of variance of oil content and protein and they found high heritability (narrow sense) for oil content (58.15%) in mustard. Highest genotypic and phenotypic coefficient of variation for seed yield followed by number of siliqua per plant was observed by (Chowdhary and Goswami 1991). Similar observations reported by Ghosh *et al*. (2001); Kumar *et al.* (1988); Singh *et al*. (2003); Misra *et al*. (2007, 2012); Singh *et al.* (2014) and Verma *et al.* (2001) that all four yield components *viz.,* primary branches per plant, secondary branches per plant, siliquae per plant and seeds per siliqua exhibited significant positive association with seed yield. Genetic variability for plant height, siliqua length, 1000-seed weight, oil content and seed yield

per plant were observed by Pant and Singh (2001). Variability, heritability and genetic advance for forty Indian mustard cultivars and the varietal differences were highly significant for plant height, days to mean flowering, siliquae per plant, seeds per siliqua, days to maturity, 1000 - seed weight and seed yield per plot (Poonam and Singh, 2004).

## Conclusions

Indian mustard is the second most important oilseed crop of India. There is a limited genetic variability available with the plant breeder for mustard improvement programme. Efforts were made to strengthen mustard germplasm from different agro-ecological regions of the country. Germplasm was evaluated for important agro-morphological traits for utilization in mustard improvement programme. Some of the promising accessions were identified as useful donors for early flowering (< 40 days) from districts Sarguja (Chhattisgarh) and Godda (Jharkhand) and high number of seeds per siliqua (>18 seeds)) from districts Patna (Bihar) and Adilabad (Andhra Pradesh) as compared to best checks. However, IC426398, IC521376 and IC395557 have been identified as donor for high oil content (> 40%) mainly from districts Nizamabad (Andhra Pradesh), Godda (Jharkhand) and Gorakhpur (Uttar Pradesh) respectively. The results concluded that Indian mustard (*B. juncea*) has wide-ranging genetic base in India. The Shannon-Weaver diversity index based on analysis of geographical distribution of morpho-agronomic traits, revealed four high diversity regions viz., Western Himalaya (Himachal Pradesh), gangetic plains (Uttar Pradesh) and eastern India (Bihar and Jharkhand). These promising genotype dwarf, early maturing, high yielding and high oil content can be used to enhance productivity of Indian mustard.

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# Selection of Homogamous Walnut from Seedling Plantation in South Kashmir

**Amit Kumar**
*Division of Fruit Science, Sher-e-Kashmir University of Agricultural Science and Technology, Shalimar-190025, Jammu and Kashmir, India*

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Thirty two homogamous walnut trees were pre-selected from a total of four hundred and eighty two trees grown naturally in fourteen villages of district Pulwama of South Kashmir. In most of the trees flowering periods of male and female are overlapping at least for six days and recorded less than 25 per cent degree of dichogamy. The quality characteristics of nuts of these selected walnut types are quite valuable. Out of these homogamous trees, more than 80 per cent varied considerably in terms of yield, nut and kernel quality. Their nut and kernel weight varied between 10.23 g to 17.73 g and 5.20 g to 9.55 g, respectively. However, kernel percentage ranged between 44.83 and 56.35 per cent. These selected walnut types are adequate for commercial growth and can be utilized in genetic improvement programmes.

**Key Words: Homogamous, Pollen shedding, Seedling, Selection, Stigma receptivity, Walnut**

## Introduction

Owing to favourable ecological conditions, to the existence of a valuable fund of germplasm which is adapted to these conditions and to a tradition of many centuries for growing this species, Kashmir is one of the regions in the whole world with an important production of walnut. The common walnut is considered to be indigenous to the region from Persia to Kashmir (Ford, 1975) which further extends to Himachal Pradesh, Uttaranchal (Hayes, 1957). Walnut is important in terms of enormous export potential and has a scope of diversification with suitable high value crop in an otherwise apple dominating region. Walnut becomes a viable alternative for commercial cultivation in hilly states. Presently the major walnut production comes from seedling trees of primitive population grown under natural forests and farmers backyards without any cultural operation. *Juglans regia* L. is heterodichogamous species i.e. having dichogamous and homogamous genotypes. Dichogamous includes protandrous and protogynous genotypes and causing outcrossing (Sutyemez, 2006). Persian walnut exhibits varying degrees of dichogamy with protandry more pronounced than protogyny in most of the genotypes (Majackaja, 1969; Germain *et al*., 1981). On the other hand, homogamy i.e. overlapping pollen shedding period and stigma receptivity periods results in good pollination and consequent higher yield, however homogamy in walnut is quite rare (Solar *et al*., 1997; Sharma and Sharma, 2000; Sutyemez, 2001; Beyhan and Ozatar, 2008; Verma *et al*., 2009) as compared to protandry and protogyny. Homogamous types of walnuts are generally more productive than the protogynous and protandrous walnuts because of synchronized blooming of male and female flowers. The present study aims in highlighting the walnut accessions with high degree of homogamy, to achieve optimum fruit set and for getting higher yields with desirable nut and kernel characters.

## Materials and Methods

In a preliminary survey four hundred and eighty two walnut trees were marked in fourteen villages of district Pulwama during 2010 and 2011. All the marked trees are of seedling origin ranging an age of between 20 to 60 years. The trees were marked on the basis of health, plant vigour, regular bearing and desirable nut and kernel characters and out of them 32 trees were pre-selected for further studies on the basis of their homogamous nature. The weather and geographical features of the studied location are represented in Figure 1.

Observations on flowering characters were recorded as per IPGRI walnut descriptors (IPGRI, 1994). Four branches on each side of the tree were selected and marked. Bearing habit of each tree was observed on the basis of terminal and lateral habit. Time of the leaf bud burst was taken on the four selected branches and noted. Number of catkins/bud was observed on four selected branches and average value was calculated. Ten catkins were randomly taken from the selected branches and

*Author for Correspondence: Email-khokherak@rediffmail.com;

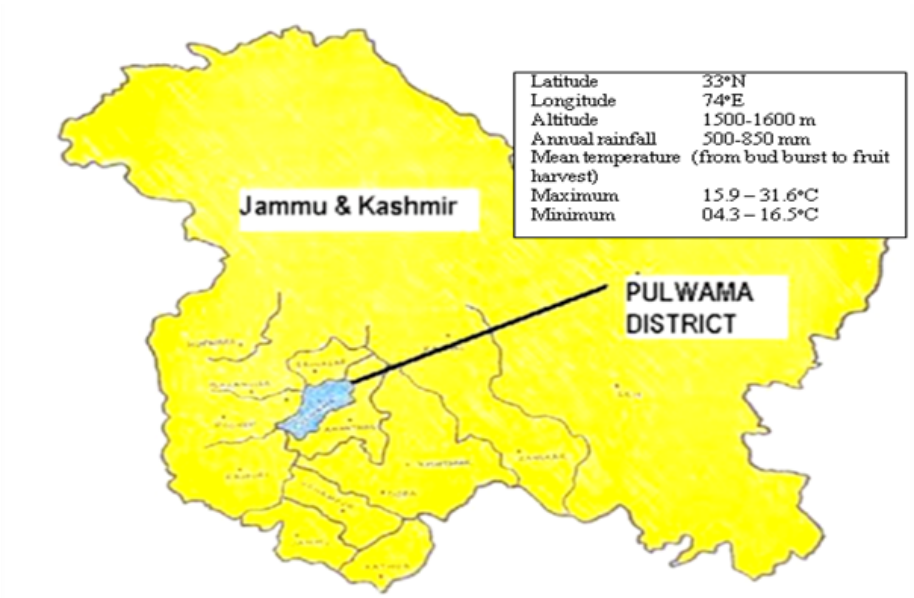



**Fig. 1. Weather and geographical features of the area surveyed**

measured with the help of digital vernier's caliper and expressed in cm. To determine the nature and degree of dichogamy, observations were recorded at the time of maturation of male catkins and female flower by selecting four branches on each tree. Degree of dichogamy was calculated as per methods of Solar *et al*. (1997).

$$\text{Degree of dichogamy (\%)} = 1 - \frac{\text{Number of days when male and female flowering coincides}}{\text{Number of days of female flowering}} \times 100$$

The selected trees showing less than 25 per cent degree of dichogamy (Kumar, 2000; Kumar *et al*., 2005) were categorized as homogamous. The homogamous selections were further evaluated for their nut, kernel and yield characteristics for two consecutive years. Nut yield (kg/tree) was calculated on the basis of total weight of all the nuts harvested after dehulling and drying. Yield efficiency and trunk cross sectional area was calculated as per Westwood (1993)

$$\text{Yield efficiency (kg/cm}^2\text{)} = \frac{\text{Yield}}{\text{Trunk cross sectional area}}$$

Trunk cross sectional area (TCSA) = $r^2$ where 'r' is the radius of the tree. For recording observations on nut and kernel characters, 20 randomly selected nuts from each selected tree were taken. Nut length and width was measured with the help of digital vernier's caliper and expressed in mm. Nut weight and kernel weight were weighed on digital balance whereas kernel percentage was calculated as:

$$\text{Kernel (\%)} = \frac{\text{Kernel weight}}{\text{Nut weight}} \times 100$$

Shell thickness was measured at near centre of half shell with the help of digital vernier's caliper. The pooled data of two year were analyzed as per method suggested by Gomez and Gomez (1985) using randomized block design.

## Results and Discussion

In the present study, the experimental trees were selected among > 1200 hundred seedling trees grown in 14 villages of district Pulwama. Out of these trees, 482 were selected as promising types from the stand point of quality of nuts, yield, disease resistance etc., according to walnut descriptors. During the selection works it was noticed that thirty two superior trees have homogamous flowering characters. All the genotypes presented in Table 1 showed terminal bearing habit, however, nature of dichogamy was homogamous. Time of leaf bud burst extended from 28$^{th}$ March (HJ-46) to 9$^{th}$ April (MD-03 and KL-29). Duration of male flowering ranges from 8 days (MD-09) to 15 days (SI-05, PA-34, MD-38, KL-29 and TL-13). However, duration of female flowering ranges from 7 days (MD-09) to 16 days (KL-29). Out of all the studied selections evaluated, thirty two trees recorded less than 25 per cent dichogamy (Table 1) ranging between

0.00 per cent (HJ-46) to 25.00 (BT-07, NO-42, PA-29, RJ-02, BS-12 and TL-12). Earlier Kumar *et al*. (2005) and Kumar and Sharma (2013) also reported less than 25 per cent dichogamy in nine selections and in three cultivars for three respective years out of 19 studied cultivars, respectively. Out of thirty two genetically diverse walnut accessions Verma *et al*. (2009) reported 13 accessions of homogamous nature, while Ghasemi *et al*. (2012) observed two genotypes, out of seventy (MS 27 and MS 29) completely homogamous.

Overlapping of pollen shedding and stigma receptivity periods in the above thirty two selections extended from 6 (MD-09) to 13 (GP-32, KL-29) i.e. the number of days which actually coincided (Table 1). Figure 2 shows that synchronization of pollen shedding and stigma receptivity was maximum (13 days) in GP-32 and KL-29 which starts from 7th April and end on 19th April, however, in accession MD-09 the synchronization

**Table 1. Bearing and flowering behaviour of selected homogamous walnut selections**

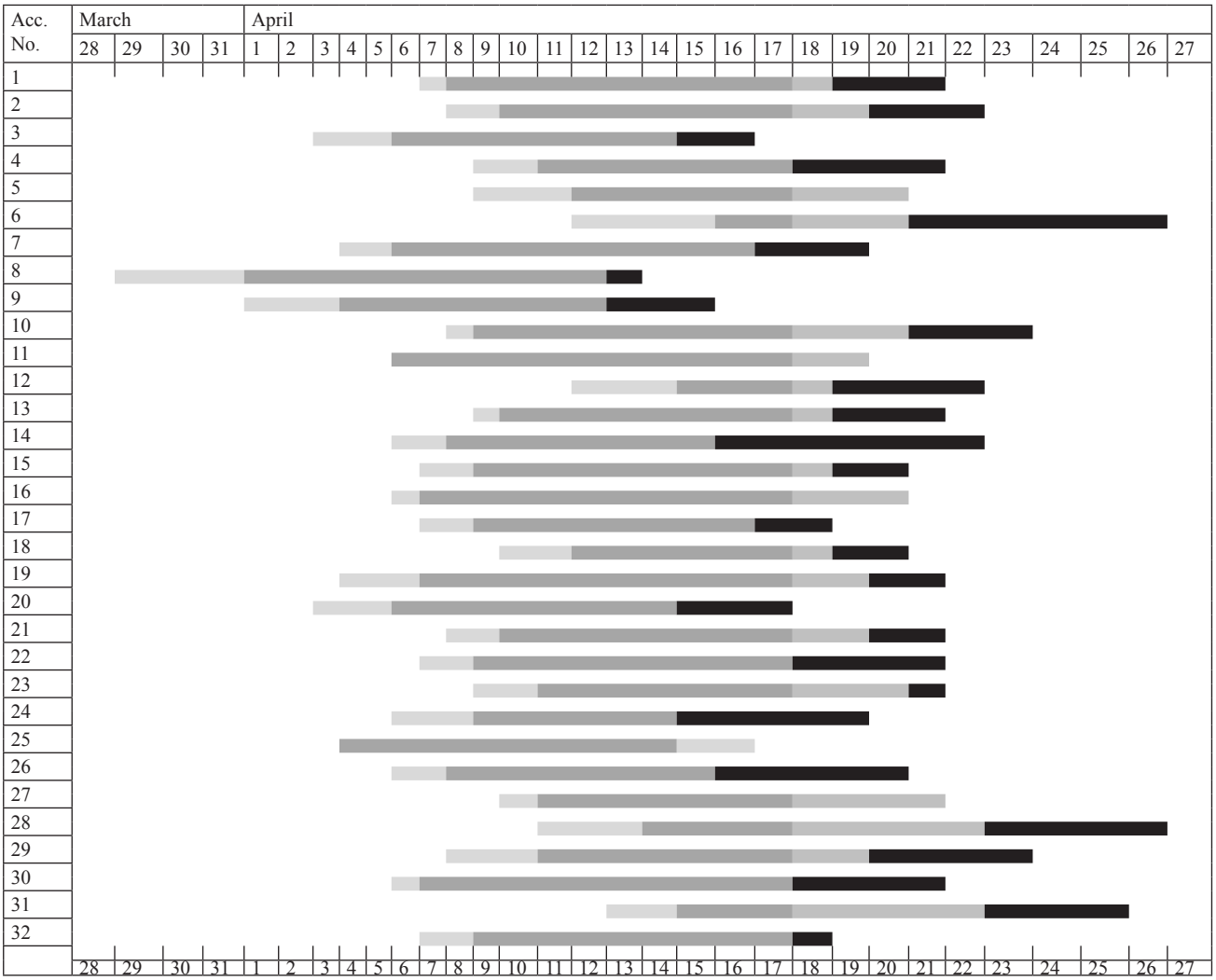
| Accession No. | Bearing habit | Date of leaf bud burst | Duration of male flowering (days) | Duration of female flowering (days) | No. of days synchronized | Degree of dichogamy | No. of catkins /bud | Catkin length (cm) | Nature of dichogamy |
|---|---|---|---|---|---|---|---|---|---|
| SI-05 | Terminal | 5th April | 15 | 12 | 11 | 8.33 | 4.36 | 9.64 | Homogamous |
| SI-19 | Terminal | 4th April | 13 | 12 | 10 | 16.67 | 3.85 | 9.90 | Homogamous |
| BT-07 | Terminal | 29th Mar | 11 | 12 | 9 | 25.00 | 4.14 | 10.08 | Homogamous |
| NO-35 | Terminal | 31st March | 11 | 9 | 7 | 22.22 | 4.10 | 7.16 | Homogamous |
| NO-42 | Terminal | 8th April | 9 | 12 | 9 | 25.00 | 5.44 | 7.65 | Homogamous |
| PA-12 | Terminal | 6th April | 11 | 9 | 7 | 22.22 | 5.18 | 7.52 | Homogamous |
| PA-17 | Terminal | 31st March | 14 | 13 | 11 | 15.38 | 3.40 | 8.10 | Homogamous |
| PA-18 | Terminal | 29th March | 13 | 15 | 12 | 20.00 | 3.85 | 7.32 | Homogamous |
| PA-29 | Terminal | 5th April | 12 | 12 | 9 | 25.00 | 4.80 | 8.44 | Homogamous |
| PA-34 | Terminal | 4th April | 15 | 13 | 12 | 7.69 | 5.80 | 7.50 | Homogamous |
| MD-03 | Terminal | 9th April | 12 | 14 | 12 | 14.28 | 4.32 | 7.00 | Homogamous |
| MD-09 | Terminal | 7th April | 8 | 7 | 6 | 14.28 | 5.39 | 8.82 | Homogamous |
| MD-15 | Terminal | 1st April | 12 | 10 | 9 | 10.00 | 5.60 | 9.36 | Homogamous |
| MD-38 | Terminal | 6th April | 15 | 10 | 8 | 20.00 | 4.98 | 10.34 | Homogamous |
| GP-19 | Terminal | 4th April | 12 | 12 | 10 | 16.67 | 6.04 | 11.16 | Homogamous |
| GP-32 | Terminal | 5th April | 13 | 15 | 13 | 13.33 | 3.20 | 7.25 | Homogamous |
| ML-01 | Terminal | 6th April | 10 | 10 | 8 | 20.00 | 6.84 | 9.15 | Homogamous |
| ML-26 | Terminal | 3rd April | 9 | 9 | 7 | 22.22 | 5.51 | 7.20 | Homogamous |
| KL-29 | Terminal | 9th April | 15 | 16 | 13 | 18.75 | 4.59 | 8.80 | Homogamous |
| RJ-02 | Terminal | 3rd April | 12 | 12 | 9 | 25.00 | 7.50 | 7.37 | Homogamous |
| RJ-24 | Terminal | 2nd April | 12 | 12 | 10 | 16.67 | 5.54 | 8.12 | Homogamous |
| RJ-38 | Terminal | 31st March | 13 | 11 | 9 | 18.18 | 7.28 | 9.49 | Homogamous |
| LP-03 | Terminal | 8th April | 11 | 12 | 10 | 16.67 | 6.54 | 10.72 | Homogamous |
| HJ-02 | Terminal | 6th April | 11 | 9 | 7 | 22.22 | 7.18 | 7.32 | Homogamous |
| HJ-46 | Terminal | 28th March | 11 | 11 | 11 | 0.00 | 7.12 | 8.79 | Homogamous |
| BS-05 | Terminal | 2nd April | 13 | 10 | 8 | 20.00 | 6.25 | 10.64 | Homogamous |
| BS-11 | Terminal | 8th April | 10 | 12 | 10 | 16.67 | 5.68 | 11.75 | Homogamous |
| BS-12 | Terminal | 5th April | 13 | 12 | 9 | 25.00 | 6.14 | 7.44 | Homogamous |
| TL-12 | Terminal | 31st March | 13 | 12 | 9 | 25.00 | 6.46 | 9.18 | Homogamous |
| TL-13 | Terminal | 2nd April | 15 | 12 | 11 | 8.33 | 6.06 | 10.89 | Homogamous |
| TL-15 | Terminal | 7th April | 11 | 10 | 8 | 20.00 | 5.62 | 8.17 | Homogamous |
| TL-28 | Terminal | 1st April | 10 | 11 | 10 | 9.09 | 6.52 | 10.39 | Homogamous |
| Mean | | | 12.03 | 11.50 | 9.50 | 17.50 | 5.48 | 8.84 | |
| SD | | | 1.87 | 1.93 | 1.81 | 6.23 | 1.71 | 1.38 | |
| CoV | | | 15.54 | 16.78 | 19.05 | 35.60 | 31.21 | 27.93 | |

**Table 2. Yield, nut and kernel characters of selected homogamous walnut selections**

| Accession No. | Nut yield (Kg/tree) | Trunk girth (cm) | TCSA (cm2) | Yield efficiency (kg/ cm2) | Nut weight (g) | Nut length (mm) | Nut width (mm) | Kernel weight (g) | Shell thickness (mm) | Kernel (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| SI-05 | 56 | 239 | 4543.06 | 0.0123 | 12.04 | 31.86 | 29.83 | 6.29 | 0.87 | 52.24 |
| SI-19 | 65 | 248 | 4891.24 | 0.0133 | 11.50 | 32.00 | 28.26 | 5.70 | 0.90 | 49.57 |
| BT-07 | 66 | 265 | 5586.32 | 0.0118 | 13.28 | 34.45 | 30.89 | 6.67 | 1.26 | 50.23 |
| NO-35 | 65 | 275 | 6015.63 | 0.0108 | 16.54 | 39.69 | 31.24 | 8.62 | 1.21 | 52.12 |
| NO-42 | 62 | 271 | 5840.91 | 0.0106 | 15.12 | 37.65 | 32.44 | 8.08 | 1.14 | 53.44 |
| PA-12 | 72 | 270 | 5797.64 | 0.0124 | 12.98 | 31.29 | 27.25 | 7.00 | 1.25 | 53.93 |
| PA-17 | 70 | 270 | 5797.64 | 0.0121 | 12.09 | 31.75 | 27.29 | 6.32 | 0.88 | 52.27 |
| PA-18 | 64 | 218 | 3779.92 | 0.0169 | 14.80 | 35.09 | 27.77 | 7.42 | 1.25 | 50.14 |
| PA-29 | 60 | 240 | 4581.38 | 0.0131 | 14.24 | 33.62 | 32.50 | 7.07 | 1.11 | 49.65 |
| PA-34 | 77 | 290 | 6690.83 | 0.0115 | 15.38 | 38.79 | 33.20 | 7.65 | 1.22 | 49.74 |
| MD-03 | 79 | 298 | 7064.23 | 0.0112 | 14.00 | 32.24 | 29.16 | 6.40 | 0.92 | 45.71 |
| MD-09 | 68 | 280 | 6237.64 | 0.0109 | 15.31 | 39.36 | 33.14 | 7.52 | 1.20 | 49.12 |
| MD-15 | 70 | 284 | 6415.30 | 0.0109 | 13.13 | 32.71 | 30.39 | 6.93 | 0.96 | 52.78 |
| MD-38 | 75 | 295 | 6921.91 | 0.0108 | 12.24 | 32.01 | 30.28 | 6.16 | 1.18 | 50.33 |
| GP-19 | 48 | 172 | 2352.65 | 0.0204 | 15.30 | 36.62 | 31.86 | 7.82 | 1.16 | 51.11 |
| GP-32 | 60 | 208 | 3441.27 | 0.0174 | 11.60 | 30.45 | 29.97 | 5.20 | 1.11 | 44.83 |
| ML-01 | 65 | 244 | 4736.26 | 0.0137 | 17.73 | 40.88 | 34.92 | 9.55 | 1.14 | 53.86 |
| ML-26 | 78 | 282 | 6324.75 | 0.0123 | 13.84 | 33.53 | 29.64 | 6.85 | 1.21 | 49.49 |
| KL-29 | 50 | 195 | 3024.18 | 0.0165 | 16.07 | 37.57 | 36.84 | 8.12 | 1.09 | 50.53 |
| RJ-02 | 45 | 192 | 2933.24 | 0.0153 | 13.24 | 32.71 | 30.39 | 6.53 | 1.20 | 49.32 |
| RJ-24 | 48 | 190 | 2872.11 | 0.0167 | 15.59 | 36.76 | 33.61 | 7.74 | 0.92 | 49.65 |
| RJ-38 | 65 | 215 | 3676.01 | 0.0177 | 14.50 | 34.27 | 32.14 | 7.64 | 1.30 | 52.69 |
| LP-03 | 62 | 204 | 3309.44 | 0.0187 | 11.84 | 31.70 | 26.12 | 6.41 | 0.92 | 54.14 |
| HJ-02 | 50 | 230 | 4207.75 | 0.0119 | 14.22 | 36.12 | 31.89 | 7.01 | 0.93 | 49.30 |
| HJ-46 | 72 | 268 | 5714.25 | 0.0126 | 12.10 | 31.18 | 28.41 | 5.60 | 0.99 | 46.28 |
| BS-05 | 65 | 270 | 5797.64 | 0.0112 | 15.16 | 38.09 | 32.52 | 7.92 | 1.15 | 52.24 |
| BS-11 | 66 | 262 | 5459.84 | 0.0121 | 12.28 | 31.93 | 30.16 | 6.92 | 1.11 | 56.35 |
| BS-12 | 72 | 285 | 6460.82 | 0.0111 | 14.28 | 34.39 | 31.34 | 7.13 | 1.26 | 49.93 |
| TL-12 | 70 | 277 | 6103.95 | 0.0115 | 10.23 | 29.26 | 26.71 | 5.73 | 1.34 | 56.01 |
| TL-13 | 62 | 232 | 4281.67 | 0.0145 | 14.45 | 35.21 | 32.50 | 7.66 | 1.14 | 53.01 |
| TL-15 | 58 | 212 | 3575.67 | 0.0165 | 13.56 | 33.72 | 29.92 | 6.72 | 1.29 | 49.56 |
| TL-28 | 64 | 226 | 4061.84 | 0.0158 | 13.58 | 33.95 | 29.25 | 6.90 | 1.12 | 50.81 |
| Mean | 64.03 | 247.09 | 4953.03 | 0.0136 | 13.82 | 34.40 | 30.68 | 7.04 | 1.12 | 50.95 |
| SD | 8.89 | 35.40 | 1354.29 | 0.003 | 1.67 | 3.06 | 3.06 | 2.54 | 0.92 | 2.63 |
| CoV | 13.88 | 14.33 | 27.34 | 22.09 | 12.08 | 8.93 | 9.93 | 36.08 | 82.40 | 5.16 |

was only for 6 days i.e. from 14$^{th}$ April to 19$^{th}$ April. In earlier reports, Lonnie *et al*. (1998) stated that the pollen shedding period coincides well with the period of pistillate flower receptivity. In their study chart of relationship of pollen shedding period and peak pistillate bloom period, it was observed that the overlapping period was more than 7 days. Sutyemez (2001) and Kumar *et al*. (2005) also reported overlapping of male and female flower between 6 to 11 days and 8 to 13 days in their respective studies. Due to this fact their self pollination occurs in a desired manner without necessity of another pollinators. With the mean values of 5.48 and 8.84, number of catkin per bud and catkin length ranges between 3.20 (GP-32) to 7.50 (RJ-02) and 7.16 cm (NO-35) to 11.75 cm (BS-11), respectively.

Data on various yield, nut and kernel characters of the selected homogamous selections are presented in Table 2. Nut yield varies from 45 kg (RJ-02) to 79 kg (MD-03) however, trunk girth and TCSA registered maximum (298 cm and 7064.23 cm$^2$) in MD-03 and minimum (172 cm and 2352.65) in GP-19. Yield efficiency in various accessions ranged from 0.0106 (NO-42) to 0.0204 kg/cm$^2$ (GP-19). The dimensions of in-shelled nuts representing selections were based on nut weight, nut length and




| S. No. | Accession No. | S. No. | Accession No. | S. No. | Accession No. | S.No. | Accession No. |
|---|---|---|---|---|---|---|---|
| 1 | SI-05 | 9 | PA-29 | 17 | ML-01 | 25 | HJ-46 |
| 2 | SI-19 | 10 | PA-34 | 18 | ML-26 | 26 | BS-05 |
| 3 | BT-07 | 11 | MD-03 | 19 | KL-29 | 27 | BS-11 |
| 4 | NO-35 | 12 | MD-09 | 20 | RJ-02 | 28 | BS-12 |
| 5 | NO-42 | 13 | MD-15 | 21 | RJ-24 | 29 | TL-12 |
| 6 | PA-12 | 14 | MD-38 | 22 | RJ-38 | 30 | TL-13 |
| 7 | PA-17 | 15 | GP-19 | 23 | LP-03 | 31 | TL-15 |
| 8 | PA-18 | 16 | GP-32 | 24 | HJ-02 | 32 | TL-28 |

Duration of pollen shedding
Overlapping duration of pollen shedding & stigma receptivity
Duration of stigma receptivity

**Fig. 2. Duration of pollen shedding and stigma receptivity in different walnut selections**

nut width. The average in-shell nut weight varied from 10.23 to 17.73 g being lowest in the accessions no. TL-12 and highest in the accessions no. ML-01. In-shell nut weight can serve as good parameter for selection provided coupled with high shelling percentage and creamish kernel colour as reported by Gautam (2000). Goughen and Weichang (1990) reported nut weight of 5.8 g as the smallest and 25-27 g as largest size in

China. Minimum standard for shell nut weight is above 12 g and all the accessions (except three) in the present study confirmed these criteria. Accession ML-01 scored maximum (40.88 mm) nut length however, minimum (29.26 mm) was of TL-12. Maximum (36.84 mm) and minimum (26.12 mm) nut width was registered in the accession KL-29 and LP-03, respectively. Most of the accessions in the present study confirmed the standard diameter laid out by Serr and Ford (1956). Pandey *et al*. (2004) and Verma *et al*. (2009) also reported similar reports with respect to various nut characters.

Kernel weight ranges from 5.20 (GP-32) to 9.55 g (ML-01); however, minimum and maximum shell thickness was registered in accession SI-05 (0.87 mm) and TL-12 (1.34 mm), respectively. Kernel percentage in various accessions ranged from 44.83 to 56.35 per cent. The highest kernel percentage (56.35 %) was obtained in accessions BS-11 followed by TL-12 (56.01 %) and LP-03 (54.14 %). Serr and Ford (1956) suggested that any accessions should have above 50 per cent shelling percentage have a reasonable goal. In the present study out of homogamous selection, nineteen selections achieved the standard along with good in-shell nut weight and kernel characteristics. Earlier Bhat *et al*. (1992) reported highest percentage ranging from 54.2 to 63.2 per cent in two indigenous selected cultivars. The extent of variations in observed nut and kernel characters is largely due to their seedling origin and varying age and is in accordance with previous studies (Sharma and Sharma, 2000; Attar, 2001; Pandey *et al*., 2004) and even in homogamous types reported (Rouskas and Zakynthinos, 2001; Sutyemez, 2001; Kumar, 2000; Kumar, *et al*., 2005). Nearly similar findings have been obtained in the present study, only thirty two selections were found to be homogamous. Homogamous types are however more productive than either protandrous or protogynous cultivars (Sutyemez, 2001). Likewise the selections made in the present study having sufficient overlapping pollen shedding and stigma receptivity yielded higher as compared to most of the remaining selections screened in the present study.

In Himalayas, most walnuts are protandrous, the inclusion of homogamous types in a walnut orchard would ensure optimum pollination to obtain higher fruit set and nut yield. The identification of homogamous walnut types indicates the possibility of developing homogamous varieties to obtain higher yield in walnut and these selections have been conserved *ex situ* in a field repository for future use in germplasm exchange, genetic improvement and commercial exploitation as direct cultivars.

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# Characterization and Evaluation of Ridge Gourd [*Luffa acutangula* (Roxb.) L.] Germplasm

**B Varalakshmi*, Y Suchitha and KS Sanna Manjunath**
*Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru-560089, Karnataka, India*

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Fifty one ridge gourd germplasm were evaluated for yield and qualitative traits during 2011-14. There were significant differences among the germplasm for all the 11 quantitative and nine out of 22 qualitative parameters studied. Regarding plant growth habit, 34 had long vines, 16 had medium long vines and only one germplasm, IC92618 had short vines. Fifteen germplasm lines recorded dark green fruit skin colour, 33 had green coloured fruits and only three germplasm had light green coloured fruits, hence this variability can be exploited for developing green and dark green coloured varieties which are very much preferred in different markets. With respect to fruit taste, 29 lines had normal fruit taste, 18 lines were sweet and four lines, viz., IC92625, IC92685, IIHR-17 and IIHR-51 had bitter fruits. Among the germplasm evaluated, IC20404 (5.2 and 41.3) showed earliness in terms of node number as well as days for appearance of first female flower followed by IC23259 (6.0 and 41.2). Arka Sumeet and Co-1 recorded highest fruit length and fruit weight which are the important yield contributing fruit parameters. IIHR-21 recorded the highest mean value for fruit yield per vine (2.8 kg) followed by IIHR-6 (2.6 kg). This variability present among the germplasm evaluated for yield and quality parameters can be effectively utilized for the improvement of ridge gourd, with IIHR-6 and IIHR-21, the most promising germplasm as common parents and 'Arka Sumeet' and 'CO-1' as partners to develop character specific hybrids with maximum yield potential.

**Key Words: Characterization, Evaluation, *Luffa acutangula* (Roxb.) L, Ridge gourd, Yield**

## Introduction

Ridge gourd [*Luffa acutangula* (Roxb.) L.] is an important cucurbitaceous summer vegetable of South East Asia and few African countries. The young tender fruits of the non-bitter types are eaten fresh like cucumbers, cooked as a vegetable or used in soups. Fruits of *Luffa* are very nutritious and good source of vitamin A, calcium, phosphorus, ascorbic acid and iron. Despite its economic importance and presence of considerable variability, development of varieties/hybrids in ridge gourd is rather limited. Identification of superior genotypes among the existing germplasm becomes imperative for promoting yield and yield related traits. Hence, collection and evaluation of germplasm is a pre-requisite for their utilization. Detailed evaluation of germplasm collected over the years determines the potential of a germplasm in specific crop improvement programme. Therefore, a trial for characterization and evaluation of presently available ridge gourd germplasm at ICAR-Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru was carried out in order to identify the potential genotypes for different horticultural characters.

## Material and Methods

The experiments were carried out at the Vegetable Farm, ICAR-IIHR during rabi-summer seasons of 2011-12, 2012-13 and 2013-14. The experiments were laid out in Randomized Block Design with 51 germplasm lines in two replications in all the three years. Ten plants per replication were raised. Two weeks old seedlings were planted at 150 × 50 cm spacing on single trelly system. The recommended agronomical practices were adopted to raise the crop. Observations were recorded on five randomly selected plants from each replication on 22 morphological traits pertaining to plant, leaf and fruit as per the NBPGR Minimal Descriptor (Srivastava *et al.*, 2001) and on 11 quantitative traits such as node number for first female flower appearance, days taken for first female flower appearance, vine length (m), branch number, peduncle length (cm), fruit length (cm), fruit girth (cm), fruit weight (g), fruit number/vine, fruit yield/vine (kg) and fruit yield/ha (t). The pooled data of three years were analysed as suggested by Panse and Sukhatme (1984) for analysis of variance.

**Author for Correspondence: E-mail: bvl@iihr.ernet.in*

## Results and Discussion

### *Qualitative Traits of Ridge Gourd Germplasm*

Qualitative characteristics of 51 germplasm of ridge gourd are presented in Table 1. Wide variability was observed for nine out of 22 qualitative traits studied among the ridge gourd germplasm such as early plant vigour, plant growth habit, leaf size, leaf pubescence nature, fruit skin colour, fruit skin luster, fruit ridge (rib) shape, seediness and fruit taste. Good early plant vigour helps in better establishment and development of good frame work of the plant which results in more flowers, fruits and ultimately high yield. In the present study, 29 germplasm had very good early plant vigour, 17 had good vigour where as only 5 germplasm lines were poor in early plant vigour (Table 1). Regarding plant growth habit, 34 had long vines, 16 had medium long vines and only one germplasm, IC92618 had short vines. Leaf size was large in 30 germplasm, medium in 20 lines and small in only one germplasm i.e., IC92618. Hard leaf pubescence was observed in 30 germplasm, where as it was intermediate in 21 lines. The fruit skin colour was light-green, green and dark-green (Table 1). Fifteen germplasm lines recorded dark-green fruit skin colour, 33 had green colour fruits and only three germplasm had light-green colour fruits. In general green and dark-green coloured varieties are preferred in the market; hence the variability for fruit skin colour present in this collection can be exploited for developing such varieties in ridge gourd. Fruit skin luster is important in ridge gourd and matt type fruits are preferred in the market than the glossy types. Sufficient variability for this trait was present among the germplasm and about 23 germplasm recorded matt type, 21 had intermediate and only seven were with glossy fruit skin lustre.

Ridges on fruit surface are significant as the deep grooved fruits will have the strength to withstand

**Table 1. Frequency distribution (%) of morphological traits of ridge gourd germplasm**

| S. No. | Morphological trait | Stage of observation recorded | Class | Germplasm (no.) | Frequency |
|---|---|---|---|---|---|
| 1 | Early plant vigour | After 30 days of sowing | Poor | 5 | 9.8 |
| | | | Good | 17 | 33.3 |
| | | | Very good | 29 | 56.9 |
| 2 | Plant growth habit | At fully grown plant | Short viny | 1 | 2.0 |
| | | | Medium viny | 16 | 31.4 |
| | | | Long viny | 34 | 66.7 |
| 3 | Leaf size | At full foliage stage | Small | 1 | 2.0 |
| | | | Medium | 30 | 58.8 |
| | | | Large | 20 | 39.2 |
| 4 | Leaf pubescence | At full foliage stage | Soft | 0 | 0.0 |
| | | | Intermediate | 21 | 41.2 |
| | | | Hard | 30 | 58.8 |
| 5 | Fruit skin colour | At marketable stage | Light green | 3 | 5.9 |
| | | | Green | 33 | 64.7 |
| | | | Dark green | 15 | 29.4 |
| 6 | Fruit skin luster | At marketable stage | Matt | 23 | 45.1 |
| | | | Intermediate | 21 | 41.2 |
| | | | Glossy | 7 | 13.7 |
| 7 | Fruit ridge (rib) shape | In cross-section at marketable stage | Superficial | 9 | 17.6 |
| | | | Rounded/grooved | 0 | 0.0 |
| | | | Intermediate | 17 | 33.3 |
| | | | Deep grooved | 25 | 49.0 |
| 8 | Seediness | At marketable stage | Low | 20 | 39.2 |
| | | | Medium | 19 | 37.3 |
| | | | High | 12 | 23.5 |
| 9 | Fruit taste | At marketable stage | Normal | 29 | 56.9 |
| | | | Sweet | 18 | 35.3 |
| | | | Bitter | 4 | 7.8 |

long distance transport on one hand and on the other hand, superficial ridge shaped fruits are preferred by the consumers with minimum wastage while peeling the fruits. In the present investigation, majority of the germplasm (25) were deep grooved, followed by intermediate (17) and nine germplasm had superficial ridge shape. Low seediness is preferred in any gourd vegetable and 20 out of 51 germplasm had this trait, 19 had medium seediness and 12 germplasm had high seediness. Similar variability for most of the qualitative traits was observed among the 55 germplasm lines of ridge gourd evaluated by Mahajan *et al.* (2005). Fruit taste is a very important qualitative trait, as cucurbits are known for the presence of the bitter principle (cucurbitacin). This bitterness poses a serious problem by contaminating other sweet lines also through their pollen (metaxenia) thus, making them also bitter. In the present study, 29 lines had normal fruit taste, 18 lines were sweet and four lines, viz. IIHR-17, IC92625, IC92685 and IIHR-51 had bitter fruits and thus these four lines are unfit for commercial utilisation.

### *Quantitative Traits of Ridge Gourd Germplasm*

The analysis of variance revealed significant differences among the 51 germplasm lines in ridge gourd for all the 11 traits studied (Table 2). The results of 47 germplasm lines are discussed excluding the four bitter fruited germplasm. Wide range of variation was observed for most of the characters like days taken for first female flower appearance (37.0-66.4), fruit length (10.5-41.3 cm), fruit number/plant (4.7-33.8), fruit weight (79.8-300.8 g) and fruit yield/ha (8.5-37.9 t). Presence of such high variability for these parameters will form the basis for effective selection of superior lines in ridge gourd. Such wide variability for many quantitative traits was reported earlier by Varalakshmi *et al.* (1995), Choudhary and Suresh Kumar (2011) and Rabbani *et al.* (2012) in ridge gourd. Earliness is a desirable trait and among the germplasm evaluated, IC20404 (5.2 and 41.3) showed earliness in terms of node number as well as days for appearance of first female flower which was followed by IC23259 (6.0 and 41.2). Similar results were observed by Krishna Prasad and Singh (1989) during the evaluation of ridge gourd germplasm.

Significant differences were observed for plant characters among the germplasm lines with the germplasm IIHR-6 and IIHR-14 (5.6 m) recording the longest vines followed by IIHR-2 (5.5 m). Varghese (1991) also found variability in vine length among 48 snake gourd genotypes. Maximum branch number was recorded by IIHR-7 (13) followed by IIHR-2 (11) which can have more flowers and fruit set. Significant differences were observed among the germplasm lines for all the fruit traits. Arka Sumeet had longest fruits (41.3cm) followed by Rekha (40.9 cm) and Co-1(37.1 cm). Maximum fruit girth (16.9 cm) was recorded by IC308561 followed by IC344652 (15.5 cm). However, some times, minimum fruit girth at marketable maturity is a preferred trait and in this direction, IIHR-14 (8.1cm) had very thin fruits. Similar variation in fruit characters was observed in bottle gourd by Suganthi (2008). Weight of a single fruit determines the overall yield performance of a vine and among the germplasm studied, Arka Sumeet (300.8 g) recorded highest fruit weight followed by Mallika (267.2 g) and Co-1 (260.8 g). Similar variability for fruit weight was reported by Alli Rani and Jansirani (2014) in ridge gourd.

Number of fruits per vine is an important character which directly contributes to higher yield and significant difference was observed for fruit number per vine among the germplasm studied. Based on the mean performance, the genotype IC110893, which is an andro-monoecious line, had higher number of fruits per vine (33.8) followed by IC308562 (24.1). Similar findings for differential fruit number by the germplasm were reported by Suganthi (2008) and Hitesh *et al.* (2012) in bottle gourd and Coccinia respectively. In the present study, among the 51 germplasm, IIHR-21 and two hybrids, NS-03 and Mallika recorded the highest mean value for fruit yield per vine (2.8 kg) followed by IIHR-6 (2.6 kg). Similar findings for variability in fruit yield per vine were reported by Hitesh *et al.* (2012) in ivy gourd and by Alli Rani and Jansirani (2014) in ridge gourd.

Selection of genotypes with the highest fruit yield is the primary objective in any crop improvement programme. Among 51 germplasm evaluated, IIHR-21 recorded the highest fruit yield/ha (37.9 t) followed by IIHR-6 with mean fruit yield of 34.8 t/ha. These germplasm can be used as one of the parents for developing hybrids with high yield potential in ridge gourd. This study clearly indicated that varieties/hybrids could be developed with earliness, higher fruit length and more fruits per vine with higher yield potential in ridge gourd.

**Table 2. Performance of ridge gourd germplasm with respect to 11 quantitative traits during 2011-14**

| S.No. | Germplasm | NFF | DFF | Vine length (m) | Branch number | Peduncle length (cm) | Fruit length (cm) | Fruit girth (cm) | Fruit weight (g) | Fruit number/ vine | Fruit yield/ vine (kg) | Fruit yield/ ha (t) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | IC92700 | 8.2 | 47.5 | 4.3 | 5.4 | 7.0 | 22.3 | 10.0 | 142.7 | 22.9 | 1.7 | 23.2 |
| 2 | IC20404 | 5.3 | 41.2 | 3.8 | 5.0 | 5.4 | 14.1 | 10.6 | 101.1 | 18.0 | 1.0 | 14.1 |
| 3 | IC92624 | 7.9 | 49.9 | 2.6 | 2.9 | 7.4 | 20.0 | 10.0 | 120.4 | 18.5 | 1.5 | 18.6 |
| 4 | IC105554 | 8.8 | 44.1 | 3.6 | 5.9 | 6.9 | 15.3 | 11.2 | 120.5 | 19.0 | 2.0 | 28.4 |
| 5 | IC23255 | 8.4 | 42.3 | 2.7 | 4.8 | 7.3 | 20.4 | 10.6 | 141.7 | 8.9 | 1.3 | 17.0 |
| 6 | IC339224 | 7.7 | 44.8 | 3.4 | 4.2 | 6.4 | 18.1 | 10.0 | 151.8 | 12.9 | 1.7 | 22.0 |
| 7 | IC23259 | 6.0 | 41.2 | 3.5 | 5.4 | 7.3 | 17.1 | 10.6 | 123.7 | 15.6 | 1.5 | 21.8 |
| 8 | IC92637 | 7.7 | 39.2 | 3.4 | 5.8 | 7.1 | 18.0 | 10.4 | 130.1 | 21.6 | 1.7 | 26.9 |
| 9 | IC92689 | 6.2 | 46.0 | 3.0 | 4.2 | 6.5 | 18.4 | 10.7 | 153.1 | 7.8 | 0.6 | 8.6 |
| 10 | IC92618 | 7.1 | 42.9 | 2.8 | 3.9 | 6.4 | 16.6 | 11.4 | 112.2 | 16.7 | 1.9 | 23.7 |
| 11 | IC93393 | 13.9 | 48.7 | 2.9 | 3.9 | 9.3 | 21.9 | 11.9 | 163.2 | 9.9 | 1.7 | 20.9 |
| 12 | IC392334 | 7.4 | 47.9 | 3.6 | 4.8 | 8.0 | 16.1 | 10.8 | 143.9 | 16.7 | 1.8 | 25.1 |
| 13 | IC308562 | 6.9 | 44.8 | 3.2 | 4.9 | 6.2 | 13.2 | 9.7 | 100.1 | 24.1 | 1.8 | 26.2 |
| 14 | IC385911 | 9.2 | 45.2 | 3.8 | 9.0 | 8.7 | 24.4 | 10.8 | 175.3 | 15.4 | 2.3 | 31.5 |
| 15 | IC385912 | 9.1 | 45.5 | 3.5 | 4.8 | 7.8 | 12.2 | 12.0 | 118.8 | 18.8 | 1.8 | 23.4 |
| 16 | IC92622 | 7.0 | 37.0 | 3.5 | 4.5 | 7.2 | 15.8 | 15.0 | 117.9 | 12.4 | 2.5 | 19.6 |
| 17 | IC105579 | 7.3 | 48.1 | 3.6 | 6.4 | 7.6 | 18.4 | 14.3 | 151.7 | 15.9 | 1.7 | 23.6 |
| 18 | IC110893 | 10.8 | 40.9 | 3.1 | 3.3 | 4.9 | 10.5 | 12.9 | 80.1 | 33.8 | 1.8 | 23.9 |
| 19 | IC146606 | 8.7 | 46.6 | 3.0 | 13.3 | 5.7 | 16.7 | 14.2 | 116.4 | 14.6 | 1.3 | 19.9 |
| 20 | IC201145 | 6.8 | 46.8 | 3.1 | 8.4 | 7.8 | 17.2 | 14.6 | 149.5 | 14.4 | 1.6 | 25.4 |
| 21 | IC308561 | 7.5 | 41.2 | 2.2 | 3.0 | 5.8 | 11.4 | 16.9 | 100.6 | 18.1 | 1.3 | 16.4 |
| 22 | IC344652 | 8.1 | 49.5 | 3.8 | 7.9 | 8.8 | 22.0 | 15.5 | 168.7 | 9.8 | 1.6 | 20.3 |
| 23 | IC146589 | 8.3 | 49.4 | 3.5 | 6.0 | 7.1 | 16.1 | 13.0 | 114.2 | 17.5 | 1.8 | 23.7 |
| 24 | IC369441 | 8.7 | 46.7 | 2.9 | 4.2 | 7.0 | 13.4 | 12.7 | 100.2 | 21.3 | 1.6 | 21.7 |
| 25 | IC395846 | 9.8 | 56.0 | 2.8 | 6.5 | 6.6 | 13.0 | 13.5 | 131.1 | 12.3 | 1.5 | 20.0 |
| 26 | IIHR-1 | 9.9 | 47.8 | 4.2 | 9.3 | 7.4 | 23.6 | 10.5 | 185.7 | 16.5 | 2.2 | 27.0 |
| 27 | IIHR-2 | 10.0 | 46.4 | 5.5 | 11.0 | 10.7 | 32.2 | 10.7 | 235.6 | 14.3 | 1.9 | 25.6 |
| 28 | IIHR-6 | 11.5 | 48.8 | 5.6 | 9.4 | 10.8 | 31.9 | 10.1 | 228.7 | 11.7 | 2.6 | 34.8 |
| 29 | IIHR-7 | 17.8 | 53.7 | 5.2 | 13.0 | 8.3 | 23.7 | 10.9 | 214.3 | 5.1 | 0.9 | 12.1 |
| 30 | IIHR-10 | 10.1 | 49.4 | 3.8 | 9.8 | 7.6 | 25.7 | 10.2 | 181.9 | 11.3 | 1.7 | 21.7 |
| 31 | IIHR-12 | 10.1 | 46.6 | 3.7 | 6.0 | 7.9 | 26.6 | 10.8 | 188.9 | 9.3 | 1.8 | 23.1 |
| 32 | IIHR-13 | 10.7 | 52.8 | 3.3 | 5.0 | 9.8 | 25.2 | 9.7 | 189.3 | 12.6 | 2.0 | 29.0 |
| 33 | IIHR-14 | 15.3 | 59.1 | 5.6 | 6.0 | 7.8 | 22.1 | 8.1 | 214.8 | 7.3 | 1.2 | 15.7 |
| 34 | IIHR-15 | 11.4 | 49.7 | 3.1 | 7.1 | 8.1 | 27.7 | 10.7 | 174.1 | 9.3 | 1.7 | 23.3 |
| 35 | IIHR-16 | 9.6 | 49.3 | 3.3 | 7.2 | 8.3 | 25.8 | 10.4 | 172.1 | 13.3 | 1.8 | 25.2 |
| 36 | IIHR-21 | 8.6 | 48.7 | 4.4 | 6.4 | 10.3 | 28.8 | 10.6 | 219.4 | 14.1 | 2.8 | 37.9 |
| 37 | IIHR-22 | 8.7 | 50.6 | 3.9 | 11.4 | 8.6 | 26.3 | 10.0 | 210.3 | 10.8 | 2.1 | 28.2 |
| 38 | IIHR-53 | 9.5 | 46.0 | 4.5 | 9.9 | 10.3 | 33.6 | 14.6 | 244.4 | 8.4 | 2.0 | 26.4 |
| 39 | Pusa Nasdar | 12.6 | 51.1 | 5.4 | 10.5 | 10.8 | 29.5 | 10.6 | 224.4 | 6.3 | 1.4 | 19.8 |
| 40 | Arka Sumeet | 15.6 | 55.2 | 5.0 | 11.3 | 9.6 | 41.3 | 11.0 | 300.8 | 5.7 | 1.5 | 20.6 |
| 41 | Arka Sujat | 14.9 | 54.7 | 4.4 | 9.7 | 9.5 | 28.5 | 10.9 | 234.6 | 7.7 | 1.5 | 19.6 |
| 42 | CO-1 | 12.4 | 60.6 | 5.0 | 10.6 | 12.7 | 37.1 | 15.0 | 260.8 | 4.7 | 1.2 | 15.3 |
| 43 | Rekha | 12.6 | 54.0 | 4.5 | 6.9 | 12.2 | 40.9 | 10.3 | 241.5 | 9.7 | 2.6 | 31.7 |
| 44 | Mallika | 8.5 | 41.8 | 5.0 | 6.2 | 11.7 | 33.5 | 11.2 | 267.2 | 12.4 | 2.8 | 36.6 |
| 45 | NS-3 | 9.5 | 42.3 | 4.3 | 6.4 | 11.4 | 32.7 | 11.7 | 258.9 | 13.4 | 2.8 | 37.0 |
| 46 | Naga | 9.5 | 48.3 | 5.0 | 10.8 | 8.1 | 12.4 | 13.4 | 102.8 | 18.1 | 2.1 | 27.1 |
| 47 | Malav-11 | 12.2 | 44.5 | 4.1 | 9.3 | 7.3 | 24.6 | 13.9 | 174.5 | 8.7 | 1.4 | 17.6 |
| 48 | IIHR-17 | 20.0 | 66.4 | 6.5 | 8.9 | 8.9 | 25.5 | 9.9 | 237.5 | 5.3 | 1.3 | 14.4 |
| 49 | IC-92625 | 8.3 | 49.0 | 3.4 | 4.2 | 7.6 | 15.2 | 15.1 | 154.8 | 10.0 | 1.5 | 17.9 |
| 50 | IC-92685 | 6.4 | 42.2 | 2.9 | 3.0 | 5.5 | 13.8 | 13.1 | 79.8 | 17.7 | 1.5 | 19.4 |
| 51 | IIHR-51 | 10.3 | 38.7 | 5.9 | 5.9 | 11.1 | 36.4 | 13.9 | 234.1 | 11.7 | 2.8 | 37.1 |
| | Mean | 9.8 | 47.7 | 3.9 | 6.9 | 8.2 | 22.5 | 11.8 | 169.8 | 13.6 | 1.8 | 23.3 |
| | Sig. | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** | ** |
| | CD at 0.01 | 2.0 | 6.1 | 0.9 | 1.5 | 1.7 | 4.6 | 2.8 | 37.5 | 4.3 | 0.5 | 6.1 |
| | CV % | 17.6 | 11.2 | 20.0 | 19.0 | 18.3 | 18.1 | 20.9 | 19.4 | 28.2 | 22.8 | 22.9 |

** Significant at P=0.01; NFF- Node number for first female flower appearance; DFF- Days taken for first female flower appearance

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# Principal Component Analysis of Growth and Biomass Characteristics for Different Progenies of *Ulmus villosa* Brandis

**Sapna Thakur* and IK Thakur**
*Department of Tree Improvement and Genetic Resources, College of Forestry, Dr YS Parmar University of Horticulture and Forestry, Nauni-Solan-173230, Himachal Pradesh, India*

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The present study was carried out in order to find out the most important character contributing towards genetic variability in 30 *Ulmus villosa* progenies on the basis of principal component analysis. Principal Component Analysis (PCA) was carried out taking 10 important parameters, proved useful in extracting the most important factors. Three principal components contributed 84.62% of total variance. First principal component contributed 40.97% of total variation whereas the second component accounted for 24.93% variation and the third explains 18.72 % of variation. In the first PCA high loadings for traits such as shoot fresh weight (0.853), shoot dry weight (0.843), collar diameter (0.764) and plant height (0.736) represented those which are important for selection and further improvement of the species. The study revealed that maximum weightage should be given to fresh shoot weight due to its maximum variable loading for the initial selection of progenies for the biomass improvement of the species.

**Key Words: Biomass, Growth, PCA, Progenies, *Ulmus villosa***

## Introduction

The elms (*Ulmus* L.) are represented by approximately 35 species distributed throughout the temperate regions of the Northern Hemisphere and into the subtropics of Central America and Southeast Asia, including six species in eastern North America (Pooler and Townsend, 2005). There are five species of *Ulmus* found in India, of which four species namely *U. wallichiana*, *U. villosa*, *U. pumila* and *U. chumlia* are from North Western Himalaya and *U. lanceifolia* from North-Eastern regions of the country. Himalayan elms are the source of best fodder and quality timber. *U. wallichiana* is lopped for fodder which causes the depletion of regeneration. It is already categorized as vulnerable species in Red Data Book (www.iucnredlist.org). *Ulmus villosa* Brandis, commonly known as marinoo in India, is a small to medium sized deciduous tree belonging to family Ulmaceae (Melville and Heybroek, 1971). It is one of the more distinctive Asiatic elms and a species capable of remarkable longevity (Singh, 1991). It grows up to 20-30 m in height at elevations from 1200 m to 2500 m with a scattered distribution in the north western Himalayas. It finds greater favor on account of its multiplicity of uses and fast growth habit. It is a multipurpose agroforestry tree species producing fodder, fuel and timber. Inspite of its immense popularity and multiplicity of its uses, less attention has been paid on the improvement of this species (Melville and Heybroek, 1971). It is considered one of the most important agro-forestry trees in the Kashmir region. It also has a great potential outside its natural range for use on degraded land (Singh 1982; Bhardwaj and Mishra 2005). It is moderately susceptible to Dutch Elm Disease (DED) (Santamour 1979) and has been introduced in Europe and North America as an ornamental tree and for breeding purposes. DED is caused by certain fungi (*Ophiostoma* spp) and is one of the most serious diseases known to trees that has ravaged elm populations all over Europe. This poses a challenge for future conservation of *elm*, which in turn necessitates more knowledge about the distribution of variation in adaptive traits in the species.

Principal component analysis is a multivariate statistical technique which helps to reduce the data with large number of correlated variable into a substantially smaller set of new variables through linear combination of variables that account most of the variation present in the original variables. Since the aim of principal component analysis is to replace the original set of variables with few variables as possible, naturally in doing so some information contained in the original variables has to be sacrificed. But principal component has an advantage that this lost information is kept to minimum. Kaiser (1958)

**Author for Correspondence: Email- sapnakullu_thakur@rediffmail.com*

suggested the dropping of those principal components of the correlation matrix with eigen value less than one. He argued that the components with variance less than one contain less information. Hence keeping these points in view the present study was carried out in order to find out the most important character contributing towards genetic variability in marinoo progeny on the basis of principal component analysis.

## Materials and Methods

Well matured seeds were collected in the month of April, 2011 from five mother trees (15-25cm DBH) each at six sites (Table 1). The progenies were then raised under nursery conditions in the experimental field. The experiment was conducted at the main campus of Dr. YS Parmar University of Horticulture and Forestry at Majhgaon experimental area. The area is situated at 30˚50' N latitude and 76˚11 E longitude at an elevation of 1100 m above mean sea level on north eastern aspect. On an average the area receives an annual rainfall of 1150 mm most of which is concentrated during monsoon rains.

The observations on morphometric traits of progenies *viz*; plant height, collar diameter, number of branches , number of leaves, petiole length, root length, leaf area, shoot fresh weight, shoot dry weight, root fresh weight and root dry weight were recorded by selecting five plants randomly in each treatment of replication and then taking the average value for each character (Table 2). The data so obtained were subjected to the principal component analysis (PCA) as per the Kaiser (1958). For principal component analysis of the data SPSS software, version 10.0 was used.

## Results and Discussion

The range of mean values with respect to these characters among different progenies is given in Table 2.

Since it was difficult to conceive 10 dimensions (number of characters on which measurements was recorded) therefore, principal component analysis was employed for data reduction. The factor pattern and summary of principal component analysis on the gathered data has been revealed in Table 3. It was observed that three out of ten components had eigen value greater than unity and as such these components are retained in further analysis. These components explained a sufficient amount of variation (84.62%) of the total variation.

**Table 1. List of different seed sources**

| Abb. | Site/ Seed Source | Location |
|---|---|---|
| $S_1$ | Jadh (800 m) | Mandi (H.P) |
| $S_2$ | Jugahan (800 m) | Mandi (H.P) |
| $S_3$ | Jhidi (1,089 m) | Mandi (H.P) |
| $S_4$ | Jagoti (1,824 m) | Shimla (H.P) |
| $S_5$ | Katouch (1,900 m) | Shimla (H.P) |
| $S_6$ | Andhra(2,200 m) | Shimla (H.P) |

Table 3 revealed that the first principal component ($\lambda_1$= 4.29) explains 40.97 percent of the total variability in the data set. The variable loadings for first principal component are highest for four characters, indicating that maximum weight was attached to shoot fresh weight (0.853) followed by shoot dry weight (0.843), collar diameter (0.764) and height (0.763), respectively. The second principal component ($\lambda_2$= 2.61) explains 24.93 percent of total variation. The variable loading for second component was observed highest in petiole length (0.692) followed by leaf area (0.684) and number of leaves (0.594), respectively. The third principal component ($\lambda_3$= 1.96) explains 18.72 per cent of total variation. Maximum loading was observed in root fresh weight (0.806) followed by root dry weight (0.780) and root length (0.745). Principal component analysis provides an insight into a complex relationship between different characters in a biological system. It reflects the importance of the largest contributor to the total variation. In the current study the three components accounted for 84.62 percent of whole variability (Table 3). Tunctaner (2002) reported five principal components on the basis of 14 traits studied in willow clones. Similar types of findings were reported by Singh and Huse (2004). Singh (2006) recorded cumulative variability of 56 % from three principal components in *Populus deltoides* clones. Isik and Toplu (2004) reported three PCA which accounts 90% of the overall variation in *Populus nigra* in which first component includes height, diameter and apical dominance. Gupta (2006) in *Salix* clones also reported maximum variable loading for the shoot fresh weight and recommended the same for the selection along with other components.

The results of the present study indicated that the maximum weightage should be given to shoot fresh weight (having maximum variable loading) for the

**Table 2. Mean values for growth and morphometric traits in 30 progenies of *Ulmus villosa***

| Site/ tree | Diameter (mm) | Plant height (cm) | Leaf area ($cm^2$) | No. of leaves | Petiole length (mm) | Root length (cm) | Fresh shoot weight (g) | Dry shoot weight (g) | Fresh root weight (g) | Dry root weight (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| $S_1T_1$ | 4.05 | 53.67 | 8.14 | 127.67 | 3.00 | 17.31 | 9.82 | 5.76 | 3.36 | 1.66 |
| $T_2$ | 4.05 | 58.63 | 7.20 | 109.00 | 3.80 | 29.83 | 21.67 | 12.74 | 8.74 | 4.39 |
| $T_3$ | 3.62 | 49.31 | 7.78 | 92.33 | 2.70 | 18.28 | 7.75 | 4.05 | 3.92 | 1.69 |
| $T_4$ | 5.22 | 67.28 | 14.40 | 150.00 | 2.50 | 24.93 | 18.34 | 9.92 | 6.28 | 2.78 |
| $T_5$ | 4.56 | 57.83 | 9.20 | 112.67 | 3.40 | 19.36 | 17.85 | 9.74 | 8.41 | 5.28 |
| $S_2T_1$ | 5.90 | 91.25 | 10.16 | 142.00 | 2.70 | 32.72 | 17.79 | 11.06 | 5.79 | 3.93 |
| $T_2$ | 6.04 | 84.44 | 8.95 | 132.00 | 3.00 | 33.58 | 20.15 | 11.95 | 10.72 | 6.99 |
| $T_3$ | 6.37 | 82.63 | 8.67 | 151.33 | 3.00 | 29.33 | 17.09 | 12.2 | 6.78 | 4.38 |
| $T_4$ | 6.66 | 81.27 | 9.84 | 191.67 | 3.00 | 32.40 | 23.01 | 13.69 | 10.81 | 7.51 |
| $T_5$ | 5.49 | 80.03 | 14.07 | 154.00 | 2.80 | 28.93 | 22.74 | 12.96 | 9.21 | 5.44 |
| $S_3T_1$ | 6.62 | 89.33 | 10.40 | 197.00 | 3.30 | 34.78 | 25.22 | 16.73 | 10.31 | 4.85 |
| $T_2$ | 5.70 | 94.33 | 9.74 | 175.00 | 3.80 | 35.17 | 21.49 | 12.46 | 8.75 | 4.39 |
| $T_3$ | 5.38 | 77.67 | 8.61 | 219.33 | 3.70 | 30.63 | 20.73 | 12.86 | 8.96 | 3.43 |
| $T_4$ | **7.51** | **96.09** | 10.66 | **243.00** | 2.20 | 26.12 | 14.93 | 7.94 | 6.51 | 3.69 |
| $T_5$ | 5.67 | 86.29 | 10.35 | 143.00 | 4.00 | 31.40 | 14.69 | 8.75 | 5.62 | 3.04 |
| $S_4T_1$ | 5.27 | 68.87 | 9.72 | 119.33 | 4.00 | 18.70 | 17.02 | 11.61 | 6.63 | 3.64 |
| $T_2$ | 7.44 | 83.83 | 10.77 | 176.00 | 3.30 | 31.80 | 23.12 | 14.09 | 10.16 | 5.23 |
| $T_3$ | 5.69 | 73.60 | 9.48 | 125.00 | 3.70 | **40.40** | 11.27 | 6.13 | 5.53 | 2.54 |
| $T_4$ | 6.06 | 78.82 | **20.20** | 147.00 | 3.80 | 32.45 | 23.37 | 15.85 | 8.97 | 5.24 |
| $T_5$ | 7.33 | 87.82 | 15.88 | 229.00 | **4.17** | 30.70 | **38.38** | **26.19** | 10.75 | 6.23 |
| $S_5T_1$ | 4.68 | 88.27 | 10.42 | 163.67 | 3.30 | 26.17 | 26.22 | 17.07 | 13.08 | **7.72** |
| $T_2$ | 4.37 | 62.67 | 7.36 | 88.00 | 2.70 | 26.55 | 9.86 | 5.42 | 3.56 | 1.67 |
| $T_3$ | 5.70 | 62.98 | 11.90 | 116.00 | 3.80 | 26.61 | 19.4 | 13.21 | 7.79 | 3.64 |
| $T_4$ | 6.40 | 84.33 | 11.05 | 114.00 | 2.90 | 32.27 | 18.06 | 9.93 | 6.93 | 3.2 |
| $T_5$ | 6.85 | 62.39 | 10.32 | 126.67 | 3.70 | 29.79 | 27.54 | 16 | 8.86 | 4.45 |
| $S_6T_1$ | 6.81 | 85.42 | 13.29 | 195.67 | 2.70 | 35.44 | 19.36 | 11.44 | 8.17 | 4.35 |
| $T_2$ | 4.42 | 66.77 | 9.25 | 154.67 | 3.70 | 23.42 | 17.02 | 11.83 | 5.28 | 2.86 |
| $T_3$ | 4.30 | 71.92 | 7.30 | 115.67 | 3.00 | 31.10 | 26.1 | 16.49 | **13.46** | 6.73 |
| $T_4$ | 5.04 | 62.76 | 9.41 | 166.00 | 3.00 | 31.40 | 26.14 | 16.28 | 9.88 | 5.02 |
| $T_5$ | 3.80 | 58.99 | 8.24 | 116.00 | 3.60 | 24.10 | 12.8 | 5.02 | 4.35 | 1.77 |

**Table 3.`Three principal components of 10 parameters of *Ulmus villosa***

| Characters | Principle components | | |
|---|---|---|---|
| | I | II | III |
| Height (cm) | 0.736 | -0.459 | 0.136 |
| Collar diameter (mm) | 0.764 | -0.537 | -0.081 |
| Leaf area ($cm^2$) | 0.543 | 0.684 | 0.284 |
| Number of leaves | 0.516 | 0.594 | 0.039 |
| Petiole length | 0.179 | 0.692 | 0.18 |
| Root length | 0.649 | -0.326 | 0.745 |
| Shoot fresh weight(g) | 0.853 | 0.448 | 0.04 |
| Shoot dry weight (g) | 0.843 | 0.452 | 0.099 |
| Root fresh weight(g) | 0.54 | 0.43 | 0.806 |
| Root dry weight (g) | 0.65 | 0.342 | 0.780 |
| Eigen value | 4.29 | 2.61 | 1.96 |
| Percent of variability | 40.97 | 24.93 | 18.72 |
| Cumulative percent of variability | 40.97 | 65.9 | 84.62 |

selection along with other characters, since it is the largest contributor towards total genetic variability in marinoo.

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SHORT COMMUNICATION

# IC0598236: A Potential Genotype of Great Headed Garlic (*Allium ampeloprasum* var. *ampeloprasum* L.)

**AC Mishra**
*Department of Vegetable Science, Uttarakhand University of Horticulture and Forestry, Ranichauri Campus, Tehri-Garhwal-249 199, Uttarakhand, India*

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The experiments on characterization and evaluation of collected germplasm of garlic were conducted at Vegetable Research Block of Uttarakhand University of Horticulture and Forestry, Ranichauri Campus, Tehri-Garhwal, during 2012-13 and 2013-14. A few plants exhibiting long, dark green, broader and leathery leaves, pink umbels with micro-cloves (bulbils), large bulbs and cloves were selected and multiplied clonally to generate population of uniform plants. The germplasm submitted to National Bureau of Plant Genetic Resources, New Delhi, was given IC0598236. Regarding morpho-agronomic performance, reactions to biotic and abiotic stresses, bulb yield and related traits indicated that IC0598236 was botanically *Allium ampeloprasum* var. *ampeloprasum* L. It exhibited about 38.9% higher mean bulb yield (239.8 q/ha) than *Agrifound Parvati* (174.2 q/ha), a commercial variety of common garlic (*A. sativum* L.), due to larger bulb size (68.4 g mean bulb weight) and cloves (62.6 g, 10 clove weight). The genotype IC0598236 was comparable with commercial cultivar *Agrifound Parvati* of *A. sativum* in relation to TSS and dry matter in cloves. Under field conditions, it can withstand moisture and biotic stresses very well. On the basis of these many beneficial characteristics, IC0598236 (*Allium ampeloprasum* var. *ampeloprasum*) could be recommended as a potential commercial crop of Uttarakhand hills.

**Key Words: *Allium ampeloprasum,* Commercialization potential, Elephant garlic, Great Headed garlic, Levant garlic**

The genus *Allium* represents a large diversity with respect to morphology of bulbs, nature of bulbing and appearance of foliage. Almost all the species of alliums are found in Mediterranean region, the adjoining areas of Western Asia and South-eastern Europe (USDA GRIN, 2011). In Indian sub-continents, two species of *Allium* viz., *A. cepa* L. and *A. sativum* have been under cultivation since ancient times. A few decades back some other species *viz., A. fistulosum* L.*, A. porrum* L.*, A. schenoprasum* L. etc. have been introduced in this country. Occurrence of *A. ampeloprasum* commonly called great headed garlic, elephant garlic or Levant garlic in India or abroad is confined to restricted areas of Himalayas. This species is reported to be under cultivation in South-western England and France (Bohanec *et al*., 2005). Some *Allium* species, producing umbels consisting of numerous bulbils identical to small cloves, have been identified as *A. ampeloprasum* but all the varieties of *A. ampeloprasum* essentially do not have bulbils (Block, 2010). However, some taxonomists identified such species bearing aerial bulbils as *Allium* species (Bohanec *et al*., 2005; Hirscheggar *et al.,* 2006). Block (2010) identified *A. tricoccum* and characterized it as broad leaved, monocloved wild leek, the progenitor of three cultivated types *viz*., leek or garden leek (*Allium porrum*), elephant or great headed garlic (*A. ampeloprasum* var. *ampeloprasum*) and kurrat or middle-eastern leek (*A. kurrat*). The controversial taxonomic position of different phenotypes of alliums many times creates confusion in identification of certain form of bulb-bulbil- and clove-bearing *Allium* species. Therefore, determining taxonomic position of all the phenotypes in alliums is indispensable for further crop improvement programmes.

To generate variability for crop improvement programme in garlic at Uttarakhand University of Horticulture and Forestry, Ranichauri Campus, Tehri-Garhwal, Uttarakhand, germplasm collection was made from different villages of Tehri district, during 2012. A few plants of *A. ampeloprasum* were identified in the population of collected lines of garlic. This species has been under cultivation in farmers' field since very

**Author for Correspondence: Email: acm24680@rediffmail.com; acm24680@gmail.com*

long as an admixture with *A. sativum*. The plants exhibiting identical growth habits bearing long, dark green, broad and leathery leaves, pink umbels with micro-cloves (bulbils) and big size of underground bulbs and cloves, were selected and multiplied clonally to generate required size of population of uniform plants at Vegetable Research Block of the University. The germplasm was sent to ICAR-National Bureau of Plant Genetic Resources, New Delhi to be assigned IC number. The genetic material was further evaluated for different morpho-agronomic traits in replicated trials along with nationally- and locally- grown checks *viz.*, *Agrifound Parvati* and *Ghansali Local*, a popular local variety of common garlic (*A. sativum*) during *Rabi* 2012-13 and 2013-14. The crop was raised by planting cloves at 15 × 10 cm spacing using 5.0 q/ha seed rate in garlic lines and 8.0 q/ha in great headed garlic during the month of October. The standard package of practices of garlic was followed to raise the experimental crop. The manure and fertilizers were applied at 15 t/ha FYM and 100:80:60 kg/ha NPK and the crop was irrigated by sprinkling water as and when required. Mulching with dried grasses was also done to conserve soil moisture and keep the field free from weeds. The bulbs were harvested during first fortnight of May.

Plants are foliaceous with dark green, flattened and leathery leaves about 46.0 cm long and 2.8 cm wide. Plants bear 10-12 leaves in the whole life span (Fig. 1). The central growing portion of shoot develops into a flowering stalk bearing terminal umbel at crop maturity during spring-summer. The umbels consist of tiny anthers, arising from the base of ovaries and developing in to micro-cloves (bulbils in the case of common garlic), by storage of food material (Fig. 2). The reproductive system in this species is non-functional. The micro-cloves have meristematic tissues differentiating into roots and shoots. Each umbel bears about 150-175 micro-cloves and one gram of it has 28-32 micro-cloves. The viability of micro-cloves varies from 10-12 months under ideal storage conditions. The newly identified line IC0598236 bears pink umbels at plant maturity and has large bulbs and cloves (Figs 2 & 4). The umbels consist of small cloves or bulbils which can generate new plantlets (Fig. 3). On the basis of detailed phenotypic resemblance described by Bohanec *et al*. (2005) and Hirscheggar *et al.* (2006), this collection was identified as belonging to genus *Allium* and species *ampeloprasum* of family Alliaceae. According to Brewster (1994), *A. ampeloprasum* does not normally produce bulbs, although the variety *ampeloprasum*

**Fig.1. Crop in the field**

**Fig. 2. Appearance of umbels during crop maturity**

**Fig. 3. Bulbs and umbels with micro-cloves**

**Fig. 4. Arrangement of cloves in the bulb**

(elephant garlic) has been found to produce a head of cloves like garlic (*A. sativum*) but with two sizes of cloves, bigger cloves like garlic, surrounded by smaller ones, on the outside. Thus, on the basis of description given by Brewster (1994, 2008), it was concluded that IC0598236 was botanically related to *A. ampeloprasum* var. *ampeloprasum,* commonly known as elephant garlic or great headed garlic.

The great headed garlic line IC0598236 is tolerant to foliar diseases like purple blotch and downy mildew. However, incidence of root rot is realized during prolonged, high soil moisture conditions (Table 2). There is no conspicuous infestation of common pests in alliums of temperate hills. This species is tolerant to frost as the area of its occurrence is fraught with severe and prolonged frost. For optimum performance this requires light rains or sprinkling at 8-10 days intervals.

As presented in Table 1, the performance of IC0598236, was compared with two genotypes of *A. sativum* viz., *Agrifound Parvati* and a locally grown landrace *Ghansali Local* for two years, during 2012-13 and 2013-14. Results indicated that IC0598236 had significantly higher bulb yield than both the genotypes of *A. sativum* during both the years (248.8 q/ha in first year and 230.7 q/ha in second year) which were higher by 47.3% and 28.5%, respectively as compared to *Agrifound Parvati* with bulb yield of 168.9 q/ha during first year and 179.5 q/ha during second year. This genotype was again promising for bulb weight (65.5 g and 71.2 g) and 10 clove weight (61.3 g and 63.8 g) during both the years. Higher bulb yield in IC 0598236 was associated with heavier bulbs and bolder cloves. Among the *A. sativum* genotypes, local cultivar exhibited higher bulb weight (35.8 g and 33.6 g) and 10 clove weight (35.4 g and 36.5 g) during both the years as compared to popular high yielding variety *Agrifound Parvati* (30.2 g and 37.8 g and 29.8 g and 31.4 g, respectively). The heavier bulbs, larger cloves and, broader, dark green and more leathery leaves in genotype IC0598236, was probably because of its tetraploid karyotype resembling different forms of *A. ampeloprasum* (Figliuolo and DiStefano, 2007). Variable ploidy level and chromosome number in *A. ampeloprasum* (16-56) has also been mentioned by Mathew (1996). As far as TSS and dry matter content in cloves was concerned, the landrace *Ghansali Local* again registered higher values for these quality traits during both the years viz., 43.5% & 44.0% TSS and 56.4% & 56.05% dry matter content during first year and second year, respectively. The IC0598236 and *Agrifound*

**Table 1. Comparative performance of great headed garlic (*Allium ampeloprasum* L. var. *ampeloprasum*) and cultivars of common garlic (*Allium sativum* L.)**

| Genotypes | Days to maturity | | Bulb weight (g) | | 10 Clove weight (g) | | Total soluble solids in cloves (%) | | Dry matter content in bulb (%) | | Marketable bulb yield (q/ha) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2012-13 | 2013-14 | 2012-13 | 2013-14 | 2012-13 | 2013-14 | 2012-13 | 2013-14 | 2012-13 | 2013-14 | 2012-13 | 2013-14 |
| *A.ampeloprasum* (IC0598236) | 180 | 180 | 65.5 | 71.2 | 61.3 | 63.8 | 41.5 | 41.0 | 46.5 | 48.2 | 248.8 | 230.7 |
| *A. sativum* L. (*Agrifound Parvati)* | 170 | 175 | 30.2 | 27.8 | 29.8 | 31.4 | 39.0 | 38.5 | 45.6 | 46.7 | 168.9 | 179.5 |
| *A. sativum* L. (*Ghansali Local*) | 185 | 180 | 35.8 | 33.6 | 35.4 | 36.5 | 43.5 | 44.0 | 56.4 | 56.05 | 108.7 | 114.6 |
| SE (m) | 1.8 | 2.2 | 0.93 | 1.2 | 1.85 | 1.7 | 1.2 | 1.3 | 0.9 | 0.76 | 6.4 | 9.2 |
| CD (0.05) | 3.9 | 4.7 | 2.0 | 2.6 | 3.96 | 3.7 | 2.6 | 2.8 | 1.9 | 1.6 | 13.7 | 19.73 |
| CV (%) | 5.0 | 7.3 | 11.6 | 13.4 | 8.6 | 10.8 | 4.5 | 5.6 | 7.2 | 5.8 | 13.5 | 10.6 |

**Table 2. Relative disease reactions of great headed garlic (*Allium ampeloprasum* L. var. *ampeloprasum*) and cultivars of common garlic (*Allium sativum* L.)**

| Genotypes | Incidence of Purple blotch (%) | | Incidence of Downy mildew (%) | | Root rot (%) | |
|---|---|---|---|---|---|---|
| | 2012-13 | 2013-14 | 2012-13 | 2013-14 | 2012-13 | 2013-14 |
| *A.ampeloprasum* (IC0598236) | 2.5 | 2.0 | 3.8 | 2.6 | 15.8 | 21.6 |
| *A. sativum* L. (*Agrifound Parvati)* | 23.9 | 19.5 | 12.4 | 11.9 | 8.7 | 13.5 |
| *A. sativum* L. (*Ghansali Local*) | 25.6 | 26.5 | 9.7 | 10.3 | 5.6 | 8.3 |
| SE (m) | 2.7 | 3.2 | 1.7 | 2.1 | 1.2 | 1.6 |
| CD (0.05) | 5.86 | 6.94 | 3.66 | 4.52 | 2.58 | 3.44 |
| CV (%) | 16.8 | 13.5 | 9.2 | 8.6 | 12.3 | 13.2 |

*Parvati* exhibited non-significant difference for TSS and dry matter content during both the years although higher values for these traits were observed in the former.

It gave about 38.9% higher bulb yield than *Agrifound Parvati*, a commercial variety of common garlic (*A. sativum*) due to larger bulb size and cloves. The genotype IC0598236 was comparable to the commercial cultivar *Agrifound Parvati* with respect to TSS and dry matter content of cloves. Under field conditions, it can withstand moisture and biotic stresses very well. On the basis of morpho-agronomic performance, reactions to biotic and abiotic stresses and, bulb yield and related traits which are beneficial characteristics, IC0598236 (*A. ampeloprasum* var. *ampeloprasum*) holds the potential as a commercial crop in Uttarakhand hills.

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SHORT COMMUNICATION

# Molecular Characterization of Cabbage (*Brassica oleracea* L. var. *capitata*) Genotypes using RAPD Markers

**Nisha Thakur and DK Srivastava**
*Department of Biotechnology, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan-173230, Himachal Pradesh, India*

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The genetic relationship among sixteen genotypes of cabbage were studied using RAPD markers. Cabbage genotypes were collected from IARI Research Centre, Kattarine, Kullu and Dr Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan. A total of 17 primers were used to generate RAPD profiles, out of these 7 primers gave reproducible banding patterns. A total of 22 bands were obtained and all were polymorphic with two cultivar specific bands. The percentage of primer polymorphism was 100%. Similarity index was computed based on Jaccard's similarity coefficient and used for cluster analysis based on UPGMA. At 62% similarity level sixteen genotypes were grouped into two clusters. RAPD technology could be useful for identification of different genotypes as-well-as accessing the genetic similarity among different accessions of cabbage.

**Key Words: Cabbage, Genetic relationships, RAPD markers**

A characteristic feature of living organisms is the immense natural variability present for various characteristics in most populations. A wide range of variability present in a species, always provides a better chance of selecting desirable genotypes. (Vavilov, 1951). Estimates of genetic diversity are important in designing crop improvement programme for management of germplasm. Assessment of genetic variation existing in a crop species is vital for revising strategies appropriate for directed genetic enhancement of the crop. Morphological characters such as leaf shape, leaf colour, flower colour and fruit colour which are robust qualitative genetic traits have been used in the past to study genetic variation and characterization of crop genotypes. Due to interaction of quantitative traits with environment, these markers were not found suitable for assessing genetic diversity.

Molecular markers thus show significant advantage in the analysis of genetic diversity. These are not influenced by the environment and proved to be useful in providing estimates of amount of genetic diversity, relationship with other variables and understanding evolution process. PCR based markers have been proved useful for genetic diversity studies. The RAPD markers are simple, fast and arbitrary markers and are appropriate for formulation of strategies for effective management of germplasm collections and estimation of diversity (Virk *et al.,*1995; Caetano *et al*.,1999; Chong *et al*., 2005; Gong *et al*., 2007; Cheng *et al*., 2009; Hoque *et al*., 2013; Sharifova *et al*., 2013). Among vegetable crops, cabbage being largely cultivated in hilly areas of H.P. Present study therefore carried out to estimate the genetic diversity between different cabbage genotypes using RAPD markers.

The plant material was obtained from IARI Research Centre Kattarine, Kullu and Dr Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, sown in glass house at Biotechnology Department in 2010. One gram of green leaves were collected and used for the DNA isolation (Table 1).

Total genomic DNA from each variety was isolated by CTAB method with slight modification using a rapid method (Doyle and Doyle 1999). The extracted DNA was purified with 10 µg/ml RNase A for 1 hour at 37$^{o}$C to remove the RNA. The purified DNA was dissolved in TE buffer and stored at -20$^{o}$C freezer for further use. Seventeen RAPD primers (Sigma Aldrich) were used to characterize 16 cultivars of cabbage. The PCR reaction having 25.0 µl volume mixture contained 17 µl sterile deionized water, 2.5 µl Taq DNA polymerase buffer (2X) with 1.5 mM $MgCl_2$(GENEI), 1.25 µl of each 2.5 mM dNTP (GENEI), 0.25 µl Taq DNA polymerase (1unit) (GENEI), 2 µl primer (13.32 µM/reaction) and 2.0 µl sample DNA (approx. 40-50 ng). The reaction mixture was subjected to the following thermal profile for amplification in a thermocycler (BioRad Amplification

*Author for Correspondence: Email-nishathakur81086@gmail.com

**Table 1. List of cabbage genotypes used in DNA study (RAPD)**

| S. No. | Name of cabbage genotypes | Abbreviation | |
|---|---|---|---|
| 1 | Golden Acre | GA | IARI, Kattraine, Kullu |
| 2 | Best of all | BA | IARI, Kattraine, Kullu |
| 3 | BC-79 | BC | IARI, Kattraine, Kullu |
| 4 | Green Emperor | GE | IARI, Kattraine, Kullu |
| 5 | Green Europium | Ge | IARI, Kattraine, Kullu |
| 6 | KGAT-3 | KG | IARI, Kattraine, Kullu |
| 7 | Pusa Drum Head | P | IARI, Kattraine, Kullu |
| 8 | Darl Cabbage | DC | IARI, Kattraine, Kullu |
| 9 | EC-30191 | EC | Dr YSPUHF, Nauni |
| 10 | AC-204 | AC | Dr YSPUHF, Nauni |
| 11 | NO-29 | NO | Dr YSPUHF, Nauni |
| 12 | NO-4 | 4 | Dr YSPUHF, Nauni |
| 13 | Giddeon | GI | Dr YSPUHF, Nauni |
| 14 | Green Kid | GD | Dr YSPUHF, Nauni |
| 15 | Cabbage Mangla | CM | Dr YSPUHF, Nauni |
| 16 | General Cabbage | GC | Dr YSPUHF, Nauni |

System): 4 min at 94$^{o}$C for initial denaturation, followed by 40 cycle of 30 second DNA denaturation at 94$^{o}$C, 1.0 min annealing at 36 ºC and 2 min at 72$^{o}$C for extension. A final extension step was done at 72$^{o}$C for 7 min. Electrophoresis was done to visualize the PCR amplified product on 1.4% agarose gel. The amplified fragments were visualized by staining with ethidium bromide.

Data analysis was carried out only for those primers which give scorable banding patterns for the genotypes under study. Co-migrating bands were considered to represent the same locus and thus treated as a same band while scoring. Presence of an amplified product was designated as "1" and absence was marked as "0". Intensity of the amplified products was not taken into account while scoring. NTSYS-pc, version 2.02 (Numerical Taxonomy System Exterer Software) was used to perform cluster analysis of the complete RAPD data (Rohlf, 2000). Similarity between accessions were estimated using the Jaccard coefficient, calculated as J = A/ (N-D) where, A is the no. of positive matches ( i.e. the presence of bands in both the samples), D is the no. of negative matches (*i.e*. the absence of bands in both the samples) and N is the total sample size including the no. of matches and unmatches. Similarity estimates were analysed by unweighted pair group method with arithmetic averages (UPGMA) and the resulting clusters were expressed as dendrogram in the cabbage genotypes.

A total of 22 bands were obtained with seven RAPD primers and all were found to be polymorphic. Two unique bands were obtained in genotype No-4 and Darl Cabbage with primers OPB-03 and OPB-07 respectively. Percentage of total polymorphic bands was 100% (Table 2). Using Jaccard's similarity coefficient maximum similarity was found to be 0.8235 between the variety Cabbage Mangla and Best of all, whereas the least similarity was found to be 0.1429 between the variety No-4 and Green Emperor. Fig. 1 shows dendrogram which was divided into two main clusters 1 and 2. The cluster 1 was further divided into two subclusters (1a and 1b). The subcluster 1a Golden acre and BC-79 genotypes were grouped together. The subcluster 1b further divided into sub-subclusters in which sub-subcluster 1ba including Best of all, Cabbage Mangla, General cabbage, Giddeon and Green kid genotypes. The subcluster Ibb includes Darl cabbage, Green Emperor, No-4, EC-30191, Green Europium and AC-204 genotypes. The main cluster B including the genotypes KGAT-3 and Pusa Drum Head.

In an attempt to examine the potential of RAPD markers for the ability to asses the variability in cabbage genotypes, 7 primers were used in genotyping. Cansian and Echevarrigaray (2000) have also used RAPD markers to characterize 16 commercial cultivars of cabbage. They selected 18 random decamer primers from the set of 100 primers, produced a total of 195 bands, out of which 105 (54%) were polymorphic that ranged from 100 to 2500 bp. Dias *et al*. (1991) used 13 random decamer primers for assessing genetic variation within *Brassica campestris* cultivars using RAPD markers. They obtained 15 unique bands with a number of primers namely OPE-01, OPF-07, OPK-01, OPK-02, OPK-03, OPK-04, OPN-01 to distinguish YSPb, Tobin, Debra and Pont toria cultivars. Zang and Zang (2014) evaluated genetic diversity in 21 cultivars of Chinese kale (*Brassica oleracea* L. var. *alboglabra* Bailey) by using rapid amplified polymorphic DNA and sequence-related amplified polymorphism markers. A total of 104 bands were detected by 11 RAPD primers, of which 66 were polymorphic in nature. Similarly, Panwar *et al*. (2009) have also studied the potential use of RAPDs in characterizing 25 genotypes of cauliflower with 12 reproducible primers.

Present study revealed that informative primers can be efficiently used for diversity analysis among cabbage genotypes at molecular level. A high value of similarity

**Table 2. Total number of amplified fragments and number of polymorphic fragments generated by PCR using seven random decamer oligonucleotide primers**

| S.No. | Primer Name | Sequence (5′-3′) | Total Number of Amplified bands | Total Number of Polymorphic amplified bands | Total Number of Monomorphic amplified bands | Genotype specific bands | Polymorphism ratio, percentage (%) |
|---|---|---|---|---|---|---|---|
| 1. | OPB-01 | GTTTCGCTCC | 2 | 2 | 0 | 0 | 100 |
| 2. | OPB-02 | TGATCCCTGG | 4 | 4 | 0 | 0 | 100 |
| 3. | OPB-03 | CATCCCCCTG | 2 | 1 | 0 | 1 | 50 |
| 4. | OPB-04 | GGACTGGAGT | 4 | 4 | 0 | 0 | 100 |
| 5. | OPB-05 | TGCGCCCTTC | 3 | 3 | 0 | 0 | 100 |
| 6. | OPB-07 | GGTGACGCAG | 4 | 3 | 0 | 1 | 50 |
| 7. | OPB-09 | TGGGGGACTC | 3 | 3 | 0 | 0 | 100 |
| | Total | | 22 | 20 | 0 | 2 | |

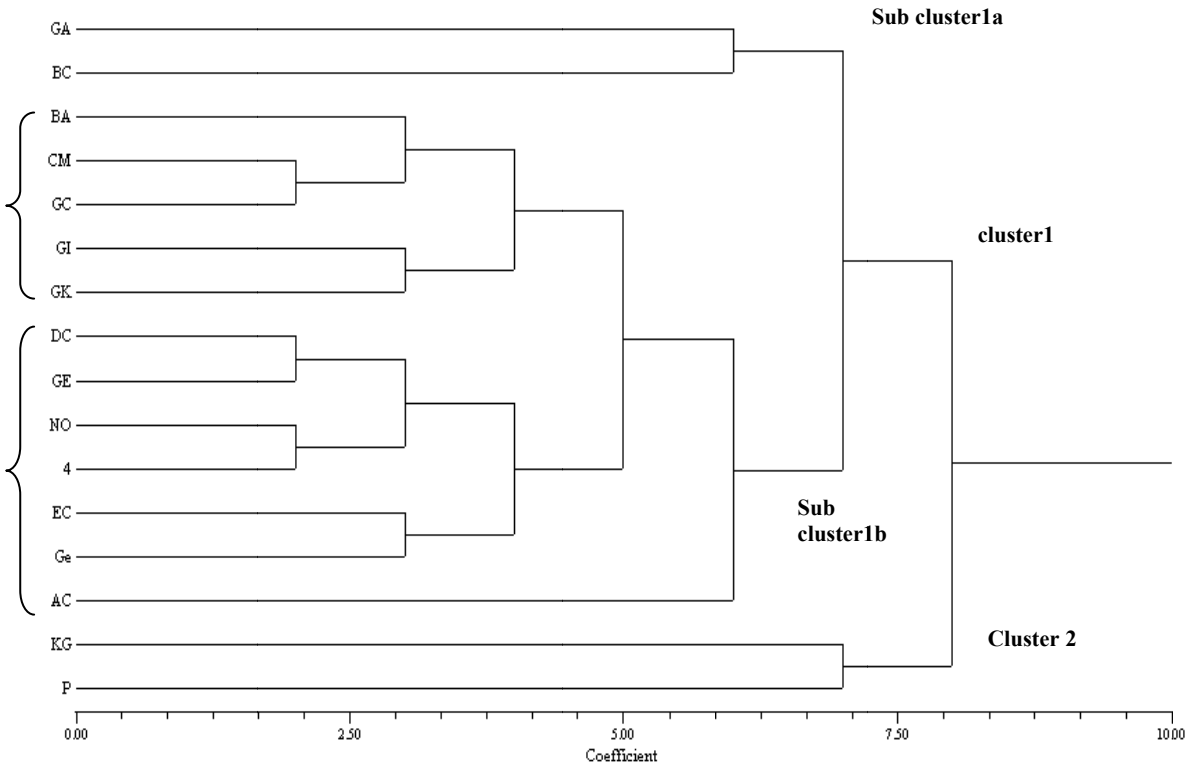


**Fig. 1. Dendrogram obtained from RAPD analysis among cabbage (*Brassica oleracea* L.var. *capitata*) genotypes**

index (0.8235) between the genotypes Cabbage Mangla and Best of all was obtained using Jaccard coefficient. The genotypes thus have same parent of origin. A least value of similarity index (0.1429) was found between the variety No-4 and Green Emperor revealed that genotypes different parents of origin. From the dendrogram it was clear that the genotypes Golden acre, BC-79, Best of all, Cabbage Mangla, General cabbage, Giddeon and Green kid, Darl cabbage, Green Emperor, No-4, EC-30191, Green Europium and AC-204 have emerged from same parents because they grouped in cluster A. The genotypes KGAT-3 and Pusa Drum Head have emerged from other parent, thus grouped into cluster B. Based on the aforesaid findings, it is concluded that cabbage genotypes collected from Katraine and Nauni are genetically diverse and the breeders can choose the most diverse parents for breeding programs for its germplasm collection and management.

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# Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXI[st] meeting held on April 21[st], 2015 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 13 germplasm lines out of 65 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. DRR-BL-150 (IC0611701; INGR15001), a Rice (*Oryza sativa* L.) Germplasm with Resistance to Leaf and Neck Blast

**Kuldeep Singh, M Sheshu Madhav*, M Srinivas Prasad, BC Virakatamath, SJS Rama Devi, B Umakanth and V Ravindra Babu**

*ICAR-Indian Institute of Rice Research (IIRR), Rajendra Nagar, Hyderabad-500030, Telangana, India*

*(Email: sheshu24@gmail.com)*

Rice blast disease, caused by *Magnaporthe oryzae*, is a major constraint for sustainable rice production. Though many resistant varieties to *M. oryzae* have been developed, the resistance is not long lasting. This is due to the high pathogen plasticity exists in the field make to breaks down single gene resistance within 3 to 5 years release of cultivation (Bonman *et al.,* 1986; Lang *et al.,* 2009). Hence, development of broad spectrum and durable blast resistant varieties is essential for combating this disease, which requires continuous efforts of breeders and pathologists. In this scenario, we identified an introgression line, DRR-BL-15 (developed using *O. glaberrima*-AA) in the background of PR114 *(indica* line) have shown consistent resistance to leaf and neck blast disease resistance when screened at multiple locations across India through All India Coordinated Rice Improvement Programme (AICRP).

**Morpho-agronomic characteristics:** DRR-BL-150 has shown the plant height of 91.4 cm, with eleven panicles per plant. The panicle length, panicle weight, yield/ plant and dry weight/ plant of DRR-BL-150 are 18.8 cm, 2.45 g, 32.02 g and 27.72g respectively. The (50%) days of flowering of the DRR-BL-150, is 110 days with long slender type of grain.

**Associated characters and cultivation practices:** The DRR-BL-150 was screened for blast resistance under UBN (artificial screening) during January year 2010 and 2011, June 2011 in two replications using artificial screening methods. The result indicated a mean resistance score of 1.0 for leaf blast.This line was screened under Donor Screening Nursery (DSN) of AICRIP 2012 and 2013 in replication for leaf and neck blast resistance.

The blast scores were recorded with reference to standard SES scale and this line showed high level of resistance to leaf and neck blast resistance across location, indicating its potential of resistance. The line also showed resistance for brown spot during AICRIP 2012 with SI 3.6. The phenotyping results of DRR-BL-150 is as follows –

*Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, ICAR–National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

| | | DRR | | AICRIP 2012 | | AICRIP 2013 | |
|---|---|---|---|---|---|---|---|
| | | Leaf Blast Score | Neck Blast Score | Leaf Blast Score | Neck Blast Score | Leaf Blast Score | Neck Blast Score |
| | **DRR-BL-150** | **1.0** | – | **3.6*@** | **3.2*#** | **2.9*$** | **2.4*#** |
| Resistant checks | TETEP | 1.8 | – | 3.0*@ | 3.5*# | 2.7*$ | 2.3*# |
| | IR64 | 1.7 | – | 4.4*@ | 3.5*# | 3.3*$ | 3.9*# |
| | C101LAC | 1.6 | – | 4.0*@ | 3.1*# | 3.1*$ | 3.8*# |
| | C101A51 | 1.6 | – | 3.9*@ | 3.6*# | 4.6*$ | 4.1*# |
| Susceptible Checks | HR12 | 9.0 | – | 6.6*@ | 6.2*# | 5.9*$ | 5.3*# |
| | TN1 | 8.5 | – | 5.2*@ | 4.1*# | 5.4*$ | 5.0*# |

* Selection of promising entries is made from the centers where Susceptible Check SI ≥5.0
@: SI calculated from 26 centers; #: SI calculated from 8 centers; $: SI calculated from 27 centers.

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# 2. DRR-BL-31 (IC0611702; INGR15002), a Rice (*Oryza sativa* L.) Germplasm with Resistance to Leaf and Neck Blast

**Kuldeep Singh, M Sheshu Madhav*, M Srinivas Prasad, BC Virakatamath, SJS Rama Devi, B Umakanth and V Ravindra Babu**

*ICAR-Indian Institute of Rice Research (IIRR), Rajendra Nagar, Hyderabad-500030, Telangana, India*
*(Email: sheshu24@gmail.com)*

Rice blast disease, caused by *Magnaporthe oryzae*, is a major constraint for sustainable rice production. Though many resistant varieties to *M. oryzae* have been developed, the resistance is not long lasting. This is due to the high pathogen plasticity exists in the field make to breaks down single gene resistance within 3 to 5 years release of cultivation (Bonman *et al.,*1986; Lang *et al.,* 2009). Hence, development of broad spectrum and durable blast resistant varieties is essential for combating this disease, which requires continuous efforts of breeders and pathologists. In this scenario, we identified an introgression line, DRR-BL-31(developed using *O. glumaepatula* (AA) as donor) in the background of PR114 (*indica* variety as recurrent parent) has shown consistent resistance to rice leaf and neck blast disease when screened at multiple locations across India through All India Coordinated Rice Improvement Programme (AICRP).

**Morpho-agronomic characteristics:** DRR-BL-31 has shown the plant height of 79.2 cm, with eighteen panicles/plant. The panicle length, panicle weight, yield per plant and dry weight/ plant of DRR-BL-31 are 21.8 cm, 1.78 g, 36.68 g and 30.84 respectively. The (50%) days of flowering of the DRR-BL-150, is 110 days with long slender type of grain.

**Associated characters and cultivation practices:** The DRR-BL-31 was screened for blast resistance under UBN (artificial screening) during January in the year 2010 & 2011, June-2011 in two replications using artificial screening methods. The result indicated a mean resistance score of 1.0 for leaf blast. The line was screened under Donor Screening Nursery (DSN) of AICRIP 2012 & 2013 in replication for leaf and neck blast resistance. The blast scores were recorded with reference to standard SES scale and this line showed high level resistance (1.9 -3.8) for neck blast and moderate resistance (2.9-4.1) to leaf blast. The result of DRR-BL-31 is as follows.

| | | DRR | | AICRIP 2012 | | AICRIP 2013 | |
|---|---|---|---|---|---|---|---|
| | | Leaf Blast Score | Neck Blast Score | Leaf Blast Score | Neck Blast Score | Leaf Blast Score | Neck Blast Score |
| | DRR-BL-31 | 1.0 | – | 4.1*@ | 3.8*# | 2.9*$ | 1.9*# |
| Resistant checks | TETEP | 1.8 | – | 3.0*@ | 3.5*# | 2.7*$ | 2.3*# |
| | IR64 | 1.7 | – | 4.4*@ | 3.5*# | 3.3*$ | 3.9*# |
| | C101LAC | 1.6 | – | 4.0*@ | 3.1*# | 3.1*$ | 3.8*# |
| | C101A51 | 1.6 | – | 3.9*@ | 3.6*# | 4.6*$ | 4.1*# |
| Susceptible Checks | HR12 | 9.0 | – | 6.6*@ | 6.2*# | 5.9*$ | 5.3*# |
| | TN1 | 8.5 | – | 5.2*@ | 4.1*# | 5.4*$ | 5.0*# |

* Selection of promising entries is made from the centers where Susceptible Check SI ≥5.0
@: SI calculated from 19 centers; #: SI calculated from 8 centers; $: SI calculated from 21 centers.

The line has shown moderate resistance for sheath rot during AICRIP 2012 with SI 3.4. Also, the line has shown moderate resistance for sheath blight during AICRIP 2013 with SI 5.8.

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## 3. Kasota (BCU 5762) (EC0532635; INGR15003), a Barley (*Hordeum vulgare* L.) Germplasm with High Antioxidant Activity

**Sneh Narwal*, Dinesh Kumar, RPS Verma and Indu Sharma**
*ICAR-Indian institute of Wheat and Barley Research (IIWBR), Karnal-132001, Haryana, India*
**(Email: snehdagar@yahoo.co.in)*

Whole grains, including wheat and barley, contain several compounds that are capable of minimizing the damaging effects of oxidation reactions. Barley and malt are now gaining renewed interests as ingredients for the production of functional foods due to their concentration of soluble fibre β-glucan and many bioactive compounds having antioxidant activity. Barley can thus serve as an excellent dietary source of antioxidants with antiradical and antiproliferative potentials for disease prevention and health promotion. Therefore, identification of barley genotypes with high antioxidant activity is the first step towards this process.

In the year 2011-12, 265 barley lines grown at DWR, Karnal farm in malt barley crossing block were screened for their antioxidant potential using two radical scavenging methods *viz.* ABTS assay and DPPH assay. Kasota is hulled, six-row spring feed barley (*Hordeum vulgare* L.). It was developed at the Field Crop Development Centre, Alberta Agriculture, Food and Rural Development, Lacombe, Alberta, Canada from the cross Celaya/ Mezquita/Godiva/3/Trompillo (Helm *et al*., 1996). Using both the assay methods, the line Kasota showed the highest antioxidant activity (11.95 μM Trolox Eq/g by ABTS assay and 70.25% discoloration by DPPH assay) (Narwal *et al*., 2014). Next two years (2012-13 & 2013-14), it was grown in multi-location trials under AICRP on Wheat & Barley along with check and another barley line. There were year to year differences in the level of antioxidant activity which is due to the variations in the climatic conditions each year. In the year 2013-14, higher activity range was obtained. But the trend was the same

at different growing centers. It showed significantly high activity than the control K551 at all the centres (Barley Network AICRP Reports, 2012-13 & 2013-14).

Although Kasota has been registered as a feed barley variety, it has been found to have very high antioxidant activity. Also, it has yellow aleurone which might be rich in many yellow pigments having high antioxidant activity. It cannot be used directly as food but the flour from its grains can be used in various food preparations to enhance the antioxidant content of the food. Also it can be used in breeding programs for developing high antioxidant food and malt barley varieties.

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# 4. DWRB-127 (IC0612434; INGR15004), a Two Rowed Barley (*Hordeum vulgare* L.) Germplasm Immune to Yellow Rust (*Puccinia striiformis* f. sp. *hordei*)

**Vishnu Kumar*[1], RPS Verma[2], R Selvakumar[1], Dinesh Kumar[1], Jogendra Singh[1], AS Kharub[1] and Indu Sharma[1]**

[1]*ICAR-Indian institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India*

[2]*International Centre for Agricultural Research in the Dry Areas, Rabat, Morocco*

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

Barley is an ancient crop and fourth largest cereal in the world with a share of 5.5-6% of the global cereal production. It is mainly used for feed, food and malt production. Like other cereals, rusts are the most devastating diseases of barley. Notably, yellow rust is an invasive disease and caused by fungus*, Puccinia striiformis* f. sp. *hordei* in barley. It is wide spread in high input production conditions *i.e*. North Western Plain Zone (NWPZ) and with high to medium natural incidences in North Eastern Plain Zone (NEPZ). In India five races of barley stripe rust are known *i.e.* 57, 24, M, G and Q. Presently, yellow rust resistance sources are very limited in barley and existing cultivars with good resistance are being utilized into breeding programmes. Chemical controls for yellow rust are available, however, inbuilt resistance mechanism is eco-friendly and best tactics for sustainable agriculture coupled with high benefit ratio.

DWRB127 (BK1222) is an advance malt barley (two-row) high yielding genotype, which was developed by pedigree method (DWR45/DWR46) at DWR, Karnal. It was screened for disease reactions at multi-locations for consecutive two seasons *viz. rabi*, 2012-13 and 2013-14 under Initial Barley Disease Screening Nursery (IBDSN) and National Barley Disease Screening Nursery (NBDSN), respectively. During *rabi,* 2012-13, the genotype DWRB127 was evaluated at four locations namely, Bajaura, Durgapura, Dhaulakuan and Ludhiana and immune response (0 reaction) was observed for yellow rust under artificial inoculations (Anonymous, 2013). The check variety K551 exhibited susceptible

**Table 1. Performance of DWRB127 and checks for yellow rust during *rabi*, 2013-14**

| 2013-14 | Yellow rust | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Genotypes | Bajaura | Dhaulakuan | Durgapura | Ludhiana | Karnal | Hisar | Almora | HS* |
| BK1222 (DWRB127) | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Infector | 80S | 100S | 100S | 60S | 80S | 80S | 60S | 100S |
| BH902 (c) | 0 | 20S | 0 | tS | 0 | 0 | 5MS | 20S |
| DWRB92 (c) | 0 | 0 | 20S | tS | 0 | 0 | 5MS | 20S |
| DWRUB52 (c) | 0 | 0 | 10S | 0 | 0 | 0 | 0 | 10S |
| K551 (c) | 30S | 0 | 80S | 5S | 20S | 20S | 40S | 80S |

*HS-highest reaction

yellow rust reactions of 60S followed by BH902 (20S), DWRB92 (5S) *etc*. in same fields under NBDSN during *rabi*, 2012-13.

Similarly, during *rabi*, 2013-14, DWRB127 was again evaluated under artificial inoculation for yellow rust and was found immune (0) at Durgapura, Dhaulakuan, Karnal, Hisar, Almora, Ludhiana and Bajaura centres (Anonymous, 2014; Kumar *et al*., 2014) (Table 1).

All the check varieties showed susceptible reactions for yellow rust during *rabi*, 2013-14. The genotype DWRB127 is not only immune for yellow rust but also depicted very high 1000 grain weight (53.8g) and overall malting quality scores (23/30) after multi-location evaluation. Therefore, it can be concluded that DWRB127 is a high yielding valuable genetic resource for yellow rust resistance and as well as for 1000 grain weight and other malting quality traits, which would be gainfully utilized in future barley improvement programmes.

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## 5. CNA-405 (IC0613959; INGR15005), a Cotton (*Gossypium arboreum* L.) Germplasm with Narrow Leaf Lobes and Brown Lint

**Punit Mohan*, BR Rode, KR Kranthi, Sujata Saxena, Ravi Nagarkar and V Santhy**
*ICAR-Central Institute for Cotton Research (CICR) Shankar Nagar, P.O., Nagpur-440010, Maharashtra, India*
**(Email: punitmohan@gmail.com)*

A light brown linted genetic stock, CNA-405 (INGR 15005) of *Gossypium arboreum* was developed by pedigree selection. The unique feature of this genotype is that it possesses: staple length (26.3mm); fibre uniformity ratio (49 %); micronaire (4.3); fibre tenacity (19.2 g/tex) and fibre maturity (76 %). The genetic stock is characterized by okra leaf shape, yellow flower petal with presence of spot, yellow pollen colour, pigmented anther filament, green and ovate boll, pitted boll surface, pointed boll tip and light brown seed fuzz colour which are major DUS characters. The lint colour is light brown with good colour stability.

## 6. NRCSFR-07-5 (IC0611700; INGR15006), a Sorghum (*Sorghum bicolor* (L.) Moench. ) Germplasm Resistant to Shoot Fly

**C Aruna*, PG Padmaja, VR Bhagwat and JV Patil**
*ICAR-Indian Institute of Millets Research (IIMR), Rajendranagar, Hyderabad-500030, Telangana, India*
**(Email: aruna@sorghum.res.in)*

Sorghum shoot fly, *Atherigona soccata* Rondani is one of the major pests that destabilizes the performance of sorghum cultivars and ultimately reduces sorghum production in many parts of the world. It causes damage to the late sown crop in *kharif* and early sown crop in *rabi.* The seriousness of the shoot fly problem in sorghum, combined with the high costs and toxicity hazards of using chemical control, renders it necessary to develop new varieties or hybrids that possess resistance to this pest. In order to incorporate resistance into sorghum parental lines, intensive breeding efforts were initiated at DSR, by crossing the elite parental lines with shoot fly resistant germplasm.

A series of crosses were made during 2003-2006 by using the elite parental lines and the shoot fly resistant sources from germplam such as IS18551, IS2312, IS2122 and RSE 03. The $F_2$ population was sown by mid July, so that the plants are exposed to sufficient shoot fly pressure. From $F_3$ onwards, selections were made in the shoot fly nursery where high pest population is build up. The seed of the resistant $F_6$ progenies was multiplied and the genotypes were tested in multilocation under AICSIP.

The line NRCSFR 07-5 is the derivative of one such cross involving 27B x IS 2122. This line was tested under AICSIP for 4 years (*Kharif* season of 2007 to 2010). NRCSFR 07-5 was observed to perform better than the elite parent, 27B which recorded 71.5% shoot fly deadhearts

The data on shoot fly eggs/ plant, flowering and plant height of this improved source of resistance is given Table 1. It showed less number of shoot fly eggs compared to its elite parent, 27B. The plant height is also less than the resistant check, IS18551 showing improvement in agronomy over the resistant check.

**Table 1. Ancillary data of the improved sources of resistance for *kharif* across years in AICSIP trials**

| Genotype | Shoot fly eggs/ 5 plants | Days to 50% flowering | Plant height (cm) |
|---|---|---|---|
| NRCSFR 07-5 | 6.13 | 68 | 154.5 |
| 27 B | 12.2 | 69 | 124.7 |
| IS18551 | 5.7 | 78.4 | 220.4 |
| DJ 6514 | 13.7 | 70.7 | 158.7 |
| CD 5% | 3.87 | 8.85 | 62.2 |
| CV (%) | 31.7 | 5.66 | 22.3 |

NRCSFR 07-5 with resistance and improved agronomy can be used as the source in the shoot fly resistance breeding program aiming at development of parental lines and genotypes with shoot fly resistance along with agronomic acceptability.

## 7. JI-258 (IC0611596; INGR15007), an Early Maturing Male Line of Castor (*Ricinus communis* L.) with Resistance to Wilt

**Rajnikant H Kavani*, Rajesh Kumar Madariya and Keshavji L Dobariya**
*Main Oilseeds Research Station (MORS), Junagadh Agricultural University, Junagadh-362001, Gujarat, India*
*(Email: rhkavani@rediffmail.com)*

Castor (*Ricinus communis* L.) is an important industrial non-edible oilseed crop grown in various countries throughout the world. Castor oil is used for number of industrial products. During the year 2014-15, the area under castor crop in India was 10.99 lakh ha, which contributed 13.51 lakh metric tonne production with a productivity of 1229 Kg/ha. Gujarat is the leading state in the country with respect to area, production and productivity of castor covering an area of 7.34 lakh ha with the production to 10.69 lakh tonne and average productivity of 1454 Kg/ha (Anonymous, 2015). Continuous cultivation of castor in the same areas has led to several fold increase in the occurrence of soil-born wilt disease caused by *Fusarium oxysporum* f.sp. *ricini* (Wr) Gordon. It is one of the major yield reducing factors in castor and cause 39-77% yield loss depending on the stage at which the plants wilt (Pushpavati, 1995). Chemical treatments are not efficient in controlling the disease (Siddaramaiah *et al*., 1980). Cultivation of wilt resistant cultivars was proved to be an effective strategy to minimize losses. There is a need for identification of diverse sources of resistance to wilt to sustain wilt resistance in castor since the existing wilt resistant cultivars are no more effective in controlling the disease as they showed moderate to high susceptibility (40-100% wilt incidence). This was because of utilization of the same source of resistance repeatedly in wilt resistance breeding programme.

The line JI-258 was developed by Junagadh Agricultural University, Junagadh using different sources for wilt resistant following pedigree selection in a segregating population of a double cross (SKP-92 x JI-85) x VP-1 x EC-97704). This genotype was found to be resistant in wilt sick plot at DOR, Hyderabad, SK Nagar and Palem during different years of testing and also early maturing with high yield potential. JI-258 was also found resistant reaction against most of the isolates of Fusarium wilt. The genetic stock has a potential to use in the heterosis breeding as a diverse source of Fusarium wilt resistance. The chief botanical and morpho-agronomic traits of JI-258 are given in Table 1.

**Table 1. Chief botanical and morpho-agronomic traits of JI-258**

| Trait | JI-258 |
|---|---|
| Stem color | Red |
| Bloom | Triple bloom |
| Capsule | Spiny |
| Nodes up to primary raceme | 16 |
| Internode type | Elongate |
| Days to 50% flowering | 49 |
| Plant height up to primary raceme | 48 cm |
| Branching nature | Divergent |
| Interspersed staminate flower | Present |
| Spike compactness | Loose |
| Capsule size | Medium |
| 100-seed weight | 34-35 g |
| Seed color | Light chocolate |
| Seed mottling | Conspicuous (High) |
| Seed caruncle | Present |

## References

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Pushapavati B (1995) Role of *Fusarium oxysporum* f.sp. *ricini* (Wr) Gordon in castor wilt complex. Hyderabad, India: Andhra Pradesh Agricultural University, *M. Sc (Ag) Thesis.*107 p.

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# 8. RG 19 (IC0612166; INGR15008), an Extra-Early Maturity, Non-Spiny Castor (*Ricinus communis* L.) Germplasm

**K Anjani**

*ICAR-Indian Institute of Oilseeds Research (IIOR), Rajendranagar Hyderabad-500030, Telangana, India*

**(Email: anjani_kammili@rediffmail.com)*

RG19 is an extra-early castor germplasm selection which flowers in 30 days and matures in 82 days after planting. It was selected in 1991 from a heterogeneous population of an exotic collection EC168752 introduced from Hungary. EC168752 segregated for low node number ranging from 5 to 14. Since node number is associated with days to maturity in castor, the plants having less than 10 nodes with similar morphological traits were selected from the source and the plants with 7-8 nodes were finally stabilized through pedigree selection for low node number. These plants were then bulked and the original ID No. RG19 was given to this bulk for maintaining as an extra-early maturing germplasm accession in castor germplasm repository. RG19 was further self-pollinated for seven generations to bring in genetic homogeneity for the unique trait. It has red stem with single bloom and elongated internodes. Its capsules are non-spiny, medium size, non-dehiscent and green in colour. It flowered and matured about 42 and 44 days earlier than the early check variety, DCS-9. It has 7-8 nodes on main stem. Its 100-seed weight was 23 g, and the yield realized at 120 days after planting was 67 g/plant and the total yield was 131 g/plant while these were 86 g/plant and 202 g/plant, respectively in the early check variety DCS 9 ( Anjani, 2010)

## References

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# 9. VRP-500 (IC610501; INGR15009), a Garden pea (*Pisum sativum)* Germplasm with Triple Pods at Every Node

**Satish Kumar Sanwal*, Rajesh Kumar and B Singh**

*ICAR-Indian Institute of Vegetable Research (IIVR), Shahanshahpur, Varanasi-221 305, Uttar Pradesh, India*

*(Email: satishsanwal@rediffmail.com)*

In garden pea, most of the varieties/germplasm lines have single pod on each node while few varieties have double pod. But this is the first genetic stock which has triple pod on every node. Due to higher number of pods, the yield/plant is just double than other pea varieties. Developing three pods per node increased yield over one pod and two pods per node (Gritton, 1986). This line was developed through hybridization between VRP-5 (single pod at each node and early in maturity) and PC-531 (double pods at each node and medium in maturity) followed by selection. Crosses were made in 2007 at research farm of Indian Institute of Vegetable Research (IIVR), Varanasi. Single plant selection was done in F3 generation and plant to row progeny was maintained. Now this line is almost homozygous and stable.

**Morpho-agronomic characteristics:** The plant height of VRP-500 varies from 130-137 cm with an average of 134.7 cm. It takes 52 days for days to 50% flowering. First flower appears on 13$^{th}$ node. First green pod harvesting can be done 70-75 days after sowing. Pods are 8-9 cm in length, green in colour and slightly curved and have 8-9 seeds/pod. Average yield/plant is 176-190 g and shelling percent is 48-49.

**Associated characters and cultivation practices:** VRP-500 is susceptible to powdery mildew but can escape if sowing is done from 25$^{th}$ October to 5$^{th}$ November. It is tolerant to leaf minor. Pea requires cold and dry climate while longer cold spell increases its yield. In north India, it is sown during October-November, while in hilly areas (Shimla), June-July is ideal sowing time. The optimum temperature for seed germination is about 22±2$^{o}$C, however, it can germinate up to 5$^{o}$C but at slow rate. Sowing should be done in lines at a spacing of 30 x 5 cm. Spraying of Stomp 30 EC (pendimethalin) @2.5 liter per ha within 72 hours of sowing checks weed population up to 30-35 days. Irrigation should be applied at flowering stage through sprinkler system. Harvesting of green pods must be done at a proper stage.

## References

Gritton ET (1986) Pea breeding. In: MJ Bassett (ed.) *Breeding Vegetable Crops*, AVI Pub. Comp. Inc., Connecticut, USA.

**Table 1. Morpho-agronomic characters of VRP-500**

| Characters/genotypes | VRP-500 | Characters/genotypes | VRP-500 |
|---|---|---|---|
| Plant height (cm) | 134.7 | Pod width (cm) | 1.46 |
| Days to 50% flowering | 52 | No. of pods/plant | 22-24 |
| First flowering node | 13.0 | 10 pod weight (g) | 80 |
| Pod colour | Green | Seed/pod | 8.0 |
| Pod shape | Slightly curved | Yield/plant (g) | 176-190 |
| Pod length (cm) | 8.2 | Shelling percent | 48.5 |

## 10. L-4602 (IC0595543; INGR15010), a Lentil (*Lens culinaris* Medikus.) Germplasm with Tolerance against Aluminium Toxicity under Low pH Conditions

**Dharmendra Singh*, Harsh Kumar Dikshit, Dayachand and Dulichand**
*ICAR-Indian Agricultural Research Institute (IARI), Pusa Campus-110112, New Delhi, India*
*(Email: dharmendrapbg@rediffmail.com)*

L-4602' is aluminium tolerant line developed at Indian Agricultural Research Institute, New Delhi, through hybridization followed by pedigree method involving parents L-830 and Precoz. The genotype is unique with respect to high level of tolerance to aluminium.

**Morpho-agronomic characteristics:** L-4602 produces light green foliage with erect and profuse branching. The plants are medium tall with light green leaf colour. The seeds are bold with light green testa and yellow cotyledons.

**Associated characters and cultivation practices:** Aluminium stress tolerant line 'L-4602' alongwith check were evaluated under hydroponic, soil culture and natural field conditions at four locations. The line 'L-4602' revealed higher root and shoot length, dry weight of root and shoot and seed yield/plant than check L-4076 under long term hydroponic and soil culture conditions. This line was also evaluated at various locations of Central Agricultural University, Imphal (Manipur) and ICAR Research Complex for NEH region, Basar centre (Arunachal Pradesh) during 2012-13 and 2013-14. 'L-4602' provided better yield than the check variety ('L-4076') under the most severe conditions (pH 5.0 and 5.1). Less retention of Al in roots of L-4602 restricting its transport to shoot suggests its efficient exclusion mechanism. The aluminium tolerance of 'L-4602' along with low accumulation of aluminium and callose makes it highly useful for incorporating aluminium tolerance in high yielding genotypes (Singh *et al.,* 2015). Standard agronomical cultural practices are required to raise the crop.

### Reference

Singh D, HK Dikshit and A Kumar (2015) Aluminium tolerance in lentil with monogenic inheritance pattern. *Plant Breeding*, **134**: 105-110

## 11. CIAHZN-J (IC0598427; INGR15011), a Ber (*Ziziphus nummularia* (Burm. f.) Wight & Arn.) Germplasm with Low Moisture Stress Tolerance

**PN Sivalingam, Dhurendra Singh, R Bhargava and SK Sharma**
*ICAR-Central Institute for Arid Horticulture (CIAH), Bikaner, Rajasthan, India*
*(Email: pnsivalingam@gmail.com)*

*Ziziphus nummularia* is well distributed and growing as wild in Jaisalmer district, the north-western parts of Rajasthan where the average annual rainfall is less than 150mm (Pareek, 2001; Pandey *et al.,* 2010). The stones of CIAHZN-J were collected and tested for moisture stress tolerance and compared with *Z. nummularia* from Bikaner and Godhra (Gujarat), *Z. mauritiana* and *Z. rotundifolia.* Seeds of CIAHZN-J had 64 per cent germination at -0.5 MPa and it has ability to germinate at- 0.73 MPa. Whereas *Z mauritiana*, *Z. rotundifolia, Z. nummularia* from Bikaner and Godhra had 10, 28, 42 and 57 per cent germination, respectively at -0.5 Mpa. Increased root length from 10 to12 cm and the ratio of root dry weight to fresh weight was 0.5 found in CIAHZN-J genotype at 0.5MPa. Withdrawing water up to 15 days to three months old seedlings of CIAHZN-J genotype showed the average cumulating morphological stress rating of 3.0, maintaining relative water content of more than 60 %, downward rolling of leaves and maintaining membrane stability at normal level during stress are the unique features of this genotype. Stomatal conductance of CIAHZN-J was 256.5 mmol/$m^2$/sec, proline level was increased by 35 fold and catalase increased by two fold during stress compared to control. Other genotypes reached average cumulating morphological stress rating of 3.0 lesser than 15 days and increased proline level by 10-25 fold during stress compared control. This genotype has very higher tolerance to moisture stress compared *Z. mauritiana* and *Z. rotundifolia*.

## References

Pandey A, R Singh, J Radhamani and DC Bhandari (2010) Exploring the potential of *Ziziphus nummularia* (Burm. f.) Wight et Arn. from drier regions of India. *Genet. Resour. Crop Evol*. **57:** 929-936.

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# 12. Sel-13 (IC0610821; INGR15012), a Makhana (*Euryale ferox* Salisb.) Germplasm with Bold Seeds (Seed Diameter: 14 mm). Highest 100-Seed Weight (141g)


**Lokendra Kumar**

*ICAR-RCER Research Centre for Makhana (RCM), Darbhanga-846005, Bihar, India*

**(Email: dr.lokendrakumar@yahoo.com)*


In makhana, the size and color of lawa (popped seeds) are the two main criteria of its market value (Choudhary *et al.,* 2003).The bigger and white lawa is considered the best one while the small and yellowish one is the poorest in its marketing. In this way, bold seeded genotypes of makhana are highly desirable as they are more remunerative for farmers.

**Morpho-agronomic characteristics:** The seeds of Sel-13 genotype are bold in size (13.47 mm) and deep black in colour (Table1). Leaves are large (142.30 cm) and green. The number of fruits/plant is low (10.25) but their size is large (7.20cm). The number of seeds /fruit is medium (42.50). Bigger size of seeds is a highly desirable trait in makhana crop. Owing to this trait, the line can be utilized as a potential material for incorporating the bold seeded trait in makhana crop.

**Table 1. Descriptor and descriptor state of Sel-13 (IC0610821) genotype of makhana (average over 4 years)**

| Descriptor | Descriptor state |
|---|---|
| Days to seedling emergence | 37.25 |
| Seedling vigor | High |
| Leaf shape | Orbicular |
| Leaf diameter | 142.3cm |
| Flower size | Large |
| Flower color | Purple |
| Days to 50% flowering | 133.75days |
| Fruit shape | Spheroid |
| Fruit color | Whitish brown |
| Status of fruit prickles | Dense |
| Size of fruit prickles | 1.3 cm |
| Fruit diameter | 7.20cm |
| Number of seeds/fruit | 2.50 |
| Number of fruits/plant | 10.25 |
| Seed yield /fruit | 55.72 g |
| Seed yield /plant | 580.62 g |
| Seed color | Deep black |
| Seed shape | Spherical |
| 100-seed weight | 134.97 g |
| Seed diameter | 13.47 mm |


## Reference

Choudhary JN, Om Prakash, PK Jha and ON Jha (2003) Economic analysis of production and marketing of Makhana in Bihar. *In:* RK Mishra, Vidyanath Jha and PV Dehadrai (eds.) *Makhana.* Indian Council of Agricultural Research, New Delhi, India, pp 107-123.

# 13. Sel-14 (IC0610822; INGR15013), a Makhana (*Euryale ferox* Salisb.) Germplasm with Irregular Seed Shape (mutant), Large Fruit Size (Fruit Diameter: 8.1 cm). Highest Number of Seeds/Fruit (139)

**Lokendra Kumar**
*ICAR-RCER Research Centre for Makhana (RCM), Darbhanga-846005, Bihar, India*
**(Email: dr.lokendrakumar@yahoo.com)*

Makhana is an important plant of low land ecosystem of north Bihar, West Bengal, Assam, Manipur and Orissa. Matured seeds are the most economic part of makhana which are transformed into their popped form for its utilization as a dry fruit commodity (Jha and Barat, 2003) .The seed yield of makhana is determined by various traits, such as, fruit diameter, number of fruits per plant, number of seeds per fruit, number of seeds /plant, seed size and 100-seed weight (Kumar *et al.,* 2011).

**Morpho-agronomic characteristics:** In contrast of round seeds (normal shape), the seeds of sel-14 genotype are irregular in shape and deep black in colour (Table1). Leaves are large and green. The diameter of fruits is large (7.9cm) and number of seeds per fruit is high (1507.7). Fruits are covered with sharp and dense green prickles. Large fruit size and high number of seeds per fruit is the two main components of seed yield in makhana. These two desirable attributes may be exploited for development of high yielding genotypes of makhana. Further, this genotype is very peculiar due to its seeds' shape (irregular shape). Owing to this trait, this genotype may be utilized for inheritance study of seed shape in makhana crop.

**Table 1. Descriptor and descriptor state of Sel-14 (IC0610822) genotype of makhana (Mean over 4 years)**

| Descriptor | Descriptor state |
|---|---|
| Days to seedling emergence | 51.75 |
| Seedling vigor | High |
| Leaf shape | Orbicular |
| Leaf diameter | 144.52cm |
| Flower size | Large |
| Flower color | Purple |
| Days to 50% flowering | 162.0days |
| Fruit shape | Spheroid |
| Fruit color | Brownish |
| Status of fruit prickles | Dense |
| Size of fruit prickles | 1.5 cm |
| Fruit diameter | 7.92cm |
| Number of seeds/fruit | 129.75 |
| Number of seeds /plant | 1507.75 |
| Number of fruits/plant | 11.75 |
| Seed yield /fruit | 73.92g |
| Seed yield /plant | 878.05g |
| Seed color | Black |
| Seed shape | irregular |
| 100-seed weight | 59.6 g |
| Seed diameter | 6.0 mm |

## References

Jha V and GK Barat (2003) Nutritional and medicinal properties of *Euryale ferox* Salisb. *In:* RK Mishra, Vidyanath Jha and PV Dehadrai (eds.) *Makhana.* Indian Council of Agricultural Research, New Delhi, India, pp 107-123.

Kumar L, VK Gupta, BK Jha, IS Singh, AK Singh and BP Bhatt (2011) Status of Makhana (*Euryale ferox* Salisb.) cultivation in India. ICAR-RCER, Patna, *Technical Bulletin* No.R- 32/ PAT-21. 31p.

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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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## CONTENTS



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