



## Development of random mating population for genetic enhancement of yield traits in Indian mustard (*Brassica juncea*)

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Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is a predominantly grown oilseed crop in India among the rapeseed-mustard group of crops. Although, this crop is considered as self pollinated but fairly a high degree of cross pollination has been reported. Chauhan *et al.* (1987) reported out crossing up to 24% in this crop, whereas many workers reported extent of out crossing from 7.6 to 18.1% (Labana and Banga 1984), 6.5 to 9.8% (Abraham 1994) and 16.6% (Ram Bhajan *et al.* 1991) which indicates certain level of heterozygosity and suggests use of population improvement as a long term breeding strategy for exploitation of hidden variability, thus making available for selection. Moreover, Brassica researchers have been successful in the development of pure line varieties or hybrid parents through exploitation of available genetic variability by direct selection and by the use of conventional methods, i.e. pedigree and backcross breeding. These methods produce varieties with a relatively narrow genetic base, accumulate linkage blocks due to rapid fixation of genes and limit recombination.

On the other hand, population improvement procedures offer more opportunities for recombination to break linkages between desired and undesired traits and provide long term breeding strategy to derive diverse and broad genetic based superior varieties/hybrid parents (Bhola Nath 1982). Review of literature indicated that a systematic population improvement programme for genetic enhancement of yield components is scanty in Indian mustard. Keeping these facts in view, a population development programme has been initiated for genetic enhancement of siliqua characteristics (siliquae/plant, seeds/siliqua and siliqua length), 1000 seed weight and seed yield as a whole.

Initial material for present investigation consisted of germplasm and advanced breeding lines which were selected on the basis of their superiority for siliqua characteristics

and 1000 seed weight from a pool of germplasm maintained at Directorate of Rapeseed Mustard Research (DRMR), Bharatpur. Seeds of twenty germplasm lines, viz. NPJ 99, SEL 2, SEL 13, SEL 15, IC 248994, IC 248995, IC 261670, IC 312514, IC 312525, IC 344294, BPR 171, MRW J-2001-18, KLM 134, NRCDR 509, RRN 609, NPJ 114, JM WR 908-1, PHJ 03, RRN 604, RL 2047 were collected from germplasm section of DRMR while seeds of 05 promising lines RH 0207, RH 0119, RH 0204, RH 0502, RH 0401 were procured from Chaudhary Charan Singh Agricultural University (CCSHAU), Hisar. Seeds of SKM 9585 and GM 2 were supplied by SDAU, Sardar Krushi Nagar. Equal amount of seed of these donors was mixed and grown at experimental area of DRMR during 2007-08 in isolation distance of 100 metre. About 500 plants were randomly selected from this isolation and tagged. Hand emasculation was done in tagged plants and about 300 plants were completely emasculated and allowed to cross pollinate/ random mate so that pollen from any other plant could pollinate the emasculated plant. At the maturity time, seed set on emasculated buds was harvested to make a population. During 2008-09, random cross pollinated seeds obtained from emasculated plants during 2007-08 were mixed again and grown in isolation. About 300 plants were completely emasculated and left open for random mating. The seeds set in emasculated plants were harvested. This seed was again mixed and grown in isolation during *rabi* 2009-10. All recommended package of practices were followed to raise a healthy crop. About 250 superior plants on the basis of phenotype were selected and tagged. While selecting plants main emphasis was given on number of siliquae/plant, siliqua length, boldness of the seed and yield potential of the plant. These individual plants were harvested and threshed separately and considered as Half Sibs because we had to control only on one parent at the time of random mating, i.e. female. Finally, 180 half sibs were used for evaluation. Half sibs (180) so developed were evaluated during *rabi* 2010-2011 in an augmented block design. The material was divided into six blocks; each block consisted of 30 progenies and 4 check varieties namely, Kranti, Maya, Bio 902 and RGN 73 and which were common to each

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block. In each block, progenies and check varieties were sown in 2 row plots of five meter length, spaced 30 cm apart with plant to plant distance of 10 cm achieved by thinning at 15-20 days after sowing. Recommended package of practices were followed to raise a healthy crop. Observations were recorded on siliquae/plant, siliquae length, seeds/siliqua, seed yield/plant and 1000-seed weight. Ten plants were randomly selected from each plot to record the data.

The mean data were subjected to analysis of variance as per the method suggested by Fedrer (Fedrer 1956). Genetic parameters were calculated as per standard procedure (Burton 1952, Johnson *et al.* 1955).

Usefulness of population improvement is realized when readily usable genetic variability for yield traits is accumulated in population which can be exploited in deriving superior pure lines or hybrid parents. In augmented design, evaluation of checks is first done to get an estimate of error, which is used for getting adjusted mean of entries. Evaluation of 180 half sib progenies showed significant differences for the traits, viz. siliquae/ plant, siliquae length, seeds/siliqua, seed yield/plant and 1000-seed weight suggesting the estimate of significant variation among the entries (Table 1). These results support scope of selection programme for high yielding genotypes. Mean sum squares due to blocks were found to be non-significant for all the characters studied which indicate less influence of environment on phenotypic expression. Check v/s progenies exhibited significant differences for all the characters this indicates differences between checks as a group and progenies as another group.

Estimation of genetic components for the characters revealed that the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters under study indicating influence of environment on character expression. However, differences between GCV and PCV in the present material are relatively narrow suggesting their relative tolerance to environmental changes. Seed yield/plant followed by siliquae/plant showed higher estimates of genotypic as well as phenotypic coefficient of variation as compared to other characters (Table 2 )

Table 1 Mean sum of squares for different morpho-physiological characters in half sib progenies of Indian mustard.

| Source             | df  | Siliquae length | Siliquae/ plant | Seeds/ siliqua | Seed yield/ plant (g) |
|--------------------|-----|-----------------|-----------------|----------------|-----------------------|
| Block              | 5   | 0.08            | 230.9           | 0.56           | 30.4                  |
| Treatment          | 183 | 0.12*           | 5283.1**        | 3.3**          | 24.6**                |
| Control            | 3   | 0.12            | 5285**          | 0.66           | 29.5**                |
| Progeny            | 179 | 0.12*           | 5282.7**        | 3.3**          | 24.0**                |
| Progeny vs control | 1   | 0.71**          | 5317**          | 7.7**          | 127.0**               |
| Error              | 15  | 0.05            | 108.8           | 0.40           | 4.80                  |

\*\* Significant at 1% level, \* Significant at 5% level

Table 2 Over all mean value of half sib progenies, their range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance expressed as % of mean

| Character             | Mean   | Range      | GCV   | PCV   | h <sup>2</sup> | GA    |
|-----------------------|--------|------------|-------|-------|----------------|-------|
| Siliquae length       | 3.94   | 3.1-5.13   | 6.76  | 8.79  | 59.16          | 10.68 |
| Siliquae/plant        | 314.17 | 166-526    | 22.89 | 23.09 | 97.94          | 46.65 |
| Seeds/siliqua         | 13.29  | 7.81-17.40 | 12.79 | 13.64 | 87.84          | 24.68 |
| Seed yield/ plant (g) | 14.51  | 4.6-32.35  | 30.19 | 33.73 | 80.13          | 55.68 |
| 1000 seed weight (g)  | 5.17   | 3.2-6.57   | 6.86  | 8.62  | 63.32          | 11.19 |

GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation; h<sup>2</sup>, Heritability; GA, Genetic advance expressed as per cent of mean

suggesting that selection may be exercised directly for these traits. Earlier Singh *et al.* (2009) made similar reports. The estimate of GCV and PCV alone is not much helpful in determining the heritable portion. The amount of advance to be expected from selection can be achieved by estimating heritability along with coefficient of variability. The estimates of heritability in present investigation were observed to be high 59.16 to 97.94% for all the characters. The high degree of estimates for these traits suggested their genetic control. These results are in agreement with earlier reports (Singh *et al.* 2009, Singh *et al.* 2011). High heritability coupled with high genetic advance and GCV were observed for siliquae/ plant and seed yield/plant. From the study of heritability and genetic advance it can be concluded that simple selection among half sib progenies can bring about significant improvement in these traits. The expected genetic advance might have been biased upward as it is based on the estimates of heritability in broad sense, secondly in the augmented design the estimation of mean squares due to the error is based on the check variety only. Hence, it might have given the high estimates of genetic variances in it.

Based on the adjusted mean values of half sib progenies, promising progenies which showed significant superiority over best check, were selected (Table 3). Range of significantly superior progenies selected for five traits varied from 1.66% (03) to 39.44% (71). Maximum number of half sib progenies showed significant superiority for 1000 seed weight (39.44%) followed by seed yield/plant (10.55%), siliquae length (5.5%), siliquae/plant (5%) and seeds/siliquae (1.66%). These progenies may be utilized for initiation of second cycle of selection/development of trait specific gene pools. Conclusion that can be drawn from this experiment states that *Brassica juncea* breeders should include population development programme as a long term strategy for creating variability and development of gene pools.

SUMMARY

A random mating population of Indian mustard

Table 3 Significantly superior half sib progenies selected for yield components in Indian mustard

| Character            | Selected superior half sib progenies   |
|----------------------|--|
| Siliquae length (cm) | YHS 1 (4.52), YHS 10 (4.49), YHS 13 (4.67), YHS 23 (4.55), YHS 26 (4.62), YHS 36 (4.85), YHS 77 (4.53), YHS 95 (4.53), YHS 117 (5.12), YHS 144 (5.13) (Total 10)<br>Value of best check (Bio 902) = 3.94, CD (5%) = 0.55   |
| Siliquae/plant       | YHS 12 (417.2), YHS 16 (482.2), YHS 67 (456.5), YHS 90 (511.4), YHS 147 (501.2), YHS 153 (417), YHS 169 (418), YHS 175 (414), YHS 177 (526) (Total 09)<br>Value of best check (RGN 73) = 384.16, CD (5%) = 26.06   |
| Seeds/siliqua        | YHS 53 (17.4), YHS 147 (16.01), YHS 149 (17.01) (Total 03)<br>Value of best check (Krantti) = 14.25, CD (5%) = 1.57  |
| Seed yield/plant     | YHS 3(25.9), YHS 7(26), YHS 9 (21), YHS 10 (21), YHS 12 (28.5), YHS 14 (26) YHS 15 (21), YHS 147 (16.01), YHS 149 (17.01), YHS 151 (15.34), YHS 152 (15.67), YHS 162 (15.45), YHS 169 (15.01) YHS 170(22.35), YHS 171(27.35), YHS 172 (27.35), YHS 174 (32.35), YHS 175 (22.35), YHS 179 (22.35)<br>Value of best check (Maya) = 15.33, CD (5%) = 5.45(Total 19)   |
| 1000 seed weight (g) | YHS 4(5.69), YHS 7(6.08), YHS 9 (5.41), YHS 21 (5.41), YHS 30 (5.53), YHS 32 (5.59), YHS 33 (5.59), YHS 34 (5.40), YHS 35 (5.93), YHS 39 (5.52), YHS 46 (5.98), YHS 47 (5.82), YHS 48 (5.44), YHS 49(5.55), YHS 54(5.67), YHS 55 (5.82), YHS 56 (5.51), YHS 57 (5.71), YHS 58 (5.94), YHS 59 (6.44), YHS 60 (6.31), YHS 61(6.04), YHS 62 (5.96), YHS 63(5.52), YHS 68 (6.02), YHS 69 (5.85), YHS 70 (5.43), YHS 76 (5.43), YHS 78 (5.39), YHS 79 (5.54), YHS 85 (5.95), YHS 86(5.73), YHS 87 (5.47), YHS 91(5.43), YHS 92(6.57), YHS 101 (6.23), YHS 102 (5.99), YHS 107 (5.59), YHS 108 (5.57) , YHS 109 (6.10) YHS 110 (5.81), YHS 111(5.40), YHS 115 (5.55), YHS 117(6.07), YHS 121 (5.42), YHS 122 (5.61), YHS 123(5.56), YHS 125 (5.52), YHS 126 (5.57), YHS 132 (5.52), YHS 133 (5.41), YHS 135(5.52), YHS 139 (5.42), YHS 141(5.68), YHS 143(5.60), YHS 146 (5.61), YHS 148 (5.96), YHS 149 (5.72), YHS 150 (5.74) , YHS 153 (6.08), YHS 155 (5.51), YHS 156 (5.61) , YHS 158 (5.38), YHS 161 (5.87), YHS 163 (5.51), YHS 165 (5.68), YHS 166 (5.40), YHS 167 (167) , YHS 173 (5.38), YHS 174 (5.73), YHS 175 (5.46) Value of best check (Maya) = 4.71, CD (5%) = 0.67 (Total 71) |

YHS, Yield half sibs

[*Brassica juncea* (L.) Czern. & Coss.] utilizing 20 germplasm accessions/promising donors for component traits, was developed from 2007-08 to 2009-10. Single plant progenies (180) termed as 'half sibs' were developed from this population and evaluated during 2010-11 in augmented block design along with standard checks. Observations were recorded on siliquae/ plant, siliquae length, seeds/siliqua, seed yield/plant and 1000-seed weight. The estimates of heritability were observed to be high 59.16 to 97.94% for all the characters. High heritability coupled with high genetic advance and GCV were observed for siliquae/plant and seed yield/plant. Maximum number of half sib progenies showed significant superiority for 1000 seed weight (39.44%) followed by seed yield/plant (10.55%), siliquae length (5.5%), siliquae/plant (5%) and seeds/siliqua (1.66%). These progenies may be utilized for initiation of second cycle of selection/development of trait specific gene pools.

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