

Original Research Article

Genetic Analysis of Siliqua per Plant and Seed Yield per Plant in Mustard (*Brassica juncea*)

Shanti Patil*, Vandana Kalamkar, R. D. Deotale, S. R. Kamdi,
Ommala Kuchanwar and Neha Chopde

College of Agriculture, Nagpur (Dr. P.D.K.V, Akola), MS, India

*Corresponding author

ABSTRACT

Genetic analysis was performed in BIP progenies developed in F₂ generation of two intervarietal crosses ACNM-2 x ACNM-11 and ACNM-2 x ACNM-5 of mustard using NCD II during 2016 to 2017 at Botany Section, College of Agriculture, Nagpur. The variance due to females (σ^2_f) were high as compared to variance due to males (σ^2_m) for both the characters in BIP progenies of ACNM-2 x ACNM-11 and variance due to males (σ^2_m) were high as compared to variance due to females (σ^2_f) in BIP progenies of cross ACNM-2 x ACNM-5. Additive variance was more pronounced than dominant genetic variance for both the traits. The broad sense heritability were high for all the characters in all the two crosses. High genetic advance was recorded for number of siliqua plant⁻¹ and seed yield plant⁻¹ in both the two crosses. Response to selection in percentage were high for number of siliqua plant⁻¹ and seed yield plant⁻¹ in both the crosses. Heritability estimates combined with genetic advance as percentage of mean revealed that, in the BIP progenies of all the two crosses, high broad sense heritability estimates were coupled with high genetic advance as per cent of mean for number of siliqua plant⁻¹ and seed yield plant⁻¹. This indicates that selection would be effective in improving number of siliqua plant⁻¹ and seed yield plant⁻¹ and hence, should be given priority for selection of significantly superior BIPs. Fourteen BIPs of ACNM-2 x ACNM-11 and six BIPs ACNM-2 x ACNM-5 were found to be significantly superior over checks and were selected for forwarding to the next generation and selection based on progeny testing through either half sib or full sib progeny should be followed till homozyosity is attained.

Keywords

Mustard, North Carolina design- II, Heritability, Genetic advance

Introduction

The oilseed crops *Brassica* are the third most important edible oil source after soybean and palm, accounting for over 13.2 per cent of the world's edible oil supply. In India, rapeseed and mustard are the second most important oilseed crops after groundnut contributing about 30 per cent of the total oilseed production (Saksena, 2001). However, the productivity of these *Brassic*as in India as compared to the world average of 1333 kg ha⁻¹ (Ganga Rao and

Gulati, 2001). Among these mustard (*B. juncea* L.) is the most important accounting for more than 75 per cent of the area under rapeseed and mustard followed by Indian rapeseed. Indian rapeseed (*B. campestris*) has three agro-morphologically distinct ecotypes namely, brown sarson, yellow sarson and toria. Genetically diverse crosses exhibit higher frequency and magnitude of heterosis for yield. A composite of such hybrid population can be developed to

initiate a population improvement programme. The extent of genotypic differences consequent upon recombination through random mating in such composite population determines the extent of gain from such selection.

The important breeding programme in mustard is oriented to develop new varieties with high yield potential, wider adaptability, disease resistance, high oil content and quality traits. Availability of variability in the germplasm is the prerequisite for making any improvement. Segregating generation obtained by crossing distant parent is one of the popular source for increasing variability out of many other sources of conventional breeding methods such as pedigree, bulk and back cross breeding with some modifications which are the principal procedures followed in the improvement of self-pollinated crops. Such procedures though significant and productive in their own way, impose restriction on the chance of releasing better recombination because of larger linkage blocks associated with the weakness of causing rapid homozygosity and low genetic variability (Clegg *et al.*, 1972). Considerable efforts have been made in past to improve the production and yield of mustard. High heterotic response observed in F_1 persisted to a considerable extent in the F_2 and subsequent advanced generations. Mating of randomly selected plants in the segregating generations of the heterotic crosses needs exploitation. This will not only be helpful in creating greater variability by breaking tight and unfavourable linkages for effective selection over a longer period but also create new populations with high frequencies of rare combinations (Dhameliya and Dobariya, 2009; Kanwar and Korla, 2004). Before such populations can be used for the genetic improvement, an efficient breeding methodology has to be formulated. For this

purpose, information would be required on the relative proportion of additive and non-additive variances.

The effectiveness of selection in different population improvement methods is based on the utilization of additive gene effects (Sprague, 1996). Comparable estimates of genetic variance components can be made in a composite population using suitable mating designs. The diallel mating design has been used more extensively than any other design for genetic analysis in Indian rapeseed. Genetic analysis using North Carolina designs of Comstock and Robinson (1948, 1952) are lacking, if not at all, in Indian rapeseed. Line x tester analysis, a factorial mating design similar to North Carolina Design II (NCD II) has been used to a limited extent in this crop. Model II analysis of NCD II experiment provides estimates of genetic variance component in a composite population for comparing gains from different methods of selection. In the present study, two crosses derived from local lines were subjected to NCD II analysis for understanding the nature and magnitude of gene action involved in the inheritance of yield and its attributes.

Materials and Methods

Present study was conducted at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur, during 2016 to 2017. Progenies were developed in two intervarietal crosses ACNM-2 x ACNM-11 and ACNM-2 x ACNM-5. Eight plants were randomly chosen from the F_2 generation of each cross and used as pollen (male) parents and eight plants were randomly chosen from the F_2 population of each cross and used as female parents. Each of the eight pollen plants (males) were crossed each of eight female plants. Resulting 32 progeny families were divided into two sets. The

seeds from each of the BIP crosses were harvested separately. Each set along with their parents and two check (Pusa bold and ACN-9) were planted in Randomized Block Design in two sets with three replications. Each biparental progeny was accommodated in a one row plot with a spacing of 45 x 15 cm. All the recommended package of practices like irrigation, plant protection measures etc. were followed to raise a healthy crop. Total five plants were chosen randomly from BIP progenies, parents and check for recording observations in each of two crosses. Observations were recorded on number of siliqua plant⁻¹ and seed yield plant⁻¹. The genetic analysis was done as per the method outlined by Comstock and Robinson (1948; 1952). Heritability, genetic advance and response to selection as per cent of mean were worked out as per method given by Robinson *et al.*, (1949).

Results and Discussion

Analysis of variance (Table1) revealed that the males in sets and females in sets were significant for seed yield plant⁻¹, in both the crosses ACNM-2 x ACNM-11 and ACNM-2 x ACNM-5 and non-significant for number of siliqua plant⁻¹. These results indicated that males and females had substantial contribution towards variation among progenies and there exist significant genetic differences among plants randomly chosen as parents. Similar to this result Dhameliya and Dobariya (2009) also reported the higher contribution of males as compared to females in brinjal.

The components of variance, ratio of additive to dominance and degree of dominance have been given in table 2. The variance due to females (σ^2_f) were high as compared to variance due to males (σ^2_m) for both the traits in ACNM-2 x ACNM-11 and the variance due to males (σ^2_m) were high

as compared to variance due to females (σ^2_f) for both the traits in ACNM-2 x ACNM-5. The estimate of genetic components of variance through NCD II analysis revealed that additive genetic variance (σ^2_A) were relatively more important for number of siliqua plant⁻¹ and seed yield plant⁻¹ in the BIP progenies of both the crosses.

These traits showed high estimate of additive genetic variance and negligible estimate of dominance genetic variance. The result indicated the predominance of additive genetic effects in the control of majority of the characters. In accordance with this result Kanwar and Korla (2004) also reported the predominance of dominant variances for most of the characters in BIP progenies of cauliflower.

Genetic advance estimated in BIP progenies of all the two crosses as observed from table 3 reveals that number of siliqua plant⁻¹ was the only trait in all the two crosses to record high genetic advance. Response to selection expressed in percentage of mean at 10% selection intensity when estimated, it was observed that, number of siliqua plant⁻¹ and seed yield plant⁻¹ exhibited high response to selection in the BIP progenies of all the two crosses. In accordance to this results the response to selection as per cent mean were reported to be high for most of the characters in sesame by Anuradha and Reddy (2004) and high response to selection for some characters and low for other characters were reported by Mitra *et al.*, (2009) in pearl millet.

Heritability estimates combined with genetic advance as percentage of mean revealed that, in the BIP progenies of the two crosses high broad sense heritability estimates were coupled with high genetic advance as per cent of mean for number of siliqua plant⁻¹ and seed yield plant⁻¹.

Table.1 Analysis of variance for NCD- II in BIP progenies of two crosses for different traits

| Sources | df | ACNM-2 x ACNM-11 | | ACNM 2 x ACNM -5 | |
|-----------------------|----|------------------------------------|------------------------------------|------------------------------------|------------------------------------|
| | | No. of siliqua plant ⁻¹ | Seed yield plant ⁻¹ (g) | No. of siliqua plant ⁻¹ | Seed yield plant ⁻¹ (g) |
| Sets | 1 | 17.015 | 2.472 | 1.562 | 0.018 |
| Replication in sets | 2 | 6908.515 | 16.805 | 3822.031 | 4.082 |
| Males in sets | 6 | 2316.619 | 15.646* | 4804.697 | 7.779* |
| Females in sets | 6 | 4722.828 | 19.869* | 4270.114 | 6.872* |
| Male x female in sets | 18 | 73.907 | 0.275 | 80.997 | 0.064 |
| Remainder | 32 | 2231.779 | 6.147 | 3758.308 | 2.907 |

Table.2 Estimates of variances, ratio of additive to dominance and degree of dominance in BIP progenies of two crosses

| Crosses | Characters | σ^2_m | σ^2_f | $\frac{\sigma^2_m}{\sigma^2_f}$ | σ^2_A | σ^2_D | $\frac{\sigma^2_A}{\sigma^2_D}$ | Degree of dominance |
|------------------|------------------------------------|--------------|--------------|---------------------------------|--------------|--------------|---------------------------------|---------------------|
| ACNM-2 x ACNM-11 | No. of siliqua plant ⁻¹ | 280.339 | 581.115 | # | 1722.91 | # | # | # |
| ACNM-2 x ACNM-5 | Seed yield plant ⁻¹ | 0.508 | 1.199 | # | 8.74 | # | # | # |
| ACNM-11 | No. of siliqua plant ⁻¹ | 590.462 | 523.639 | # | 2228.20 | # | # | # |
| ACNM-5 | Seed yield plant ⁻¹ | 0.964 | 0.663 | # | 3.631 | # | # | # |

Not estimated due to the negative values of either dominance variance

Table.3 Mean and range for different traits in the BIP progenies of two crosses

| Crosses | Characters | No. of siliqua plant ⁻¹ | Seed yield plant ⁻¹ |
|------------------|---------------------|------------------------------------|--------------------------------|
| ACNM-2 x ACNM-11 | Maximum | 278.50 | 10.24 |
| | Minimum | 120.00 | 2.35 |
| | Range | 158.50 | 7.89 |
| | Mean (BIPS) | 193.87 | 6.60 |
| | GCV (%) | 13.77 | 22.55 |
| | PCV (%) | 21.45 | 28.47 |
| | h ² (BS) | 41.21 | 62.74 |
| | GA | 30.17 | 2.07 |
| | GA (as % of mean) | 15.56 | 31.44 |
| ACNM-2 x ACNM-5 | Maximum | 291.50 | 8.37 |
| | Minimum | 120.00 | 3.37 |
| | Range | 172.50 | 5.00 |
| | Mean (BIPS) | 198.44 | 4.97 |
| | GCV (%) | 16.11 | 20.76 |
| | PCV (%) | 22.12 | 28.20 |
| | h ² (BS) | 53.06 | 54.20 |
| | GA | 40.09 | 1.34 |
| | GA (as % of mean) | 20.65 | 26.90 |

Table.4 Mean performance for different traits in the BIP progenies of two crosses

| Sr. No | Progenies | ACNM-2 x ACNM-11 | | Sr. No | Progenies | ACNM-2 x ACNM-5 | |
|--------|-----------------|------------------------------------|------------------------------------|--------|-----------------|------------------------------------|------------------------------------|
| | | No. of siliqua plant ⁻¹ | Seed yield plant ⁻¹ (g) | | | No. of siliqua plant ⁻¹ | Seed yield plant ⁻¹ (g) |
| 1 | ACNM211- 1 | 156.00 | 2.35 | 1 | ACNM25-1 | 189.50 | 4.84 |
| 2 | ACNM211- 2 | 227.50 | 8.32** | 2 | ACNM25-2 | 181.50 | 3.61 |
| 3 | ACNM211- 3 | 220.00 | 6.82 | 3 | ACNM25-3 | 156.50 | 4.17 |
| 4 | ACNM211- 4 | 194.00 | 6.42 | 4 | ACNM25-4 | 209.50 | 3.37 |
| 5 | ACNM211- 5 | 184.50 | 8.55** | 5 | ACNM25-5 | 261.00 | 7.21** |
| 6 | ACNM211- 6 | 240.00 | 4.48 | 6 | ACNM25-6 | 291.50 | 8.37** |
| 7 | ACNM211- 7 | 198.00 | 7.88** | 7 | ACNM25-7 | 159.50 | 5.56 |
| 8 | ACNM211- 8 | 206.00 | 7.47** | 8 | ACNM25-8 | 277.00 | 6.91* |
| 9 | ACNM211- 9 | 190.00 | 8.60** | 9 | ACNM25-9 | 263.00 | 5.48 |
| 10 | ACNM211- 10 | 183.50 | 6.75 | 10 | ACNM25-10 | 197.00 | 4.30 |
| 11 | ACNM211- 11 | 164.50 | 5.56 | 11 | ACNM25-11 | 187.50 | 4.13 |
| 12 | ACNM211- 12 | 202.50 | 6.09 | 12 | ACNM25-12 | 173.00 | 3.44 |
| 13 | ACNM211- 13 | 179.50 | 7.17* | 13 | ACNM25-13 | 220.50 | 7.11** |
| 14 | ACNM211- 14 | 181.50 | 7.41** | 14 | ACNM25-14 | 182.00 | 3.79 |
| 15 | ACNM211- 15 | 206.50 | 8.91** | 15 | ACNM25-15 | 136.00 | 3.55 |
| 16 | ACNM211- 16 | 215.00 | 7.60** | 16 | ACNM25-16 | 152.50 | 3.49 |
| 17 | ACNM211- 17 | 195.50 | 5.84 | 17 | ACNM25-17 | 176.50 | 5.01 |
| 18 | ACNM211- 18 | 256.00 | 7.75** | 18 | ACNM25-18 | 179.50 | 4.63 |
| 19 | ACNM211- 19 | 155.00 | 5.78 | 19 | ACNM25-19 | 211.00 | 5.13 |
| 20 | ACNM211- 20 | 131.50 | 4.66 | 20 | ACNM25-20 | 195.50 | 4.80 |
| 21 | ACNM211- 21 | 179.50 | 6.22 | 21 | ACNM25-21 | 195.50 | 6.74* |
| 22 | ACNM211- 22 | 201.00 | 7.70** | 22 | ACNM25-22 | 190.50 | 4.51 |
| 23 | ACNM211- 23 | 159.00 | 5.12 | 23 | ACNM25-23 | 218.50 | 4.47 |
| 24 | ACNM211- 24 | 154.50 | 4.07 | 24 | ACNM25-24 | 259.50 | 5.15 |
| 25 | ACNM211- 25 | 218.50 | 7.49** | 25 | ACNM25-25 | 200.00 | 6.77* |
| 26 | ACNM211- 26 | 235.50 | 8.36** | 26 | ACNM25-26 | 206.50 | 4.60 |
| 27 | ACNM211- 27 | 193.00 | 6.15 | 27 | ACNM25-27 | 201.00 | 4.03 |
| 28 | ACNM211- 28 | 226.50 | 5.82 | 28 | ACNM25-28 | 215.00 | 4.59 |
| 29 | ACNM211- 29 | 278.50 | 10.24** | 29 | ACNM25-29 | 219.50 | 5.92 |
| 30 | ACNM211- 30 | 231.00 | 8.85** | 30 | ACNM25-30 | 193.50 | 4.34 |
| 31 | ACNM211- 31 | 154.00 | 4.83 | 31 | ACNM25-31 | 175.00 | 4.14 |
| 32 | ACNM211- 32 | 196.50 | 5.21 | 32 | ACNM25-32 | 195.50 | 5.05 |
| Ch | ACN-9 | 157.00 | 5.10 | Che | ACN-9 | 157.00 | 5.10 |
| ec | Pusabold | 120.00 | 4.70 | cks | Pusabold | 120.00 | 4.70 |
| ks | S.E.(m)± | 22.55 | 0.81 | | S.E.(m)± | 21.27 | 0.67 |
| | C.D.(5%) | 64.87 | 2.33 | | C.D.(5%) | 61.19 | 1.93 |

This indicates that selection would be effective in improving number of siliqua plant⁻¹ and seed yield plant⁻¹. The findings of Gangappa *et al.*, (2003) in sesame and Naik *et al.*, (2009) in safflower, gave sufficient support to the present results. Hence, number of siliquae plant⁻¹ and seed yield plant⁻¹ should be given priority for selection of significantly superior BIPs. The mean performance of BIP progenies of the two crosses are presented in table 4. Fourteen

BIPs of ACNM 2 x ACNM 11 and six BIPs ACNM 2 x ACNM 5 were found to be significantly superior over checks.

In this study as additive gene effect were predominant for the two traits, broad sense heritability were high and response to selection as per cent of mean were high, it is suggested here that these selected BIP progenies should be forwarded to next generation and selection based on progeny

testing through either half sib or full sib progeny should be followed till homozygosity is attained.

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