COMBINING ABILITY ANALYSIS OF SOME YIELD ATTRIBUTES IN INDIAN MUSTARD (BRASSICA JUNCEA L.)

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ABSTRACT:- Eight promising genotypes were crossed in all possible combinations using 8×8 diallel system for combining ability analysis. Data was recorded for seed yield and some important yield attributes. The results for combining ability analysis indicated significant general combining ability for most of the traits except plant height and siliqua length. UCD-8/4, KJ-119 and BRS-2 were good general combiners for yield related traits. A cross BRS-2 \times UCD-8/4 showed best desired SCA for number of primary branches and siliquae per plant. S-9 × Canola Raya for siliqua length, Canola Raya × UCD-8/4 for number of seeds per siliqua, KJ-119 × BRS-2, BARD-1 × NIFA Raya for 1000-seed weight while cross BRS-2 × UCD-8/4 for seed yield showed good positive SCA, involving at least one of the promising general combiner parents. It was suggested that selection should be delayed up to sixth segregating generation for number of primary branches, number of siliqua per plant, siliqua length and seed yield due to highly significant genotypic mean square and pre-dominant role of nonadditive type of gene action while for number of seeds per siliqua and seed weight, selection in early generations would be suitable due to prominance of additive gene action.

Key Words: Indian Mustard; Cultivars; Diallel; Combining Ability; Yield Attributes; Gene Action; Pakistan.

INTRODUCTION

In Pakistan, existing *Brassica juncea* varieties are low yielding. There is great potential for improvement of seed yield in this crop and it is requirement of the time to develop varieties with higher per unit area seed yield. Cultivars of *B. juncea* perform better than those of *B. napus* for production in lowerrainfall environments. It has more heat and drought tolerance and resistance to pod-shatter as

*PMAS-Arid Agriculture University, Rawalpindi, Pakistan ** Barani Agricultural Research Institute, Chakwal, Pakistan. Corresponding author: m.arifullah79@gmail.com compared to *B. napus* (Woods et al., 1991; Burton et al., 1999; Oram et al., 1999). Mustard cultivars have more seed and dry matter production than rapeseed under semi-arid conditions (Chauhan and Bhargava, 1984). For seed yield, *B. juncea* is also better performer than *B. rapa* and *B. napus* under the conditions of Islamabad, Pakistan (Munir, 1987). There is great potential for improvement of seed yield and oil percentage in this crop and to develop varieties with higher per unit

area seed yield and oil percentage with improved quality. Breeders are required to hybridize present high yielding and widely-adapted cultivars and to select desirable genotypes in segregating generations to develop varieties with these improved characters.

Combining ability studies have significant importance in determining the type of gene action present in controlling a character. Additive type of gene action is indicated by general combining ability variance while non-additive type of gene action is shown by specific combining ability variance, originating mainly from dominance and epistasis deviations (Malik et al., 2004). The overall performance of a genotype in a series of crosses is called general combining ability while the performance of specific combinations of genotypes in crosses in relation to the average performance of all combinations is known as specific combining ability. Present studies were done to ascertain the presence of additive and non-additive type of gene action to carry out selection for yield attributes in early or late segregating generations in studied promising Indian mustard genotypes.

MATERIALS AND METHOD

The experimental material comprised total eight promising genotypes of *Brassica juncea L.* i.e., S-9, KJ-119, BARD-1, BRS-2, 95102/51, NIFA Raya, UCD-8/4 and UCD-6/23 obtained from National Agricultural Research Centre (NARC), Islamabad, Barani Agricultural Research Institute (BARI), Chakwal and Nuclear

Institute for Food and Agriculture (NIFA), Peshawar. BARD-1 and BRS-2 were bold-seeded with greater 1000-seed weight. Seeds with greater 1000-seed weight have the advantage of higher oil content and seed yield. S-9 and KJ-119 were yellow seeded. Yellow seed coat colour is generally related with higher oil and protein contents as vellow seed coats are significantly thinner than brown seed coats. 95102/51 and NIFA Raya had low erucic acid and glucosinolate contents. High erucic acid and glucosinolates are anti-nutritional. UCD-8/4 and UCD-6/23 were early maturing genotypes as early maturity is a desired trait in a B. juncea breeding programme to counter with environmental stresses. Four 5m long rows of the mentioned Indian mustard genotypes were sown in the research area of BARI, Chakwal, maintaining plant to plant and row to row distances of 30 cm and 90 cm, respectively, during rabi 2006-07. Fertilizer, DAP @ 75 kg and Urea @ 60 kg ha-¹ at the time of sowing was applied to provide the nutrients. All plant protection measures were taken to avoid insect pests and irrigation was carried out when it was necessary to avoid drought stress. At the flowering, these eight genotypes were crossed in all possible combinations under complete diallel system through hand emasculations and controlled pollinations. Kraft paper bags were used for avoiding the out crossing. Pollinations to emasculated florets were repeated once after two days for maximum seed setting.

The seeds of F_1 crosses, reciprocal and selfed parents were

sown under a Randomized Complete Block Design with three replications during rabi 2007-08 in the field. Row to row distance of 75 cm and plant to plant distance of 25 cm were maintained, respectively. Each 5m long row was accommodating about 19 plants. All standard agronomic practices were carried out as mentioned earlier.

The data was recorded on five randomly selected plants of each genotype per replication and then average was calculated for plant height (cm), number of primary branches per plant, number of siliquae per plant, siliqua length (cm), seeds per siliqua, 1000-seed weight (g) and seed yield per plot (g). The data collected from 64 genotypes (eight parents and 56 F_1 crosses) for yield related traits were subjected to analysis of variance (Steel and Torrie. 1980) to determine the significance of difference among various genotype means. The combining ability analysis was carried out for all the parents and F_1 genotypes according to procedure outlined by Griffing (1956) method-I, model-II and elaborated by Singh and Chaudhary (2004). Total variability was partitioned into component like general combining ability (GCA), specific combining ability (SCA) and error. Information was derived regarding the type of gene action controlling different traits and pattern of selection for improvement of the Indian mustard genotypes.

RESULTS AND DISCUSSION

In present study, analysis of variance showed highly significant genotypic mean square values for all the traits indicating significant variability among all the genotypes studied for all the yield related traits (Table 1). The results for combining ability analysis revealed that the mean squares for general and specific combining abilities were highly significant (Table 2) except for siliqua length, for which mean square value for general combining ability was non-significant indicating that selection would not bring about significant improvement in this trait due to absence of significant variations. Higher value of variance for general combining ability than specific combining ability for number of seeds per siliqua and 1000-seed weight revealed that these traits were predominantly controlled by additive gene action (Table 3) and it was supported by Parmar et al. (2005) and Singh et al. (2008) as they denoted prominance of additive gene action for these traits. However, Lohia (2008) reported that both additive and non-additive types of gene action were involved in controlling seed weight. It was also

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|----------------|-------|---------------|------------|---------|-----------|--------|-------------|
| | | No. of | No. of | Siliqua | No. of | 1000 - | Seed yield |
| Source of | df | primary | siliquae | length | seeds per | seed | per plot |
| variation | | branches | per plant | | siliqua | weight | |
| | | | | | | | |
| Replications | 2 | 0.63 | 3634.40 | 0.02 | 2.22 | 0.01 | 9153.94 |
| Genotypes | 63 | 4.85** | 17593.76** | 2.59** | 9.33** | 0.54** | 176559.50** |
| Error | 126 | 0.48 | 1424.80 | 0.03 | 0.86 | 0.03 | 20260.21 |
| ** Cignificant | at 1% | nrohobility l | aval | | | | |

Table 1. Mean squares for analysis of variance of different yield attributes in Indian mustard

** Significant at 1% probability level

| Source of variation | df | No. of primary branches | No. of siliquae per plant | Siliqua length | No. of seeds per siliqua | 1000 - seed weight | Seed yield per plot |
|---------------------|-----|-------------------------------|---------------------------------|-------------------|--------------------------------|--------------------------|------------------------|
| GCA | 7 | 7.04** | 26519.41** | 2.26 | 13.86** | 1.16** | 222109.98** |
| SCA | 28 | 1.59** | 5674.78** | 1.04** | 1.18** | 0.09** | 48883.33** |
| Error | 126 | 0.16 | 474.93 | 0.01 | 0.29 | 0.01 | 6753.40 |

Table 2. Mean square values from combining ability analysis (Griffing's approach) for Different yield attributes in 8x8 diallel cross of Indian mustard

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

found from present investigations that all other traits were under the influence of non-additive type of gene action. Singh et al. (2004) and Parmar et al. (2005) also indicated prevalence of non-additive gene action for number of primary branches, number of siliqua per plant and seed yield. Singh et al. (2005) found results similar to present findings and described that additive gene effects were prevalent in governing seeds per siliqua.

The results for GCA estimates (Table 4) showed that KJ-119 and UCD-8/4 showed maximum positive general combining ability values for number of primary branches and number of siliquae per plant. Canola Raya and UCD-6/23 showed highest GCA value for siliqua length. UCD-8/4 was best general combiner for number of seeds per siliqua followed by KJ-119. Only BRS-2 and BARD-1 showed positive GCA values for seed weight while KJ-119 and UCD-8/4 showed maximum positive GCA values for seed yield per plot respectively. UCD-8/4, KJ-119 and BRS-2 could be utilized as potential donors for more than one yield attributes for varietal improvement. Crosses BRS-2 × UCD-8/4, KJ-119 × Canola Raya and KJ-119 × BRS-2 showed high positive SCA (Table 5), involving at least one of the good general combiner parents for number of primary branches. Crosses BRS-2 \times UCD-8/4. BARD-I × UCD-8/4 showed desired SCA for number of siliquae per plant while S-9 × Canola Raya, Canola Raya × UCD-8/4, and UCD-8/4 × UCD-6/23 showed high SCA, involving at least one of the good general combiner parents for siliqua length. Crosses Canola Raya \times UCD-8/4, NIFA Raya

Table 3. Estimation of genetic components of variance due to general combining ability (Vg), specific combining ability (Vs) and GCA/SCA ratio (Vg/Vs)

| Variance component | No. of primary branches | No.of siliquae per plant | Siliqua length | No. of seeds per siliqua | 1000 - seed weight | Seed yield per plot |
|-----------------------|-------------------------------|--------------------------------|-------------------|--------------------------------|--------------------------|------------------------|
| Vg | 0.34 | 1308.49 | 0.08 | 0.79 | 0.07 | 10872.86 |
| Vs | 0.80 | 2919.21 | 0.58 | 0.50 | 0.04 | 23651.89 |
| Vg/Vs | 0.43 | 0.45 | 0.13 | 1.58 | 1.53 | 0.46 |
| Ratio | | | | | | |

| Genotypes | No. of primary branches | No.of siliquae per plant | Siliqua length | No. of seeds per siliqua | 1000 - seed weight | Seed yield per plot |
|-------------|-------------------------------|--------------------------------|-------------------|--------------------------------|--------------------------|---------------------------|
| S-9 | 0.27 | 12.29 | 0.11 | -0.01 | -0.06 | - 2.26 |
| KJ-119 | 1.10 | 67.74 | -0.43 | 0.78 | -0.06 | 191.31 |
| BARD-1 | -0.15 | -10.48 | -0.11 | -0.76 | 0.26 | 31.20 |
| NIFA RAYA | -0.05 | - 2.09 | -0.16 | 0.05 | -0.23 | -101.40 |
| CANOLA RAYA | -0.70 | -42.67 | 0.80 | 0.04 | -0.10 | -127.88 |
| BRS-2 | -0.31 | -20.46 | -0.22 | -1.77 | 0.55 | 20.68 |
| UCD-8/4 | 0.70 | 45.27 | -0.18 | 1.24 | -0.19 | 121.58 |
| UCD-6/23 | -0.85 | -49.59 | 0.20 | 0.43 | -0.18 | - 133.23 |

Table 4. Estimates of general combining ability (GCA) effects for different yield attributes in 8 x 8 diallel of Indian mustard.

 \times UCD-8/4, BARD-1 \times UCD-8/4 and S-9 \times KJ-119 showed desired SCA, involving at least one of the best general combiner parents for number of seeds per siliqua. Crosses KJ-119 \times BRS-2, BARD-1 \times NIFA Raya and BRS-2 × UCD-8/4 showed desired SCA, for 1000-seed weight, crosses BRS-2 × UCD-8/4, KJ-119 × BRS-2, KJ-119 × Canola Raya and NIFA Raya × UCD-8/4 for seed yield showed good positive SCA, involving

Table 5.Estimates of specific combining ability effects for different yield attributes in8 ×8 diallel of Indian mustard

| CROSSES | No. of | No.of | Siliqua | No. of | 1000seed | Seed yield |
|-------------------------|----------|-----------|---------|-----------|----------|------------|
| | primary | siliquae | length | seeds per | weight | per plot |
| | branches | per plant | | siliqua | | |
| S-9 x KJ119 | -0.93 | -45.35 | -0.47 | 0.61 | -0.06 | -47.22 |
| S-9 x BARD1 | -1.14 | -72.95 | -0.19 | -0.70 | -0.12 | -268.62 |
| S-9 xNIFA RAYA | 1.62 | 100.82 | -0.09 | 0.74 | -0.20 | 143.32 |
| S-9 x CANOLA RAYA | -0.10 | -9.27 | 0.74 | -0.37 | 0.08 | -8.37 |
| S-9 x BRS2 | -0.85 | -54.97 | 1.09 | 0.35 | 0.07 | -53.27 |
| S-9 x UCD8/4 | -0.33 | -15.20 | -0.15 | -0.63 | 0.06 | -43.16 |
| S-9 x UCD6/23 | 1.48 | 84.98 | 0.08 | 0.61 | 0.07 | 260.98 |
| KJ-1 19 x BARD1 | -0.90 | -56.24 | -0.02 | 0.33 | 0.27 | 64.15 |
| KJ-119 x NIFA RAYA | 0.446 | 31.69 | 1.20 | -0.02 | -0.19 | -62.91 |
| KJ-119 x CANOLA RAYA | 0.85 | 44.61 | 0.31 | 0.31 | -0.01 | 125.73 |
| KJ-119 x BRS2 | 0.84 | 38.07 | -0.04 | -0.84 | 0.39 | 185.67 |
| KJ-119 x UCE8/4 | 0.24 | 6.01 | -0.50 | 0.03 | -0.14 | -61.89 |
| KJ-119 x UCE6/23 | 0.18 | 5.20 | -0.58 | -0.58 | -0.19 | -148.74 |
| BARD-1 x NIFA RAYA | 1.07 | 63.26 | 0.70 | -0.88 | 0.35 | 200.53 |
| BARD-1 x CANOLA RAYA | 1.26 | 82.84 | 0.42 | 0.50 | 0.00 | 226.67 |
| BARD-1 x BRS2 | -0.19 | -9.37 | -0.80 | 1.30 | -0.02 | 80.94 |
| BARD-1 x UCD8/4 | 0.39 | 21.40 | -0.97 | 0.81 | -0.16 | 83.38 |
| BARD-1 x UCD6/23 | 0.79 | 48.92 | 0.03 | -0.20 | -0.43 | -107.47 |
| NIFA RAYA x CANOLA RAYA | -0.53 | -40.22 | -1.01 | 0.55 | 0.04 | -9.56 |
| NIFA RAYA x BRS2 | -0.41 | -34.43 | -0.01 | 0.62 | -0.41 | -163.79 |
| NIFA RAYA x UCD-8/4 | -0.01 | -0.66 | -1.25 | 0.81 | 0.09 | 111.82 |
| NIFA RAYA x UCD-6/23 | -0.98 | -48.47 | -0.23 | -0.25 | 0.23 | -9.70 |
| CANOLA RAYA x BRS2 | 0.34 | 16.98 | -0.47 | -0.80 | 0.00 | -62.64 |
| CANOLA RAYA x UCD-8/4 | -1.37 | -79.58 | 0.52 | 0.88 | -0.12 | -175.54 |
| CANOLA RAYA x UCD-6/23 | -0.83 | -45.56 | 0.06 | -0.53 | 0.07 | -97.56 |
| BRS-2xUCD-8/4 | 1.12 | 81.05 | 0.72 | -1.15 | 0.31 | 229.23 |
| BRS-2xUCD-6/23 | -0.12 | -4.77 | -1.11 | 1.33 | 0.09 | 161.05 |
| UCD-8/4x UCD-6/23 | -0.73 | -44.33 | 0.49 | -0.77 | 0.07 | -129.85 |

at least one of the promising general combiner parents as found by Lohia (2008) and Nigam and Alka (2009) . The results of the present study might be used for the improvement of certain traits of Indian mustard.

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