Combining ability analysis for seed yield and its components in Indian mustard (*Brassica juncea* L)

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Abstract

Ten diverse lines of Indian mustard (*Brassica juncea* L.) genotypes were crossed in diallel mating design excluding reciprocals to study combining ability. The mean squares due to genotypes including parents, crosses and parents vs. crosses were significant for seed yield/ plant, days to 50% flowering, days to maturity, main raceme length, siliquae on main raceme, siliquae per plant, siliqua length, seeds per siliqua, harvest index. The analysis of variance revealed significant mean sum of squares of general combining ability (GCA) and specific combining ability (SCA) for all the characters. The estimates of GCA effects revealed that parents, viz. NRCDR-02, RH-749, RH-761 and Brijraj were good general combiners for yield contributing traits. The best specific cross combinations for yield and its attributing traits were crosses DRMR IJ-31 × Pusa Bold, DRMR 150-35 × RH-761, DRMR 150-35 × Brijraj, DRMR 150-35 × RH-406, Pusa Bold × JM-2, NRCDR-02 × RH-761, DRMR 1165-40 × Brijraj on the basis of pooled analysis. These F_1s may be exploited for obtaining transgressive segregants for development of hybrid varieties in Indian mustard.

Keywords: *Brassica juncea, diallel analysis, GCA, SCA, yield components*

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] belongs to family Cruciferae. The Indian mustard is commonly known as rai. Cytologically, *B. juncea* is an amphidiploid (2n=36) derived from interspecific cross of *Brassica nigra* (2n=16) and *Brassica campestris* (2n=20) (Rout *et al*, 2018). Indian mustard is an important oilseed crop of the Indian subcontinent and contributes more than 80% of the total rapeseed-mustard production of the country. It is the second important oilseed crop at national level in terms of production and contributes nearly 26% of edible oil pool of the country (Jat *et al.,* 2019). In mustard yield is one of the most important economic characters and is product of multiplicative interaction of contributing characters (Kant and Gulati, 2001). Consequently, the primary goal in mustard improvement is the development of high-yield potential varieties. Concurrent objectives aim to create new cultivars with broader adaptability, early maturity, robust disease resistance, and high oil content, all while maintaining high yield potential.

Diallel mating design has been widely used in self and cross-pollinated plant species to understand the nature of gene action involved in the expression of quantitative traits. It yields reliable information on the components of variance and general combining ability (GCA) and specific combining ability (SCA) variances and their effects. Thus, it helps in the selection of suitable parents for hybridization as well as in the choice of appropriate breeding procedures (Griffing, 1956). Combining ability analysis is one of the powerful tools to test the value of parental lines to produce superior hybrids and valuable recombinants (Singh *et al.,* 2013). The principle of combining ability contributes an important role in determining the existence of parents and the development of superior lines or hybrids. Studies have shown that the genotypes found with excellent performance might not constantly produce desirable offspring when used in hybrid development. It is, consequently, essential to identify promising lines on the basis of combining abilities within hybrid combinations through suitable mating design. These lines could be used for the production of hybrid to enhance the productivity and production of oilseed crop (Fasahat *et al.,* 2016). Therefore, the present investigation was undertaken with an objective to assess the nature of gene action involved and combining ability of parental genotypes for various traits for evolving productive genotypes in Indian mustard.

Materials and Methods

The study was conducted at the field experimentation centre of Institute Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (UP) during *Rabi* seasons of 2021-22 and 2022-23. The

experimental material consisted of 45 F_1s of Indian mustard (*B. juncea*) involving 10 genotypes namely DRMRIJ-31 (HB-9908 × HB-9916), DRMR 150-35 (RH 819 × Pusa Bold), DRMR 1165-40 (EC552583 × BPR897-4-3), NRCDR-02 (MDOC-43 × NBPGR-36), Pusa Bold (Varuna × BIC 1780), RH-749 (RH-781 × RH-7617), RH-761 (JMR 9738 × RH 30), JM-2 (Varuna × L-4), Brijraj (NRCHB 101 × Pusa Swarnim) and RH-406 (RH-6908 × RH-8812), were crossed in diallel fashion (excluding reciprocals) during *Rabi* 2021-22. Genotypes were collected from ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan. The aim of the present study was to evaluate GCA and SCA of high yielding varieties and breeding lines. The crosses along with their parents were planted in randomized complete block design with three replications at three different dates of sowing with different environments (1, 15 and 30 November, 2022) during *Rabi* 2022–23. Analysis is done by polled data. The treatments were raised in rows with 45 cm between rows and 10-15 cm between plants, where each treatment was represented by two rows. Standard agronomic practices were followed to raise the good crop. Recommended doses of fertilizers viz., 80:40:40:40 kg/ha of N:P:K:S, respectively, were applied. Observations were recorded on fourteen quantitative traits, viz., days to flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, main shoot length (cm), number of siliquae on main shoot, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, seed yield per plant (g), harvest index (%), test weight (g) and oil content (%). Observations on days to flowering and maturity were recorded on per plot basis, and the observations on remaining traits were recorded on randomly selected five competitive plants in each replication. The mean values were used for the analysis of variance. The combining ability analysis was carried out on polled basis as per the method of Kempthorne (1957). The combining ability for 10 × 10 diallel analysis (excluding reciprocals) was carried out by Method II and Model I of Griffing (1956). The calculations were performed through computer generated programme WINDOW STAT version 8.6 from INDOSTAT Services, Hyderabad, India.

Results and Discussion

The analysis of variance (Table 1) for combining ability revealed that the mean squares due to parents, hybrids were highly significant for all the traits. This shows that sufficient genetic variability was present in the experimental material and both GCA and SCA were involved in the genetic expression of traits studied. The variation due to parents vs. crosses was significant for seed yield/ plant, days to 50% flowering, days to maturity, main raceme length, siliquae on main raceme, siliquae per plant, siliqua length, seeds per siliqua, harvest index, suggesting the presence of heterosis for these traits in the series of crosses. Similarly, highly significant variance due to crosses revealed that the sufficient amount of genetic variability was generated in the hybrids. The estimates of GCA and SCA variances for most of the traits indicate the operation of both additive and non-additive components of gene action in the materials under study. Similar results were earlier reported by many workers Gupta *et al.* (2011), Meena *et al.* (2015) and Maurya and Singh (2018) in Indian mustard.

General combining ability

The estimates of general combining ability (GCA) effects are presented in Table 2. The combining ability estimates showed that four parents viz., NRCDR-02, RH-749, RH-761 and Brijraj exhibited significant positive GCA effects for seed yield per plant. Parents Pusa Bold, DRMR IJ-31 and RH-749 exhibited significant desirable GCA effects for oil content; Brijraj and DRMR IJ-31 for days to 50% flowering, Brijraj and RH-761 for days to maturity, RH-761 and RH-749 for plant height, Pusa Bold, RH-749 and RH-406 for primary branches per plant, Pusa Bold, RH-749 and DRMR 150-35 for secondary branches per plant, DRMR 150-35, DRMR IJ-31 and RH-761 for main raceme length, RH-761, DRMR 1165-40, Brijraj and RH-749 for siliquae on main raceme length, RH-749, NRCDR-02 and DRMR 150-35 for siliquae per plant, Pusa Bold, RH-749 and Brijraj for siliqua length, NRCDR-02 and RH-749 seeds per siliqua, JM-2 for harvest index and Similarly, for test weight, significant and positive GCA effects were possessed by RH-761, DRMR IJ-31 and Pusa Bold. Among all the parents, RH-749 was observed as the best general combiner as it had good GCA effects for almost all the characters. Others parents such as RH-761, Pusa Bold, NRCDR-02 and Brijraj also possessed high GCA for seed yield and yield contributing traits like early flowering, early maturity, number of primary and secondary branches per plant, long main shoot length, siliquae on main raceme, siliquae par plant, more number of seeds per siliqua and greater test weight. These parents could be included in the breeding programme for the accumulation of favorable alleles in a single genetic background. Singh *et al.* (2005), Yadava *et al.* (2012), Singh *et al.* (2013) and Meena *et al.* (2017) reported similar results in Indian mustard with a different set of material.

Specific combining ability

Estimation of specific combining ability (SCA) effects of 45 crosses for yield and its component traits are given in Table 3. An overall appraisal revealed that none of the

Table 1: Mean squares for morphological traits in half diallel analysis in Indian mustard

Source variation	DF	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ plant	Secondary branches/ plant	Main raceme length	Siliquae on main raceme	Siliquae/ plant	Siliqua length	Seeds/ siliqua	Seed yield/ plant	Harvest index	Test weight	Oil content
Replication	2	0.8	12.8**	163.6	0.7**	0.04	59.1**	23.6**	564.5**	0.43**	10.9**	7.7**	1.1	0.2*	0.2
Treatment	54	15.2**	8.7**	216.3**	0.5**	10.8**	107.1**	30.7**	7104.9**	0.6**	2.2**	21**	26**	0.3**	1.83**
Parent	9	17.1**	5.1**	418.4**	0.6**	10.7**	44.8**	19.2**	2941**	0.4**	3**	5.5**	23.5**	0.2**	1.89**
Cross	44	14.3**	9.3**	179.9**	0.4**	11.1**	120.7**	33.2**	7540.8**	0.4**	1.9**	22.7**	25.3**	0.3**	1.86**
Parent vs. crosses	1	36**	16.9**	0.06	0.02	0.002	68.9**	23.1*	25397.6**	8**	6.9**	89.9**	79.4**	0.01	0.03
GCA	9	5.5**	2.7**	198.9**	0.2**	6.0**	29.2**	18.7**	2409.3**	0.3**	1**	9.5**	7.9**	0.2**	1.13**
SCA	45	4.9**	2.9**	46.7**	0.1**	3.1**	37**	8.5**	2360.1**	0.17**	0.6**	6.5**	8.8**	0.09**	0.5**
Error	108	1.3	1.6	67.6	0.1	0.9	9.4	3.8	99.1	0.03	0.3	0.6	3.9	0.04	0.14
Total	164	5.9	4.1	117.8	0.2	4.2	42.2	12.9	2411.6	0.23	1.1	7.4	11.1	0.1	0.7

*Where; *: Significant at 5% level of significance, **: significant at 1% level of significance*

Table 2: Estimate of general combining ability effects of fourteen characters in 10- parents half diallel cross in Indian mustard F₁

Source variation	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ plant	Secondary branches/ plant	Main raceme length	Siliquae on main raceme	Siliquae/ plant	Siliqua length	Seeds/ siliqua	Seed yield/ plant	Harvest index	Test weight	Oil content
DRMR IJ-31	-1.1**	0.7**	-6.9**	-0.4**	-1.8**	2.2**	-0.9**	0.3	-0.1**	0.0	-0.0	0.3	0.1**	0.3**
DRMR 150-35	-0.0	0.2	-1.9	0.1	0.5**	2.4**	-0.1	7.7**	-0.1**	-0.3**	-0.3**	-1.8**	-0.2**	-0.2**
DRMR 1165-40	-0.1	0.1	-3.9**	0.1	0.3	-0.1	1.1***	-19.5**	-0.2**	-0.1	-1.6**	-1.0**	-0.2**	-0.1
NRCDR-02	0.8**	0.1	-2	-0.0	-0.3	-0.8	-1.1**	10.6**	0.1	0.4**	0.6**	0.2	0.1	-0.2**
Pusa Bold	0.3	0.1	2.1	0.1*	0.7**	-1.6**	-2.5**	-7.2**	0.4**	-0.5**	-0.6**	0.3	0.1*	0.6**
RH-749	0.4	0.5*	4.4**	0.1*	0.6**	-1.5**	0.7*	29.6**	0.2**	0.4**	1.3**	-0.0	-0.1	0.3**
RH-761	0.3	-0.5**	7.1**	0.0	-0.0	1.3**	1.9**	0.2	-0.0	0.0	1.1**	0.6	0.3**	-0.3**
JM-2	0.0	0.0	-0.8	0.0-	0.1	-1.1*	0.1	-7.2**	-0.1**	0.1	-0.2	1.0**	-0.1**	0.1
Brijraj	-1.2**	-0.6**	1.4	-0.1	0.1	0.9	0.8*	2.0	0.1**	0.0	0.3**	0.4	0.0	-0.3**
RH-406	0.6**	-0.5**	0.4	0.1*	0.1	-1.5**	-0.0	-16.2**	-0.2**	-0.1	-0.6**	0.1	-0.0	-0.0
SEm± (Gi)	0.4**	0.4**	2.9**	0.1*	0.4**	1.1**	0.7**	3.6**	0.1**	0.2**	0.3**	0.7**	0.1**	0.1**
SEm± (Gi-Gj)	0.6**	0.6**	4.3**	0.2**	0.4**	1.6**	1.0**	5.3**	0.1**	0.3**	0.4**	1.1**	0.1**	0.2**

*Where; Where; *: Significant at 5% level of significance, **: significant at 1% level of significance, gi: GCA effects for line I, gj: GCA effects for line j*

Table 3: Estimates of specific combining ability effects for F$_1$ offspring of 10 Indian mustard parents for various agro-morphological traits

Source variation	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ plant	Secondary branches/ plant	Main raceme length	Siliquae on main raceme	Siliquae/ plant	Siliqua length	Seeds/ siliqua	Seed yield/ plant	Harvest index	Test weight	Oil content
DRMR IJ-31× DRMR 150-35	1.4*	2.8**	-4.2	-0.60**	-2.16**	7.37**	-0.20	-59.1**	0.12	-0.70*	-3.27**	1.46	-0.25*	-0.26
DRMR IJ-31× DRMR 1165-40	0.2	1.1	-4.9	-0.17	-1.30*	6.20**	1.80	-9.1	0.54**	-0.03	-0.86	1.07	-0.12	0.50*
DRMR IJ-31× NRCDR-02	1.7**	-1.6*	5.9	-0.25	-0.53	-2.16	4.08**	-43.7**	-0.23*	0.28	-2.00*	2.67*	-0.26*	-0.09
DRMR IJ-31× Pusa Bold	-2.9**	-2.7**	15.7**	0.16	2.92**	2.65	-3.03**	85.2**	0.02	0.10	2.30**	2.38*	-0.42**	-0.89**
DRMR IJ-31× RH-749	0.7	-1.0	-4.9	-0.32	-2.18**	2.03	-0.02	-36.8**	-0.03	0.86*	1.49**	1.54	0.40**	-0.39
DRMR IJ-31× RH-761	-1.2	1.4*	0.9	0.20	2.50**	2.50	0.53	68.4**	0.18	0.63	1.70**	-0.59	-0.01	1.32**
DRMR IJ-31× JM-2	1.5*	-0.8	-2.8	-0.33	-1.19*	-5.50**	-3.50**	18.8**	-0.25*	-0.27	1.54**	2.32*	0.39**	0.08
DRMR IJ-31× Brijraj	-0.4	0.1	4.0	1.14**	2.58**	-4.83**	0.93	81.4**	-0.14	0.12	3.00**	-1.18	-0.30*	-0.90**
DRMR IJ-31× RH-406	-1.4*	-0.1	-3.1	-0.02	-0.53	-1.70	-0.07	-25.1**	0.24*	-0.10	-1.60**	0.46	0.20	0.12
DRMR 150-35× DRMR-1165-40	3.0**	0.7	2.6	-0.02	0.83	-5.62**	0.86	67.2**	0.36**	-1.70**	1.79**	3.30**	0.00	-0.31
DRMR 150-35× NRCDR-02	-1.7**	-2.9**	9.7*	0.21	1.02	-4.60**	4.40**	-10.5	0.31**	0.82*	-1.58**	-1.16	-0.12	-0.21
DRMR 150-35× Pusa Bold	0.3	-1.2	-10.8**	-0.18	-0.26	0.47	-2.60*	-40.3**	-0.54**	2.09**	-1.58**	-1.45	-0.11	-0.54*
DRMR 150-35 × RH-749	0.9	-2.0**	-0.8	0.36	1.23*	1.87	1.94	32.9**	-0.15	0.12	-0.10	-2.60*	-0.05	0.84**
DRMR 150-35 × RH-761	-2.4**	-0.1	8.2	0.14	1.18*	4.40**	5.54**	38.7**	-0.55**	0.96**	2.44**	-1.47	0.17	-0.48*
DRMR 150-35 × JM-2	0.8-	0.8	2.9	0.41**	1.89**	3.70**	3.18**	12.1*	0.39**	0.82*	0.21	-0.60	0.25*	0.17
DRMR 150-35 × Brijraj	-0.6	-0.7	6.7	-0.21	1.56**	3.20	3.60**	45.4**	0.40**	0.47	4.10**	0.48	0.38**	-0.24
DRMR 150-35 × RH- 406	0.8	-0.9	9.8*	0.73**	2.11**	-2.00	-6.06**	61.1**	0.20*	0.43	3.90**	5.39**	-0.15	-0.01
DRMR 1165-40 × NRCDR-02	1.3*	0.1-	3.7	-0.52**	-1.20*	7.90**	-1.49	-49.3**	-0.37**	0.76*	-1.90**	2.46*	0.47**	-0.97**
DRMR 1165-40 × Pusa Bold	-0.5	0.2	2.3	0.32	-0.65	-16.00**	1.46	-30.4**	0.29**	-0.29	-1.70**	-2.80**	-0.12	-0.31
DRMR 1165-40 × RH-749	0.7	2.2**	-7.4	-0.14	-1.96**	-7.80**	-1.78	-23.4**	-0.22*	0.56	-2.31**	-3.19**	-0.20	-0.87**
DRMR 1165-40 × RH-761	0.7-	2.5**	-0.4	0.36	0.00	8.04**	-0.13	-4.8	-0.19	0.02	0.78	0.02	-0.36**	-0.19
DRMR 1165-40 × JM-2	1.4*	-0.2	-8.2	-0.06	0.99	-5.16**	3.58**	-33.2**	-0.14	-0.88*	-1.65**	0.44	-0.74**	-0.35
DRMR 1165-40 × Brijraj	-2.5**	-1.3	7.7	0.35	2.99**	6.82**	-0.23	91.0**	0.67**	0.59	4.74**	-0.16	-0.15	-0.05
DRMR 1165-40 × RH-406	1.1	-1.1	3.8	-0.22	-0.25	-5.18*	3.88**	-10.1	0.08	-0.61	0.49	-8.44**	0.34**	0.26
NRCDR-02 × Pusa Bold	0.7	-1.8*	-2.3	-0.08	2.82**	2.70	1.53	82.2**	0.02	0.63	4.20**	-1.70	-0.50**	-0.27
NRCDR-02 × RH-749	0.5	-0.4	-3.7	-0.04	-0.08	6.90**	1.66	43.3**	0.30**	-0.66	1.23**	0.03	-0.50**	-0.49*

NRCDR-02 × RH-761	1.7**	-0.4	0.5	-0.14	0.59	3.83*	-3.42**	66.0**	0.34**	0.17	2.60**	-0.07	0.28*	0.05
NRCDR-02 × JM-2	2.2**	3.1**	-4.3	-0.07	-2.50**	-5.51**	-6.46**	69.6**	-0.04	0.24	3.90**	-0.01	0.07	-0.46*
NRCDR-02 × Brijraj	-3.4**	0.7	8.2	0.25	0.06	5.10**	-0.10	-14.6**	0.83**	0.39	2.90**	1.07	0.48***	-0.14
NRCDR-02 × RH-406	-3.5**	0.4	-4.2	0.08	-3.05**	-3.60*	-2.30*	-43.0**	0.03	-0.50	-2.50**	-3.14**	0.20	0.36
Pusa Bold × RH-749	-1.4*	-1.5*	-0.5	0.30	0.46	-0.60	3.15**	-46.0**	0.24*	0.15	-0.70	6.31**	0.45**	0.82**
Pusa Bold × RH-761	-2.2**	2.4**	-9.7*	-0.24	-0.70	1.50	-1.60	-15.4**	0.07	-0.90**	-3.06**	-2.57*	-0.11	0.39
Pusa Bold × JM-2	-4.2**	0.8	4.6	0.15	-0.46	-0.05	-0.173	4.5**	0.58**	0.90**	3.02**	3.98**	0.35**	0.89**
Pusa Bold × Brijraj	3.8**	2.1**	-14.3**	-0.18	-1.50**	-7.60**	-4.58**	-63.3**	-0.35**	-0.07	-1.90**	2.51*	0.19	0.98**
Pusa Bold × RH-406	1.1	2.5**	-4.1	-0.25	0.01	-2.56	0.83	8.3	0.89**	-1.16**	-0.06	1.59	0.09	0.02
RH-749 × RH-761	-4.1**	-1.8*	-2.4	-0.51**	1.30*	-13.70**	-0.57	-36.6**	0.13-	0.95**	-0.02	1.17	0.24*	0.12
RH-749 × JM-02	-3.1**	1.1	-2.9	0.11	1.49**	8.90**	3.38**	-14.6**	0.42**	0.10	1.15*	1.80	0.40**	1.55**
RH-749 × Brijraj	2.1**	1.7*	0.7	0.02	-0.91	-3.90*	-1.58	35.1**	0.01	-0.12	1.60**	0.41	-0.08	-0.36
RH-749 × RH-406	-0.2	1.2	1.5	0.02	1.12*	1.39	-1.01	47.9**	0.01	0.30	3.12**	4.03**	-0.38**	0.27
RH-761 × JM-2	2.8**	1.9**	4.7	0.6**	-1.17*	-2.08	1.36	15.3**	0.23*	-1.26**	-0.50	2.68*	-0.05	0.52*
RH-761 × Brijraj	-0.8	-1.5*	2.9	0.012	-2.36**	-1.40	0.02	-59.8**	-0.05	1.19**	-3.00**	1.15	-0.10	-0.24
RH-761 × RH-406	0.9	0.9	6.0	-0.40*	-1.05	0.30	0.05	-1.7	0.35**	0.95**	1.30**	-0.13	0.13	-0.89**
JM-02 × Brijraj	-2.7**	-2.7**	0.8	-0.21	-1.48**	-8.20**	1.01	-44.3**	-0.20*	-0.18	-3.40***	-1.12	-0.37**	0.66**
JM-02 × RH-406	-3.3**	-3.0**	-3.7	-0.82**	-2.15**	3.30*	0.05	-26.7**	0.19	-0.17	-2.28**	-2.80*	-0.12	-0.80**
Brijraj × RH-406	0.2	-0.9	-6.7	-0.15	0.13	5.05**	0.09	0.6	-0.37**	0.22	-1.90**	-0.68	-0.07	1.24**
Sij <> 0 at 95%	1.2	1.3	8.8	0.37	1.07	3.30	2.09	10.6	0.19	0.60	0.87	2.12	0.23	0.41
Sij--Sik at 95%	1.8	2.0	12.9	0.55	1.57	4.80	3.08	15.6	0.29	0.90	1.28	3.11	0.34	0.60
Sij--Skl at 95%	1.7	1.9	12.3	0.52	1.50	4.62	2.93	14.9	0.27	0.90	1.20	2.97	0.30	0.57

*Where; *: Significant at 5% level of significance, **: significant at 1% level of significance*

crosses had significant SCA effects for all the characters. The crosses DRMR IJ-31 × Pusa Bold, DRMR 150-35 × RH-761, DRMR 150-35 × Brijraj, DRMR 150-35 × RH- 406, Pusa Bold × JM-2, NRCDR-02 × RH-761, DRMR 1165-40 × Brijraj also had recorded high single plant yield along with more number of primary and secondary branches per plant, more number of siliquae per plant, siliqua length and test weight, these crosses emerged as good specific cross combinations for seed yield per plant. These results were supported by studies of Singh *et al.* (2010), Gupta *et al.* (2011) and Kumar *et al*. (2020). Therefore, these above new cross combinations are useful populations for obtaining transgressive sergeants.

Conclusion

In this study, general combining ability and specific combining ability were highly significant. The genotypes NRCDR-02, RH-749, RH-761 and Brijraj possessed significantly high general combining ability for seed yield as well as yield related traits, could be exploited in practical plant breeding. Specific crosses combinations namely DRMR 150-35 × RH-761, Pusa Bold × JM-2, DRMR 150-35 × Brijraj should be exploited through heterosis breeding or should be used in recombination programme for tapping desirable transgressive segregants in segregating generations. The intermating between selected segregants in advance generations of segregation would help to accumulate favorable, desirable alleles for further improvement in seed yield and its component characters in Indian mustard.

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