

GENETIC ANALYSIS OF SEED YIELD AND RELATED TRAITS IN *BRASSICA JUNCEA* L.

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Abstract

Best parents and F1 hybrids were identified based on general combining ability (GCA), specific combining ability (SCA), and high heterotic performance by analyzing the yield characters of 19 Indian mustard lines crossed with three male parents (testers). Significant genetic variability was observed among genotypes for all traits except 1000-seed weight and oil content. The highest GCA effects were recorded for main shoot pods, seed yield/plant and secondary branches. The lines LES 60, JC 36, JC 33, PM 29, and PDZ 12 exhibited significant positive GCA effects for seed yield and major yield-contributing traits, identifying them as good general combiners for hybrid breeding. The crosses PDZ 12 × RLC 3 and PM 29 × RLC 3 showed the highest positive SCA effects for seed yield. Based on performance and heterosis estimates, the hybrids PM 29 × RLC 3, LES 61 × RLC 9, and PDZ 12 × RLC 3 were identified as promising for developing high-yielding hybrids and exploiting hybrid vigour.

Introduction

Brassica juncea L. plays a crucial role in the edible oil economy in India. More than 80% of the area of rapeseed mustard cultivation in the Indian subcontinent is devoted to this oilseed crop. In India, mustard cultivation has significantly increased in recent years, with output growing by 40% between 2019-20 and 2022-23, and productivity raised by 11%. The area under rapeseed and mustard cultivation also increased by 29%. Due to the growing demand for edible oil, there is a compelling need to increase and stabilize the productivity of Indian mustard. The main objective of mustard improvement is to develop varieties with high yield potential.

Knowledge of combining ability and genetic architecture is essential for developing superior breeding lines in *B. juncea*. Combining ability analysis helps to identify parents with desirable gene effects, enabling the development of high-performing hybrids and recombinants (Allard 1960, Meena *et al.* 2015). Heterosis breeding is a promising approach to overcome the current yield plateau in Indian mustard by improving productivity and input-use efficiency. Therefore, identifying parents with high combining ability and heterotic potential is a prerequisite for generating superior hybrids and transgressive segregants. Integrating combining ability with estimates of genetic variance provides an effective basis for parent selection and the development of improved, high-yielding mustard cultivars. A well-planned breeding program leading to rapid improvement and selection of desirable parents for hybridization is crucial for plant breeders.

The Indian mustard crop is autogamous. In early generations, combining ability analysis can be an efficient way to select parents. The combining ability should be considered during the selection of parents and crossing partners, as well as for identification of offspring for developing high-yielding varieties. The general and specific combining ability effects of inbred lines are important indicators of hybrid combination potential in the mustard breeding program. Various mating designs have been used to assess the breeding value of parents by estimating variance and combining ability. Considering these, the present study was undertaken to determine the combinability of genotypes and heterosis of different cross combinations in Indian mustard, as well as to provide material for mustard improvement.

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Materials and Methods

The experiments were conducted at the experimental Farm, Department of Plant Breeding and Genetics, PAU, Ludhiana, Punjab, India, located at 30.90° N, 75.86°E. The experimental material comprised of nineteen mustard genotypes (PM 29, JC 32, PDZ 1, LES 61, JC 33, PDZ 13, DRMRQ 5-2, 9IJ5001, LES 60, LES 59, PDZ 12, RH 749, LES 54, PDZ 14, RH (OE) 1705, PDZ 11, RH (OE) 1706, RCH 1 and JC 36 and crossed with three testers (RLC 3, RLC 9 and JC 21) resulting in a total of 57 crosses. This study examined GCA and SCA of high yielding varieties and breeding lines that mature early and yield more. Nineteen elite lines and three testers of the mustard were raised in the field with staggered sowing in the crossing block for production of F₁'s and crossed in line x tester mating design during *Rabi* season of 2022-23. The seeds of 57 F₁ hybrids were produced by hand emasculation and pollination. All F₁s and parents (lines and testers) were evaluated in 2023-24 during *Rabi* season. Experiment was conducted in randomized block design with two replications under timely sown irrigated conditions. The experimental plot of each treatment consisted of one row of 2m length. Row to row and plant to plant distances were maintained at 30 and 10 cm, respectively. All the recommended package of practices were followed to raise a good crop. The observations were recorded on randomly taken five competitive plants from each entry in each replication for thirteen quantitative traits, viz., days to 50% flowering, days to 100% flowering, maturity, plant height, primary branches per plant, secondary branches per plant, main shoot length, main shoot pods, pod length, total pods per plant, 1000-seed weight (g), seed yield (g) and oil content (%). Observations on days to flowering and maturity were recorded on per plot basis. Data were subjected to combining ability analysis as per the method given by Kempthorne (1957) and better parent heterosis was calculated as deviation of F₁ value from the better parent through a computer generated program using INDOSTAT software.

Results and Discussion

The analysis of variance for combining ability indicated significant differences among hybrids for most of the traits except secondary branches, main shoot length, pod length, 1000 seed weight and oil content (Table 1). The mean squares due to crosses were partitioned into three components, viz. lines, testers and lines x testers interaction. Mean squares due to lines were significant for plant height, secondary branches, main shoot length, main shoot pods, total pods and seed yield per plant. Mean squares due to testers were non-significant for all the traits except main shoot length, pod length and total pods. Mean squares due to lines x testers interactions were significant for all the traits except secondary branches, pod length, 1000-seed weight and oil content suggested that the experimental material possessed considerable variability and that both GCA and SCA were involved in the genetic expression of these factors thereby indicating that they are suitable for combining ability studies. According to the significant differences between line-tester interactions, specific combining ability was heavily involved in the expression of these traits, and non-additive variance is important for all traits. Similar findings were reported by Kant and Gulati (2001), Choudhary *et al.* (2020) and Ram *et al.* (2023). In addition, significant mean squares due to lines and testers revealed additive variance. Selection of parents and breeding procedures play a major role in the success of any breeding program.

The estimates of GCA effects were worked out for all the traits and presented in Table 2. The significant negative GCA effects were observed for two lines for days to 50 and 100% flowering and one line for days to maturity. In case of days to 50% flowering, genotype LES 59 was found to be the best general combiner as it showed the highest significant negative GCA effects. In case of days to 100% flowering, genotype PDZ 11 was the best general combiner as it showed the highest negative GCA effects. The female PM 29 was also found to be a good general combiner for earliness in maturity. For seed yield and yield contributing traits, genotypes PM 29 and PDZ 12 were the best general combiner as these genotypes exhibited the highest positive GCA effects.

Table 1. Analysis of variance and estimates of combining ability components for seed yield and related traits.

Source of variations	DF	DF (50%)	DF (100%)	DM	PH	PB	SB	MSL	MSP	PL	TP	SY/plant (g)	1000 Seed weight	OC
Replicates	1	0.71	0.03	1.48	234.52*	12.76	16.95	244.56*	1117.53	0.63	2046.39	21.91	0.09	0.03
Crosses	56	3.29*	4.75*	21.52**	509.78*	1.48*	18.22	95.13	138.99*	0.30	2473.54**	46.16*	0.11	1.06
Line Effect	18	3.17	4.58	13.05	502.63**	1.59	37.20*	172.26**	251.15**	0.32	2447.85**	60.64**	0.09	1.38
Tester Effect	2	2.87	15.97	29.71	442.80	0.21	2.09	175.54**	1.64	0.83**	5224.85**	63.79	0.27	1.96
Line * Tester Eff.	36	3.37*	4.21*	25.29*	517.07**	1.51*	9.63	52.10**	90.54**	0.26	2333.54**	52.95**	0.10	0.86
Error	56	3.60	2.96	21.23	618.88	2.24	16.26	176.85	72.02	0.22	1700.75	47.61	0.12	1.29
Total	113	3.42	3.82	21.19	561.41	1.96	17.24	136.96	114.47	0.26	2086.78	61.36	0.11	1.17

DF: Days of flowering, DM: Days of maturity, PH: Plant height, PB: Primary branches, SB: Secondary branches, MSL: Main shoot length, MSP: Main shoot pods, PL: Pod length, TP: Total pods per plant, SY: Seed yield, OC: Oil content.

Table 2. Estimation of GCA effect for various characters in Indian mustard.

Genotypes	DF (50%)	DF (100%)	Maturity	PH	PB	SB	MSL	MSP	PL	TP	SY (g)	1000 Seed-weight (g)	OC
PM 29	0.307	0.088	-1.044*	14.912	0.529	-3.424*	3.140	2.691	0.233	-3.877	5.620*	-0.195	-0.161
JC 32	0.974	0.588	0.623	-0.700	0.714	0.611	-7.469	1.401	0.134	20.456	-2.213	-0.148	-0.191
PDZ 1	-1.526	0.754	0.623	6.800	-0.619	-0.944	1.756	-2.045	0.044	9.289	-0.913	-0.132	0.107
LES-61	-0.860	-0.079	0.289	-2.088	-0.008	0.111	5.755	-0.934	-0.48*	19.956	4.570	-0.082	0.264
JC-33	-0.193	0.088	-0.711	-7.560	0.519	2.805	1.253	20.123**	-0.272	-24.877	2.204	0.085	0.314
PDZ-13	0.807	1.754*	-0.044	-8.702	0.021	-1.222	-3.579	-1.045	-0.106	3.456	-0.246	-0.015	0.200
DRMRQ 5-2	0.474	0.254	1.123	1.855	0.109	0.666	4.535	2.233	0.173	9.123	-0.430	0.018	-0.461
9II5001	0.974	-0.912	-1.544	-0.033	0.492	0.723	1.090	-0.822	-0.52*	1.789	2.037	0.135	0.179
LES-60	0.140	-1.246	-0.044	7.077	0.881	6.501**	5.533	-1.100	-0.034	19.956	0.920	-0.215	-0.898*
LES-59	-1.193*	-1.42*	-1.211	19.188	0.324	0.780	6.755	3.956	0.018	-17.044	1.454	0.118	0.049
PDZ 12	-0.360	-0.412	-0.211	2.243	0.047	-2.000	-2.857	-1.044	-0.166	-23.711	7.520**	0.168	-0.221
RH 749	-0.526	1.588*	-0.544	6.522	-0.841	1.223	1.531	0.176	0.181	19.456	-2.380	-0.098	0.227
LES 54	-0.026	0.088	-3.544	9.965	0.159	1.056	0.810	-2.989	0.236	-30.044	-2.330	0.202	0.224
PDZ 14	-0.026	-0.079	0.789	-6.090	-0.343	-4.334**	1.141	-0.935	0.206	-14.211	-2.396	0.018	0.639
RH (OE) 1705	0.640	0.588	-1.544	-15.088	-0.119	-0.722	-2.579	0.731	0.274	17.623	-2.363	0.085	0.882
PDZ-11	-0.974*	-1.59*	0.456	-7.643	-1.008	-1.720	-2.467	-15.044**	-0.141	-36.211*	-3.946	0.035	0.552
RH (OE) 1706	-0.193	-0.412	2.456	-13.200	-0.229	-2.390	-7.745	-5.599	0.134	20.956	-2.663	-0.132	-0.555
RCH 1	0.140	-0.079	2.789	-1.755	-0.119	-0.890	-13.190*	-4.434	0.084	24.956	-2.196	0.035	-0.270
JC 36	-0.526	0.254	1.289	-5.700	-0.508	3.166 *	6.588	4.676	0.003	-17.044	-2.246	0.118	-0.880

The estimates of SCA effects revealed that all the cross combinations were average combiners for different traits. For days to maturity and plant height, PM 29 x JC 21 and RH 749 x RLC 3 showed the highest significantly negative SCA effect, respectively and was the best combination for early maturity and proper plant height. For positive significant SCA effects, three crosses PM 29 x RLC 9 (1.41*), 9IJ5001 x RLC 9 (1.24*), RH (OE) 1705 x RLC 9 (1.52*) were recorded significant positive SCA effects for primary branches. Similar results were reported by Yadava *et al.* (2012) and Dahiya *et al.* (2018) in Indian mustard. In hybridization, a parent's potential can be assessed by its per se performance and GCA effects. In most genotypes, there was a relatively high degree of correspondence between per se performance and GCA effects for observed characters. As a result, additive and additive x additive gene action was dominant in the inheritance of these traits. These findings are consistent with Patel *et al.* (2024).

Table 3. Significant positive specific combining ability effects for yield and yield attributing characters of *Brassica juncea*.

Traits	Specific combining ability (SCA)
50% Flowering	PM 29 X RLC-9 (-1.52*), JC-33 X RLC-9 (-3.02*), PDZ-13 X JC-21 (-1.02*)
100% Flowering	PM 29 X RLC-9 (-2.06*), PDZ 12 X RLC-9 (-2.56*)
DM	PM 29 X JC-21 (-5.01*), PDZ 1 X JC-21 (4.83*), JC-33 X RLC-9 (7.92*)
PH	RH 749 X RLC-3 (-10.72 *)
PB	PM 29 X RLC-9 (1.41*), 9IJ5001 X RLC-9 (1.24*), RH (OE) 1705 X RLC-9 (1.52*)
SB	JC-33 X JC-21 (2.62*), PDZ 12 X JC-21 (2.35*), RH 749 X JC-21 (2.46*), RH (OE) 1705 X RLC-3 (3.35*)
MSL	JC-33 X RLC-9 (6.89*), PM 29 X RLC-9 (4.83*)
MSP	RH 749 X RLC-9 (7.46*), LES 54 X JC-21 (8.39*)
PL	RH 749 X JC-21 (0.75*)
TP	RH 749 X RLC-9 (46.28*), PDZ 14 X RLC-3 (68.59*)
SY/plot (g)	PM 29 X RLC-3 (7.83*), PDZ 12 X RLC-3 (24.18**), PDZ 12 X RLC-9 (-12.49**), PDZ 12 X JC-21 (-11.68*)
1000 seed weight	JC-33 X RLC-9 (-0.27*), LES-59 X RLC-9 (-0.35*), PDZ 12 X RLC-9 (-0.25*), RH (OE) 1705 X RLC-9 (0.38*)
OC	JC 32 X RLC-3 (-0.58*), PDZ 1 X JC-21 (-0.47*)

*Significant at 5% level of significance.

The estimates of specific combining ability effects revealed that two cross combinations exhibited significant and positive SCA effects for seed yield per plant (Table 3). The maximum significant positive SCA effects were exhibited by hybrid PDZ 12 x RLC 3 followed by PM 29 x RLC 3. Thus they were good hybrid combinations, contributing towards higher seed yield. When two good combiners are crossed with poor or average combiners, transgressive segregants may be produced. Because of the high magnitude of non-additive components for the superiority of the pertinent cross combination, poor x poor crosses may be better than good x good and good x poor. The best combiners for seed yield were PDZ 12 x RLC 3 and PM 29 x RLC 3. As a result of the SCA effects on yield per plant for the top two crosses in the present study, PDZ 12 x RLC 3, did not involve one good general combiner, suggesting an additive x dominance type of gene interaction which is expected to result in desirable transgressive segregants in the future. Barupal *et al.* (2016) have demonstrated that additive x additive, additive x dominance, and epistasis types of gene expression play a role in Indian mustard yield and its traits. Genetic diversity in the form of heterozygous loci for specific traits may be responsible for crosses where poor x poor and poor x good general combiners produced high SCA effects. The best F₁ combination would have good per se performance, high heterobeltiosis, at least one good general combiner, and high SCA effects. Dholu *et al.* (2014) observed that the best crosses involving at least one good combining parent can produce transgressive segregants, which is also true in many crosses studied in the current investigation. When SCA effects predominate in self-pollinated crops, the majority of variability is due to additive x additive effects. It is therefore advisable to delay selection for later

generations. Furthermore, for all traits, the per cent contribution of lines was higher than the corresponding testers and their interaction. Accordingly, lines played a significant role in expressing different characters in various cross-combinations. These crosses clearly demonstrate that the parents were useful specific combiners, but their relative contributions to the effect of specific combining ability on seed yield were attributed to diverse yield-attributing traits in different hybrids. Similarly, SCA effects are not directly related to heterobeltiosis/better parent heterosis. Hybrid vigour has not been extensively exploited in self-pollinated crops as compared to cross-pollinated crops. Nevertheless, Indian mustard has been extensively studied as a way to increase productivity through heterosis.

Summary of superior F_1 hybrids identified based on desirable heterosis for key agronomic and yield traits in Indian mustard is presented in Table 4. Overall, the hybrid PDZ-12 x RLC-3 emerged as the most promising cross because of its highly significant positive heterosis for seed yield per plant. Crosses PM 29 x RLC-3, LES-61 x RLC-9, and JC-33 x JC-21 also demonstrated desirable heterotic performance for seed yield. For earliness, JC-33 x RLC-9 and PDZ-1 x JC-21 were identified as the best hybrids owing to their significant negative heterosis for days to 50% flowering. Furthermore, JC-33 proved to be an excellent parent for improving the number of main shoot pods, as all three of its hybrids exhibited high positive heterosis for this trait. These hybrids represent valuable genetic materials for the development of high-yielding and early-maturing Indian mustard hybrids. Similar findings were also reported by Kaur *et al.* (2020). As a further step, the high yielding cross combinations may be exploited for their commercial application, and the parents involved in developing heterotic hybrids will be converted to well-adapted cytoplasmic male sterile or restorer lines.

Table 4. Superior F_1 hybrids identified based on desirable heterosis for different traits.

Traits	Best hybrid (s)	Desirable heterosis (%)
Days to 50% flowering	JC-33 x RLC-9	-10.15 (SC)
	PDZ-1 x JC-21	-9.15 (SC)
Days to maturity	PM 29 x JC-21	-8.45 (BP)
	JC-33 x RLC-9	76.32 (SC)
Main shoot pods	JC-33 x RLC-3	62.41 (SC)
	JC-33 x JC-21	48.91 (SC)
	PDZ-12 x RLC-3	18.74 (BP), 36.65 (SC)
	PM 29 x RLC-3	13.57 (BP), 19.20 (SC)
Seed yield per plant	LES-61 x RLC-9	11.99 (BP), 14.75 (SC)
	JC-33 x JC-21	12.36 (BP), 11.26 (SC)

BP: Better parent, SC: Standard check.

The most outstanding parental lines such as LES 60, JC 36, JC 33, PM 29 and PDZ 12 were found to be good general combiners for most of the traits. Cross combinations like RH 749 x RLC 9, PDZ 14 x RLC 3, JC 33 x RLC 9, PM 29 x RLC 9, RH 749 x RLC 9, LES 54 x JC 21, PDZ 12 x RLC 3, PM 29 x RLC 3 were the best specific combiners which may give desirable transgressive segregates if the additive effect of one parent and complementary epistatic effect act in the same direction and maximize desirable plant characters.

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