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LINE × TESTER ANALYSIS REVEALS PREDOMINANCE OF NON-ADDITIVE GENE ACTION FOR YIELD IMPROVEMENT IN TARAMIRA (*ERUCA SATIVA* MILL.)

Mahipal Yadav[1]*, Manohar Ram[1], Deepak Gupta[1], A.C. Shivran[2], G.K. Mittal[3] and M.K. Sharma[4]

[1]Department of Genetics and Plant Breeding, Sri Karan Narendra Agricultural University, Jobner-303 329, Jaipur, Rajasthan, India.
[2]Department of Agronomy, Sri Karan Narendra Agricultural University, Jobner-303 329, Jaipur, Rajasthan, India.
[3]Department of Biochemistry, Sri Karan Narendra Agricultural University, Jobner-303 329, Jaipur, Rajasthan, India.
[4]Department of Horticulture, Sri Karan Narendra Agricultural University, Jobner-303 329, Jaipur, Rajasthan, India.
*Corresponding author E-mail: starmy97@gmail.com

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ABSTRACT

The present investigation was conducted to assess heterosis, combining ability, and gene action in taramira (*Eruca sativa* Mill.) using a line × tester mating design. The experimental material comprised 44 genotypes, including 10 female lines and 3 male testers, which generated 30 F_1 hybrids during Rabi 2023–24. These hybrids, along with parents and a standard check (RTM-1351), were evaluated in a Randomized Block Design with three replications during Rabi 2024–25 at S.K.N. College of Agriculture, Jobner, Rajasthan. Observations were recorded for 13 agronomic, yield, and quality traits. Analysis of variance revealed significant genetic variability among genotypes, parents, and crosses for all characters. Combining ability analysis indicated that specific combining ability (SCA) variance was higher than general combining ability (GCA) variance for all traits, suggesting the predominance of non-additive gene action. Several parents, notably RTM-2211, RTM-2223, RTM-2011 and RTM-1624, were identified as good general combiners for seed yield and its contributing traits. Among the hybrids, RTM-2202 × RTM-2011, RTM-2206 × RTM-314, and RTM-2221 × RTM-1624 exhibited superior per se performance, high SCA effects, and significant heterosis for seed yield. The results highlighted that crosses with high SCA effects also demonstrated improved performance for yield-attributing traits. The predominance of non-additive gene action suggests the potential for exploiting heterosis in taramira breeding. The hybrid RTM-2202 × RTM-2011 was identified as the most promising genotype for yield improvement. The study recommends selection based on per se performance and GCA effects, followed by biparental mating and reciprocal recurrent selection to effectively utilize non-additive genetic variance for crop improvement.

Key words : *Eruca sativa* Mill., Heterosis, GCA, SCA.

Introduction

Taramira (*Eruca sativa* Mill.) is an important *Rabi* oilseed crop. Rajasthan is most important and leading state for the taramira cultivation in India. In Rajasthan, area grown under taramira is 1.28 lakh ha, producing 0.66 lakh tonnes with a productivity of 521 kg/ha (Anonymous, 2022-23). The oil content of taramira varies between 31.6% and 41.31% (Yadav *et al.*, 1980; Ola *et al.*, 2021) and this variation is influenced by factors such as fertilization, irrigation and disease control practices. The seed oil had a specific gravity of 0.910, refractive index of 1.4680 (at 40 degree celcius), iodine value of 137.0, saponification value of 168.1 and a free fatty acid content of 2.3% (as oleic acid). Gas chromatographic analysis of the oil revealed high levels of linolenie acid (36.2%) and relatively low levels of erucic acid (10.3%) (Flanders and Abdulkarim, 1985; Kumar and Ohlsson, 1988).

The overall productivity of taramira remains low and inconsistent because it is typically cultivated under minimal input conditions on marginal and sub-marginal soils. Contributing factors include the absence of well-defined production packages, limited availability of improved varieties, poor siliqua formation, restricted genetic variability, and insufficient understanding of the genetics underlying yield and its related traits (Sharma *et al.*, 1991). The crop thrives on low-fertility soils and is favored over related species because of its strong tolerance to stress and its adaptability to harsh environmental conditions (Gupta *et al.*, 1998). Creation of variability and exploitation of heterosis has been recognized as an important tool for genetical improvement of yield and yield related traits: and also serve as an important fruitful technique to break existing morphological and biochemical barriers.

Materials and Methods

The experimental material comprised of fourty-four genotypes includes ten females lines *viz*., RTM - 2201, RTM - 2202, RTM – 2204, RTM – 2206, RTM – 2208, RTM – 2209, RTM – 2211, RTM – 2221, RTM – 2223 and RTM – 2270, and three male parents *viz*., RTM - 1624, RTM - 314 and RTM – 2011 were crossed (*Rabi* 2023-24) and thus resultant 30 hybrids were analysed with RTM- 1351 as a check were sown in a Randomized Block Design with three replications during *Rabi* 2024-25 at instruction farm S.K.N. College of Agriculture, Jobner, Jaipur, Rajasthan, India. Each genotype was sown in two row of 2 m length with inter and intra row distance were 30 cm and 10 cm, respectively. All the recommended agronomic practices and plant protection measures were adopted for raising a good crop.

The observations *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliquae per plant, siliquae density, siliqua length (cm), seeds per siliqua, test weight (g), seed yield per plant (g), oil content (%) and chlorophyll values (SPAD), were recorded on randomly selected ten plants of each genotype in each replication except days to flowering and days to maturity, test weight (g) and oil content (%) which were recorded on plot basis. The replication wise mean values of each genotype for various traits were subjected to statistical analysis as per the procedure of Randomized Block Design as suggested by Panse and Sukhatme (1978). Analysis for the per cent heterosis over better parent (heterobeltiosis) and economic heterosis was calculated as deviation of F_1 value from better parent and line x tester analysis were followed as under combining ability and effects were computed as per Kempthorne (1957) by Windostat version 9.5.

Results and Discussion

The analysis of variance revealed highly significant values for genotypes, parents, crosses and parents vs. crosses indicating wide genetic variability in the studied material for all the characters. These findings were in close agreement with those reported by Ahsan *et al.* (2013); Alpaslan and Sincik (2025). Likewise mean sums of squares due to lines and testers were found significant for most of the traits except siliqua per plant, whereas the mean sums of squares due to line vs. testers revealed that all the characters were significant except plant height and oil content (Table 1) similar findings were reported by Ahsan *et al.* (2013).

The analysis of variance for combining ability revealed that the mean squares due to crosses were significant for all the traits these results were in close agreement with Gami and Chauhan (2013). The mean sums square due to tester effect were found significant for oil content. The mean square due to line x tester effect interaction was significant for all the characters under study (Table 2) these results were also obtained earlier by Akabari and Sasidharen (2017), Datta *et al.* (2024).

Further variance due to sca observed to be higher than that of due to gca for all the characters under study. This revealed the role of non-additive gene action in the inheritance of traits under study. Similar, results were concluded earlier by Makwana and Patel (2010). Likewise the ratio of σ^2 gca / σ^2 sca was less than unity for all the thirteen traits, this suggested greater role of non-additive genetic variance in the inheritance of these traits. Similar results were recorded by Solanki *et al.* (2009), Gami and Chauhan (2013), Akabari and Sasidharen (2017) and Afrose *et al.* (2025) (Table 2).

Among the genotypes mean values observed for the parents RTM- 2011 recorded the maximum number of branches (primary and secondary) per plant, siliqua per plant, siliqua length, seeds per siliqua, seed yield per plant and oil content. Likewise RTM- 314 recorded maximum number of primary branches per plant, siliquae per plant, siliquae density, seeds per siliqua, 1000-seed weight and seed yield per plant. Whereas, RTM-1624 recorded maximum number of secondary branches per plant, siliquae density, siliqua length, 1000-seed weight and seed yield per plant. Mean values among the crosses *i.e.*, RTM-2202 X RTM- 2011, RTM- 2211 X RTM- 1624 and RTM-2211 X RTM- 2011 recorded highest seed yield per plant.

Parents RTM- 2211, RTM- 2223, RTM- 2011, RTM-314 and RTM- 1624 were good general combiners for seed yield per plant. An overall appraisal of general combining ability effects of parents revealed that RTM-

Table 1 : Analysis of variance showing mean squares in first date of sowing for parents and F_1's for yield and its contributing traits.

Sources of variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Siliqua density
Replication	2	0.008	0.442	160.076	2.957	2.789	85.875	0.002
Genotypes	42	12.581**	28.209**	478.266**	9.583**	56.497**	3449.651**	0.050**
Parents	12	12.603**	20.842**	221.737**	3.317**	8.594**	431.747**	0.022**
Lines	9	11.411**	19.319**	213.901**	2.236*	6.711**	244.818	0.016**
Testers	2	7.000*	10.111*	265.325*	5.668**	5.560*	413.303	0.015**
Lines vs Testers	1	34.531**	56.014**	205.088	8.343**	31.606**	2150.996**	0.091**
Parents vs Crosses	1	67.368**	132.924**	3598.901**	139.932**	561.852**	62722.386**	0.560**
Crosses	29	10.682**	27.646**	476.807**	7.680**	58.893**	2654.552**	0.044**
Errors	84	1.786	2.958	60.626	0.964	1.686	139.515	0.002

Sources of variation	d.f.	Siliqua length (cm)	Seeds per siliqua	1000-seed weight (g)	Seed yield per plant (g)	Oil content (%)	Chlorophyll values
Replication	2	0.010	1.043	0.022	4.699	0.418	2.023
Genotypes	42	0.428**	17.286**	0.539**	109.905**	5.570**	59.574**
Parents	12	0.328**	17.714**	0.167**	11.493**	5.182**	43.321**
Lines	9	0.270**	13.876**	0.129**	4.585*	6.292**	38.868**
Testers	2	0.407**	16.101**	0.272**	6.677*	2.378**	53.519**
Lines vs Testers	1	0.685**	55.490**	0.299**	83.291**	0.799	62.997**
Parents vs Crosses	1	4.587**	239.472**	9.647**	1900.539**	8.928**	21.948**
Crosses	29	0.327**	9.447**	0.379**	88.882**	5.615**	67.597**
Errors	84	0.080	2.385	0.015	1.981	0.473	2.665

* and ** represent level of significance at 5 and 1%, respectively.

2211 was good general combiner for most of the traits except days to 50 per cent flowering, days to maturity, oil content (%) and chlorophyll content. Likewise, parents RTM- 2204 found to be good general combiner for days to 50 per cent flowering, primary branches per plant, secondary branches per plant, number of siliquae per plant, siliquae density, seeds per siliqua and 1000-seed weight. Parent RTM- 2221 was good general combiner for days to maturity, secondary branches per plant, number of siliquae per plant, length of Siliqua and 1000-seed weight. Good general combiner for these traits were also reported earlier by Akabari and Sasidharen (2017) and Alpaslan and Sincik (2025).

A perusal of data resulted that none of the crosses had high ranking sca effects for all the traits under study. Out of thirty crosses nine crosses expressed significant and positive sca effects for seed yield per plant. Earlier similar results were also reported by Patel *et al.* (2014). Out of nine crosses the cross RTM- 2202 × RTM- 2011 revealed highest sca effects for seed yield per plant followed by RTM- 2206 × RTM- 314 and RTM- 2221 × RTM- 1624. The cross RTM- 2221 × RTM- 1624 also expressed significant sca effects for secondary branches per plant, siliquae per plant, siliquae density and 1000-seed weight. Whereas, cross RTM- 2202 × RTM- 2011showed significant negative sca effects for days to flowering and days to maturity. Thus, these two crosses RTM- 2221 × RTM- 1624 and RTM- 2202 × RTM- 2011 can be used in practical plant breeding for exploitation of heterosis and selection of better transgressive segregant for earliness.

The cross RTM- 2208 × RTM- 2011 registered significant and positive sca effects for yield component, *i.e.*, number of siliquae per plant, siliqua density, number of seeds per siliqua and 1000-seed weight; and the cross RTM- 2204 × RTM- 1624 recorded significant and favourable sca effects for branches per plant (primary and secondary), siliqua per plant, siliqua density and 1000-seed weight. Thus, it could be concluded that crosses exhibiting high sca effects for seed yield per plant also manifested high sca effects for one or more yield attributing traits earlier reported by Bhateria *et al.* (1995),

Table 2 : Analysis of variance for combining ability for thirteen characters in taramira in every date of sowing.

Sources of variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Siliqua density
Replication	2	0.278	0.133	95.407	1.730	5.379	39.786	0.004
Crosses	29	10.682**	27.646**	476.807**	7.680**	58.893**	2654.552**	0.044**
Line Effect	9	4.915	29.600	243.560	4.553	61.748	2332.181	0.029
Tester Effect	2	22.011	9.433	1070.738	3.902	42.357	2267.787	0.004
Line * Tester effect	18	12.307**	28.693**	527.439**	9.664**	59.304**	2858.711**	0.055**
Error	58	1.990	3.179	63.710	1.069	1.880	148.215	0.002
Components of variances								
σ^2 Lines		0.821	0.101	31.542	0.568	0.272	58.503	0.003
σ^2 Testers		0.323	0.642	18.11	0.192	0.565	19.697	0.002
σ^2 GCA		0.498	0.541	13.432	0.76	0.293	78.201	0.005
σ^2 SCA		3.439**	8.504**	154.576**	2.865**	19.141**	903.498**	0.018**
σ^2 GCA/ ó^2 SCA		0.145	0.064	0.087	0.265	0.015	0.087	0.257

Sources of variation	d.f.	Siliqua length (cm)	Seeds per siliqua	1000-seed weight (g)	Seed yield per plant (g)	Oil content (%)	Chlorophyll values
Replication	2	0.023	0.310	0.010	4.864	0.113	5.829
Crosses	29	0.327**	9.447**	0.379**	88.882**	5.615**	67.597**
Line Effect	9	0.464	10.666	0.505	65.776	6.052	18.219
Tester Effect	2	0.356	8.911	0.258	92.457	17.042*	131.945
Line * Tester Effect	18	0.255**	8.896**	0.329**	100.037**	4.126**	85.136**
Error	58	0.088	2.234	0.016	2.347	0.411	2.467
Components of variances							
σ^2 Lines		0.023	0.197	0.019	3.807	0.214	7.435
σ^2 Testers		0.003	0.001	0.002	0.253	0.431	1.56
σ^2 GCA		0.027	0.197	0.017	4.059	0.645*	5.875
σ^2 SCA		0.056**	2.221**	0.105**	32.563**	1.238**	27.556**
σ^2 GCA/ σ^2 SCA		0.478	0.089	0.164	0.125	0.52	0.213

* and ** represent level of significance at 5 and 1%, respectively.

Ahsan *et al.* (2013). The crosses RTM- 2201 × RTM- 1624 and RTM- 2209 × RTM- 1624 exhibited significant and positive sca effects for oil content with seed yield per plant. While cross combination RTM- 2204 × RTM- 1624 manifested significant and negative sca effects for days to 50 per cent flowering and days to maturity. Therefore, these cross combinations can be further exploited for genetic improvement by advancing them through successive generations of selection and selfing, facilitating the stabilization and enhancement of desirable quality traits.

The analysis of data presented in Table 3 demonstrated that hybrids expressing high specific combining ability (SCA) effects did so independently of the general combining ability (GCA) status of their parental lines. Notably, crosses involving superior general combiners did not invariably yield the best hybrid combinations, while hybrids derived from poor × poor general combiners were not consistently inferior.

This observation underscores the significant contribution of non-additive gene action, coupled with inter-allelic interactions, in governing SCA effects. The superior performance of hybrids originating from poor × poor or average × poor general combiners suggests the predominance of dominance × dominance interactions, indicative of epistatic gene action. These findings further emphasize the critical role of intra-allelic interactions in the genetic regulation of these traits. Additionally, hybrids exhibiting high SCA effects with at least one good general combiner parent imply the involvement of additive ×

Table 3 : Top three ranking parent with respect to *per se* performance and gca effects and hybrids with respect to *per se* performance and sca effects and heterosis over better parent and standard check (RTM-1351) in Taramira.

Characters	Best performing parent (*per se* performing)	Best combiners	Best performing hybrids (*per se* performing)	Hybrid with high sca effects	Sca effects	Heterosis (%) over	
						Better parent	Standard Check
Days to 50% flowering	RTM-2202	RTM-2202	RTM-2202 X RTM-2011	RTM-2206 X RTM-314	-2.544**	-9.26 **	-3.92
	RTM-2204	RTM-2204	RTM-2211 X RTM-1624	RTM-2202 X RTM-2011	-2.378**	-4.58 *	-4.58 *
	RTM-2208	RTM-314	RTM-2211 X RTM-2011	RTM-2204 X RTM-1624	-2.189**	-5.13 *	-3.27
Days to maturity	RTM-2204	RTM-2221	RTM-2202 X RTM-2011	RTM-2208 X RTM-314	-3.433**	-5.91 **	-2.45 *
	RTM-2211	RTM-2223	RTM-2208 X RTM-314	RTM-2204 X RTM-1624	-3.200**	-2.88 **	-0.98
	RTM-2223	RTM-2270	RTM-2209 X RTM-1624	RTM-2223 X RTM-2011	-3.144**	-1.95	-1.23
Plant height (cm)	RTM-2202	RTM-2209	RTM-2201 X RTM-2011	RTM-2221 X RTM-2011	-23.652**	-21.70 **	-23.58 **
	RTM-2208	RTM-2211	RTM-2221 X RTM-2011	RTM-2223 X RTM-314	-19.862**	-18.06 **	-21.84 **
	RTM-2211	RTM-1624	RTM-2223 X RTM-314	RTM-2211 X RTM-1624	-16.691**	-2.78	-1.31
Primary branches per plant	RTM-2211	RTM-2204	RTM-2204 X RTM-1624	RTM-2206 X RTM-2011	1.851**	19.22 *	17.31 *
	RTM-314	RTM-2209	RTM-2211 X RTM-314	RTM-2208 X RTM-2011	1.851**	11.73	9.94
	RTM-2011	RTM-2211	RTM-2211 X RTM-2011	RTM-2221 X RTM-314	1.776**	29.86 **	19.87 *
Secondary branches per plant	RTM-2223	RTM-2204	RTM-2211 X RTM-314	RTM-2206 X RTM-2011	5.765**	34.07 **	31.47 **
	RTM-1624	RTM-2211	RTM-2211 X RTM-2011	RTM-2201 X RTM-314	4.807**	41.11 **	14.66 *
	RTM-2011	RTM-2221	RTM-2221 X RTM-314	RTM-2211 X RTM-2011	4.798**	59.12 **	56.03 **
Siliquae per plant	RTM-2209	RTM-2204	RTM-2204 X RTM-1624	RTM-2206 X RTM-2011	51.511**	37.70 **	42.68 **
	RTM-314	RTM-2211	RTM-2211 X RTM-314	RTM-2201 X RTM-314	43.903**	41.26 **	40.72 **
	RTM-2011	RTM-2221	RTM-2221 X RTM-1624	RTM-2208 X RTM-2011	24.300**	23.37 **	27.82 **
Siliquae density	RTM-2223	RTM-2204	RTM-2204 X RTM-1624	RTM-2201 X RTM-314	0.190**	23.30 **	16.67 **
	RTM-1624	RTM-2211	RTM-2211 X RTM-314	RTM-2206 X RTM-2011	0.163**	48.61 **	15.05 *
	RTM-314	RTM-2223	RTM-2211 X RTM-2011	RTM-2211 X RTM-2011	0.133**	62.50 **	25.81 **
Siliqua length (cm)	RTM-2206	RTM-2211	RTM-2211 X RTM-314	RTM-2211 X RTM-2011	0.423*	18.53 **	13.23 *
	RTM-1624	RTM-2221	RTM-2211 X RTM-2011	RTM-2201 X RTM-314	0.326	18.69 *	-1.41
	RTM-2011	RTM-314	RTM-2221 X RTM-314	RTM-2223 X RTM-1624	0.254	1.83	-0.52

Table 3 continued...

Table 3 continued...

Seeds per siliqua	RTM-2206	RTM-2204	RTM-2204 X RTM-314	RTM-2208 X RTM-2011	1.776*	-3.50	5.08
	RTM-314	RTM-2209	RTM-2209 X RTM-1624	RTM-2206 X RTM-2011	1.553	-3.94	4.60
	RTM-2011	RTM-2211	RTM-2211 X RTM-314	RTM-2223 X RTM-314	1.510	15.58 *	13.02 *
1000-seed weight (g)	RTM-2202	RTM-2204	RTM-2211 X RTM-314	RTM-2206 X RTM-2011	0.409**	23.69 **	8.58 **
	RTM-1624	RTM-2211	RTM-2221 X RTM-1624	RTM-2201 X RTM-314	0.375**	11.05 **	9.42 **
	RTM-314	RTM-2221	RTM-2221 X RTM-314	RTM-2202 X RTM-1624	0.310**	3.39	3.31
Seed yield/plant (g)	RTM-1624	RTM-2211	RTM-2202 X RTM-2011	RTM-2202 X RTM-2011	8.625**	100.08 **	95.19 **
	RTM-314	RTM-2223	RTM-2211 X RTM-1624	RTM-2206 X RTM-314	7.484**	78.83 **	64.15 **
	RTM-2011	RTM-2011	RTM-2211 X RTM-2011	RTM-2221 X RTM-1624	6.948**	145.07 **	84.20 **
Oil content (%)	RTM-2204	RTM-2202	RTM-2202 X RTM-314	RTM-2211 X RTM-314	2.097**	3.37 *	9.81 **
	RTM-2211	RTM-2209	RTM-2211 X RTM-314	RTM-2223 X RTM-2011	1.227**	-0.07	4.53 **
	RTM-2011	RTM-314	RTM-2270 X RTM-314	RTM-2201 X RTM-1624	1.183**	0.99	4.16 **
Chlorophyll content	RTM-2202	RTM-2208	RTM-2221 X RTM-2011	RTM-2221 X RTM-2011	8.415**	25.03 **	-7.63 **
	RTM-2208	RTM-2223	RTM-2223 X RTM-314	RTM-2211 X RTM-2011	6.682**	25.92 **	-10.92 **
	RTM-2223	RTM-314	RTM-2270 X RTM-314	RTM-2208 X RTM-2011	5.250**	10.51 **	-10.97 **

dominance gene interactions, which are instrumental in generating desirable transgressive segregants in subsequent generations. Therefore, for effective mustard breeding programs, the most desirable cross combinations are those that exhibit strong per se performance, high heterobeltiosis, and standard heterosis, along with the inclusion of at least one parent possessing superior GCA and a high magnitude of SCA effects, thereby ensuring enhanced hybrid performance.

The crosses exhibited high sca effect for yield per plant also exhibited high or average sca effect for yield contributing characters. Considering these aspects, out of 30 crosses RTM- 2202 × RTM- 2011, RTM- 2206 × RTM- 314 and RTM- 2221 × RTM-1624 were identified as promising for obtaining higher seed yield per plant.

The data for seed yield per plant revealed that twenty-four and twenty-one crosses manifested significant and positive heterosis and heterobeltiosis, respectively, while, nineteen crosses showed significant and positive heterosis over standard check RTM- 1351. For seed yield per plant (g), high relative heterosis and heterobeltiosis expressed by the crosses RTM- 2221 × RTM- 1624 and RTM- 2211 × RTM-1624, respectively these results were in close agreement with Ahsan *et al.* (2013). These hybrids are useful for exploitation of heterosis in development of high yielding with super inbred lines of taramira. They also possessed high heterosis for many yield attributing characters in desirable direction. The expression of heterosis for seed yield arises from the combinations of favorable yield components. *Per se* performance, heterosis and combining ability effects, the parents RTM- 2211, RTM- 2223, RTM- 2011 and RTM- 1624 and the hybrids RTM- 2202 × RTM- 2011, RTM- 2206 × RTM- 314 and RTM- 2221 × RTM-1624 were found to be promising for the development of high yielding genotypes.

Conclusion

The expression of most quantitative as well as qualitative traits was primarily governed by non-additive gene action. The predominance of such gene effects can be efficiently harnessed in mustard hybrid reeding programs, particularly when a stable fertility restorer line is available. Based on the comprehensive evaluation of experimental results, the hybrid RTM-2202 × RTM-2011 was identified as a highly promising genotype. This hybrid exhibited superior *per se* performance and secured the top rank with respect to positive specific combining ability (SCA) effects for seed yield. Furthermore, it is recommended that the initial selection of parental genotypes should be carried out based on their *per se* performance in conjunction with general combining ability (GCA) effects. Subsequently, the adoption of biparental mating followed by reciprocal recurrent selection would be an effective breeding strategy to exploit non-additive genetic variance. This approach would facilitate the accumulation and fixation of desirable allelic combinations, thereby contributing to the genetic enhancement of economically important traits in Taramira.

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