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Assessing Genetic Variability in Taramira (*Eruca sativa* Mill.) Germplasm for Enhanced Breeding Strategies

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Abstract

The present research was carried out to estimate the genetic variability for 13 characters among 30 different germplasm of Taramira (*Eruca sativa* Mill.) in a randomized block design with three replications over four artificially created environments through different dates of sowing (timely sown 17 Oct. and late sown 5 Nov.) with (*Orobanche* free and *Orobanche* infested field) *i.e.* timely sown, *Orobanche* free (E_1), timely sown, *Orobanche* infested (E_2), late sown, *Orobanche* free (E_3), late sown, *Orobanche* infested (E_4) at Research farm of SKN College of Agriculture, Jobner (SKNAU, Jobner) during the *rabi* 2022–23. Pooled Anova revealed significant differences among germplasm, environments and G×E interaction significant for all the traits except days to maturity, primary branches per plant, siliqua length (cm). Therefore, analysis of variance is carried out separately for each environment, indicated significant differences among all traits. In all four environments, the PCV>GCV value for all characters. After comparing the mean and range for yield and different yield attributing traits in all four environments, it was found that both were highest in E_1 for most of the traits. The high heritability coupled with high genetic advance as percentage of mean for all four environments revealed that characteristics such as height of first branch emergence (cm), seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g) had high value. As a result, they might be under the control of additive gene action. Therefore, selection for these characters will be highly responsive.

Keywords: Genetic variability, GCV, heritability, PCV, siliqua, yield

1. Introduction

Taramira (*Eruca sativa* Mill.) is an important rainfed winter season oil seed crop in the Brassicaceae family Noor et al. (2020). It is believed to have originated in South Europe and North Africa before being introduced to India Bailey (1949). It contains a diploid number of chromosomes (2n=22) and chromosomes are very small Srivastava (2020). Taramira possesses excellent characteristics, especially resistance to powdery mildew, which can be transmitted to *Brassica campestris* and *Brassica juncea*, both of which are important crops Sastry (2003); Nitin and Sharma (2023). In India, it is known by many names such as tara, trara, schwan, duan, turra, tirwa, merha, merkai, chara, ushan and Sondha as per Singh (1958). The oil content of taramira varies between 31.60 to 41.31% Yadav (1980); Ola et al. (2022). Taramira oil is mostly used to increase the pungency of mustard oil Kuri et al. (2022). Taramira cake may be used as manure to improve soil physical condition and fertility, as well as nutritional feed for animals Elizabeth et al. (2021).

Taramira cultivated primarily for its high-quality oil content and nutritional value Singh et al. (2022). Originating from the Mediterranean region, Taramira has gained prominence in various parts of the world due to its adaptability to diverse climatic conditions and soil types. The crop holds significant agricultural and economic importance, particularly in regions with arid and semi-arid climates where other oilseed crops

may struggle to thrive Dagar and Yadav (2017). Taramira seeds contain a rich composition of essential fatty acids, vitamins, and minerals, making them valuable for human consumption and industrial applications Sharma et al. (2022). Additionally, Taramira oil is renowned for its medicinal properties and culinary uses, contributing to its growing demand in global markets. Despite its potential, Taramira cultivation faces challenges such as susceptibility to pests and diseases, necessitating further research and development initiatives to enhance its productivity and sustainability Singh et al. (2022). The success of any breeding programme relies on genetic variability for economically important traits in the population and its management for exploitation. Germplasm with genetic variation are able to adapt themselves in changeable environment and insured the plants to meet the harsh environment conditions Bibi et al. (2022).

Any strategy to increase yield must begin with the choice of selecting superior parents showing higher heritability and genetic advance for specific traits Sharma et al. (2022). Estimation of heritability in combination with genetic advance are usually more useful than heritability alone for forecasting genetic gain under selection Heera et al. (2023). However, a trait with a high heritability does not always have a high genetic advance Johnson et al. (1955). It is impossible to begin an effective breeding programme without first establishing genetic variability using appropriate metrics including the coefficient of variation (phenotypic and genotypic), genetic advance and broad sense heritability (h^2b) Raju et al. (2023) and Tutlani et al. 2023. Due to lack of variability and a limited knowledge on genetics of yield and its contributing traits, no concerted efforts have been made on the genetic improvement of Taramira Rai et al. (2007); Yadava et al. (2022). Development of new high yielding varieties requires knowledge of the existing genetic diversity and extent of association among the yield contributing characters Keer and Jakhar (2012). The estimate of heritability alone does not provide an idea of the expected gain in the next generation, however the variation could be find along with the greater degree of accuracy when heritability in conjunction with genetic advance Hill (2010); Meena et al. (2021).

Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotype. Hence an experiment was planned to assess the variability, heritability and genetic advance for yield and other characters in a set of taramira germplasm.

2. Materials and Methods

This investigation was conducted during *rabi,* 2022–23 at Research Farm, S.K.N. College of Agriculture, Jobner (Rajasthan). Jobner is located at 26.97°N and75.38°E. It has an average elevation of 400 m above mean sea level (1312 feet).

2.1. Genetic material

The material for the present investigation were consist of a set of 30 germplasm lines including five checks which were released varieties *i.e.* RTM-314, RTM-1351, RTM-1355, RTM-1624, RTM-2002 obtained from the collection being maintained at the AICRP Rapeseed-Mustard (Taramira Unit), Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner (Table 1).

Table 1: List of germplasm lines used under investigation

Sl. No.	Germplasm	Sl. No.	Germplasm
1.	RTM-314	16.	RTM-1613
2.	RTM-644	17.	RTM-1616
3.	RTM-715	18.	RTM-1624
4.	RTM-754	19.	RTM-1626
5.	RTM-1119	20.	RTM-1651
6.	RTM-1120	21.	RTM-1660
7.	RTM-1206	22.	RTM-1822
8.	RTM-1351	23.	RTM-1826
9.	RTM-1355	24.	RTM-1829
10.	RTM-1396	25.	RTM-2002
11.	RTM-1475	26.	RTM-2107
12.	RTM-1530	27.	RTM-2110
13.	RTM-1587	28.	RTM GP-35
14.	RTM-1591	29.	RTM GP-41
15.	RTM-1598	30.	RTM GP-47

These 30 germplasms was sown in four different environments created by manipulating sowing date and *Orobanche* infestation. Envionment-1 (timely sown *Orobanche* free field), Envionment-2 (timely sown *Orobanche* infested field), Envionment-3 (late sown *Orobanche* free field), Envionment-4 (late sown *Orobanche* infested field) in randomized block design with three replications in each environment during *rabi,* 2022–23. The date of timely sown environment was 17th October, 2022 and date of late sown was 5th November, 2022. The inter row spacing's followed would be 80 cm and planttoplantdistanceweremaintainedat15cmbythinningafter 15 days of sowing.

Five plants were randomly selected and tagged before flowering from each plot and data were taken on plant height (cm), primary branches plant^{-1}, height of first branch emergence (cm), siliqua on main shoot, siliqua density, siliqua length(cm), seeds per siliqua, chlorophyll content 35 DAS (SPAD), chlorophyll content 70 DAS (SPAD) and 1000-seed weight (g) while data relating to days to 50% flowering and days to maturity was recorded on whole plot basis. SPAD is used to measure cholophyll content (Kumari et al., 2023)

2.2. Statistical analysis

The data were subjected to analysis of variance as per the procedure suggested by Panse and Sukhatme (1985). The

genotypic coefficient of variation (GCV) and phenotypic coefficient Variation (PCV) computed by the formula suggested by Burton (1952). The PCV and GCV values were ranked as low (0–10%), medium (10–20%) and high (>20%). Heritability (h^2) in the broad sense was calculated according to the formula given by Johnson et al. (1955). Heritability values are categorized on the basis of range of percentage as low (<30%), moderate (30–60%) and high (>60%). Genetic advance for each character was predicted by the formula given by Johnson et al. (1955). Genetic advance as percent of mean was classified as low (0–10%), moderate (10–20%) and high (>20%).

3. Results and Discussion

The pooled analysis of variance was estimated from pooled data of three replications of four environments for all germplasm. Pooled analysis of variance showed highly significant difference among the germplasm for each character. The environmental effects were, also highly significant for all characters. The majority of the parameters with the exception of days to maturity, primary branches per plant and siliqua length (cm) were, significantly influenced by G×E interactions. It indicated differential effects of environments on the germplasm for all the traits. These results showed presence of substantial amount of G×E interaction (Table 2). Therefore, analysis of variance was carried out environment wise which revealed significant variance due to germplasm for all the characters indicating the presence of ample amount of variability in the germplasm (Table 3). These results are similar with earlier findings of Jat et al. (2014) and Kamdi et al. (2022).

Comparative study of different environments depicted that mean values in E_2 and E_4 were lower in relation to E_1 and E_3 for all the traits except height of first branch emergence (cm) indicated that late sowing, *Orobanche* infested had adverse effect on the performance of taramira germplasm for most of the traits. Further it was also observed that E_1 had higher mean in comparison to E_3 for most of the traits except height of first branch emergence and siliqua on main shoot whereas, E_2 in comparison to E_4 had similar trend for all traits except height of first branch emergence (Table 4). Based on the above result, it can be concluded that taramira germplasm should be tested under a timely sown, *Orobanche* free environment for a clear distinction between superior and inferior germplasm because this environment was found to be better for the expression of most of the component traits.

Comparison of range over environments for all the traits indicated that E_1 was most favourable for the expression of traits *viz.* days to maturity, height of first branch emergence (cm), siliqua length (cm), 1000-seed weight (g) and Seed yield per plant (g) which revealed that these traits had higher range in this environment. Similarly, E_3 was favourable for expression of siliqua on main shoot, siliqua density, seeds per siliqua and chlorophyll content 35 DAS (SPAD meter) and E_4 had wider range for the traits days to 50% flowering, plant height (cm) and primary branches per plant. E_2 wider range for only trait Chlorophyll content 70 DAS (SPAD meter) (Table 4). Conclusively it can be advocated that to obtain clear-cut discrimination in screening of taramira germplasm for different traits should be carried out under timely sown, *Orobanche* free (E_1) conditions.

In all four environments, the phenotypic coefficient variation

Table 2: Pooled analysis of variance for yield and yield determining traits in Taramira germplasm

Source	d.f	DFF	PH	DM	PBPP	HFBE	SMS
Environments	3	1654.24**	4456.27**	1091.89**	5.18**	0.15**	139.81**
Rep in Env.	8	9.76	35.83	18.18	0.25	0.04	2.33
Germplasm	29	82.60**	339.86**	253.47**	3.48**	0.99**	17.94**
G×E Interaction	87	35.44**	55.61**	28.53	0.17	0.29**	4.07**
Pooled Error	232	7.48	26.53	25.59	0.20	0.02	1.22

Table 2: Continue...

Source	SD	SL	SPS	CC-35	CC-70	TW	SY/P
Environments	0.119**	0.51**	457.04**	204.29**	2504.10**	19.98**	177.76**
Rep in Env.	0.003	0.06	2.30	10.32	8.03	0.01	0.04
Germplasm	0.022**	0.30**	72.63**	37.87**	33.51**	0.80**	1.03**
G×E Interaction	0.004**	0.01	4.00**	11.07**	18.05**	0.07**	0.26**
Pooled Error	0.002	0.03	1.46	6.63	6.63	0.02	0.05

DFF: Days to 50% flowering; PH: Plant height (cm); DM: Days to maturity; PBPP: Primary branches plant^{-1}; HFBE: Height of first branch emergence (cm); SMS: Siliqua on main shoot; SD: Siliqua density; SL: Siliqua length (cm); SPS: Seeds siliqua^{-1}, CC-35- Chlorophyll content 35 DAS (SPAD meter), CC-70- Chlorophyll content 70 DAS (SPAD meter); TW: 1000 seed weight (g); SY/P: Seed yield plant^{-1} (g); *, **: Significant at (p=0.05) and (p=0.01) levels, respectively

Table 3: Environment wise analysis of variance for 30 germplasm of Taramira tested under four environments

Environment	Source	d.f	DFF	PH	DM	PBPP	HFBE	SMS
Environment-1 (Timely sown and Orobanche free)	Rep.	2	9.30	48.05	20.58	0.21	0.01	0.83
	Germ.	29	15.52**	102.60**	112.02**	1.23**	0.52**	7.06**
	Error	58	7.06	31.64	26.53	0.21	0.02	1.48
Environment-2 (Timely sown and Orobanche infested)	Rep.	2	15.23	10.83	10.73	0.16	0.04	2.38
	Germ.	29	21.36**	168.39**	56.03**	0.66**	0.37**	6.27**
	Error	58	9.18	23.58	26.16	0.18	0.03	1.01
Environment-3 (Late sown and Orobanche free)	Rep.	2	11.91	49.66	22.71	0.42	0.06	3.43
	Germ.	29	67.28**	82.44**	88.95**	1.11**	0.59**	9.28**
	Error	58	9.27	29.78	25.85	0.20	0.03	1.46
Environment-4 (Late sown and Orobanche infested)	Rep.	2	2.61	34.78	18.71	0.20	0.05	2.67
	Germ.	29	84.78**	153.26**	82.04**	0.97**	0.36**	7.53**
	Error	58	4.41	21.13	23.83	0.19	0.02	0.92

Table 3: Continue...

Environment	Source	SD	SL	SPS	CC-35	CC-70	TW	SY/P
Environment-1 (Timely sown and Orobanche free)	Rep.	0.002	0.103	4.30	17.50	3.61	0.02	0.054
	Germ.	0.005**	0.102**	30.00**	21.66**	14.52**	0.39**	0.670**
	Error	0.002	0.037	1.81	7.59	4.34	0.04	0.092
Environment-2 (Timely sown and Orobanche infested)	Rep.	0.005	0.066	2.55	6.19	7.01	0.01	0.049
	Germ.	0.007**	0.079**	13.15**	15.36**	35.87**	0.25**	0.322**
	Error	0.002	0.032	1.09	6.10	12.33	0.02	0.032
Environment-3 (Late sown and Orobanche free)	Rep.	0.005	0.091	4.06	22.37	4.69	0.01	0.041
	Germ.	0.013**	0.095**	30.35**	21.04**	14.21**	0.21**	0.818**
	Error	0.002	0.034	1.84	8.72	4.03	0.02	0.058
Environment-4 (Late sown and Orobanche infested)	Rep.	0.002	0.070	2.09	7.15	16.82	0.01	0.002
	Germ.	0.008**	0.067**	11.13**	13.08**	23.05**	0.15**	0.008**
	Error	0.002	0.030	0.98	3.66	5.84	0.01	0.002

*, **: Significant at (p=0.05) and (p=0.01) levels, respectively

was higher than the genotypic coefficient of variation for all characters. High PCV and GCV were observed for height of first branch emergence in E_1 and E_3 (Table 5). Similar findings pertaining to presence of high genetic variability were reported by Kumar et al. (2023) for first branch initiation height. Moderate GCV and PCV were recorded for plant height (cm) in E_2 and E_4, also for traits siliqua on main shoot, seeds siliqua^{-1}, 1000-seed weight (g) and seed yield plant^{-1} (g) in all four environment. Similar findings have also been reported by Kumar et al. (2023) for plant height (cm), Chaurasia et al. (2014) for siliqua on main shoot, Yadav (2017) seeds siliqua^{-1}, Bahadur et al. (2021) for 1000-seed weight and Nishad et al. (2022) for seed yield plant^{-1} (g) Kumar et al., 2023. The results demonstrated a significant level of genetic variability in the examined germplasm for the primary yield contributing characteristics, as well as seed yield, suggesting that further improvement for these traits is possible. Likewise, lower GCV and PCV were recorded for days to 50% flowering, days to maturity, siliqua length (cm), chlorophyll content 35 DAS (SPAD meter) and chlorophyll content 70 DAS (SPAD meter) (Table 5). These similar findings were reported by Choudhary et al. (2023) for days to 50% flowering, days to maturity, Nisar et al. 2024; Ola et al. (2023) for days to 50% flowering and days to maturity, Sultana et al. (2020) for siliqua length and Padra and Lal (2021) for chlorophyll content.

Johnson et al. (1955) suggested the heritability estimates combined with genetic advance would be more effective in estimating yield under phenotypic selection than heritability estimates alone. In the present investigation, estimate of high heritability along with high genetic advance as per cent of mean were reported for characteristics such as height of first branch emergence (cm), seeds siliqua^{-1}, 1000-seed weight (g)

Table 4: Range and mean for yield and related traits in Taramira germplasm in different environments

Sl. No.	Characters	Range				Mean			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
1.	Days to 50% flowering	52-61.33 (9.33) IV	51-61.33 (10.33) III	42.33-59.67 (17.34) II	41.24-59.74 (18.50) I	57.23	56.10	49.66	48.95
2.	Plant height (cm)	65.13-84.33 (19.2) III	51.6-75.93 (24.33) II	66.27-81.33 (15.06) IV	49-73.73 (24.73) I	76.01	63.94	74.23	62.18
3.	Days to maturity	1 1 6 . 6 7 - 139.67 (23) I	119.33-135.33 (16) IV	114.33-134.67 (20.34) II	112.33-131.67 (19.34) III	128.76	127.52	123.54	121.24
4.	Primary branches plant^{-1}	5.20-7.27 (2.07) II	5.07-6.47 (1.40) IV	5-7 (2) III	4.13-6.40 (2.27) I	6.09	5.76	5.94	5.53
5.	Height of first branch emergence (cm)	1.25-2.70 (1.45) I	1.35-2.51 (1.16) IV	1.43-2.87 (1.44) II	1.42-2.60 (1.18) III	1.86	1.92	1.96	1.92
6.	Siliqua on main shoot	13.07-19.87 (6.80) II	11.33-16.47 (5.14) III	12.6-19.87 (7.27) I	11.13-15.93 (4.80) IV	15.72	13.87	15.81	13.39
7.	Siliqua density	0.56-0.72 (0.16) IV	0.48-0.68 (0.20) III	0.31-0.69 (0.38) I	0.43-0.64 (0.21) II	0.63	0.57	0.60	0.54
8.	Siliqua length (cm)	2.25-2.91 (0.66) I	2.21-2.81 (0.60) II	2.24-2.84 (0.60) II	2.15-2.71 (0.56) III	2.63	2.51	2.55	2.45
9.	Seeds siliqua^{-1}	13.6-23.80 (10.20) II	11.27-17.67 (6.40) III	12.33-22.60 (10.27) I	11.20-16.93 (5.73) IV	18.69	14.50	17.36	14.01
10.	Chlorophyll content 35 DAS (SPAD meter)	39.98-47.88 (7.90) III	37.85-46.27 (8.42) II	38.63-47.15 (8.52) I	37.36-44.75 (7.39) IV	44.12	41.57	42.52	40.57
11.	Chlorophyll content 70 DAS (SPAD meter)	37.60-45.89 (8.29) IV	29.72-42.89 (13.17) I	36.92-46.16 (9.24) III	22.32-32.63 (10.31) II	41.12	36.15	39.73	29.32
12.	1000 seed weight (g)	2.40-3.57 (1.17) I	1.85-2.80 (0.95) II	2.30-3.25 (0.95) II	1.56-2.30 (0.74) III	3.00	2.31	2.76	1.96
13.	Seed yield plant^{-1} (g)	2.77-4.90 (2.13) I	1.64-3.09 (1.45) III	2.34-4.24 (1.90) II	0.43-0.63 (0.20) IV	3.61	2.28	3.39	0.54

(Bracket value shows the difference between the highest and lowest values of ranges and I,II,III and IV shows ranking)

Table 5: Genotypic coefficient of variation and phenotypic coefficient variation for yield and related traits in Taramira germplasm in different environments

Sl. No.	Characters	Genotypic coefficient of variation (%)				Phenotypic coefficient variation (%)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
1.	Days to 50% flowering	2.93	3.59	8.86	10.57	5.49	6.49	10.77	11.41
2.	Plant height (cm)	6.4	10.87	5.64	10.67	9.78	13.26	9.27	12.98
3.	Days to maturity	4.15	2.47	3.71	3.63	5.76	4.71	5.54	5.42
4.	Primary branches plant^{-1}	9.58	6.99	9.25	9.24	12.23	10.12	11.97	12.14
5.	Height of first branch emergence (cm)	21.9	17.7	22.16	17.49	23.14	19.54	23.64	19.03
6.	Siliqua on main shoot	8.68	9.55	10.22	11.08	11.62	11.99	12.76	13.2
7.	Siliqua density	4.55	7.74	10.38	8.69	8.74	10.5	12.77	11.41

Sl. No.	Characters	Genotypic coefficient of variation (%)				Phenotypic coefficient variation (%)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
8.	Siliqua length (cm)	5.51	4.92	5.58	4.52	9.3	8.76	9.1	8.43
9.	Seeds siliqua^{-1}	16.36	13.82	17.76	13.13	17.97	15.61	19.4	14.92
10.	Chlorophyll content 35 DAS (SPAD meter)	4.83	4.23	4.77	4.37	8.03	7.29	8.42	6.43
11.	Chlorophyll content 70 DAS (SPAD meter)	4.48	7.75	4.64	8.17	6.76	12.43	6.86	11.61
12.	1000 seed weight (g)	11.45	12.01	9.31	10.82	13.12	13.21	10.38	12.33
13.	Seed yield plant^{-1} (g)	12.16	13.66	14.83	8.53	14.78	15.78	16.44	11.32

Table 6: Heritability (%) and Genetic advance as per cent of mean for yield and related traits in Taramira germplasm in different environments

Sl. No.	Characters	Heritability (%)				Genetic advance as per cent of mean			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
1.	Days to 50% flowering	29	31	68	86	3.23	4.10	15.00	20.19
2.	Plant height (cm)	43	67	37	68	8.62	18.35	7.08	18.07
3.	Days to maturity	52	28	45	45	6.15	2.68	5.12	5.01
4.	Primary branches plant^{-1}	61	48	60	58	15.45	9.94	14.72	14.49
5.	Height of first branch emergence (cm)	90	82	88	85	42.68	33.03	42.79	33.13
6.	Siliqua on main shoot	56	63	64	71	13.35	15.65	16.85	19.17
7.	Siliqua density	27	54	66	58	4.88	11.74	17.39	13.65
8.	Siliqua length (cm)	35	32	38	29	6.72	5.70	7.05	5.00
9.	Seeds siliqua^{-1}	83	78	84	77	30.70	25.20	33.48	23.81
10.	Chlorophyll content 35 DAS (SPAD meter)	36	34	32	46	5.97	5.05	5.56	6.11
11.	Chlorophyll content 70 DAS (SPAD meter)	44	39	46	50	6.11	9.96	6.47	11.85
12.	1000 seed weight (g)	76	83	80	77	20.58	22.50	17.19	19.56
13.	Seed yield plant^{-1} (g)	68	75	81	57	20.62	24.36	27.56	13.23

and seed yield plant^{-1} (g) in all the environments (Table 6). As a result, they might be under the control of additive gene action. Therefore, selection for these characters will be highly responsive. Similar findings have been recorded by Padra and Lal (2021) for test weight (g) and seed yield (g), Sultana et al. (2020) for seeds siliqua^{-1}, seed yield plant^{-1} (g) in, Sharma et al. (2023) for seeds siliqua^{-1}, test weight (g) and seed yield (g). The trait siliqua on main shoot and siliqua density showed high heritability along with moderate genetic advance (except in E_1 for siliqua density) in all the four environments. Choudhary et al. (2023) also reported this result for siliqua on main shoot.

4. Conclusion

There was sufficient genetic variability present in the experimental material for most of the traits in all the environments. Therefore, this variability could be used to establish segregating generations by using these germplasm for both timely and late planting situations. For yield and its attributing traits in all four environments, E_1 for most of the traits H^2b and GAM revealed highest values governed by additive gene action and direct selection based on these traits could be beneficial.

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