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RESEARCH ARTICLE

Estimation of variation, heritability and genetic advance in taramira (*Eruca sativa* Mill)

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SUMMARY

Fourty two genotypes of taramira (*Eruca sativa* mill.) were evaluated for genetic parameters of variation heritability and genetic advance of yield and its related traits over three different environments created by three dates of sowing during *Rabi* 2009-10. Environment wise analysis of variance revealed that in first environment significant differences were observed for all the characters except oil content, in second environment significant difference were observed for all the characters except seed yield and test weight whereas in third environment, days to maturity showed non-significant difference.

Key Words : Heritability, Genetic advance, Variation, Taramira

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Oil seeds, as a group comprises a variety of crops producing edible oils like groundnut, mustard, soybean and a number of non-edible oil like castor and linseed which have an established industrial uses.Oil seeds occupy a significant place in national economy next only to food grains. The bulk of the country's edible oils are derived from two major oil seeds namely; groundnut and rapeseed-mustard which together account for about 14.7 million tones which is about 52.12% of the total oil seeds production (28.2 million tones) (Anonymous, 2009 and 2010). Taramira (*Eruca sativa* Mill.) is an important winter season oil seed crop of the family Brassicaceae. It is an introduced crop in India. South Europe and North Africa are believed to be the native place of it (Bailey, 1949 and Prakash, 1980). It has diploid number of chromosomes 2n = 22 and the chromosomes are very small. Taramira has desirable traits particularly resistance to powdery mildew that can be transferred to *Brassica compestris* and *Brassica juncea* both of which are important crops (Sastry, 2003). In india, it is known by many names such as tara, schwan, seoha, duan, turra, tirwa, merha, merkai, chara, ushan and sondha (Singh, 1958). In Europe it is known as rocket salad, rocket, roquuette or arrugula, where it is generally grown for young leaves that are eaten as green salad. In India taramira is mainly grown in the states like Rajasthan, Haryana, Punjab, Gujarat and Madhya Pradesh.

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MATERIAL AND METHODS

A set of 40 germplasm lines along with two check varieties namely RTM-314 and RTM-2002 were selected at random from the collection being maintained at the AICRP on oilseeds (Taramira Unit), Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner. The details of the lines selected are given in Table 1. All the 42 entries were sown at three different dates, representing three environments. The sowing dates were 20th October, 5th November and 20th November, 2009. In each environment, all the genotypes were evaluated in Randomized Block Design

with three replications. Plot size was 0.6 x 5.0 m^2 accommodating two rows of each entry. The row to row distance was kept at 30 cm and plant to plant distance was maintained 10 cm by thinning at 25 days after sowing. ten competitive plants were randomly selected at the time of maturity (excepting the days to 50% flowering) from each plot to record the following observations: days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, seed yield per 10 plant (g), test weight (g), oil content (%).

RESULTS AND DISCUSSION

The experimental findings obtained from the present study have been discussed in following heads:

Variation:

Analysis of variance was carried out for pooled data (Table 1) which indicated significant differences between the three environments created by three different dates of sowing for all the characters. Variance due to genotypes was highly significant. variance due to genotype x environment (dates of sowing) interaction was also highly significant for all the characters except for days to maturity. Thus, genotypes had variable performance over the environments. The significant variance due to environment and genotype x environment indicated need of estimation and analysis of genetic parameter of variation for each of the environment independently. Thus, analysis of variance was carried out environment wise which has been presented in Table 2. Analysis of variance for first environment (first date of sowing) indicated significant variance due to genotypes for all the characters except for oil content. Analysis of variance for second environment had indicated significant variance due to genotypes for all the characters except test weight and seed yield whereas in third environment the variance was also significant for all the characters except days to maturity.

Heritability and genetic advance:

In first environment high heritability was recorded for secondary branches per plant, test weight, days to 50% flowering, number of siliquae per plant, plant height and primary branches per plant. For seed yield and number of seeds per siliqua it was moderate whereas for days to maturity and oil content it was low (Table 3). High heritability along with high genetic advance as percentage of mean was recorded for secondary branches per plant, number of siliquae per plant, primary branches per plant. Characters like days to 50% flowering, test weight and plant height had high heritability and moderate genetic advance as percentage of mean whereas low heritability coupled with low genetic advance for days to maturity and oil content.

In second environment heritability estimates were high

Table 1 : Pooled analysis of variance for various morphological traits

Source	d.f.	Mean sum of squares								
		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches / plant	Secondary branches / plant	No. of siliquae / plant	No. of seeds / siliqua	Seed yield (g)	Test weight (g)	Oil content (%)
Environment	2	2881.6376**	2173.0115**	28011.9556**	331.9992**	7782.5919**	30347095.15**	745.2926**	24142.6223**	1.2130**	3.2157*
Rep / Env.	6	6.0370*	3.6322	28.9073	1.2517	2.0664	69.8307	4.5291	375.8290**	0.1941**	0.8848
Genotypes	41	34.0406**	13.7223**	319.2331**	15.9731**	79.4124**	3793.4340**	62.0133**	142.6219**	0.1195**	2.5789**
Gen. x Env.	82	13.1877**	3.4809	241.5486**	13.7001**	69.1482**	3479.5869**	40.0494**	105.2513**	0.1014**	1.3605*
Error	246	2.706	3.15	27.24	1.248	3.589	149.3	3.04	41.03	0.0281	0.9606

* and ** indicate significance of values at P=0.05 and 0.01, respectively

for number of siliquae per plant (98.29) followed by number of seeds per plant siliqua (92.67), plant height (78.01), secondary branches per plant (76.48), primary branches per plant (73.91), days to 50% flowering (60.54) and days to maturity (51.01), whereas heritability for seed yield and test weight was low. High genetic advance as per cent of mean was recorded for number siliquae per plant (58.44%) followed by number of seeds per siliqua (47.37%), primary branches per plant (40.22%) and secondary branches per plant (39.45%). While plant height (18.22%) had moderate genetic advance as per cent of mean. Whereas low genetic advance as percentage of mean was recorded for seed yield, days to 50% flowering, days to maturity, test weight, plant height and oil content. High heritability alongwith high genetic advance as per cent of mean was recorded for number of siliquae per plant, number of seeds per siliqua, primary branches per plant and secondary branches per plant. High heritability with moderate genetic advance as percentage of mean was recorded for plant height whereas high heritability coupled with low genetic advance as percentage of mean was observed for days to 50% flowering and days to maturity. Moderate heritability with low genetic advance was recorded for oil content and low heritability with low genetic advance as percentage of mean was recorded for seed yield and test weight. %).

In third environment high heritability was recorded for number of siliquae per plant (98.29%), secondary branches per plant (96.92%), primary branches per plant (92.91%), number of seeds per siliqua (92.67%), plant height (91.04%), seed yield (65.81%) and days to 50% flowering (57.58%) whereas moderate heritabilitobserved for test weight and low heritability was recorded for oil content and days to maturity (Table 3). High genetic advance as per cent of mean was observed for secondary branches per plant (87.00%), primary branches per plant (77.64%), number of siliquae per plant (65.59%), number of seeds per siliqua (46.94%) and seed yield (41.67%), whereas low genetic advance as per cent of mean was observed for test weight (5.14%), days to 50% flowering (3.62%), oil content (1.48%) and days to maturity (0.50%). High heritability coupled with high genetic advance as per cent of mean was recorded for secondary branches per plant, primary branches per plant, number of siliquae per plant, number of seeds per siliqua and seed yield. High heritability along with low genetic advance as per cent of mean was observed for days to 50% flowering and moderate heritability along with low genetic advance as percentage of mean was observed for test weight.

Heritability estimates along with genetic advance as per cent of mean were considered together, primary branches per plant, secondary branches per plant and number of siliquae per plant had high heritability along with high genetic advance as per cent of mean for all the three environments. While, number of seeds per siliqua had high heritability coupled with high genetic advance as per cent of mean in the second and

Table 2 : Environmental wise analysis of variance for forty two genotypes over three environment for different characters

Environment	Source	d.f.	Days to 50% flowering	Days to maturity	Plant height	Primary branches / plant	Secondary branches / plant	No. of siliquae / plant	No of seeds / siliqua	Seed yield (g)	Test weight (g)	Oil content (%)
I	Replication	2	8.667	8.000	47.231	2.129	4.805	176.177	10.676	7.089	0.034	1.211
	Genotypes	41	32.708**	5.159*	298.598**	9.046**	106.293**	4397.796**	16.663**	187.942**	0.177**	2.852
	Error	82	3.024	2.967	49.961	1.750	6.225	413.718	5.628	58.683	0.015	1.803
II	Replication	2	4.675	1.301	22.459	1.333	1.274	23.634	1.876	1117.079**	0.048	1.239*
	Genotypes	41	19.679**	9.328**	291.134**	14.215**	41.008**	4451.988**	76.576**	89.821	0.056	0.841**
	Error	82	3.512	2.262	25.009	1.496	3.882	23.111	2.238	53.287	0.039	0.305
III	Replication	2	4.770	1.595	17.025	0.243	0.133	9.682	1.059	3.318	0.499**	0.204
	Genotypes	41	8.029**	6.197	212.204**	20.113**	76.433**	1902.824**	48.873**	75.361**	0.089**	1.607*
	Error	82	1.583	4.221	6.738	0.499	0.733	10.984	1.256	11.125	0.030	0.774

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 3 : GCV Heritability and genetic advance (%)

Sr. No.	Characters	Genotypic coefficient variation			Heritability			Genetic advance (%)		
		E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
1.	Days to 50% flowering	5.85	3.97	2.31	76.59	60.54	57.58	10.55	6.37	3.62
2.	Days to maturity	0.65	1.24	0.66	19.76	51.01	13.49	0.60	1.83	0.50
3.	Plant height	9.14	10.01	11.58	62.43	78.01	91.04	14.89	18.22	22.76
4.	Primary branches / plant	16.29	22.71	39.10	58.15	73.91	92.91	25.61	40.22	77.64
5.	Secondary branches / plant	24.68	21.89	62.62	84.27	76.48	96.92	46.67	39.45	87.00
6.	No. of siliquae / plant	20.70	28.58	32.11	76.25	98.46	98.29	37.25	58.44	65.59
7.	No. of seeds / siliqua	9.00	24.00	23.67	39.53	91.72	92.67	11.66	47.37	46.94
8.	Seed yield (g)	15.30	8.27	24.93	42.34	18.60	65.81	20.51	7.35	41.67
9.	Test weight (g)	6.75	2.05	3.94	77.83	12.45	39.92	12.27	1.49	5.14
10.	Oil content (%)	1.56	1.12	1.19	16.24	36.92	26.43	1.29	1.39	1.48

third environment, whereas seed yield had high heritability with high genetic advance in the third environment. Thus characters like primary branches per plant, secondary branches per plant, number of siliquae per plant, number of seeds per siliqua and seed yield might be under the control of additive gene action. Plant height had high heritability with moderate genetic advance as per cent of mean in all the three environments and also for the pooled data, while test weight had high heritability with moderate genetic advance in first environment. The characters days to 50% flowering had high heritability with low genetic advance as per cent of mean for all the three environments, whereas days to maturity and oil content had moderate heritability alongwith low genetic advance as per cent of mean for all the three environments and also for the pooled data.

Conclusion:

In any breeding programme assessment of genetic variability is the foremost requirement. In absence of genetic variability in the material the selection is not effective. Moreover, response to selection is directly proportional to the genetic variability present in the material. In taramira only limited varieties like ISTA, T-27, RTM-314 and RTM-2002 were released for commercial cultivation during past 50 years. Looking to the depleting water availability, there is an urgent need to breed an improved variety of taramira with high seed yield alongwith high heritability over environments and wider adaptability.

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