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Evaluation of Half-sib Progenies Developed From RTM 314 in *Eruca sativa* for Seed Yield and its Components

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Abstract: Variability, heritability and correlations were studied in 150 half-sib families generated from RTM-314 variety of taramira, in RBD with two replications. The estimates of σ^2_A and σ^2_P for plant height, number of secondary branches, number of siliquae per plant and number of seeds per siliquae were very low. The estimates of heritability (narrow sense) were very high for plant height, number of secondary branches, number of siliquae per plant and number of seeds per siliquae. The expected selection gain between families was lower in comparison to expected gain from within family selection. Correlation analysis has shown positive association of plant height and number of siliquae per plant with seed yield per plant in the half-sib progenies. It is suggested that, based on secondary branches and number of seeds per siliquae, superior progenies may be used to reconstitute new populations for the improvement of seed yield in RTM 314.

Key words: Taramira, *Eruca sativa*, half-sib progenies, heritability, variability.

Taramira (*Eruca sativa*) is a cross pollinated crop with sporophytic type of self-incompatibility (Verma *et al.*, 1977). To improve such crops, population improvement is the recommended method. Commonly used methods for population improvement are mass (individual phenotypic) selection, full-sib, half-sib and S_1 progeny selection where selfing is possible. These methods help in the exposure of hidden variability which can be used either to generate further variability or to improve the population (Narooka, 1985; Sastry *et al.*, 1987).

Taramira being a cross pollinated crop, S_1 progeny selection is not effective. Of the remaining methods, half-sib selection is the easiest to employ. The present investigation was planned to test the efficacy of half-sib method in exposing the residual variability or its use in further improvement of taramira.

Materials and Methods

Investigation was carried out on RTM 314, a variety developed through mass selection from material collected from Sri Ganganagar. A large number of single plants were selected randomly from a large field of RTM 314 which was growing in isolation. The produce of each plant was harvested separately. In the succeeding *rabi* season, 150 selected single plants forming half-sib families were evaluated in RBD with 2 replications. Each family was sown in a single row plot of 3 m length.

The source population, i.e., variety RTM 314, was repeated after every 20 families as a check variety. Row to row distance was 30 cm with 10 cm distance between

Table 1. Analysis of variance of half-sib families

Characters	Mean squares			
	Replication (df = 1)	Family M_1 $\sigma^2w+\sigma^2+r\sigma^2f$ (df=149)	Error M_2 σ^2w2 (df=149)	Within M_3 σ^2_w (df=2700)
Plant height (cm)	362.00	8539.41**	2435.93	159.23
Primary branches per plant	518.36**	9.35	30.85	2.43
Secondary branches per plant	486.88	3124.52**	179.76	36.66
Siliquae per plant	287.00	75878.98**	20430.56	1573.23
Seeds per siliqua	5.82	365.19**	95.61	8.94
Siliqua length (cm)	0.02	0.63	0.78	0.07

Based on family means:

	Mean squares		
	Replication	Family	Error
Days to 50% flowering	0.187	11.64	7.59
Test weight(g)	0.201	0.10	0.05
Seed yield per plant(g)	0.03	0.60	2.14
Oil content (%)	1.90	4.157*	0.88
Harvest index	1.72	14.57	11.94

* significant at P = 0.05, ** significant at P = 0.01.

plants within row. Data on randomly selected 10 plants were recorded for plant height, number of primary branches, number of secondary branches, number of siliquae per plant and siliquae length, biological yield, while data on whole plot basis was taken for days to 50% flowering, test weight (g), seed yield per plant (g), oil content (%) and harvest index.

Results and Discussion

Among the progenies, the family sum of squares (Table 1) was significant for four characters, namely, plant height, number of secondary branches, number of siliquae per plant and number of seeds per siliquae indicating inherent differences between the families for these characters. The family mean square of these characters was significant when tested against within mean sum of squares, indicating that inter-family variance was higher in comparison to intra-family variance. In such cases, the between-family selection is supposed to be more effective to within-family selection. Significant differences between families existed only for oil content. In open pollinated progenies, significant differences between families are expected if the original population is highly heterogeneous. Earlier also, significant differences between half-sib families have been reported by Narooka (1985) and Sastry *et al.* (1987).

In 7 out of 11 characters, the families did not show significant variation. This can be ascribed to the population structure of RTM 314 itself. Taramira is cultivated on marginal lands in Rajasthan, where fertilizer use is very limited. Under such conditions only such genotypes which are best suited for marginal conditions might have

Table 2. Estimation of phenotypic variances, heritability (narrow sense) and genetic advance for taramira yield (based on individual plant data)

Parameter	Characters					
	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seed per siliqua	Siliqua length
σ^2_F	305.17	-1.08	147.23	27772.42	13.48	-0.01
σ^2_{HS}	1451.49	13.26	220.62	12279.75	57.26	0.35
σ^2_A	1220.63	–	588.95	11089.68	53.92	–
σ^2_P	1379.93	–	625.61	12662.91	62.86	–
$h^2_{(NS)}$ as %	88.40	–	94.10	87.50	85.70	–
GA among families as % mean	0.22	–	5.23	0.29	1.36	–
GA within families as % mean	5.96	–	94.42	6.78	26.19	–
GA among + GA within families as % mean	6.18	–	99.65	7.07	27.55	–

From the mean squares of M_1, M_2 and M_3 of Table 1, σ^2_A, σ^2_P, σ^2_{HS}, h^2_{NS}, were estimated as per the following formulae (Hallaeur and Miranda, 1988).

$$\sigma^2_A = 4\sigma^2_f = \frac{M_1 - M_2}{nr} \qquad \sigma^2_P = \sigma^2_A + M_3$$

GA when selection is done among families is determined by $= \left[\left(k\frac{1}{8}\frac{\sigma^2_A}{\sigma^2_{HS}}\right) \div \overline{X}\right] \times 100$

GA when selection is done within families was estimated $= \left[\frac{k\left[\frac{3/8\sigma^2_A}{M_3}\right]}{\overline{X}}\right] \times 100$

GA among + within is estimated by $= \frac{\text{GA among families + within families}}{\overline{X}} \times 100$

where, $\overline{X}$, the general mean of the character; n = number of plants per family; r = number of replications.

evolved. Further, since taramira is cultivated on limited area, the amount of variability present in this group should also be limited. Similar views are reported by Sastry *et al*. (1995). RTM 314 has been developed by mass selection from the material from Sri Ganganagar. Therefore, it is possible that the original population itself is less variable for most of the traits, which is reflected from non-significant differences between families.

In six characters where single plant data were available, the difference between σ^2_A and σ^2_P estimates (Table 2) of plant height, number of secondary branches, number of siliquae per plant and number of seeds per siliquae was very low, indicating the importance of additive variance in the inheritance of these characters.

The heritability (narrow sense) was very high for plant height, number of secondary branches, number of siliquae per plant and

Table 3. Correlations in half-sib families between different characters of taramira

Character	Plant height	Primary branches	Secondary branches	Siliquae per plant	Seed per siliqua	Siliqua length	Test weight	Seed yield per plant	Oil content	Harvest index
Days to 50% flowering	-0.33**	-0.11	-0.09	-0.27**	0.00	-0.05	0.09	-0.31**	0.00	-0.12
Plant height		0.07	0.02	0.29**	0.01	0.09	0.13	0.31**	0.05	-0.04
Primary branches			0.67**	0.060**	-0.02	0.06	-0.11	0.17**	-0.19**	-0.13
Secondary branches				0.66**	0.07	0.12	-0.07	0.18**	-0.13	-0.06**
Siliquae per plant					0.05	0.12	-0.01	0.42**	-0.09	-0.19**
Seeds per siliqua						0.67**	0.06	0.04	-0.03	-0.05
Silique length							0.14**	0.07	-0.02	-0.15*
Test weight								0.09	0.06	0.02
Seed yield per plant										-0.07

** Significant at P = 0.05.

number of seeds per siliquae, which indicates that selection for these traits should be effective. The expected selection gain, because of selection between families was low in comparison to the expected gain from selection within the families. Among the above four characters, the total expected gain (both within and among) is highest in number of secondary branches, followed by number of seeds per siliquae. For the other traits, the gain was very low.

As most of the characters exhibited non-significant differences, only simple correlations using family mean were estimated among characters in all possible combinations. The correlations were estimated in the parent population and the half-sib families separately. In the parent population, most of the correlations were significant and positive. Seed yield per plant was found to be positively associated with all the traits, similar to the reports of Rathore (1995) and Meena (1996). Most of the associations were also found to be positive. The correlation of harvest index was, however, found to be non-significant except for its association with test weight and oil content. Such type of associations have also earlier been reported by Nehra *et al.* (1989), Rathore (1995) and Meena (1996).

Among half-sib families, very few correlations were found to be significant. Seed yield was found to be significant and positively correlated with plant height, number of primary branches, number of secondary branches, number of siliquae per plant, biological yield and harvest index.

In conclusion, it can be pointed out that significant between-family variance for major yield components is still present in RTM 314, which can be exploited. Further, this can be exposed and exploited even with simple population improvement methods like half-sib method, because development of hybrid varieties is a far cry in taramira due to economic considerations, as well as the development of inbred lines because of the presence of self incompatibility. Correlation analysis indicated that the associations of plant height, number of primary branches, number of secondary branches, number of seeds per siliqua in general had positive correlation with the seed yield in both the parent (RTM 314) and half-sib progenies.

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