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DIVERGENCE ANALYSIS IN TARAMIRA (*ERUCA SATIVA* MILL.)

S. N. SODANI, E. V. D. SASTRY AND M. R. NEHRA

Department of Genetics and Plant Breeding, S. K. N. College of Agriculture, Jobner

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ABSTRACT

Genetic divergence of 99 lines of taramira (*Eruca sativa* Mill.) was assessed using Mahalanobis' D^2 statistic. These lines could be grouped in 13 clusters. Grouping of lines in different clusters was not related to their geographic origin. Pods/plant, seed yield/plot, seed yield/plant and test weight contributed maximum towards total genetic divergence. Based on mean performance, genetic distance and clustering pattern, hybridization involving parents RTM-136, 176, 91, 345 and 465 belonging to clusters III, VIII, X and XII may give higher yielding varieties.

Key words: *Eruca sativa*, taramira, genetic divergence.

Taramira is mainly grown on very poor and sandy soils with low rainfall areas of Rajasthan. It is a highly drought resistant crop with efficient root system to extract moisture from deep soils. During the years of severe drought with very late rabi rains, taramira is the only alternative crop available for sowing. In view of its importance in the region, crop improvement work has been started at the S. K. N. College of Agriculture, Jobner. The germplasm lines were collected from different parts of Rajasthan. For identifying diverse parents for hybridization, multivariate analysis by means of Mahalanobis' D^2 statistic has been used in several crops. It is a powerful tool in quantifying the degree of genetic divergence among parents. However, such information is lacking in taramira (*Eruca sativa* Mill.). An attempt was, therefore, made to study the genetic diversity in this crop.

MATERIALS AND METHODS

A large number of taramira germplasm collections are being maintained at the S. K. N. College of Agriculture, Jobner (Rajasthan). From this collection, 99 lines were selected on the basis of their geographic diversity. The experiment was sown in RBD with three replications in rabi (winter) 1987-88. Each line was sown in four rows of 2 m length, spaced at 30 cm. The plant-to-plant distance was 10 cm. From the two central rows, 10 plants were randomly taken and observations recorded for plant height, primary and secondary branches/plant, pods/plant, pod length, seeds/pod, seed yield/plant, test weight, and oil content. The observations on days to flowering, days to maturity and seed yield were recorded on plot basis.

Analysis of variance for different characters was done as per standard procedures. Mahalanobis' D^2 statistic was used to assess divergence. Lines were grouped on the basis of minimum generalized distances using Tocher's method as described by Rao [1].

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the lines for all the characters studied, indicating adequate genetic variability among the lines.

Table 1. Cluster composition in taramira

Cluster	Number of lines included	Lines included in cluster with place of collection
I	69	RTM-57, 61, 64, 234, 248, 253, 327, 329, 330, 336, 337, 346, 345, 547 (Jaipur); RTM-85, 88, 107, 119, 180, 181, 183, 187, 192, 193, 196, 453, 455, 457, 459 (Tonk); RTM-199, 201, 204, 437, 440, (Bundi); RTM-28, 37, 126, 132, 140 (Bhilwara); RTM-23, 283, 290, 293, 294 (Alwar); RTM-5, 10, 20, 118, (Ajmer); RTM-67, 210, 214, 446 (Kota); RTM-169, 170, 174, 175 (Chittorgarh); RTM-257, 278, 373 (Sikar); RTM-309, 316, 473 (Sriganganagar); RTM-1, 413, 419, 427 (Bharatpur); RTM-2 (I) Job TC-2 (Jobner, Jaipur); T-27 (Hisar, Haryana)
II	6	RTM-100, 152, 575 (Udaipur); RTM-125 (Bhilwara); RTM-263 (Sikar); RTM-423 (Bharatpur)
III	7	RTM-342, 324, 333, 345 (Jaipur); RTM-304, 465 (Sriganganagar); RTM-109 (Tonk)
IV	5	RTM-145, 168 (Udaipur); RTM-141 (Bhilwara); RTM-341 (Jaipur); RTM-430 (Bharatpur)
V	2	RTM-354 (Sikar); RTM-461 (Tonk)
VI	2	RTM-3 (Ajmer); RTM-99 (Tonk)
VII	2	RTM-31, RTM-41 (Bhilwara)
VIII	1	RTM-176 (Chittorgarh)
IX	1	RTM-236 (Jaipur)
X	1	RTM-91 (Tonk)
XI	1	RTM-188 (Tonk)
XII	1	RTM-136 (Bhilwara)
XIII	1	RTM-218 (Kota)

The 99 lines were grouped into 13 clusters (Table 1). The maximum number of lines (69) were included in cluster I, followed by 7 in III, 6 in II, 5 in IV, and 2 each in V, VI and VII. The clusters VIII to XIII consisted of only one line each. Interestingly, the lines from Tonk, Bhilwara and Jaipur were grouped in 6, 5 and 4 clusters, respectively, having maximum genetic diversity. The clustering pattern of the lines suggested that geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity [2]. In contrast, all lines from Alwar (5) and Bundi (5) were grouped into a single cluster, viz. I, indicating genetic similarity among lines coming from the same geographic area, as was also observed by Jeswani et al. [3].

On the basis of the present findings it can be suggested that though geographic diversity may not necessarily be an index of genetic diversity, due attention should also be paid to geographic diversity if sufficient genetic diversity has to be accumulated in the germplasm [4].

Table 2. Average inter- and intracluster (in bold) distances (D) in taramira

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**5.00**	6.49	7.07	6.86	7.29	7.61	6.55	6.19	7.63	7.61	6.00	8.86	7.63
II		**4.67**	9.54	9.05	7.14	10.06	9.35	6.75	9.37	8.10	6.12	12.18	7.90
III			**4.94**	6.74	11.44	9.37	7.78	9.39	8.53	11.26	7.00	7.45	10.32
IV				**4.81**	10.03	10.58	7.13	8.92	10.70	10.41	6.38	6.82	9.88
V					**4.38**	8.97	9.85	6.45	10.01	5.84	8.92	11.56	8.95
VI						**4.78**	7.20	6.57	6.19	8.89	10.81	11.06	8.52
VII							**5.32**	7.60	8.02	9.19	8.22	9.21	8.31
VIII								**0.00**	7.06	8.12	8.24	11.71	7.79
IX									**0.00**	8.27	8.61	12.55	10.51
X										**0.00**	7.95	12.47	9.48
XI											**0.00**	10.08	9.94
XII												**0.00**	11.87
XIII													**0.00**

The average intercluster (D) values ranged from 5.84 to 12.55 (Table 2). The maximum intercluster (D) value (12.55) was observed between clusters IX and XII with one genotype each. The minimum intercluster average (D) value (5.34) was found between cluster V with 2 genotypes and cluster X with 1 genotype, indicating that the genotypes of these two clusters were genetically close.

Table 3. Character means of 99 taramira genotypes belonging to different clusters

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Pod length (cm)	Seeds per pod	Test weight (g)	Seed yield per plant (g)	Seed yield per plot (g)	Oil content (%)
I	52.6	120.8	69.22	5.06	9.75	112.8	1.87	18.3	3.01	5.28	244.6	34.1
II	52.0	119.8	57.23	4.56	8.10	69.1	1.82	18.8	3.19	3.87	184.1	33.8
III	53.1	121.0	70.55	5.00	8.32	149.8	1.94	17.9	2.60	8.06	353.2	34.2
VIII	50.7	121.3	69.13	5.66	14.13	119.2	1.71	18.9	3.88	7.85	247.1	35.8
IX	54.7	124.3	84.03	4.40	12.07	124.8	2.13	13.1	2.91	9.15	259.9	35.4
X	55.7	123.7	73.80	5.17	14.17	86.9	2.19	19.3	2.69	3.15	167.7	35.0
XI	52.0	121.7	67.23	4.17	7.03	90.9	2.10	17.8	2.77	4.00	248.2	35.7
XII	53.0	120.0	74.10	6.33	12.17	181.8	1.69	16.3	2.25	6.50	388.0	33.1
XIII	55.0	118.7	66.23	5.17	9.47	104.5	1.78	16.9	3.69	4.70	198.3	32.2

Cluster means for different characters indicated that seed yield/plot and pods/plant were highest in cluster XII (RTM-136) with earlier maturity (Table 3). Cluster VIII (RTM-176) showed earliest flowering, highest oil content, and high test weight combined with higher number of seeds/pod and secondary branches. Seed yield/plot and pods/plant were higher in cluster III (RTM-345 and RTM-465), whereas cluster X (RTM-91) had the highest values for seeds/pod and pod length, and also higher number of secondary branches than clusters III, VIII, and XII (Table 3).

Hybridization between accessions falling in the most distant clusters (RTM 236 and RTM 136) should result in maximum hybrid vigour and eventually desirable segregates. Also, based on mean performance, genetic distance and clustering pattern, hybridization involving RTM-136, 176, 91, 345 and 465 should result in desirable combinations leading to development of useful genetic stocks and varieties.

REFERENCES

1. C. R. Rao. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York.
2. A. N. Asthana and V. K. Pandey. 1980. Genetic divergence in linseed. Indian J. Genet., **40:** 247–250.
3. L. M. Jeswani, B. R. Murty and R. B. Mehra. 1970. Divergence in relation to geographical origin in a world collection of linseed. Indian J. Genet., **30:** 11–25.
4. J. Ram and D. V. S. Panwar. 1970. Intraspecific divergence in rice. Indian J. Genet., **30:** 1–10.