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Genetic Divergence in Taramira (*Eruca sativa* Mill.)

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Abstract

One hundred and fifty genotypes of taramira (*Eruca sativa* Mill.) were evaluated to estimate genetic divergence for seed yield and its component characters. All the genotypes and check varieties were grouped in to 10 clusters. Cluster composition indicated that geographic diversity was not related to genetic diversity. Among all the characters, plant height contributed the most towards total D^2 followed by number of siliquae per plant and number of seed per siliqua. Cluster 10 had highest mean value for seed yield per plant and number of secondary branches per plant while cluster VII had highest mean value for number of siliquae per plant. On the basis of D^2 analysis, nine genetically diverse cluster pairs, 12 genetically diverse and superior genotypes were identified.

Key words: *Eruca sativa, Genetic diversity, Cluster mean and Seed yield*

Introduction

Taramira (*Eruca sativa* Mill) is an important oilseed crop of the rapeseed-mustard group. It is grown on marginal lands with poor fertility. Due to its drought tolerant nature and adaptability to adverse environmental conditions, it is preferred over *Brassica* species under water scarce conditions (Gupta *et al.*, 1998). In spite of the fact that it is an oil seed crop, it was always given minor importance and thus, efforts at improving the yielding ability are very much limited in this crop (Gupta *et. al*., 1998). Even the basic important studies involving evaluation of germplasm lines in order to identify the genetically superior and diverse parents for hybridization programme are very much limited. Thus, in the present investigation an attempt was made to identify genetically diverse genotypes, which will be very useful to develop superior population and also to develop superior inbreds in order to generate superior hybrids.

Materials and Methods

In the present investigation 146 germplasm lines collected from different places of Rajasthan along with four check varieties (RTM-910, RTM-314, RTM-969 and T-27) were evaluated in RBD with three replications in single row plot of size 4.5 m length, for seed yield and its component characters. The row to row and plant to plant distance was kept 30 cm and 10 cm, respectively. Observations for various characters except days to flowering and days to maturity were recorded on 10 randomly selected plants of each genotype in each replication on plot basis. Mean values over 10 randomly sampled plants of each genotype in each replication for various characters were used for D^2 analysis. D^2 analysis was carried out as per the method given by Mahalanobis (1936). Grouping of genotypes into different clusters was carried out by Tocher's method as suggested by Rao (1960).

Results and Discussion

Identification of genetically diverse parents is an important aspect in hybridization programme aiming to evolve wide spectrum of genetic variability, to get more heterotic expression in F_1 and to combine desirable and diverse genes. Analysis of variance was carried out for all the characters, which indicated the presence of substantial amount of genetic variability among the genotypes. Aggregate effect of all the nine characters was tested by Wilk's criterion, which indicated highly significant differences among the genotypes and hence, analysis of genetic divergence based on D^2 values was considered relevant. Moreover, the D^2 values for almost all (98.8%) the pairs of genotypes were significant. Sodani *et. al.* (1989) and Ahmad *et al.*

(2009) also reported wide diversity in the taramira and mustard germplasm accessions. All the 146 germplasm lines and 4 check varieties were grouped into 10 clusters (table 1).

Table 1: Composition of clusters

Cluster	Number of genotypes	Composition of cluster with place of collection
1	111	**Shriganganagar:** RTM-570, RTM-571, RTM-572. RTM-573, RTM-668, RTM-669, RTM-670, 671, RTM-672, RTM-673, 674, RTM-675, RTM-676, RTM-677, RTM-680, RTM-682, RTM-683, RTM- 684, RTM-685, RTM-686, RTM-687, RTM-689, RTM-691, RTM-697, RTM-698, RTM-701, RTM-702, RTM-703, RTM-704 **Udaipur:** RTM-574, RTM-575, RTM-576, RTM-577, RTM-578, RTM-579, RTM-580, RTM-581, RTM-582, RTM-583, RTM-587 **Hanumangarh:** RTM-589, RTM-590, RTM-591, RTM-592, RTM-593, RTM-594, RTM-596, RTM-600, RTM-601, RTM-602, RTM-603, RTM-605, RTM-606, RTM-607, RTM-608, RTM-609, RTM-611, RTM-616, RTM-613, RTM-618, RTM-620, RTM-621, RTM-622, RTM-623, RTM-624, RTM-628, RTM-629, RTM-630, RTM-631, RTM-632, RTM-633, RTM-634, RTM-635, RTM-636, RTM-638, RTM-639, RTM-642, RTM-644, RTM-645, RTM-646, RTM-648, RTM-649, RTM-650, RTM-651, RTM-653, RTM-654, RTM-655, RTM-656, RTM-659, RTM-660, RTM-662, RTM-663, RTM-664, RTM-665, RTM-667, RTM-667, RTM-705, RTM-706, RTM-709, RTM-710, RTM-RTM-711, RTM-712, RTM-713, RTM-714 **Jobner:** RTM-661 RTM-96 (Check) **Nagaur:** RTM-681, RTM-910 **Checks:** RTM-31, T-27 **Udaipur:** RTM-588 **Checks:** RTM-314, T-27
II	12	**Udaipur:** RTM-588 **Hanumangarh:** RTM-625, 643, RTM-658 **Sriganganagar:** RTM-688, RTM-690, RTM-692, RTM-693, RTM-69, RTM-695, RTM-696, RTM-700
III	16	**Udaipur:** RTM-58 **Hanumangarh:** RTM-595, RTM-597, RTM-598, RTM-604, RTM-610, RTM-612, RTM-617, RTM-619, RTM-637, RTM-640, RTM-641, RTM-647, RTM-652, RTM-657, RTM-715
IV	3	**Hanumangarh:** RTM-599, RTM-614, RTM-615
V	3	**Hanumangarh:** RTM-626, RTM-666 **Sriganganagar:** RTM-679
VI	1	**Sriganganagar:** RTM-699
VII	1	**Sriganganagar:** RTM-678
VIII	1	**Hanumangarh:** RTM-708
IX	1	**Udaipur:** RTM-586
X	1	**Hanumangarh:** RTM-627

Cluster 1 had the most or 111 genotypes. The cluster II had 12 genotypes, cluster III had 16, cluster IV and V each had three genotypes while all other collected from different places were genetically diverse. Also, genotypes collected from different places were grouped in the same cluster. Thus, geographical diversity of the genotypes was not related to genetic diversity. In taramira, Sodani *et al*. (1989), Wilson *et. al* (1990) and Shanmuganathan *et al.* (2006) also reported that grouping of germplasm lines into different clusters was not related to their geographical origin. Moreover, the grouping of genotypes collected from same place in the genetically diverse clusters might have occurred due to genetic drift or mutation in the population. On analyzing relative magnitude of intra cluster D^2 values (table 2), it revealed that cluster VI, VII, VIII, IX and X had intra-cluster D^2 values of zero. Whereas, maximum intra-cluster D^2 value was recorded for cluster III followed by cluster II, Cluster V, Cluster IV and Cluster I. On comparing the number of genotypes in a particular cluster with its magnitude of average intra-cluster D^2 values, it revealed that number of genotypes in a cluster does not decide the average intra-cluster D^2 value but the degree of divergence among the genotypes in a cluster decides about the number of genotypes in a cluster. Average inter-cluster values (Table 2) showed a very wide range, which indicated that there was high degree of genetic diversity among the genotypes. Highest average inter-cluster value was recorded between cluster VI and X, each having single genotype RTM-699 and RTM-627, respectively. Thus, these clusters were genetically most diverse. The results of average inter-cluster D^2 values indicated that cluster X was having highest five inter-cluster D^2 values with clusters VI, IV, V VIII and cluster II. Thus, genotype RTM-627 of cluster X was genetically more diverse with respect to genotypes of clusters VI, IV, V, VIII and cluster II. Similarly, cluster VI was genetically more diverse with genotypes of cluster VII and IX.

Table 2: Average intra and inter cluster D^2 and D^2 (parentheses) values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	50.05 (7.70)	83.06 (9.11)	94.65 (9.72)	109.91 (10.48)	130.25 (11.41)	112.34 (10.59)	118.05 (10.86)	96.60 (9.82)	135.08 (11.62)	271.45 (16.47)
II		74.82 (8.64)	127.52 (11.29)	180.60 (13.43)	193.23 (13.90)	99.85 (9.99)	138.86 (11.78)	113.88 (10.67)	164.77 (12.83)	295.96 (17.20)
III			82.96 (9.10)	143.73 (11.98)	170.84 (13.07)	209.48 (14.47)	84.59 (9.19)	172.03 (13.11)	114.69 (10.71)	213.10 (14.59)
IV				60.16 (7.75)	178.28 (13.35)	140.26 (11.84)	248.59 (15.76)	185.16 (13.60)	216.77 (14.72)	434.47 (20.84)
V					66.18 (8.13)	221.29 (14.87)	153.60 (12.39)	122.60 (11.07)	127.97 (11.21)	392.28 (19.80)
VI							295.18 (17.18)	129.25 (11.36)	280.73 (16.75)	522.65 (22.86)
VII								168.87 (12.99)	102.81 (10.14)	171.46 (13.09)
VIII									127.16 (11.27)	389.19 (19.72)
IX										162.29 (12.73)
X										0

Table 3: Cluster mean values for yield and its components

Cluster	Day to flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	No. of secondary branches/ plant	No. of siliquae/ plant	No. of seeds/ siliquae	1000 seed weight (g)	Seed yield/ plant (g)
I	70.83	115.27	55.59	3.46	3.69	36.34	18.12	2.62	1.32
II	72.00	114.14	47.79	3.27	3.49	38.12	23.23	2.52	0.87
III	71.0	115.62	58.82	4.11	4.56	60.49	19.43	2.69	2.20
IV	72.22	115.77	89.38	3.75	3.62	49.46	17.08	3.03	2.04
V	62.11	114.66	67.75	5.87	5.25	43.35	16.87	2.45	1.18
VI	74.00	114.33	73.23	3.07	2.17	28.43	24.47	2.03	0.23
VII	66.33	115.00	38.73	4.53	4.50	66.27	18.68	2.47	1.81
VIII	60.00	115.00	53.80	2.40	2.37	30.97	23.97	2.44	0.73
IX	62.33	117.00	53.90	4.87	6.53	54.1	24.73	2.80	2.56
X	71.67	115.33	25.00	3.40	9.80	61.73	18.27	2.67	3.13

The mean values of the clusters for all the characters were calculated (table 3), which indicated that cluster IV had highest mean values for plant height and 1000 seed weight. Cluster V had highest mean values for primary branches per plant and lowest values for days to flowering.

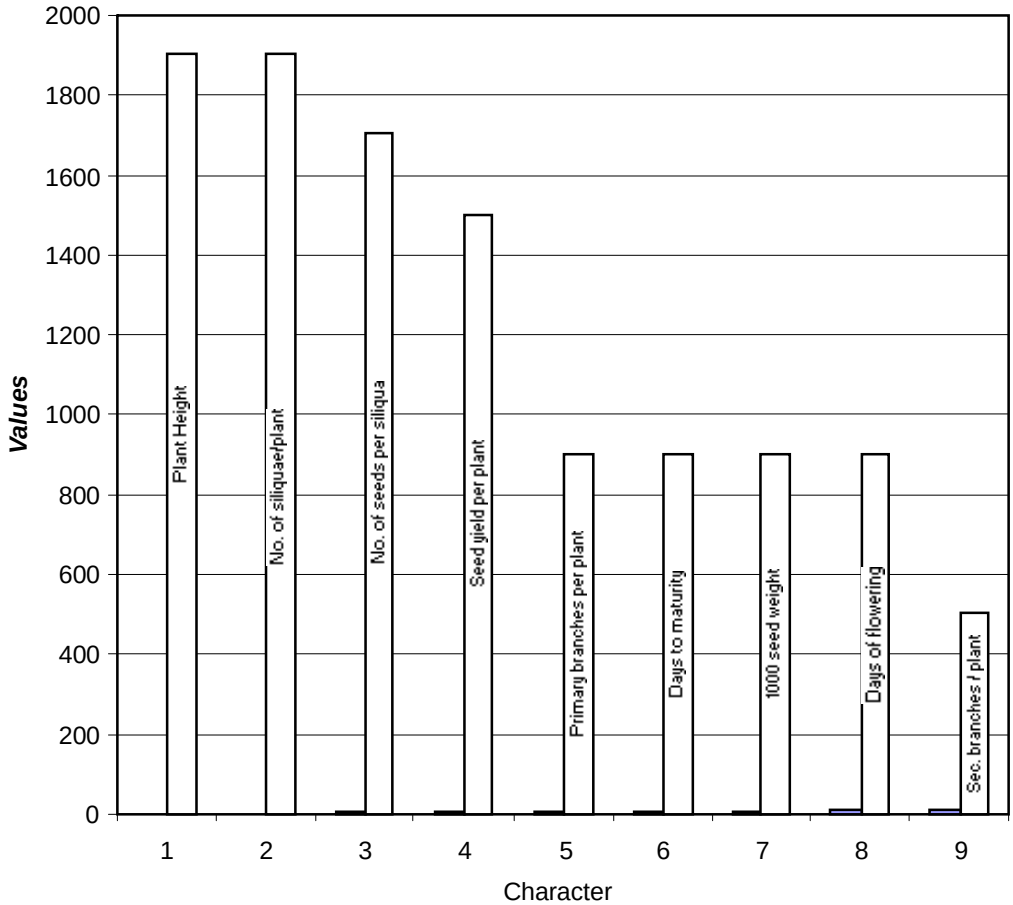

Figure 1: Contribution of different characters towards total (D^2)

Cluster VII had highest mean values for number of siliquae per plant. Cluster X had highest mean values for number of secondary branches per plant and seed yield per plant while second highest mean values for number of siliquae per plant. Cluster IX had highest mean values for number of seeds per siliquae and days to maturity. Cluster VI had highest mean values for days to flowering. Thus, genotypes in the cluster X, IV, V and VII had highest mean performance for the major seed yield components.

Contribution of various characters towards total divergence (figure1) indicated that plant height and number of siliquae per plant had highest contribution while number of seeds per siliqua and seed yield had substantial contribution. In taramira, Sodani *et al.* (1989) also reported that pods per plant, seed yield per plot, seed yield per plant and 1000 seed weight contributed the most towards genetic divergence. Thus, it indicated that the characters plant height, siliquae per plant and seeds per siliquae might be important in the evolutionary history of taramira.

In the present investigation, D^2 analysis indicated substantial amount of genetic diversity. Thus, genetically diverse parents were selected for hybridization programme on the basis of higher average inter-cluster distances, cluster means for major seed yield components, mean performance of genotypes for major components and complementary nature of genotypes for major seed yield components. Thus, on the basis of above mentioned criteria, nine cluster pairs were identified for hybridization programme.

Out of them, cluster X was involved in five cluster pairs. From these cluster pairs superior genotypes with highest mean performance for major seed yield components and seed yield per plant were identified. Moreover character complementation for major seed yield components was also considered.

Thus, on the basis of present investigation a hybridization programme involving RTM-627 x RTM-699, RTM-627 x RTM-599, RTM-627 x RTM-615, RTM-627 x RTM-626, RTM-627 x RTM-708, RTM-627 x RTM-658, RTM-678 x RTM-699, RTM-586 x RTM-699, RTM-627 x RTM-628, RTM-627 x RTM-618, RTM-627 x RTM-685, RTM-615 x RTM-678, RTM-599 x RTM-678 may be planned. Which may provide good base material for development of population for direct exploitation or for developing inbreds for generating superior hybrids. However, developing hybrids is still a distant dream in taramira till methods to overcome self-incompatibility are available.

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