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GENETIC DIVERGENCE IN RAPE MUSTARD

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ABSTRACT

Nineteen strains of rape mustard (*Brassica campestris* L.) were grouped into five clusters using D^2 statistic. Cluster I was the largest, consisting of two-thirds of the total population. Cluster III showed maximum genetic distance from cluster IV, suggesting wide diversity between them. Test weight, days to maturity and seed yield were the highest contributors to D^2 values. Strains Pusa Bold and Pusa Barani of cluster III and NDT 8503 of cluster IV were found important for varietal improvement programme on the basis of their genetic distances and higher cluster mean values for the aforesaid three characters.

Key words: Genetic divergence, D^2 statistic, rape mustard.

Precise information about the extent of genetic divergence and on characters used for discrimination among populations is crucial in any crop improvement programme, because selection of parents based on genetic divergence has become successful in several crops [1–3]. Therefore, the nature and magnitude of genetic divergence and the characters contributing to genetic diversity were studied among nineteen strains of rape mustard using D^2 statistic.

MATERIALS AND METHODS

Nineteen strains of rape mustard collected from the Directorate of Oilseed Research, Hyderabad, were evaluated in a randomized complete block design with three replications during 1986–87 winter season. Each plot consisted of 4 rows of 5.5 m length with inter- and intrarow spacings of 30 cm and 15 cm, respectively. Ten plants were selected at random from each plot for recording observations on nine characters, namely, days to 50% flowering and maturity, plant height, number of branches, pods per branch, pods per plant, seeds per pod, 1000-seed weight, and seed yield. Following analysis of variance, the data were subjected to multivariate analysis of D^2 statistic [4]. On the basis of magnitude of D^2 values,

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the strains were grouped into a number of clusters following Tocher's method [5]. The relative contributions of different characters towards genetic divergence were also worked out.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences among the strains for all the nine characters and after comparing D^2 values for all possible 171 pairs of populations, the 19 strains were grouped into five clusters (Table 1). Cluster I was the largest having 13 strains while clusters II and III had two clusters, IV and V had one strain each, suggesting that the cultivars NDT 8503 (cluster IV) and PT 303 (cluster V) diversed most from others. The intracluster distance was maximum in cluster III and minimum in clusters IV and V, therefore, two strains in cluster III indicated to be the most heterogeneous (Table 2). As regards intercluster distance, cluster III showed maximum genetic distance from cluster IV, suggesting wide diversity between them [6].

Table 1. Cluster composition based on D^2 statistic in rape mustard

Cluster	No. of strains	Strains falling in cluster
I	13	TK 8601, TK 8602, TFD 5, TFD 19, TH 100, TH 103, PT 86-1, PT 86-2, TW 2113-1 TW 9692, TW 3-63-LS, B 54, T 9
II	2	TFD 4, PT 86-3
III	2	Pusa Bold, Pusa Barani
IV	1	NDT 8503
V	1	PT 303

The characters contributing maximum to the divergence are given greater emphasis for deciding on the clusters for the purpose of further selection and choice of parents for hybridization [3]. The highest contributors in this regard were test weight, days to maturity, and seed yield. On considering cluster means in respect of these three characters, the importance of cluster III for test weight and seed yield, and that of cluster IV for days to maturity became obvious (Table 3). The crosses involving parents belonging to most divergent clusters are expected to manifest maximum heterosis and also wide variability in genetic architecture. The clusters comprising only one cultivar with specific traits could also be used in a hybridization programme for exploiting hybrid vigour as reported in opium poppy [7]. Thus, crosses between the cultivars of cluster III (Pusa Bold and Pusa Barani) with that of cluster IV (NDT 8503) would exhibit high heterosis and is also likely to produce new recombinants with desired traits in rape mustard.

Table 2. Intracluster (in bold) and intercluster genetic distances ($\sqrt{D^2}$) among five clusters in rape mustard

Cluster	I	II	III	IV	V
I	**4.4**	5.9	36.5	7.4	7.7
II		**3.0**	34.9	6.7	6.5
III			**5.0**	39.0	33.5
IV				—	9.5
V					—

Table 3. Cluster means and relative contribution to D^2 values of different characters in rape mustard

Character	Character means in different clusters					Contribution to D^2 values (%)
	I	II	III	IV	V	
Days to 50% flowering	39.0	36.0	48.0	32.0	38.0	5.44
Days to maturity	79.0	78.0	97.0	75.0	81.0	32.54
Plant height (cm)	75.9	78.9	122.1	54.3	83.2	2.47
Branches per plant	3.6	3.4	3.8	2.7	2.5	5.99
Pods per branch	21.1	26.5	18.9	27.2	21.6	2.88
Pods per plant	77.2	91.0	71.3	72.8	55.9	2.06
Seeds per pod	15.4	18.3	10.6	16.3	16.9	1.79
1000-seed weight (g)	2.7	2.27	7.4	2.7	2.5	33.21
Seed yield (q/ha)	3.8	2.9	0.0	2.2	3.0	13.62

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