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GENETIC DIVERGENCE STUDIES IN RADISH (*RAPHNUS SATIVUS L.*) UNDER KASHMIR CONDITIONS

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Radish (*Raphnus sativus* L.) is an important root vegetable used mostly as salad. Due to continuous cultivation of this highly cross-pollinated crop a large variation in vegetative and root characters has occurred. With the result a wealth of radish germplasm is available in India. But for maximizing heterosis information regarding nature and magnitude of genetic distance among the genotypes and choosing diverse parental combinations is necessary. The multivariate analysis using Mahalanobis D^2 statisticswas followed to obtain quantitative estimates of divergence.

The experiment with 21 genotypes of radish was laid out in a randomized block design with three replication during rabi 2003-04 and 2004-05 at Vegetable Experimental Field, S.K. University of Agricultural Sciences & Technology (K), Srinagar. Each entry was sown accommodating 50 plants in two rows of 2.5 m length per replication at 30 x 10 cm spacing. Observations were recorded on 10 randomly selected plants for eight characters *viz.*, leaf length (cm), number of leaves/plant, average leaf weight/plant (g), root length (cm), root diameter (cm), average root weight (g), top root ratio and root yield q/ha. Genetic diversity between groups was estimated by using D^2 statistic given by Mahanalobis's (1936) following the procedure given by Rao (1952). The grouping of genotypes was done by using Tocher's method (Rao 1952). Canonical analysis (Singh and Chaudhary, 1979) was carried out by calculating the first two vectors of canonical roots, which accounted for 94.74 per cent of the total variability.

The divergence for traits within the genotypes tested by Wilk's criterion was significant (÷2 = 1248.04 for 160 d.f.), thus the analysis of genetic divergence among the genotypes used in the study was considered relevant.

The genotypes of radish under evaluation were grouped into seven clusters (Table 1). Maximum number of genotypes was grouped in cluster II (six genotypes) followed by cluster I (five genotypes), cluster III and IV (three genotypes each), cluster V (two genotypes) and cluster VI and VII (one genotype in each). Distribution of genotypes into various cluster showed no uniformity and those belonging to the same place were distributed among different clusters, thus ruling out the association between geographical distribution of genotypes and genetic divergence. Present results are also supported by the findings of Rai *et al.* (1998) and Parphasarathy and Aswath (2002) in tomato and Mehta *et al.* (2004) in brinjal.

Canonical analysis was employed to obtain the spatical positions of all the 21 genotypes on a graph (Fig. 1). Arbitrarily these were grouped into 7 clusters, thus confirming the clustering pattern obtained by D^2 statistics. The proportion of variation accounted for by the first two canonical roots were 88.62 and 6.12 per cent. The results suggests that classification of a number of genetic stock using D^2 statistics provides a set of groups from which parents can be chosen for further breeding programmes and points to the potency of the method of grouping.

Intra and inter cluster (D) values among the seven clusters are given in Table 2. Cluster V had maximum intra cluster distance (24.98) while cluster III had minimum distance (18.73). The intra cluster distance for other cluster were 23.57 (cluster IV), 20.84 (cluster I) and 20.54 (cluster II). Maximum inter cluster distance was between cluster I and IV (145.68) and minimum was between cluster V and VII (29.83). The inter cluster distance was also maximum between cluster I and V (118.42) followed by cluster III and IV (115.85) and cluster IV and VI (106.38). Low intra cluster and high inter cluster distance suggested that populations grouped were nearly homogeneous between clusters. Selection of parents from such clusters for hybridization would result in novel recombinants (Varalakshmi and Haribabu, 1991).

On analyzing cluster means for different characters (Table 3), it was observed that cluster I, which included the genotypes SKAU-R-3, SKAU-R-4, Early Milano,

Table 1: Composition of clusters based on D^2 values in 21 genotypes of radish

Cluster	Number of genotypes	Genotype
I	5	SKAU-R-3, SKAU-R-4, Early Milano, Japnese White Long, Scarlet Long
II	6	All Season, SKAU-R-7, Pusa Himani, Mino Early, SKAU-R-6, SKAU-R-1
III	3	SKAU-R-2, Selection – 9, SKAU-R-8
IV	3	SKAU-R-5, SKAU-R-10, Palam Hriday
V	2	Chinese Pink, SKAU-R-9
VI	1	French Break Fast
VII	1	Radish Newar

Table 3: Cluster wise means performance of 21 genotypes of radish for 8 characters.

Character	I	II	III	IV	V	VI	VII
Leaf length (cm)	26.11	23.64	28.19	28.57	24.41	20.87	32.09
Number of leaves/plant	12.94	13.70	11.56	12.27	13.24	8.40	14.82
Average leaves weight (g)	97.58	88.05	70.84	117.33	98.00	53.33	127.00
Root length (cm)	22.05	21.39	17.97	14.44	17.22	6.13	20.02
Root diameter (cm)	4.48	3.59	4.41	2.60	2.97	5.76	3.06
Average root weight (g)	236.93	154.89	174.77	56.44	71.79	127.00	106.11
Root shoot ratio	1.41	1.57	1.40	2.98	2.35	1.42	2.20
Root yield (q/ha)	758.19	495.11	559.26	180.62	229.74	406.40	339.55

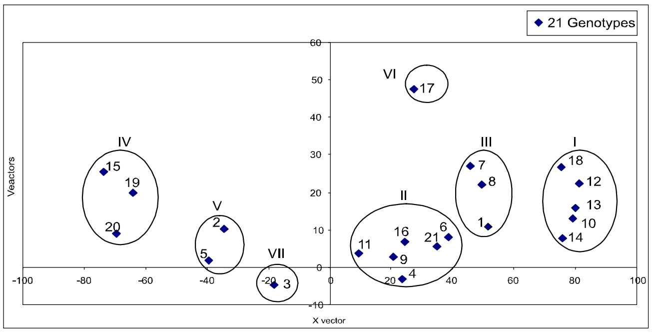

Fig. 1: Canonical diagram of the first two vectors showing relative position of 21 genotypes of radish

Table 2: Intra and inter cluster distance (D value) in 21 genotypes of radish.

Cluster	I	II	III	IV	V	VI	VII
I	20.84	57.50	39.28	145.68	118.42	66.27	98.07
II		20.54	30.23	99.82	68.20	47.97	46.20
III			18.73	115.85	86.54	37.64	67.44
IV				23.57	41.05	106.38	62.31
V					24.98	80.09	27.83
VI						00.00	70.42
VII							00.00

Table 4: Per cent contribution of different yield and its traits in 21 genotypes of radish

Character	Number of time appearing as first in the rank	Per cent contribution towards total divergence	Canonical vectors	
		D^2 Statistics	Vector I	Vector II
Leaf length (cm)	35	16.67	-0.007	0.089
Number of leaves/plant	37	17.61	-0.000	-0.168
Average weight of leaves (g)	21	10.00	-0.026	-0.098
Root length (cm)	27	12.85	0.056	-0.586
Root diameter (cm)	29	13.80	0.029	0.684
Average root weight (g)	26	12.38	0.707	0.143
Root shoot ratio	28	13.33	-0.218	0.350
Root yield (q/ha)	07	3.33	0.670	-0.021
Total	210	100	88.62 %	6.12 %

Japnese White Long and Scarlet Long recorded the highest mean value for root length, average root weight and root yield, while minimum mean value for root shoot ratio. In contrast, cluster IV which consist of SKAU-R-5, SKAU-R-10 and Palam Hriday recorded minimum value for root length, root diameter, average root weight and root yield, while maximum mean value for root shoot ratio, thus contributing to high inter cluster distance between cluster I and IV. However, cluster VII recorded the maximum mean value for leaf length, number of leaves/plant and average leaf weight. The maximum mean values for root diameter was recorded with cluster VI but root length was minimum.

The relative contribution of different plant characters towards diversity was also investigated (Table 4).The character number of leaves/plant contribute maximum percentage (17.61) towards diversity followed by leaf length (16.67), root diameter (13.80), root shoot ratio (13.33), root length (12.85), average root weight (12.38). The principal components corresponding to the two largest eigen values supplied by the two best orthogonal vectors indicated that average root weight (0.707), root yield q/ha (0.670), and root length (0.056) were the most important primary cause of divergence, recorded high linear functions in the first component (Table 4). The secondary cause of divergence was root diameter (0.684), root shoot ratio (0.350) and average root weight (0.143) as they had highest linear function in the second component, thus indicating that these are the basic common attributes of plant architecture. De *et al.* (1988) proposed that traits contributing maximum towards the D^2 values need to be given greater emphasis for deciding on the cluster to be chosen for the purpose of further selection and choice of parents for hybridization. Hence, selection for divergent parents based on above mentioned characters will be useful for heterosis breeding in radish.

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