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Morphological variability among low chilling peach genotypes under Dehradun conditions

P.L. Saran*, A.K. Godara and S.K. Sehrawat****
GB Pant University of Agriculture & Technology, Horticulture Research and Extension Centre,
Dhakrani, Dehradun 248 142, Uttarakhand

ABSTRACT

Meagre information is available on the genetic diversity on low chilling peach cultivars. On 11 genotypes, 13 morphological traits were recorded and data analyzed using Mahalanobis's D^2 statistics. All the genotypes were classified into five distinct clusters, grouping together the less divergent genotypes. The accessions showed sufficient variability to select genotypes for further breeding and grouping. Cluster-II and IV had three genotypes each, followed by Cluster-I and V with two each and Cluster III had one genotype. The maximum inter-cluster distance (7.63) was observed between Clusters III and V. The parents for hybridization could be selected on the basis of their inter-cluster distance for isolating useful recombinants in the next generation. To improve the yield traits in peach, selection and hybridization programme may be initiated utilizing the Fla 16-33, Saharanpur Prabhat and Pratap owing to their distinct genetic diversity.

Key words: Peach genotypes, diversity, *Prunus persica.*

INTRODUCTION

Peach (*Prunus persica*) is a widely cultivated and popular stone fruit crop of temperate regions of the world. In India, it is commercially grown in the mid hill zones of Himalayas. Low chilling peaches and nectarines (mutants closely related to peach) are grown in warm temperate zones and sub-tropical regions particularly in Uttarakhand, western Uttar Pradesh, Haryana, Punjab and NE states. These cultivars are important for integration into rising temperatures due to global warming under transition zones of temperate regions. There is a wide diversity in peach cultivars for cultivation in these regions. In the recent past, some exotic peach cultivars were also introduced which performed well under sub-tropical Doon Valley conditions, Uttarakhand. Among them, Saharanpur Prabhat, Sarbati and Sanpedro (Fla 16-33) were the heavy bearer and early maturing cultivars. These cultivars were also around 35-40 days earlier than the temperate peaches and thus provided high returns to growers (Krishna *et al*., 3). The fruits are rich source of sugars, vitamins and minerals. It is also a good source of malic acid (1.2%). Prunacin is the principal glycoside present in the pulp while the glycoside, amygdalin is present in the peach seed (Voldrick and Kyzlink, 7). The present study was undertaken to assess the casual components of peach tree which contribute directly or indirectly towards fruit yield. The information on nature and degree of morphological divergence could be helpful for further improvement through hybridization of most diverse genotypes.

MATERIALS AND METHODS

The present investigation was carried out at the experimental orchard of GBPUA&T, Horticulture Research and Extension Centre (Dhakrani), Dehradun during 2006-07. This place is located (latitude 28° 42' N and longitudes 73.35° to 81.5° E) in the northern region of India about 200 km north of New Delhi. The altitude of Dehradun is 600 m above mean sea level with the winter quite cold (1°C) and summer very hot (42°C).

Saharanpur Prabhat, Pratap, Sarbati, Safeda, Shan-i-Punjab, Fla 16-33, Flordaking, Flordasun, Marivillha, Armking and Sunred genotypes of peach were introduced from different parts of India and other countries. Eleven peach accessions were chosen for the present study. The morphological traits, such as the yield (kg/tree), number of shoots (per main branch), number of flowers / shoot, number of fruit set, fruit weight (g), fruit length (cm), fruit diameter (cm), stone weight (g), tree height (m), tree spread (m), stem girth (cm) were observed by using standared methods. The chlorosis (%) was measured by counting all the chlorotic leaves and aphid infestation (%) by counting all the curled leaves from randomly selected shoots.

The selected genotypes were 18-year-old trees, budded on Kabul Greengage rootstock planted in RBD with three replicates, planted at 6 m × 6 m spacing received uniform training and pruning contributed as experimental plant material.

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*Corresponding author's E-mail: saranpl@rediffmail.com
**Department of Horticulture, CCS HAU, Hisar, Haryana 125 004

Thirteen morphological traits were observed during 2006 and 2007. From analysis of variance and covariance, the effort variance and covariance values were subjected to multivariate analysis. The original correlated variables (X's) were first transformed to uncorrelated ones (Y's as linear function of X's) and then D^2 values were worked out. Pivotal condensation method was used to compute inverse matrix of the error dispersion matrix. The generalized distance function (D^2) between two genotypes is simply the sum of squares of differences in Y's (Rao, 4).

Divergence between any two populations was obtained as sum of squares of difference in the values of corresponding entries using D^2 statistics. Based on the D^2 value, the genotypes were classified into distinct clusters, grouping together the less divergent genotypes according to Tocher's method given by Rao (4). Dendogram and pairwise dissimilarities were calculated according to Euclidean's square distance.

RESULTS AND DISCUSSION

The significant values of mean sum of squares from the analysis of variance (Table 1) revealed the presence of variability among the genotypes for all the traits investigated but such analysis is unable to infer anything about the extent of genetic diversity present among the genotypes.

To overcome this problem and simultaneously to quantify genetic divergence between any two genotypes or group of genotypes, Mahalanobis D^2 statistics was used and the grouping of genotypes into different clusters was done by following Tocher's method (Rao, 4). The peach genotypes were grouped into five clusters on the basis of their relative magnitude of D^2 values, in such a way that the D^2 value within the cluster had been much lower than those belonging to different clusters.

The distribution pattern of genotypes in different cluster is presented in Table 2 and Fig. 1. The cluster II and IV had three genotypes each, followed by Cluster I and V with two genotypes each and cluster III had one genotype. The unweighted pair group using arithmetic mean (Mahalanobis Euclidean square distance) cluster analysis, the eleven peach genotypes fell into five clusters. First cluster comprised genotypes Saharanpur Prabhat and Pratap, while second cluster comprised Sarbati, Safeda and Shan-i-Punjab genotypes. Cluster third comprised only Fla 16-33. Fourth comprised Flordaking, Flordasun and Maravillha, while fifth comprised Armking and Sunred (nectrine) genotypes.

The intra- and inter-cluster average D^2 values have been depicted in Table 2. Intra-cluster distances ranged from 0.97 (II) to 6.58 (III), which indicated the presence of diversity within clusters. The maximum inter-cluster distances varied from 0.00 (III) to 7.63 (V) followed by Cluster III and cluster IV which was 6.75 as given in Table 4 & Fig. 1. The inter-cluster average D^2 value was higher than any intra-cluster average D^2 value. Genotypes representing clusters separated by the high genetic distance should be used in hybridization to obtain a wide spectrum of variance among the progenies

Table 1. Mean sum of square obtained from the analysis of variance for various traits in peach genotypes.

Source of variation	d.f.	Yield (kg/ tree)	No. of shoots	No. of flowers/ shoot	No.of fruit set	Fruit weight (g)	Fruit length (cm)	Fruit dia. (cm^2)	Stone weight (g)	Height (m)	Spread (m^2)	Stem girth (cm)	Chlorosis (%)	Aphid infestation (%)
Replication	2	0.20	42.54	867.84	33.57	10.19	0.01	0.00	0.01	0.05	0.31	23.12	11.93	3.98
Treatment	10	397.61*	1202.09*	4599.80*	549.89*	997.68*	1.38*	1.04*	4.93*	5.08*	12.73*	1477.81*	1418.85*	1673.79*
Error	20	6.88	104.74	216.81	52.64	22.23	0.01	0.02	0.06	0.23	0.59	98.85	11.29	9.61
CV (%)		12.88	20.96	10.18	15.42	12.22	2.72	3.90	7.08	10.31	13.61	13.47	7.42	6.31

Table 2. Classification of peach genotypes in different clusters.

Cluster No.	No. of genotype (s)	Name of genotype (s)
I	2	Saharanpur Prabhat, Pratap
II	3	Sarbati, Safeda, Shan-i-Punjab
III	1	Fla 16-33
IV	3	Flordaking, Flordasun, Marivillha
V	2	Armking, Sunred

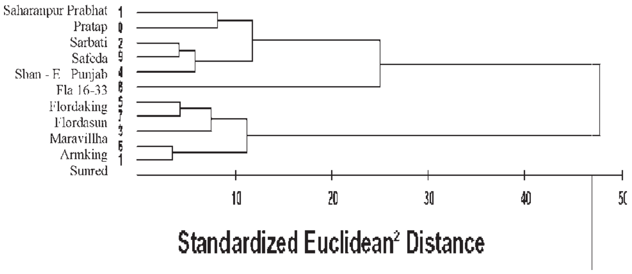


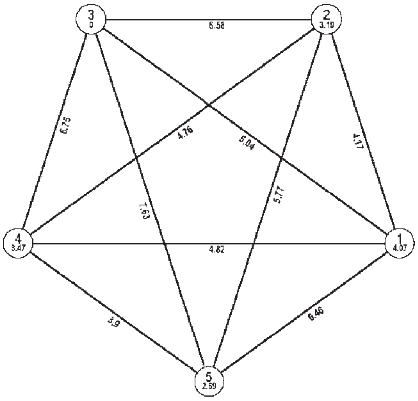
Fig. 1. Ward's minimum variance dendrogram of the low-chill peach genotypes.

Table 3. Intra- (diagonal) and inter-cluster D^2 (average) values among low chill peach genotypes.

Cluster	I	II	III	IV	V
I	**4.07**	4.17	5.04	4.82	6.46
II		**3.20**	6.58	4.77	5.77
III			**0.00**	6.75	**7.63**
IV				**3.47**	3.90
V					**2.69**

(Bhat, 1). Similar findings were also observed in Indian jujube (Saran *et al*., 5).

The genetic diversity among the genotypes depends upon the extent of variability present in the population for different traits under investigation for fruit characters. The magnitude of heterosis is largely governed by the degree of genetic diversity resting among the parental lines. In the present investigation, the maximum genetic diversity was observed in between Cluster III and V followed by Cluster II and III (3.38), which is indicative of getting more heterotic F$_1$s promising segregants in the subsequent segregating generations. The cluster mean values of different traits under study are presented in Table 4 and fruit are shown in Fig. 3.



Euclidean Distance (Not to the Scale)

Fig. 2. Euclidean distance dendrogram among low chill peach genotypes.

The cluster means for different traits were reflection of genetic differences among the clusters. The clusters Showed differences with each other for one or more traits. Cluster III had the highest yield (39.50 kg/tree), number of shoots (68.33), fruit weight (75.48 g), fruit length (5.85 cm), fruit diameter (5.32 cm) and stone weight (7.00 g). Cluster II had the maximum number of flowers / shoot (183.11), stem girth (99.11 cm), height (5.94 m) and spread (7.81 m). Cluster I had maximum

Table 4. Cluster-wise mean values of different traits in low chill peach genotypes.

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Yield (kg/tree)	27.61	23.91	39.50	11.29	11.93
No. of shoots	44.33	38.44	68.33	51.33	55.33
No. of flowers / shoot	130.50	183.11	173.00	132.67	104.50
No. of fruit set	63.00	44.89	58.00	49.78	24.67
Fruit weight (g)	55.98	34.58	75.48	27.46	25.33
Fruit length (cm)	4.57	4.04	5.85	3.79	3.64
Fruit diameter (cm)	4.52	4.06	5.32	3.86	4.48
Stone weight (g)	3.77	3.03	7.00	2.93	3.23
Height (m)	5.73	5.94	4.40	3.78	3.18
Spread (m)	7.13	7.81	5.44	4.12	3.31
Stem girth (cm)	85.00	99.11	55.67	68.33	41.83
Chlorosis (%)	63.12	58.26	41.71	35.71	24.09
Aphid infestation (%)	30.40	68.39	40.02	31.03	70.38

Table 5. Diverse and superior genotypes selected from clusters.

Genotype	Cluster	Traits
Fla 16-33	III	Yield, number of shoots, fruit weight, fruit diameter, stone weight, number of fruit set
Saharanpur Prabhat	I	Number of fruit set, fruit weight
Pratap	I	Yield, number of fruit set, low chlorosis

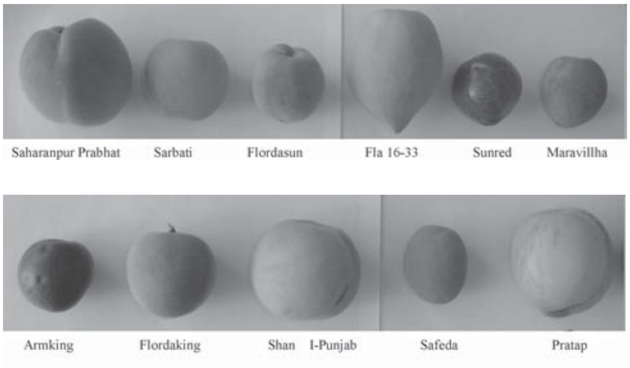


Fig. 3. Morphological variability of peach fruits.

number of fruit set (63.00) and chlorosis (63.12%), while highest cluster mean value for aphid infestation (70.38%) was observed in case of Cluster V. Cluster III and I performed outstanding on the basis of better cluster means for most of traits. Cluster means represents an interesting picture of the existing diversity among the material under study observed by Sardana *et al.* (6) in rice and Zaffar *et al.* (8) in apricot.

Pair-wise dissimilarities of peach genotypes according to squared Euclidean's distance showed that genotypes Fla 16-33 and Armking observed with maximum dissimilarity (Fig. 1). As given in Table 5, the genotypes Fla 16-33 (Cluster III) had highest cluster mean value for yield, number of shoots, fruit weight, fruit diameter, stone weight and number of fruit set. The Saharanpur Prabhat (Cluster I) also performed better for number of fruit set and fruit weight while Pratap had better mean value for yield, number of fruit set and chlorosis, whereas mean of Clusters IV and V was not satisfactory. Great emphasis for deciding such type of superior genotypes was given for the purpose of further selection and crossing to evolve noval cultivars. Variation for fruit yield in some low chilling peach introductions was also reported by Khajuria *et al.* (2). Such findings were supported by Saran *et al.* (5) in 35 *ber* germplasm.

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