

Genetic divergence analysis for vegetative, flowering, fruit quality and yield characters in strawberry, *Fragaria x ananassa* Duch

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ABSTRACT

Fourteen genotypes were evaluated for different vegetative, floral, fruit quality and yield characters to study genetic divergence by employing D² analysis. The genotypes were grouped into 3 diverse clusters. Cluster III consisted of maximum six genotypes followed by cluster I and II both of which consisted of four genotypes. The maximum inter-cluster distance was recorded between cluster II and cluster III hence genotypes belonging to these clusters can be used as parents for hybridization programme for the development of high yielding strawberry genotypes. Highest intra-cluster distance was observed in cluster II.

Keywords: Strawberry; D² analysis; genetic divergence

INTRODUCTION

Strawberry is known as the most delicious and refreshing fruit of the world to millions of peoples. Its plant is also cherished in gardens and commercial plantations for its beautiful and attractive red fruits. The added advantage with strawberry is that it gives early and very high returns per unit area compared to other fruits because crop is ready for harvesting within six months after planting. Varieties from geographically diverse localities are generally included in hybridization programmes presuming genetic diversity and greater likelihood of recovering

promising segregants. However this being an inferential criterion it can not be successfully utilized for discrimination between parents. The problem of selection may further be simplified if one could identify the characters responsible for discrimination between parents. Genetic divergence analysis by using cluster statistics is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components to the total divergence (Sikarvar et al 2006). The reports available on this aspect in strawberry are rather

scanty. Therefore the present investigations were aimed at ascertaining the nature and magnitude of genetic diversity among a set of strawberry genotypes.

MATERIAL and METHODS

The present investigations were carried out at experimental farm of the Department of Fruit Science, College of Horticulture, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh during 2011 to 2013. To carry out the investigations the planting of runners was done on raised (15 cm) beds on 1 November 2011 and 2012. Individual plants were spaced at 30 cm between the rows and plant to plant distance was also kept at 30 cm. Sixteen plants of each of the fourteen strawberry cultivars were planted in 1.5 x 1.0 m raised beds for detailed investigations. During the course of study recommended cultural practices were followed. Vegetative characters like plant spread, number of leaves per plant, days to runner formation after planting and floral characters viz days to flowering, duration of flowering and fruit characters like fruit length, fruit breadth, number of achenes per fruit, days to maturity (duration), number of fruits per plant, average berry weight, TSS, total sugars and yield per plant were recorded by adopting standard procedures.

Mahalanobis D^2 statistic was used for assessing the genotypic divergence

between populations (Mahalanobis 1936). The generalized distance between any two populations is given by the formula:

$$D^2 = \sum \sum \lambda_{ij} \sigma_{ai} \sigma_{aj}$$

where D^2 = Square of generalized distance; λ_{ij} = Reciprocal of the common dispersal matrix, $\sigma_{ai} = (\mu_{i1} - \mu_{i2})$; $\sigma_{aj} = (\mu_{j1} - \mu_{j2})$; μ = General mean

Since the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (X_s) to standardized uncorrelated variable (Y_s) was done to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (gs) values of any two uncorrelated genotypes of D^2 value. All $n(n-1)/2$ D^2 values were clustered using Toucher's method described by Rao (1952). The intra-cluster distances were calculated by the formula given by Singh and Choudhary (1997):

$$\text{Square of the intra-cluster distance} = \sum D_i^2 / n$$

where D_i^2 is the sum of distance between all possible combinations of the entries included in a cluster and n is number of all possible combinations. The inter-cluster distances were calculated by the formula described by Singh and Choudhary (1997):

Square of the inter-cluster distance = $D^2_i / n_i n_j$

where D^2_i is the sum of distances between all possible combinations ($n_i n_j$) of the entries included in the clusters under study. n_i is number of entries in cluster I and n_j is number of entries in cluster j.

The criterion used in clustering by this method was that any two genotypes belonging to the same cluster, at least on an average show a small D^2 value than those belonging to two different clusters.

RESULTS and DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the characters studied indicating thereby the existence of genetic variability among the genotypes. Overall 14 genotypes were grouped into three clusters showing sufficient variability for selecting the genotypes for future breeding programmes. This cluster composition is presented in Table 1. The cluster III consisted of maximum six genotypes (Douglas, Etna, Catskill, Shasta, Addie and Ofra) whereas cluster I (Torrey, Elasantha, Fern and Gorella) and II (Belrubi, Selva, Chandler and Sweet Charlie) both consisted of four genotypes.

The various combinations of different cluster distances are presented in Table 2. Results of cluster analysis indicated that the highest intra-cluster distance was

observed for cluster II (3.092) followed by cluster III (2.254) and cluster I (2.172). Moreover the highest inter-cluster distance was measured between cluster II and III (5.265) followed by cluster I and II (5.203) whereas the minimum distance was observed between cluster I and III (2.465).

The average intra-cluster distance in cluster II was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves however in all cases the inter-cluster distances were greater than the intra-cluster distances implying presence of greater degree of genetic diversity between the genotypes of two cluster than the genotypes present within the cluster (Singh et al 2006).

On the basis of results it is inferred that subsequent hybridization between the genotypes having broad genetic base should result in maximum heterotic performance and eventually the desirable transgressive recombinants as broad genetic base is a fundamental requirement for any crop improvement programme (Sharma et al 2013).

Mean performance of individual cluster for different characters is presented in Table 3. For plant spread and number of leaves, cluster II possessed the highest mean value and lowest values were recorded for cluster I and cluster III respectively. The cluster I took maximum days to runner formation whereas days to

Table 1. Clustering pattern of 14 genotypes of strawberry on the basis of genetic divergence

Cluster	# genotypes	Genotype
I	4	Torrey, Elsantha, Fern, Gorella
II	4	Belrubi, Selva, Chandler, Sweet Charlie
III	6	Douglas, Etna, Catskill, Shasta, Addie, Ofra

Table 2. Intra- and inter-cluster distance (D^2)

Cluster	I	II	III
I	2.172		
II	5.203	3.092	
III	2.465	5.265	2.254

Table 3. Cluster means for different characters among 14 genotypes of strawberry

Character	Clusters		
	I	II	III
Plant spread (cm)	28.82	36.08	31.22
# leaves	26.12	30.79	24.03
Days to runner formation	209.21	196.58	197.78
Days to flowering	124.61	118.00	129.70
Duration of flowering	77.19	88.65	79.90
Fruit length (mm)	27.05	31.84	27.13
Fruit breadth (mm)	20.09	24.58	20.27
# achenes/fruit	205.25	234.79	187.58
Days to maturity	41.25	43.67	44.25
# fruits/plant	14.40	25.62	16.32
Average berry weight (g)	8.98	11.69	8.73
TSS (°Brix)	8.89	10.27	9.37
Total sugars (%)	7.26	7.09	6.39
Yield/plant (g)	130.17	300.62	140.56

runner formation were minimum in cluster II. Days to flowering exhibited the highest mean performance for cluster III. The cluster II possessed the maximum duration of flowering, fruit length, fruit breadth and number of achenes per fruit. The cluster means for fruit length and breadth were found to be minimum for cluster I whereas cluster III showed the minimum value for number of achenes per fruit. The genotypes of cluster II took the maximum days to fruit maturity whereas it was lowest in cluster I. Cluster means for number of fruits per plant, average berry weight, TSS and yield per plant were found to be highest in cluster II while cluster I had the maximum cluster mean for total sugars.

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