Electronic Journal of Plant Breeding, 8(1): 306-310 (March 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00044.8

Research Note

Cluster analysis for fruit yield components in grapes

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(Received: 09 March 2016; Revised: 10 Feb 2017; Accepted: 22 Feb 2017)

Abstract
For any plant improvement programme, different genotypes are to be classified into clusters based on genetic diversity. Further the extent of genetic divergence between them needs to be estimated. D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, to quantify the degree of divergence and to choose genetically diverse parents for obtaining desirable recombinants. The present study was conducted at Punjab Agricultural University, Regional Research Station, Bathinda from 2011-13 on 20 genotypes of grapes for genetic divergence with respect to nine yield contributing traits *viz*., bunch length, bunch breadth, bunch weight, berry length, berry breadth, berry weight, TSS (%), acidity (%) and fruit yield per vine. The analysis of variance exhibited significant differences among genotypes for all the nine characters studied. Twenty genotypes were grouped into five clusters. The cluster size varied from single genotype (cluster V) to seven genotypes (cluster I). Cluster II, III, IV had 4, 5 and 3 genotypes respectively. No relationship between geographic and genetic diversity was revealed as genotypes from same geographic area fell in different clusters and vice versa. The intercluster distances were more than intracluster distances. The highest intercluster distance was observed between cluster I and cluster IV followed by clusters I and V. The other intercluster distances were of low magnitude. Hence crossing between genotypes of cluster I with those from cluster IV and V will be rewarding. Based on intercluster distances and cluster mean for different characters, parents were identified which upon crossing may yield desirable recombinants.

Key words
Grapes, fruit yield components, D^2 analysis

Genetic variability in a base population is a prerequisite for effective selection and recombination breeding. When existing variability has been exploited, a breeder resorts to creation of variability through hybridization as a population with more diverse genotypes is of considerable value for the success of any breeding programme. The relatedness and genetic distance between accessions can be obtained through cluster analysis. Cluster analysis is grouping accessions which have the same characteristics in homogeneous categories of each stratum (Crossa *et al.*, 1995). Commercial grape cultivation in India is one of the most remunerative, which is mainly confined to table grapes. More than 80 per cent are cultivated under the tropical conditions of the Southern peninsular region, while viticulture in North India is under subtropical conditions. Due to the diversity of climate, different cultivars are planted in different regions (Chadha and Shikhamany, 1999).

Information on the nature and degree of divergence among the genotypes helps the breeders in choosing right type of parents for initiating a breeding programme to recover better varieties or hybrids, since the degree of heterosis is believed to be correlated with genetic divergence among the parents. Earlier geographic diversity was considered to be an index of genetic diversity. However genetic diversity of parents is not necessarily associated with geographic diversity or place of origin. Multivariate analysis using Mahalanobis D^2 technique is a powerful tool in identifying the degree of divergence among the genotypes. The present study was undertaken to assess genetic relatedness of 20 genotypes of grapes into different clusters based on genetic divergence.

The experimental material consisted of 20 diverse genotypes of grapes representing the broad spectrum of variation from different parts of India *viz.*, Angur Early, Arka Hans, Arka Kanchan, Arka Shyam, Arkavati, Banquiabyad, Beauty Seedless, Bharat Early, Black Muscat, Black Prince, Cardinal, Delight, Khalili, Lomanto, Madeliene Anguvine, Perlette, Ruby Red, Shadipur Local, Tas-e-Ganesh and Selection 7. The experiment was planted in randomized complete block design with 3 replications at PAU, Regional Research Station, Bathinda, Punjab during 2011-13. In each replication 3 plants of each cultivar were grown at geometrical spacing of 3 x 3 meters. The average annual rainfall at the experimental site was 400 mm, the annual maximum temperature was 31.5°C and annual minimum temperature was 16.9°C. The soil was sandy loam and characterized with pH (8.31), organic carbon (0.32%), electrical conductivity (0.24 dS/m), available N (212 kg/ ha), available P (21.5 kg/ ha) and available K (357.0 kg/ ha). Data were recorded on bunch length (cm), bunch breadth (cm), bunch weight (g), berry weight (g), berry length (cm), berry breadth (cm), total soluble solids (TSS), acidity (%), bunch number and fruit yield per vine (kg). The TSS was measured with the digital refractometer (0-85%) and acidity was estimated by 0.1 N NaOH method

(AOAC, 2000). The analysis of variance was carried out for all characteristics and data were analysed following multivariate analysis of Mahalanobis (1936) and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

The analysis of variance (ANOVA) exhibited significant differences among the genotypes for all the characters studied. Based on D^2 values, 20 genotypes were grouped into 5 clusters (Table1). The cluster strength varied from single/solitary genotype (cluster V) to 7 genotypes (cluster I). The clusters II, III and IV had 4, 5 and 3 genotypes respectively. The pattern of distribution of genotypes into five clusters confirmed the existence of diversity among the genotypes, as indicated by analysis of variance. It also revealed that geographic diversity was not related to genetic diversity as genotypes of same geographic region were grouped into different clusters and vice versa. It may be due to distribution of different gene constellations within a geographic region or due to differences in adaptation, selection criteria, selection pressure and environmental conditions. This genetic diversity among the genotypes could be due to factors like heterogeneity, genetic architecture of the populations and developmental traits (Murty and Arunachalam, 1966).

The average intra and intercluster distances are given in table 2. The intracluster distances ranged from 0 (cluster V) to 28.05 (cluster I). The cluster II and IV also had sufficient intracluster distances (25.55 and 25.75 respectively). The cluster III had minimum intracluster distance (16.79) indicating limited genetic diversity among the genotypes of this cluster. Similar findings were also reported by Rajan *et al.* (2007) in guava The intercluster distances were higher than intracluster distances. The maximum intercluster distance was found between cluster I and IV (149.31) followed by I and V (123.93). Genotypes from such clusters may be utilized in the hybridization programme as crossing between diverse parents is likely to produce wide variability and transgressive segregants with heterotic effects. The minimum intercluster distance was observed between clusters II and V (47.12) revealing that the genotypes of these clusters were relatively closer. Similar findings in grapes genotypes were also reported by Tamhankar *et al*. (2001).

The cluster means for different characters under study revealed considerable differences between the groups (Table 3). Cluster I recorded the highest mean value for berry weight (2.72g) and berry length (1.77cm), while cluster II had the highest mean value for berry breadth (1.62 cm), cluster III possessed minimum acidity percentage (0.93) and hence maximum TSS: acidity ratio while cluster IV had maximum bunch number (90.22). It is strange to note that cluster V with a solitary genotype, Beauty Seedless recorded the highest value for six traits *viz*., bunch length (20.01cm), bunch breadth (12.61 cm), bunch weight (320.29g), TSS (17.33%), brix yield (3.93g) and fruit yield per vine (23.12kg). It indicated that this cluster (or genotype) with most of the desirable characters could be selected as such. However genotypes superior for specific characters from different clusters are required to be selected for utilization in recombination breeding programme to recover transgressive segregants, as genotypes within a cluster are considered similar with respect to aggregate effect of genes and the hybridization between them is not expected to be rewarding (Mishra *et al.*, 2007).

The superior genotypes for specific characters from different clusters are listed in Table 4. Potential parents for crossing programme should belong to diverse clusters characterized by large intercluster distances. Keeping in view, the large intercluster distances (Table 2) along with high mean values of different genotypes (Table 4), the promising cross combinations identified are Banquiabyad x Perlette, Banquiabyad x Lomanto, Arkavati x Perlette, Arkavati x Lomanto, Tas-e-Ganesh x Perlette, Tas-e-Ganesh x Lomanto, Banquiabyad x Beauty Seedless, Arkavati x Beauty Seedless, Tas-e-Ganesh x Beauty Seedless. However in order to accommodate maximum desirable characters scattered over different genotypes into a single genotype, complex crosses are required.

Acknowledgement
The authors are thankful to Dr KS Brar, Senior Plant Breeder, PAU Regional Research Station, Bathinda, for helping in data analysis and interpretation.

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Table 1. Clustering pattern of 20 grapes genotypes

Cluster	No. of genotypes	Genotype (s)	Geographic origin
I	7	Angur Early	India,
		Banquiabyad,	India
		Arkavati ,	India
		Bharat Early	-
		Arka Hans	India
		Tas-e Ganesh	India
		Black Prince	France
II	4	Cardinal	USA
		Madeliene Anguivine	France,
		Ruby Red	USA
		Black Muscat	Germany
III	5	Khalili, ,	Azerbaijan
		Shadipur local,	India
		Delight	USA
		Arka Shyam,	India
		Selection 7	India
IV	3	Perlette, ,	USA
		Arka Kanchan	India
		Lomanto	USA
V	1	Beauty Seedless	USA

Table 2. Intra and intercluster distances (D values) among five cluster of grapes

Cluster	I	II	III	IV	V
I	**28.05**	90.85	53.53	149.31	123.93
II		**25.55**	43.85	63.85	47.12
III			**16.79**	95.66	79.00
IV				**25.75**	28.99
V					**0.0**

Bold values are intracluster distances

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Table 3. Cluster means for twelve component trails in grapes

Cluster	Bunch length (cm)	Bunch breadth (cm)	Bunch weight (g)	TSS (%)	Acidity (%)	Berry weight (g)	Berry length (cm)	Berry breadth (cm)	Bunch number	TSS/Acid ratio	Brix yield (g)	Fruit yield per vine (kg)
I	17.36	10.96	291.74	17.25	1.06	2.72	1.77	1.59	26.79	17.99	1.23	7.14
II	16.47	10.30	224.54	15.54	1.07	2.70	1.71	1.62	68.00	17.66	2.34	14.89
III	15.93	10.83	291.14	16.81	0.93	2.27	1.72	1.49	45.66	20.30	2.13	12.55
IV	16.45	10.47	253.19	15.95	1.18	2.15	1.57	1.51	90.22	15.55	3.43	21.27
V	20.01	12.61	329.29	17.33	1.16	1.66	1.55	1.32	68.35	15.35	3.93	23.12

Table 4. List of Superior genotypes selected from different clusters

S. No.	Genotypes	Cluster No.	Superior for character (s)
1	Banquiabyad	I	Berry weight (4.14g), Berry breadth (1.92 cm)
2	Arkavati	I	Bunch length (20.22cm)
3	Tas-e-Ganesh	I	TSS (18.19%)
4	Cardinal	II	Acidity (0.64%), Berry weight (4.77g), Berry length (2.11cm), Berry breadth (2.01cm)
5	Delight	III	Acidity (0.75%), TSS: acidity ratio (25.68)
6	Selection-7	III	Bunch breadth (14.20cm), Bunch weight (560g), Berry length (2.09cm)
7	Perlette	IV	Berry yield (5.01g), Fruit yield per Vine (29.83kg)
8	Lomanto	IV	Bunch number (104.91)
9	Beauty Seedless	V	Bunch length (20.01cm), TSS (17.33g), Brix yield (3.93g), Fruit yield per vine (23.12kg)