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Short communication

Genetic divergence analysis of pear using qualitative traits as per DUS guidelines

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ABSTRACT

Genetic divergence was studied among 18 pear accessions being grown at Experimental Farm of CITH, Srinagar, J&K. Highest number of genotypes were groped in cluster II. Average cluster mean was recoreded maximum in cluster IV for most of the characters. Inter cluster D^2 values were higher than intra cluster value. Highest intra-cluster value (2.513) was noted in cluster II and minimum values intra-cluster distance were exhibited in IV, III and I clusters.

Keywords: Genetic diversity, DUS pear, qualitative traits.

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The pear genus *Pyrus* belongs to family Rosaceae, contains 22 widely recognized primary species all indigenous to Europe, temperate Asia and mountainous areas of North Africa .It is cultivated wide range of soil and climatic conditions from typical temperate zone to sub temperate and sub tropical areas. Jammu and Kashmir has highest area and production in India but average productivity is just 3.8 t/ha (Anon, 1). The need of parental diversity to the optimum magnitude to obtain superior genotypes to recover transgressive segregants has also been repeatedly emphasized by Arunachalam and Bandyopadhyay (2). Characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistic and cluster analysis. This procedure characterizes genetic divergence using the criterion of similarly or dissimilarly based on the aggregate effect of a number of horticulturally important characters. More diverse parent within a reasonable range, better the chances of improving economic characters under consideration in the resulting offspring. *Pyrus* is genetically diverse and the gene pool available for the breeders is well documented (Westwood, 10). The present investigation was conducted to indentify the diverse genotypes for qualitative traits and their relation to yield and density associating characters.

The present experimental was carried out at Experimental Farm of Central Institute of Temperate Horticulture, Srinagar, J&K , the site is located at Karewa Belt of Kashmir at 34°45^{1}N latitude and 74°50^1 E, longitude and the elevation is 1649 masl. The area experienced average minimum and maximum temperate 6.52° - 19.63°C, with amount of rainfall 650-1000 mm. Eighteen accessions of pear, *i.e.* Red Bartlett (NBPGR), Bar Battira Giffard (NBPGR), Pyasua Behapa (NBPGR), Doyenne-du-Comice (NBPGR), Santya Baiskage (NBPGR), Hayward (NBPGR), Gent Drouard (NBPGR), William Bartlett (NBPGR), Starkrimson (NBPGR), Z.H. Copacea (NBPGR), Kashmiri Nakh (Kashmir), CITH-PW 03 (Kashmir), CITH-PW 04 (Kashmir), CITH-PW 05 (Kashmir) and CITH-PW 06 (Kashmir). The trees were planted at 4 m × 4 m spacing and grafted on Kainth (*P. pashia*) rootstock. The characteristics chosen for this study were selected among a larger set defined by UPOV (International Union for the Protection of New Varieties of Plants) (6) and IBGRI (International Board of Plant Genetic Resources (5) descriptor for pear. Qualitative observations were recorded for the three consecutive years. Fruit length, fruit diameter, were recorded with the help of digital Vernier callipers, fruit weight with electronic balance, firmness with penetrometer, depth of stalk cavity, depth of eye basin, length of fruit stalk with scale. Procedure for recording various observations were done using UPOV, DUS guideline for pear. Three years data recorded were pooled and subjected to D^2 analysis. The Mahalanobis'D^2 (7) statistics analysis was conducted to estimate the intra- and inter- cluster distance and to group the genotype into different clusters as suggested by Rao (9).

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Data apparently have significant differences and wide range of variation for all the fruit characters. Mean fruit length recorded 63.25, whereas fruit thickness 0.32 and fruit firmness (21.10 lb/cm^2) petiole length, diameter recorded 2.44 and 0.97 mm, respectively and depth of stalk cavity and eye basin depth noted 0.50 and 0.57, respectively. Coefficient of variation recorded highest 80.00% in depth of stalk cavity followed by 71.82% in fruit weight (Table 1). Configuration of genotypes in to various clusters are depicted in the Table 2. Cluster II possess maximum (10) genotypes followed by cluster III (5), whereas cluster IV is mono-genotypic (Table 2). Table 3 indicates maximum within intra-cluster D^2 value (2.51) was noted in cluster II, followed by cluster III (0.89), whereas intra-cluster distance (0.88) noted in cluster I. It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance Bose and Pradhan (4). Cluster II had high intra-cluster distance (2.513) because the accessions in this cluster belongs to diverse origin. Therefore, crossing within cluster could produce desirable recombinants. The maximum inter-cluster distance noted between cluster I (1.92) and cluster IV (4.43) and least inter-cluster D^2 value recorded between cluster I and cluster III. Inter-cluster distance was greater than intra cluster distance which indicate high genetic diversity between clusters. Similar trend of grouping was noted by Panday and Tripathi (8) in walnut and Barua and Sharma (3) in apple. The grouping of variety into one cluster from different geographical location might be due to presence of common gene. The closest distance between clusters indicated that varieties of these cluster had maximum number of common gene complexes. High statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Inter crossing of divergent genotypes with desirable traits would lead to greater opportunity for maximum amount of heterosis.

Table 1. Cluster mean, SD, CD and CV for various fruit characters in pear.

Character	Mean	SD	CV (%)
Fruit length (mm)	63.25	26.83	42.42
Fruit diameter (mm)	53.45	19.11	35.75
Fruit weight (g)	121.17	87.02	71.82
Fruit skin thickness (mm)	0.32	0.04	12.50
Firmness (lb/cm^2)	21.10	9.61	45.55
Petiole length (cm)	2.44	1.07	43.85
Petiole dia. (mm)	0.92	0.36	39.13
Length of fruit stalk (cm)	0.37	0.12	32.43
Thickness of stalk (cm)	1.07	0.50	46.73
Depth of stalk cavity (cm)	0.50	0.40	80.00
Fruit: depth at eye basin (cm)	1.57	0.70	44.59

Table 2. Distribution of various pear genotypes into various clusters.

Cluster No.	No. of genotype (s)	Genotype(s)
1	2	CITH-PW = 01, CITH-PW = 02
2	10	Bar Battira Giffard, Pyasua Behapa, Doyenne-du-Comice, Santya Baiskage, Hayward, Gent Drouard, William Bartlett, Starkrimson, Z.H. Copaceae, Kashmiri Nakh.
3	5	CITH–PW = 03, CITH-PW-04, CITH-PW-5, CITH-PW = 06
4	1	Red Bartlett

Table 3. Mean intra-cluster (diagonal and bold) and inter-cluster distances among four clusters.

Cluster	1	2	3	4
1	0.88			
2	4.164	2.513		
3	1.924	4.435	0.891	
4	6.814	5.606	6.36	0.000

Table 4. Cluster mean of various characters of pear germplasm.

Character	Cluster No.			
	1	2	3	4
Fruit length (mm)	34.98	81.28	32.77	91.79
Fruit diameter (mm)	30.29	67.46	31.88	67.54
Fruit weight (g)	42.56	175.93	31.62	178.6
Fruit skin thickness (mm)	0.27	0.35	0.28	44.67
Firmness (lb/cm^2)	22.9	18.56	21.51	40.83
Petiole length (cm)	1.32	3.16	1.53	2.00
Petiole diameter (mm)	0.70	1.12	0.63	0.87
Length of stalk (fruit)	0.29	0.33	0.43	0.59
Thickness of stalk (cm)	1.37	1.28	0.63	0.60
Depth of stalk cavity (cm)	0.28	0.65	0.21	0.80
Fruit: depth at eye basin (cm)	0.82	1.99	0.93	2.10

Cluster wise various mean characters are presented in Table 4. Average fruit length, dia. weight, fruit thickness and firmness 91.79, 67.54, 178.60, 44.67, 40.83, respectively registered in cluster IV, followed by cluster II, except fruit firmness. Mean petiole length and diameter registered in cluster II fruit stalk length, and thickness was noted in cluster IV and cluster I respectively, whereas mean highest eye basin noted in the cluster II.

On the basis of findings it can be concluded that maximum number of varieties find place in cluster II where as cluster IV is monogenetic. Most of the wild strain grouped in cluster III which indicates that these genotypes having common gene responsible for various characters. The genotypes of different geographic origin were randomly distributed in the clusters which means that geographical diversity does not necessarily represents genetic diversity. Hence, it is suggested to cross between the genotypes selected from most distant clusters with high mean performance to get desirable transgressive segregants.

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