

Genetic studies on variability, heritability, genetic advance and cluster analysis in pear (*Pyrus* spp.)

Z.A. Bhat* and W.S. Dhillon

Department of Fruit Science, Punjab Agricultural University, Ludhiana 141004

ABSTRACT

Data on 21 quantitative traits were subjected to genotypic and phenotypic coefficient of variation, heritability, genetic advance and clustering using D² analysis with group constellation following Tocher's method. Phenotypic and genotypic coefficients of variation were high for fruit yield (46.58 and 46.55%), fruit length (47.06 and 42.69%), fruit weight (46.53 and 45.17%), pedicel length (38.47 and 37.82%) and TSS (39.62 and 36.1%) and medium to low for other traits. The estimates of heritability and genetic advance were maximum for fruit yield. High heritability estimates accompanied with greater genetic advance were observed for yield, fruit weight, pedicel length and fruit length indicating that these traits may be considered for selecting promising parents. Test genotypes were grouped into four clusters with maximum number of genotypes (6) in cluster I, 2 genotypes in cluster IV and one genotype each in clusters II and III. Highest inter-cluster distance (153.05) was between cluster II and IV, while highest intra-cluster distance was observed in cluster IV (36.24).

Key words: Genetic variability, genetic advance, heritability, pear.

INTRODUCTION

Pear is one of the most important temperate fruits of the world next to apple. Total world pear production reached 21 million metric tonnes in 2013 (FAO STAT, 6) ranking second after apple, among global production of deciduous fruit tree species. In India the annual pear production is 2.17 lakh metric tonnes from an area of 39,700 ha (Anon, 2). In Punjab, it ranks 4th among fruit crops in terms of area after citrus, guava and mango and occupies an area of 2,598 ha with an annual production of 58,643 MT (Aulakh and Gill, 3). The area can be increased further and cultivation of this crop may prove to be a best alternative for diversification of agriculture.

The basic information which a fruit breeder usually needs for improvement in a particular plant species is the nature and magnitude of genetic variation present in the available germplasm and extent to which the desirable characters are heritable. However, little efforts have been made for genetic characterization of diversity in the commercially grown pear cultivars, and their potential for continued breeding success in applied pear breeding is indistinct. Furthermore, quantitative studies enable breeders to understand the racial affinities and evolutionary pattern in various species of cultivated plants. In addition, it also helps in making decisions in selection of the best parental

combinations in hybridization programme. It serves as a basis of grouping of two or more genotypes based on minimum divergence or resemblance between them. Information on divergence *vis-à-vis* fruit traits of pear is lacking, therefore, the present investigation was undertaken to assess the genetic variability, heritability, genetic advance and to group the available genotypes based on their genetic distances for various fruit and tree characteristics.

MATERIALS AND METHODS

The present study was conducted on 10 pear cultivars collected from different sources and conserved in a field gene bank at Horticultural Farm of PAU, Ludhiana. The plants were maintained under uniform cultural conditions. The observations were recorded for three consecutive years (2009-2011) on 21 quantitative characteristics. There were three replications to determine these traits. For evaluation a random sample of twelve fruits per tree was collected with four fruits from each replication. The pooled mean values of three years for all 21 characters were subjected to biometric analysis.

The variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (GCV) and heritability (h^2) were computed according to methods suggested by Burton and de Vane (4), genetic advance by Allard (1), while genetic divergence by D² statistics (Rao, 12). Group formation was estimated using Tocher's method.

*Corresponding author's present address: Ambri Apple Research Centre, SKUAST-K, Srinagar; E-mail: zahoormano@gmail.com

RESULTS AND DISCUSSION

The perusal of data on phenotypic and genotypic coefficient of variation, heritability and genetic advance (Table 1) revealed that mean was high for number of days from flowering to harvest (125.07) followed by fruit set per cent (114.31), yield (64.77) and flower intensity (45.47). Phenotypic and genotypic coefficients of variation were high for fruit yield (46.58 and 46.55%), fruit length (47.06 and 42.69%) fruit weight (46.53 and 45.17%), pedicel length (38.47 and 37.82%) and TSS (39.62 and 36.1%) and medium to low for other traits. The estimates of GCV were lower in magnitude than PCV and the range was nominal indicating that there is lesser influence of environment on the traits studied and consistency in the expression of these traits irrespective of growing conditions, except for trunk increment and flower duration where the difference in magnitude indicates more influence of environment. The higher values of both PCV and GCV for various traits like fruit weight, fruit length, fruit yield and TSS indicate that greater

Table 1. Pear genotypes used in present study.

Genotype	Pedigree	Origin
Patharnakh	<i>Pyrus pyrifolia</i>	India
Punjab Beauty	<i>Pyrus pyrifolia</i> × <i>Pyrus communis</i>	India
Shinseiki	<i>Pyrus pyrifolia</i>	Japan
YaLi	<i>Pyrus bretschneideri</i>	China
Kainth	<i>Pyrus pashia</i>	India
Shiara	<i>Pyrus serotina</i>	India/Pakistan/ Nepal
Smith	<i>Pyrus communis</i> × <i>Pyrus pyrifolia</i>	New York
LeConte	<i>Pyrus communis</i> × <i>Pyrus pyrifolia</i>	Georgia
Keifer	<i>Pyrus communis</i> × <i>Pyrus pyrifolia</i>	Pennsylvania
Baggugosha	<i>Pyrus communis</i> × <i>Pyrus pyrifolia</i>	India

Table 1. Estimates of various genetic parameters of pear genotypes.

Trait	Mean	Coefficient of variation (%)		Heritability (%)	Genetic advance as percent of mean
		PCV	GCV		
Tree height (m)	6.05 (1.02)	10.67	10.33	93.64	20.58
Tree spread (m)	5.75 (0.89)	18.3	17.85	95.15	35.88
Trunk increment (cm)	2.11 (0.70)	18.19	15.47	72.33	27.1
Leaf length (cm)	9.29 (1.10)	17.79	16.91	90.37	33.12
Leaf breadth (cm)	5.77 (0.76)	22.86	21.76	90.64	42.68
Flower intensity (No./m of branch length)	45.47 (3.24)	22.33	22.07	97.75	44.96
Flower duration (days)	8.65 (1.04)	31.63	24.8	61.5	40.07
No. of days from flowering to harvest	125.07 (4.36)	26.93	26.7	39.64	54.53
Fruit set (%)	114.31 (3.67)	32.52	29.48	98.31	26.56
No. of lenticels (No./cm ²)	0.63 (0.09)	31.86	31.4	97.16	63.76
No. fruits per spur	3.68 (0.68)	24.02	21.13	77.39	38.3
Yield (kg/tree)	64.77 (2.13)	46.58	46.55	99.88	95.84
Pedicel length (cm)	2.5 (0.31)	38.74	37.82	95.34	76.08
Pedicel diameter (mm)	6.17 (1.21)	22.92	22.37	95.26	44.99
Fruit weight (gm)	5.73 (0.54)	46.53	45.17	94.21	90.31
Fruit length (cm)	7.06 (0.47)	47.06	42.69	82.3	79.79
Fruit diameter (cm)	11.73 (1.05)	27.79	27.51	98.02	56.11
Fruit firmness (kg/cm ²)	0.44 (0.03)	30.54	30.07	96.91	60.97
TSS (°Brix)	32.55 (2.61)	39.62	36.1	83.02	67.75
Acidity (%)	17.37 (2.01)	11.44	9.99	76.24	17.96
TSS/ acid ratio	32.1 (1.89)	15.39	15.37	99.81	31.63

Note: Data in parenthesis is SE

improvement be expected in the selection for these characters. The estimates of heritability in broad sense was more than 95 per cent for fruit yield (99.88%), TSS/acid ratio (99.81%), fruit set (98.31%), fruit diameter (98.02%), flower intensity (97.75%), number of lenticels (97.16%), fruit firmness (96.91%), pedicel length (95.34%) and tree spread (95.15%). Heritability estimates were low for number of days from flowering to harvest (39.64%). High heritability indicates that the traits under study had great scope for genetic improvement. The computation of genetic advance revealed that highest value was observed for fruit yield (95.84), fruit weight (90.31), fruit length (79.79), pedicel length (76.08) and TSS (67.75), whereas, acidity had the least value (17.96). High value of genetic advance indicates that heritability is due to additive gene action.

Since most of economic characters like yield are complex in their inheritance and are greatly influenced by environmental conditions, the study of heritability and genetic advance is very useful to estimate the scope of improvement by selection. Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotypic expression. The heritability estimates were high (>80%) for characters like tree height, tree spread, leaf length, leaf breadth, flower intensity, fruit set, number of lenticels, fruit yield, pedicel length, pedicel diameter, fruit weight, fruit diameter, fruit firmness and TSS/acid ratio. High heritability indicates that the traits under study had great scope for genetic improvement. Many workers have observed high heritability for different characters in several fruit crops (Verma *et al.*, 15; Rajan *et al.*, 11). Moderate to low estimates indicates that improvement through selection would be limited. However, the computation of heritability alone will not be capable to emphasize in improving fruit traits unless there is a higher genetic gain, which indicates additive gene action. It also indicates that improvement in these traits can be achieved through selection. According to Johnson *et al.* (7), an estimated heritability associated with genetic advance is more reliable than heritability alone for prognosticating the impact of selection.

In the present study, high heritability estimates accompanied with greater genetic advance were observed for yield, fruit weight, fruit length, pedicel length, TSS and number of lenticels which revealed that these characters had additive gene effect and, therefore, have more roles in proficient selection. Comparatively low genetic advance accompanied with high heritability estimates for tree height, tree spread, leaf length, leaf breadth, flowering intensity, fruit set, acidity and TSS/ acid ratio may be due to non-additive gene action, which associated epistasis

and dominance. Several workers (Kumar *et al.*, 8; Rajan *et al.*, 10; Doss *et al.*, 5) are also of the similar opinion in case of estimates as well as relation of GCV, PCV, heritability and genetic advance in various crops. A low genetic advance indicates that heritability was mainly due to non-additive gene action, whereas, high heritability due to additive gene action would be associated with high genetic advance (Shadakshari *et al.*, 13).

On the basis of relative magnitude of D^2 values, the test genotypes were grouped into four clusters (Table 2) based on 21 quantitative traits using Tocher's method with variable number of entries in each cluster indicating the presence of genetic diversity in the genotypes of present study. Cluster I had maximum number of genotypes (6) comprising Punjab Beauty, Smith, Baggugosha, LeConte, Keifer and YaLi followed by cluster IV with 2 genotypes (Kainth and Shiara), cluster II and III with one genotype in each cluster (Patharnakh and Shinseiki, respectively). The formation of different clusters with variable number of entries in each cluster indicates diversity among genotypes. The genotypes from different countries or agro-ecological zones were found to scattered in different clusters. This suggests that a pattern of clustering of accessions was independent of their geographic origin. No parallelism was found between genetic and geographic diversity. This mixed grouping of genotypes from different origins in same cluster could be due to extensive utilization of few donor species to generate pear genotypes across world or due to unidirectional selection pressure practised by the breeders in tailoring the promising cultivars. The results on similar lines were also reported by Sharma and Sharma (14) in walnut.

The intra-cluster distances ranged from 0.00 to 36.24 (Table 3) indicating that the genotypes in clusters have dissimilarity for morphological features and performance. The members of cluster II and IV exhibited maximum divergence (inter-cluster distance 153.05) followed by the members of cluster

Table 2. Clustering pattern of various genotypes based on D^2 analysis.

Cluster No.	No. of genotype(s)	Genotype(s)
I	6	Punjab Beauty, Smith, Baggugosha, LeConte, Keifer, YaLi
II	1	Patharnakh
III	1	Shinseiki
IV	2	Kainth, Shiara

Table 3. Inter- and intra-cluster (bold) average D² values and distances ($\sqrt{D^2}$) among pear genotypes.

Cluster No.	I	II	III	IV
I	24.36	61.42	72.81	137.92
II		0.00	73.50	153.05
III			0.00	135.67
IV				36.24

I and IV (inter-cluster distance 137.92) and cluster III and IV (inter-cluster distance 135.67). The members of cluster I and II were least divergent (inter-cluster distance 61.42). The inter-cluster distances were larger than the intra-cluster distances indicating a wider genetic diversity between genotypes of clusters with respect to trait considered. Maximum inter-cluster distance is indicative that genotypes falling in these clusters had wide diversity and can be used for hybridization programme to get better recombinants in the segregating generations. Low levels of intra-cluster distances were indicative of narrow genetic variation within the cluster. Hence, selection of parents from this cluster is to be avoided

(Rai and Mishra, 9). Genotypes of same cluster would not yield desirable recombinants. It is concluded that genotypes of pear with wide genetic variation accompanied with useful characteristics could be effectively employed in intra specific crosses with the hope that this would lead to the transmission of higher genetic gain for different putative traits major being yield related traits from practical utility point of view. On the basis of the performance of different genotypes and the cluster analysis, the pear genotypes have been identified for different characters could serve as an outstanding genetic basis and a source of germplasm for pear breeding programmes.

The cluster mean value for twenty one characters is presented in Table 4. The perusal of data indicated considerable differences for all the characters among clusters. It can be seen from the cluster means that each cluster has its uniqueness that separated it from other characters. cluster I was characterized by maximum tree height (6.35 m), flower intensity (47.02), yield (76.08 kg), fruit length (7.23 cm) and low mean value for number of lenticels per cm² of fruit surface (26.80). Maximum mean value for tree

Table 4. Mean performance of different clusters.

Trait	Cluster			
	I	II	III	IV
Tree height (m)	6.35	6.26	4.60	5.73
Tree spread (m)	6.13	6.58	3.73	5.18
Trunk increment (cm)	2.26	2.43	2.05	1.51
Leaf length (cm)	9.35	12.65	9.00	7.52
Leaf breadth (cm)	5.87	8.00	5.60	4.43
Flower intensity (No./m branch)	47.02	40.33	45.50	43.33
Flower duration (days)	17.16	14.00	20.33	18.16
No. of days from flowering to harvest	117.27	142.66	96.33	154.00
Fruit set (%)	9.08	6.50	3.50	11.00
No. of lenticels (No./cm ²)	26.80	39.16	34.83	43.08
No. fruits per spur	2.13	2.50	2.83	3.41
Yield (kg/tree)	76.08	57.84	14.51	59.44
Pedicle length (cm)	4.06	2.32	3.00	3.55
Pedicle diameter (cm)	0.70	0.96	0.51	0.28
Fruit weight (gm)	138.82	160.98	121.30	15.26
Fruit length (cm)	7.23	7.23	4.80	3.13
Fruit diameter (cm)	6.31	6.96	5.43	3.50
Fruit firmness (kg/cm ²)	6.32	5.02	4.46	11.59
TSS (°Brix)	13.08	12.90	14.30	5.78
Acidity (%)	0.35	0.43	0.31	0.80
TSS/ acid ratio	38.86	30.28	47.03	7.72

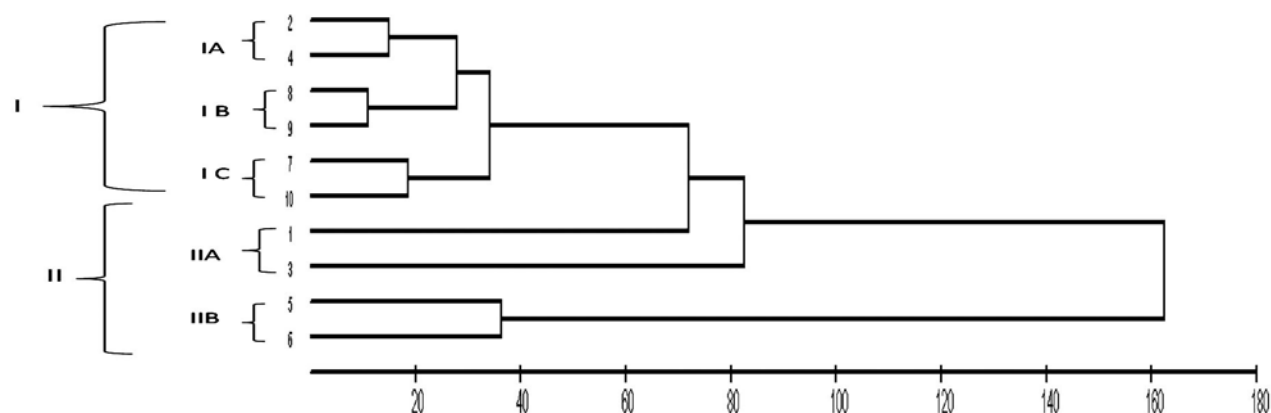


Fig. 1. Dendrogram based on morphological parameters in pear genotypes.

spread (6.58 m), leaf length (12.65 cm), pedicel diameter (0.96 mm), fruit weight (160.98 g) and fruit diameter (6.96 cm) and minimum mean values for pedicel length (2.32 cm) were represented by cluster II. Cluster III was characterized by highest mean value for TSS (14.30°Brix), TSS/ acid ratio (47.03) and least value for tree spread (3.73 m), number of days from flowering to harvest (96.33) and acidity (0.31%). Cluster IV was characterized by maximum mean value for number of days from flowering to harvest (154.00), fruit set per cent (11.00), number of lenticels per cm² of fruit surface (43.08), fruit firmness (11.59 kg/cm²) and acidity (0.80%). In present study, cluster I was better with respect to higher yield per plant and low number of lenticels, while cluster II for maximum fruit weight and size. Cluster III was better due to low tree spread, minimum number of days from flowering to harvest, high TSS and low acidity, whereas, cluster IV was better due to low incremental trunk girth, high fruit set per cent and maximum fruit firmness.

The dendrogram of 10 pear genotypes was also constructed based on morphological data in order to examine the genetic diversity (Fig. 1). The cluster analysis grouped the genotypes into three major clusters, i.e. I, II and III. The cluster I was further sub-divided in IA and IB, whereas, cluster II was sub divided into IIA and IIB. The sub group IA comprised of 4 genotypes (Punjab Beauty, YaLi, LeConte and Keifer), whereas subgroup IB included two pear genotypes (Smith and Baggugosha). The sub group IIA and IIB included one genotype each (Patharnakh and Shinseiki, respectively). Rootstocks, viz., Kainth and Shiara were grouped in one group (III). The clustering pattern shows the influence of environment, pedigree and center of origin.

The study revealed that GCV, PCV, heritability and genetic advance are more important for selecting

parents for hybridization than eco-geographical isolation. Better recombinants may be obtained if cultivars are chosen between cluster I and IV.

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Received : September, 2013; Revised : February, 2015;
Accepted : April, 2015