

# Genetic variation, heritability and correlation analysis of forty seven pear genotypes under subtropics

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## Abstract

A study was undertaken to analyze the variation, heritability and correlation for vegetative and fruit characters for forty seven genotypes of pear at PAU, Ludhiana. Highest range of variation was recorded in fruit weight (70.0-213.0), TSS/acid ratio (19.7-69.0) and acidity (0.2- 0.5) with the mean of 151.11g, 43.70, and 0.29%, respectively. The PCV and GCV were observed maximum for the fruits number per spur, acidity, fruit weight and TSS/acid ratio. Heritability estimates were observed high for fruit weight (100%), flower number per spur (99.95%), TSS/acid ratio (99.79%), leaf breadth (99.73%) and fruit breadth (99.24%). A highly significant positive genotypic and phenotypic correlation was observed for fruit length with fruit weight (0.7463 and 0.7439), fruit breadth (0.5345 and 0.5318), TSS (0.2684 and 0.2667) and low significant with TSS/acid ratio (0.1796 and 0.1740). Similarly, positive significant genotypic correlation of fruit number per spur and flower number per spur was recorded with leaf breadth (0.2816 and 0.2814) and leaf length (0.5823 and 0.3598), respectively.

**Key words:** *Pyrus species*, correlation, heritability, genetic advance, variability

## Introduction

Pear is one of the most important fruit crops of the world owing its fine fruit quality and varied uses. An ancient Greek poet Homer praised pears as one of the 'gifts of God'. Pear fruit is blessed with many pharmacological properties like anti-inflammatory, anti-tumour, antiallergic etc and also help in reducing risk of cardiovascular diseases and preferred by diabetic patients (Gorinstein *et al.*, 2002). About 72% of all commercially cultivated species of genus *Pyrus* are native to Asia. Pear genotypes are hardy in nature and grow in a wide range of climatic conditions and can tolerate temperature as low as -26 °C in dormant and as high as 45°C in growing period. Its adaptation to many diverse uses and environments is a reflection of the extent of genetic variability existent in the genus *Pyrus* (Verma *et al.*, 2014), which can be exploited in the breeding programme.

Information on the heritability of characters is one of the prerequisite for proper planning of breeding program for which screening of germplasm for target traits and subsequent selection of appropriate parents are helpful in harnessing the natural variability in the germplasm (Doss *et al.*, 2012). To boost the production in India both for home and export, development of improved varieties and hybrids is required. For this, information on genetic variability, heritability and genetic advance in pear need to be generated by the systematic studies. The utmost tool for breeder is the variability present in the germplasm. An attempt was, therefore, made to estimate the genetic variability components in the pear germplasm which may further help in identifying the promising types on the basis of their performance under subtropical environment.

## Material and methods

The field experiment was conducted on 47 genotypes including four major groups *viz.*, hard pear strains, semi soft pear strains and

Asian soft pear and other varieties raised at New Orchard, Punjab Agricultural University, Ludhiana (Table 1). The experiment was premeditated in Randomized Complete Block Design (RCBD) with three replications. A single tree of each genotype having uniform size and shape considered as unit of replication. The genotypes were evaluated for vegetative, flowering and fruiting behaviour. The data on fruit characters and quality attributes were recorded in quantitative terms. Genotypic and phenotypic coefficients of variations were calculated according to the methods suggested by Burton and DeVan (1953). For the estimates of heritability and genetic advance (percent mean), the methods of Johnson *et al.* (1955) were followed.

## Results and discussions

The data on genotypic mean, range, genotypic coefficient of variation, phenotypic coefficient of variation along with the per cent of heritability ( $h^2$ ), expected genetic advance and genetic gain are given in Table 2. A wide range of variability was observed for most of the characters. Higher range of variation was recorded in fruit weight (70.0-213.0), TSS/acid ratio (19.7-69.0), acidity (0.2-0.5) with the mean of 151.11g, 43.70, and 0.29%, respectively. Moderate to low range of variability was found in remaining characters and these findings were in concordance with studies done in pear germplasm (Kajiura and Suzuki, 1980). The characters which showed high range of variation should be given priority in the selection (Vijay and Manohar, 1990). The phenotypic coefficient of variation was observed higher than genotypic coefficient of variation and also closely corresponding to PCV and GCV for all the traits revealed that genotypic effects were important in the expression of the character. The PCV and GCV were observed maximum for the fruit number per spur (42.30 and 31.95), acidity (23.40 and 24.16), fruit weight (21.38 and 21.40) and TSS/acid ratio (27.18 and 27.77), indicating better scope of phenotypic selection to enhance the cultivar

Table 1. Pedigree and origin of different pear genotypes

Genotypes	Pedigree	Origin
<b>Asian soft pear and other varieties</b>		
Nijisseiki	<i>P. pyrifolia</i>	Japan
Shinseiki	<i>P. pyrifolia</i>	Japan
YaLi	<i>P. pyrifolia</i>	China
Hosui	<i>P. pyrifolia</i>	Japan
Kosui	<i>P. pyrifolia</i>	Japan
T-Su-Li	<i>P. pyrifolia</i>	China
Florda Home	<i>P. communis</i>	North America
Tenn	<i>P. communis</i>	North America
Peckham's Triumph	<i>P. communis</i>	Australia
Orient	<i>P. communis</i>	North America
Saharanpuri	<i>P. sp.</i>	India
<i>P. species</i>	<i>P. sp.</i>	India
<b>Strains of hard pear (Patharnakh)</b>		
Strain I	<i>P. pyrifolia</i>	India
Strain II	<i>P. pyrifolia</i>	India
Strain III	<i>P. pyrifolia</i>	India
Strain IV	<i>P. pyrifolia</i>	India
Strain V	<i>P. pyrifolia</i>	India
Strain VI	<i>P. pyrifolia</i>	India
Strain IX	<i>P. pyrifolia</i>	India
Strain X	<i>P. pyrifolia</i>	India
Strain XI	<i>P. pyrifolia</i>	India
Strain XII	<i>P. pyrifolia</i>	India
<b>Strains of semi-soft pear</b>		
S I	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S II	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S III	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S IV	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S V	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S VI	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S VII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S VIII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S IX	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S X	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XI	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XIII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XIV	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XV	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XVI	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XVII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XVIII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XIX	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XX	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XXI	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XXII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XXIII	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XXIV	<i>P. communis</i> x <i>P. pyrifolia</i>	India
S XXV	<i>P. communis</i> x <i>P. pyrifolia</i>	India

Table 2. Estimates of variability for various traits in pear

Characters	Range	Grand mean	CV	Coefficient of variation		Heritability (h <sup>2</sup> %)	Genetic advance (GA)	GA as percent mean
				GCV	PCV			
Leaf length (cm)	5.6-12.0	8.37	1.89	15.21	15.33	98.48	2.60	31.09
Leaf breadth (cm)	3.22-7.51	5.45	1.06	20.25	20.28	99.73	2.27	41.67
Flower (cm)	2.6-4.0	3.17	1.14	10.69	10.75	98.87	.69	21.89
Flower number per spur	5.0-11.7	7.45	0.42	19.46	19.46	99.95	2.98	40.08
Fruit number per spur	1.0-4.0	1.77	27.71	31.95	42.30	57.07	.88	49.73
Fruit length (cm)	4.8-7.9	6.68	0.93	11.74	11.78	99.38	1.61	24.11
Fruit breadth (cm)	4.2-7.2	6.12	0.70	7.94	7.97	99.24	1.00	16.29
Fruit weight (g)	70.0-213.0	151.11	0.10	21.38	21.38	100.00	66.55	44.04
Acidity (%)	0.2-0.5	0.29	6.00	23.40	24.16	93.84	0.14	46.70
Total soluble solids	9.0-15.1	12.06	0.60	13.16	13.18	99.79	3.27	27.09
TSS/acid ratio	19.7-69.0	43.70	5.72	27.18	27.77	95.75	23.94	54.78

improvement in pear. The magnitude of heritability reveals the extent of reliability in identifying the genotypes on the basis of phenotypic expression. Thus in present studies heritability estimates were observed high for fruit weight (100%), flower number per spur (99.95%), TSS/acid ratio (99.79%), leaf breadth (99.73%) and fruit breadth (99.24%). In spite of high heritability for most of the traits genetic advance as percentage of mean ranged from 16.29 to 54.78. The highest genetic advance was observed for TSS/acid ratio (54.78) followed by fruit number per spur (49.73), acidity (46.70) and fruit weight (44.04). High heritability and genetic advance had also been reported in mulberry (Rahman *et al.*, 2006), peaches and nectarines (Colaric *et al.*, 2005). Chen *et al.* (2007) found that pear cultivars have different heritability of traits, often low to moderate, influenced by prevailing environmental conditions. High heritability with high value of genetic advance as percentage mean observed for TSS/acid ratio, flower number per spur, fruit weight and acidity indicated that these characters were less influenced by environment demonstrating either these were simply inherited characters governed by a few major genes because total genetic variance on which these estimates are based is made up of three parts, namely, additive genetic variance, non-additive genetic variance due to dominance, and non-additive genetic variance due to nonallelic gene interactions and therefore, selection of these characters would be more effective for cultivar improvement (Kumar *et al.*, 2014). Thus, present study revealed that high heritability along with high genetic advance as percent mean and high GCV for characters indicate the possibility of improvement in pear by using these characters as a tool for selection.

Correlation study among different characters revealed that all genotypic coefficients were significantly higher than the phenotypic coefficients (Table 3). A highly significant positive genotypic and phenotypic correlation was observed for fruit length with fruit weight (0.7463 and 0.7439), fruit breadth (0.5345 and 0.5318), TSS (0.2684 and 0.2667) and low significant with TSS/acid ratio (0.1796 and 0.1740). These results indicated that fruit weight, fruit breadth and TSS would be increased with increase in fruit length. Positive correlation was observed for breadth with leaf length (0.6715 and 0.6657) but was negatively correlated with TSS and TSS/acid ratio depicted that there would be no effect of increase in leaf breadth and length on quality characters of fruit. TSS/acid ratio showed highly positive and significant correlation with TSS (0.6706 and 0.6566). Positive significant correlation of fruit number per spur was recorded with leaf breadth (0.5094 and 0.3830) and leaf length (0.5823 and 0.4294). Likewise flower number per spur were correlated

Table 3. Genotypic and phenotypic correlation coefficient among various characters studied in pear genotypes

Characters		Acidity	Flower size	Flower number per spur	Fruit number per spur	Fruit length (cm)	Fruit weight (g)	Fruit breadth (cm)	Leaf breadth (cm)	Leaf length (cm)	TSS/ acid
Flower Size	G	0.4150**									
	P	0.4013**									
Flower number per spur	G	0.4460**	0.3279**								
	P	0.4316**	0.3258**								
Fruit number per spur	G	-0.2334	0.2388**	0.0442							
	P	-0.1761	0.1724*	0.0343							
Fruit length (cm)	G	-0.0530	-0.3997	0.0249	-0.2586						
	P	-0.0500	-0.3955	0.0249	-0.1902						
Fruit weight (g)	G	0.1410	-0.1261	0.2200**	-0.2931	0.7463**					
	P	0.1367	-0.1253	0.2199**	-0.2216	0.7439**					
Fruit wreadth(cm)	G	0.0924	0.0729	0.2188**	-0.2137	0.5345**	0.5727**				
	P	0.0888	0.0731	0.2181**	-0.1616	0.5318**	0.5705**				
Leaf breadth (cm)	G	0.2160**	0.4234	0.2814**	0.5094**	-0.4431	-0.2799	-0.3015			
	P	0.2082**	0.4204	0.2816**	0.3830**	-0.4405	-0.2795	-0.2995			
Leaf length(cm)	G	0.1584	0.5303**	0.3598**	0.5823**	-0.6185	-0.4404	-0.2915	0.6715**		
	P	0.1567	0.5251**	0.3573**	0.4294**	-0.6125	-0.4371	-0.2885	0.6657**		
TSS/acid Ratio	G	-0.8635	-0.5813	-0.4472	0.1977	0.1796*	-0.0409	-0.0932	-0.3492	-0.2606	
	P	-0.8685	-0.5663	-0.4372	0.1507	0.1740*	-0.0400	-0.0908	-0.3406	-0.2561	
TSS	G	-0.2901	-0.4409	-0.2128	-0.0466	0.2684**	0.1875*	-0.0632	-0.3564	-0.2370	0.6706**
	P	-0.2803	-0.4371	-0.2124	-0.0349	0.2667**	0.1874*	-0.0627	-0.3554	-0.2346	0.6566**

\* =5 % level of significance \*\*= 1 % level of significance. G (genotypic correlation) and P (phenotypic correlation)

with leaf breadth (0.2814 and 0.2816) and length (0.3598 and 0.3573). Thus both results depicted that increase in leaf length and breadth would enhance the source sink relation for increasing fruit number and yield and were found in line with the findings of Saran (2007) in ber germplasm and Osekita *et al.* (2014) in tomato genotypes.

Considerable genetic variability was present among pear genotypes selected in the study. The highest range of variability was recorded in fruit weight followed by TSS/acid ratio, fruit number per spur and acidity. High heritability estimates coupled with high and moderate genetic advance was observed for fruit weight, fruit length, TSS, acidity, TSS/acid ratio and flower number per spur. Correlation analysis suggested that fruit weight, fruit length, fruit number per spur, flower number per spur, TSS and TSS/acid ratio would be effective characters for selection and improvement of pear.

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