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Genetic diversity of pomegranate genotypes for important horticultural traits

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ABSTRACT

The present study assessed genetic relatedness based on 12 phenotypic traits among 60 pomegranate genotypes representing 20 indigenous and 40 exotic types. Per se, performance was measured for plant height, number of branches, thorn length, rind thickness, fruit weight, fruit length, fruit breath, etc. The phenotypic correlation coefficients were higher in magnitude than the genotypic correlation coefficients. Using principal component analysis, the first principal component (PC1) explained 28.73% of the total variance, mainly consisting of fruit breadth, length, and weight predominantly. In comparison, PC2 explained 21.28% variability, mainly including plant height and the number of branches and fruit length up to some extent. Further, PC3 and PC4 showed the remaining 15.16% and 11.48%, respectively, for traits like, thorn length, number of stems, and rind thickness. A phylogenetic tree constructed based on phenotypic characteristics by applying Squared Euclidean Distance and group average clustering method showed two diverse groups. However, it partially divided the genotypes based on their type into two significant groups or clusters. The present results could be further utilized for screening parents for a particular trait in future breeding programs.

Keywords: *Punica granatum* L., morphological traits, PCA, horticultural traits

INTRODUCTION

Pomegranate, one of the oldest known fruit trees has gained an increasing importance especially because of its medicinal and nutritional value (Kalaycıoglu and Erim, 7), belonging to family Lytheraceae of order Myrtales. The family contains a single genus *Punica* so it is considered to be the smallest family consisting two species*: P. granatum* and *P. protopunica* that are originated from central Asia exclusively the Transcaucasia- Caspian area in Iran and Socotra Island close to horn of Africa, respectively. Maximum diversity and optimal conditions for its growth and development are found in Iran owing to historical cultivation and other predisposing environmental factors (Chandra *et al.* 2; Holland *et al.* 5; Jalikop, 6). It is spread to different countries of the world including Mediterranean region, India, China, Pakistan and Afghanistan through primordial trade passage (Jalikop, 6; Saroj and Parmar, 12). Ornamental Japanese dwarf pomegranate (*Punica granatum v*ar. nana) is also popular among south-east Asian countries besides cultivated and wild types. South Asian countries have been reported to be the major center of genetic diversity for pomegranate (Holland *et al.*, 5). The scattered plantation of wild form of pomegranate (*Daru*) can be seed profusely in the mid hill conditions of North Western Himalayan region comprising of some parts of Shimla, Solan, Sirmour districts in HP, Udhampur, Doda and Jammu in J&K and Dehradun, Nanital in Uttarakahnd (Rana *et al.*, 11).

Genetic diversity evaluation provides the basis for selection of crop through distinguishing the donor accession for productivity enhancement, efficient utilization of nutrient under scarce resource conditions, breeding for novel purposes and climate resilience fruit cultivars and hybrids with increased biotic and abiotic stress potential (Dhillon *et al.*, 3). Tools including morphological, biochemical and molecular markers have been successfully applied for the evaluation of genetic diversity in different crop plants including horticultural and forest trees. Because of the perennial nature, specific climatic and edaphic conditions of these crops, it takes around 15 years to develop a new variety. With all these challenges, it is more evident that before taking up any crop improvement program in pomegranate, assessment of the genetic diversity and the source of the gene pools to be used as donors needs to be worked out. The specific breeding objective forms the framework for evolving new elite selections or hybrids. Being single fruit crop genus of Lytheraceae family, the genomic resources needs to be strengthened first so as to assess the genetic diversity using morphological traits.

MATERIALS AND METHODS

The experimental plant material comprising of 40 different cultivars maintained at Dr YS Parmar

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University of Horticulture & Forestry, Nauni, Solan (HP) orchard and 20 wild pomegranate genotypes procured from the various locations of Himachal Pradesh were considered for morphological characterization (Table 1). The research was carried out in randomized block design (RBD) with 3 replications, each with 1 tree. The genotypes were described based on the pomegranate descriptor developed by Protection of Plant Varieties and farmers' Right Authority New Delhi. Twelve different attributes including growth habit (geometry of plant crown), plant height (using scale), thorn length (using scale), number of secondary stem (visual observations), fruit weight (using digital weighing balance), fruit shape index

Table 1. List of the Pomegranate germplasm used in the study.

Districts	Location	Altitude above mean sea level	Genotypes	Wild/Cultivated
Solan (HP)	Dr YSP UHF, Nauni	1275 m	Saharnyi	Cultivated
			Chawla	Cultivated
			Vina	Cultivated
			Purple Heart	Cultivated
			Rosamia	Cultivated
			Alk Pust Ghernez Sveh	Cultivated
			Sogdiana	Cultivated
			Haku-botan	Cultivated
			Parfyanets	Cultivated
			Pink	Cultivated
			20090265	Cultivated
			Ambrosia	Cultivated
			Blaze	Cultivated
			Golden globe	Cultivated
			Phoenica	Cultivated
			Green Globe	Cultivated
			Loffani	Cultivated
			Loulou	Cultivated
			Al-sirin-nar	Cultivated
			Kaim-anar	Cultivated
			Bala mursal	Cultivated
			Apseronski	Cultivated
			Kazeake	Cultivated
			Cloud	Cultivated
			Crab	Cultivated
			Cranberry	Cultivated
			Sour	Cultivated
			Dewey	Cultivated
			Dkfromshevlan	Cultivated
			Podarok	Cultivated
			Nusai	Cultivated
			Ovadan	Cultivated
			Eve	Cultivated
			G-137	Cultivated

Contd...

Table 1 contd...

Districts	Location	Altitude above mean sea level	Genotypes	Wild/Cultivated
			Anar srin	Cultivated
			Ganesh	Cultivated
			Kandharihasi	Cultivated
			Mridula	Cultivated
			Kandari kabuli	Cultivated
			Gulyalek	Cultivated
	Kandaghat	1150 m	Kandaghat-1	Wild
			Kandagaht-2	Wild
			Kandaghat-3	Wild
			Kandaghat-4	Wild
Sirmour (HP)	Rajgarh	1345 m	Rajgarh-1	Wild
			Rajgarh-2	Wild
			Rajgarh-3	Wild
			Rajgarh-4	Wild
	Narag	1250 m	Narag-1	Wild
			Narag-2	Wild
			Narag-3	Wild
			Narag-4	Wild
Shimla (HP)	Shoghi	950 m	Shoghi-1	Wild
			Shoghi-2	Wild
			Shoghi-3	Wild
			Shoghi-4	Wild
	Badiyal	1050 m	Badiyal-1	Wild
			Badiyal-2	Wild
			Badiyal-3	Wild
			Badiyal-4	Wild

(using standard descriptors), fruit colour (using colour charts of Royal Horticulture Society), fruit length & breadth (from stalk end to persistent calyx end using Vernier Caliper), fruit cracking (visual observations), rind thickness (using Vernier Calliper) and aril colour (using colour charts of Royal Horticultural Society) were taken into considerations. Analysis of variance (ANOVA), comparison of mean values, simple correlations, and dendrogram analyses were carried out using SPSS and SAS software to reveal the genetic relatedness among the genotypes (Karimi and Mirdehghan, 8; Sheikh Akbar Mehr *et al.* 13).

RESULTS AND DISCUSSION

The performance of various pomegranate genotypes for different plant and fruit characters was studied during the course of present studies (Table 2). The range of average plant height varied from 1.57 to 3.59 m, number of branches ranged from 2.33 to 5.67, rind thickness varied from 2.00 mm to 4.40 mm and variation in thorn length ranged from 4.08 to 10.20 mm. Similarly, a wide variation among the genotypes was observed for fruit weight (168.17g to 341.67 g), fruit length (56.65 to 95.33 mm) and fruit breadth (64.78 to 98 mm). Different types of growth habits were observed in the tested pomegranate genotypes including spreading, erect, semi erect and semi spreading. Fruit shape was either round or square round. The problem of fruit cracking was mostly absent but present in Balamiusral and Sogdiana. A huge variation was also observed in fruit colour ranging from yellowish green to dark red and likewise in aril, colour varied from white to dark red. The possible cause for this huge variation may be the environmental factors and xenia effect which is commonly found in pomegranate (Gharaghani *et al*., 4).

Table 2. Mean performance of phenotypic traits studied in genetic diversity evaluation of pomegranate genotypes.

Genotypes	Growth habit	Plant height (m)	No. of branches	Thorn length (mm)	Fruit shape	Rind thickness (mm)	Fruit cracking	Fruit weight (g)	Fruit length (mm)	Fruit breadth (mm)	Fruit colour	Aril colour
Saharnyi	Spreading	2.53	4.33	7.22	Round	2.99	Absent	168.20	68.25	72.27	Pink red	Red
Chawla	Spreading	2.37	5.33	4.83	Round	4.40	Absent	183.33	72.67	72.33	Yellow pinkish	Red
Vina	Spreading	2.46	4.67	5.13	Round	2.10	Absent	219.17	80.67	77.33	Pinkish red	Red
Purple Heart	Upright	1.90	2.67	5.23	Round	2.40	Absent	223.63	73.04	90.58	Green yellowish	Red
Rosamia	Spreading	2.42	3.00	5.22	Round	2.20	Absent	168.17	66.97	73.79	Pink red	Red
Alk Pust Ghernez Sveh	Spreading	2.03	2.67	5.23	Round	2.30	Absent	191.02	60.50	70.58	Yellow red	Red
Sogdiana	Upright	2.02	4.00	4.77	Round	2.13	Present	184.54	70.69	68.79	Green yellowish	Red
Haku-botan	Spreading	2.38	4.00	7.22	Round	2.92	Absent	218.14	64.98	80.81	Yellowish green	Red
Parfyanets	Drooping	2.53	3.67	6.93	Round	2.99	Absent	233.71	62.69	71.00	Green yellowish	Red
Pink	Upright	2.90	4.00	4.98	Round	2.42	Absent	182.87	70.60	69.50	Green yellowish	Pink
20090265	Spreading	1.57	2.33	4.83	Round	2.21	Absent	195.37	58.65	68.87	Green yellowish	Red
Ambrosia	Erect	1.93	3.67	5.33	Round	2.27	Absent	198.33	68.67	70.00	Yellow pink	Light red
Blaze	Spreading	2.70	3.00	5.62	Round	2.21	Absent	221.20	57.27	65.12	Yellow pinkish	Red
Golden globe	Spreading	3.59	4.67	5.90	Round	3.30	Absent	301.67	76.23	96.73	Yellow green	Light red
Phoenica	Spreading	2.17	4.00	6.93	Round	2.92	Absent	188.33	69.50	72.17	Yellowish red	Red
Green Globe	Spreading	3.38	3.67	5.33	Round	2.22	Absent	332.89	77.81	94.64	Yellow orange	Pink
Loffani	Upright	2.22	4.67	5.43	Round	2.60	Absent	196.73	69.23	72.37	Green yellowish	Light red
Loulou	Upright	3.33	3.33	5.43	Round	2.00	Absent	209.34	68.98	70.87	Yellowish green	Dark red
Al-sirin-nar	Spreading	2.12	2.33	5.22	Round	2.17	Absent	264.90	63.91	75.12	Pink red	Red
Kaim-anar	Upright	1.95	2.33	5.17	Round	4.40	Absent	226.68	69.95	80.23	Yellowish green	Red
Bala mursal	Upright	2.83	3.33	9.17	Round & squarish	2.85	Present	222.50	72.95	69.47	Pink red	Pink
Apseronski	Spreading	2.28	4.33	5.17	Round	2.17	Absent	223.33	80.17	73.00	Pink red	White
Kazeake	Spreading	2.17	4.33	5.17	Round	2.02	Absent	217.67	76.33	65.50	Green yellowish	Red
Cloud	Upright	1.87	3.00	4.77	Round	2.85	Absent	191.94	66.10	72.33	Green yellowish	Red
Crab	Spreading	2.28	3.67	5.37	Round	2.08	Present	180.92	63.22	70.04	Green yellowish	Red
Cranberry	Spreading	2.27	3.33	10.17	Round & squarish	2.27	Absent	221.53	69.00	77.92	Yellowish green	Red

Contd...

Table 2 contd...

Genotypes	Growth habit	Plant height (m)	No. of branches	Thorn length (mm)	Fruit shape	Rind thickness (mm)	Fruit cracking	Fruit weight (g)	Fruit length (mm)	Fruit breadth (mm)	Fruit colour	Aril colour
Sour	Upright	3.15	5.67	10.20	Round	2.18	Absent	201.83	70.03	72.41	Green yellowish	Pinkish
Dewey	Spreading	3.32	3.00	5.20	Round	2.60	Absent	285.96	71.01	79.11	Pink red	Pink
Dkfromshevlan	Erect	2.37	3.33	5.14	Round	2.13	Absent	223.33	78.83	70.17	Yellowish green	Red
Podarok	Upright	2.55	3.67	4.83	Round	2.33	Absent	207.15	69.85	68.73	Green yellowish	Red
Nusai	Upright	2.37	2.67	5.33	Round	2.12	Absent	224.14	72.87	68.11	Pink red	Dark red
Ovadan	Spreading	1.90	3.33	7.22	Round	2.25	Absent	243.89	61.76	69.24	Pink red	Red
Eve	Spreading	2.52	3.67	5.27	Round	2.27	Absent	248.90	56.65	65.41	Yellow red	Pink
G-137	Spreading	3.17	4.67	5.08	Round	4.13	Absent	235.00	85.00	84.33	Yellow red	Pink
Anar shrin	Spreading	2.23	4.33	5.25	Round	3.02	Absent	341.67	95.33	98.00	Pinkish red	Pink
Ganesh	Semi erect spreading	2.48	4.67	5.12	Round	2.53	Absent	211.67	80.40	76.15	Yellowish red	Pink
Kandharihasi	Erect	2.00	4.33	5.00	Round	2.28	Absent	213.33	76.00	72.67	Pink red	Pink
Mridula	Spreading	2.73	4.33	4.62	Round	2.93	Absent	203.33	76.33	70.67	Dark red	Dark red
Kandari kabuli	Spreading	2.46	3.33	4.08	Round	2.33	Absent	236.67	90.00	90.00	Pinkish red	Dark red
Gulyalek	Spreading	2.55	4.33	10.20	Round	2.99	Absent	183.24	57.46	64.78	Yellowish green	Red
Kandaghat-1	Spreading	3.38	4.00	5.63	Round	2.42	Absent	215.25	59.77	67.95	Yellowish green	Red
Kandagaht-2	Spreading	3.25	4.33	5.40	Round	2.50	Absent	216.67	63.00	69.83	Yellowish green	Red
Kandaghat-3	Spreading	3.33	4.00	5.60	Round	2.46	Absent	219.00	66.50	68.63	Yellowish green	Red
Kandaghat-4	Spreading	3.27	4.33	5.45	Round	2.47	Absent	210.00	65.67	68.67	Yellowish green	Red
Rajgarh-1	Upright	3.11	4.33	5.23	Round	2.00	Absent	175.00	72.17	70.17	Green yellowish	Red
Rajgarh-2	Upright	2.80	4.33	5.22	Round	2.08	Absent	211.41	74.50	68.35	Green yellowish	Red
Rajgarh-3	Upright	3.00	4.67	5.77	Round	2.13	Absent	221.67	76.00	71.67	Green yellowish	Red
Rajgarh-4	Upright	2.93	4.00	4.77	Round	2.12	Absent	215.17	74.67	70.67	Green yellowish	Red
Narag-1	Upright	2.78	3.00	5.37	Round	2.63	Absent	206.23	84.23	76.73	Yellow orange	Dark red
Narag-2	Upright	2.97	3.67	5.20	Round	2.42	Absent	207.33	82.63	75.83	Yellow orange	Dark red
Narag-3	Upright	2.95	4.67	5.16	Round	2.57	Absent	206.77	83.28	76.33	Yellow orange	Dark red
Narag-4	Upright	2.97	4.00	5.27	Round	2.50	Absent	214.33	82.25	73.67	Yellow orange	Dark red
Shoghi-1	Upright	3.43	5.00	5.29	Round	2.27	Absent	194.91	70.03	72.07	Yellow pinkish	Red
Shoghi-2	Upright	3.40	4.00	5.32	Round	2.25	Absent	195.00	70.35	71.50	Yellow pinkish	Red

Table 2 contd...

Genotypes	Growth habit	Plant height (m)	No. of branches	Thorn length (mm)	Fruit shape	Rind thickness (mm)	Fruit cracking	Fruit weight (g)	Fruit length (mm)	Fruit breadth (mm)	Fruit colour	Aril colour
Shoghi-3	Upright	3.47	4.67	5.33	Round	2.33	Absent	194.00	70.33	69.83	Yellow pinkish	Red
Shoghi-4	Upright	3.45	4.67	5.30	Round	2.30	Absent	193.50	71.67	71.00	Yellow pinkish	Red
Badiyal-1	Upright	3.36	5.33	5.52	Round	2.38	Absent	217.17	79.70	77.17	Yellow pinkish	Pink
Badiyal-2	Upright	3.43	5.67	5.57	Round	2.33	Absent	221.67	81.33	77.67	Yellow pinkish	Pink
Badiyal-3	Upright	3.37	5.00	5.50	Round	2.27	Absent	225.00	81.00	78.00	Yellow pinkish	Pink
Badiyal-4	Upright	3.38	4.33	5.48	Round	2.42	Absent	221.33	80.67	77.50	Yellow pinkish	Pink
Minimum		1.57	2.33	4.08		2.00		168.17	56.65	64.78		
Maximum		3.59	5.67	10.20		4.40		341.67	95.33	98.00		
Mean ± Standard Error		2.70 ± 0.06	3.96 ± 0.1	5.69 ± 0.16		2.51 ± 0.06		216.79 ± 4.28	72.17 ± 1.06	74.07 ± 0.94		
CV		6.00	25.96	5.14		5.06		7.80	4.43	2.71		
$CD_{(0.05)}$		0.26	1.67	0.47		0.21		27.37	5.12	3.25		

Data studied for all the attributes demonstrated that the phenotypic coefficient of variation was greater in magnitude as compared to genotypic coefficient of variation, though difference was very less but was considerable for most of the characters which indicated the less environmental impact on the characteristics assessed for phenotypic traits. The phenotypic coefficient of variation was recorded highest for growth habit (50.00), thorn length (23.89), rind thickness (23.58), plant height (22.01), number of branches (21.54), fruit weight (15.35), fruit length (12.70) and fruit breadth (10.75) (Table 3). Similarly, genotypic coefficient of variations was observed highest for growth habit (47.03), thorn length (22.72), rind thickness (20.53), number of branches (20.39), plant height (19.93), fruit weight (15.32), fruit length (11.45) and fruit breadth (9.90). High and moderate phenotypic coefficient of variation revealed the existence of significant variability indicating better scope for their enhancement through selection process. Greater advancement therefore, could be achieved for these traits. Low phenotypic coefficient of variation illustrated high substantial nature of these traits among distinctive genotypes, considered for the study, and provided least scope for improvement in these phenotypic traits.

Genetic gain was recorded as low to moderate for maximum number of traits taken into consideration for research purpose. Genetic gain was moderate for thorn length (46.81), growth habit (42.88), rind thickness (42.30), number of branches (42.01), plant height (41.05), fruit weight (31.57) and lower values for fruit length (23.59) and fruit breadth (20.40). It ranged from 20.40 % to 46.81 %. Heritability magnitude revealed that the genotype could be identified by its phenotypic expression. Estimation of heritability (broad sense) indicated that the heritability for traits under investigation ranged from 86.66 to 99.45 per cent. In the present research, high heritability was observed for all the traits studied (Table 3). High heritability estimation was evident to prove that selection for these characters provide effective variability, and was not affected by environmental conditions. High heritability accompanied with high genetic gain suggested that selection for these traits could be useful in breeding programme in pomegranate. High heritability and moderate genetic gain showed that these traits were greatly influenced by additive gene action, and hence selection process based on phenotypic expression of these traits provides a reliable approach in pomegranate breeding (Mishra, 9).

At genotypic level, the correlation coefficients were almost similar to those observed at phenotypic level for most of the attributes, but the values were

Table 3. Variability parameters for morphological and fruit characteristics of different pomegranate genotypes.

Parameters	Coefficient of variation (%)		Heritability (%)	Genetic advance	Genetic gain (%)
	Phenotypic	Genotypic			
Growth habit	50.00	47.03	88.57	0.72	42.88
Plant height	22.01	19.93	90.62	1.10	41.05
Number of branches	21.54	20.39	92.85	1.66	42.01
Thorn length	23.89	22.72	97.09	2.66	46.81
Rind thickness	23.58	20.53	86.66	1.06	42.30
Fruit weight	15.35	15.32	99.45	68.45	31.57
Fruit length	12.70	11.45	91.13	17.03	23.59
Fruit breadth	10.75	9.90	89.70	15.11	20.40

higher than the corresponding phenotypic ones. Fruit length (+0.33) and fruit breadth (+0.68) were positively correlated with fruit weight, which were taken as dependent variables in the study, and it was observed that the larger the length and breadth of fruit, the more will be the weight. Furthermore, correlation coefficients among eight quantative phenotypic attributes (Table 4) measured showed significantly positive correlation with fruit length and plant height (+0.21), and negative for growth habit and plant height (-0.31) because of the reason that more the spreading type less the height. Likewise, number of branches showed the positive correlation with fruit length (+0.34), however, fruit length showed the negative correlations with thorn length (-0.29). It may be due to reason that the luxuriant vegetative growth affect reproductive growth. The fruit breadth was found to have the positive correlation with rind thickness (+0.30). The results were found similar to the findings of Yazici and Sahin (15) who observed twenty-one morphological for assessing the genetic diversity in 67 pomegranate lines.

In this study, fruit weight was considered as dependent variable for morphological attributes studied, because it helps in selection for better genotype according to fruit size which are suitable for export as well as for domestic purposes. Fruit weight showed positive direct effect with fruit breadth

Table 4. Phenotypic and genotypic correlation coefficient for the different morphological and fruit traits.

Characters		Plant height	Number of branches	Thorn length	Rind thickness	Fruit weight	Fruit length	Fruit breadth	Growth habit
Plant height	P	1.00							
	G	1.00							
Number of branches	P	0.49	1.00						
	G	0.52	1.00						
Thorn Length	P	0.01	0.08	1.00					
	G	0.01	0.11	1.00					
Rind thickness	P	-0.05	0.06	0.05	1.00				
	G	-0.07	0.08	0.07	1.00				
Fruit weight	P	0.13	-0.09	-0.04	0.07	1.00			
	G	0.14	-0.10	-0.06	0.09	1.00			
Fruit length	P	0.19*	0.32*	-0.27*	0.05	0.30*	1.00		
	G	0.21*	0.34*	-0.29*	0.09	0.33*	1.00		
Fruit breath	P	0.07	0.02	-0.09	0.28*	0.64*	0.54	1.00	
	G	0.09	0.03	-0.11	0.30*	0.68*	0.59	1.00	
Growth habit	P	-0.30*	-0.05	0.04	0.11	0.15	-0.15	0.01	1.00
	G	-0.31*	-0.09	0.07	0.13	0.18	-0.17	0.01	1.00

*Significant at 5% level of significance; P-Phenotypic coefficient, G-Genotypic coefficient

(0.69), plant height (0.25), growth habit (0.24), thorn length (0.03) and fruit length (0.001). However, rind thickness (-0.11) and number of branches (-0.22) depicted direct negative effect on fruit weight (Table 5). Fruit breadth showed positive indirect effect via fruit length (0.41), and plant height showed indirect positive effect with fruit length (0.05) and fruit breadth (0.02). Unexplained effects are treated as residual effects. Low value of residual effect at genotypic level determined that the traits included in the present investigation accounted for most of the variation for the dependent variable that is fruit weight. The studies on path coefficient analysis suggested that selection for fruit weight could be possibly dependent on growth habit, plant height, thorn length, fruit length and fruit breadth. In the study of Sinha *et al.* (14), fruit weight was considered as dependent variable to select a genotype having bigger fruit size which could be utilized for export purpose. In conclusion, path analysis showed that growth habit, number of branches and rind thickness had strong influence on fruit weight, that could be utilized by breeder to select a genotype with good quality fruit.

It was observed that the first principal component (PC1) explained 28.73 % of the total variance that mainly consisted of fruit breadth, fruit length and fruit weight predominantly while, PC2 explained 21.28 % variability that mainly included plant height and number of branches and fruit length up to some extent. Further, PC3 and PC4 showed remaining 15.16% and 11.48%, respectively for traits like, thorn length, number of stem and rind thickness as given in Table 6. Furthermore, results of PCA analysis was confirmed by creating biplot of first two principal components as shown in Fig. 1. The diversity observed among the genotypes for phenotypic characters like fruit weight, fruit length and breadth and rind thickness was possibly due to xenic effect (effect of pollen on seed and fruit of the fertilized plant) in pomegranate (Gharaghani *et al*., 4). Among all the phenotypic traits, plant height and number of

Table 6. Principal component analysis based on morphological and fruit traits in pomegranate genotypes.

Principal component	Eigen value	Variability (%)	Cumulative (%)
1	2.29	28.73	28.73
2	1.70	21.28	50.02
3	1.21	15.16	65.18
4	0.91	11.48	76.66
5	0.81	10.21	86.88
6	0.60	7.56	94.45
7	0.24	3.05	97.50
8	0.20	2.49	100.00

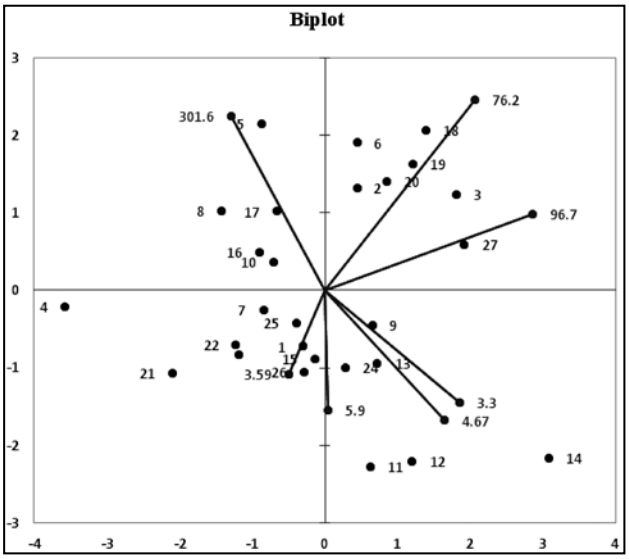

Fig. 1. Bi-plot of pomegranate genotypes for first two principal components.

Table 5. Estimates of direct and indirect effects of different traits on fruit weight of pomegranate genotypes.

	Growth habit	Plant height	Number of branches	Thorn length	Rind thickness	Fruit length	Fruit breadth	Correlation with fruit weight
Growth habit	0.244	-0.075	-0.024	0.017	0.031	-0.041	0.003	0.18
Plant height	-0.077	0.250	0.129	0.001	-0.017	0.052	0.024	0.13
Number of branches	0.022	-0.116	-0.224	-0.024	-0.018	-0.077	-0.006	-0.10
Thorn length	0.002	0.000	0.003	0.031	0.002	-0.009	-0.004	-0.06
Rind thickness	-0.014	0.008	-0.008	-0.008	-0.113	-0.011	-0.034	0.09
Fruit length	0.000	0.000	0.000	-0.001	0.000	0.001	0.001	0.32
Fruit breadth	0.008	0.068	0.019	-0.077	0.211	0.413	0.696	0.68

Residual effect = 0.6609

branches predominantly disseminated in all eight components with maximum positive values as given in Table 6 hence, important factor for selection in pomegranate breeding programmes.

Phylogenetic tree constructed on the basis of phenotypic characteristics by applying squared Euclidean distance and group average clustering method showed two diverse groups but partially divided the genotypes on the basis of their type into two major groups or clusters as shown in Fig. 2. Group I which was further divided in two sub-groups contained all the five cultivated varieties which include Dewey, Al-sirin-nar, Golden globe, Green globe, Anarsrin and rest of thirty-five cultivated varieties and twenty wild germplasm accessions obtained from different locations were placed in Group II. Group II was further divided two sub clusters of which one having maximum of genotypes including both wild and cultivated types. The results of morphological based dendrogram revealed that cultivated and wild germplasm are associated with each other phenotypically. Further selection pressure which include both artificial selection and natural selection, environmental condition and geographical isolation created phenotypic variability among these genotypes and are the important factors which are responsible in generating phenotypic diversity among different subjected genotypes. Furthermore, in the study conducted by Noormohammadi *et al*. (10), eighteen landraces of pomegranate were taken into consideration for morphological study, and clustering analysis of pomegranate based on phenotypic traits showed no correlation between geographical localities and morphological grouping of cultivars.

The present study revealed evolutionary relationship among cultivated pomegranate and wild genotypes that can be further utilized for choice of parents in breeding pomegranate breeding programmes. This study provides information regarding narrow genetic base existing among the pomegranate genotypes as observed during clustering on basis of morphological traits. Being a self-pollinated it has less scope for developing hybrids, the success and crossing for important traits would be also limited due to the narrow genetic back ground but xenia effect can be utilized to improve phenotypic traits like aril color, fruit shape, fruit size and rind color. Thus, genetic diversity analysis has revealed the widening the genetic base is essential for developing improved hybrids and varieties in pomegranate.

AUTHORS' CONTRIBUTION

Conceptualization of research (Rajnish Sharma), Designing and Execution of experiment (Himanshu Pandey), Contribution in data analysis

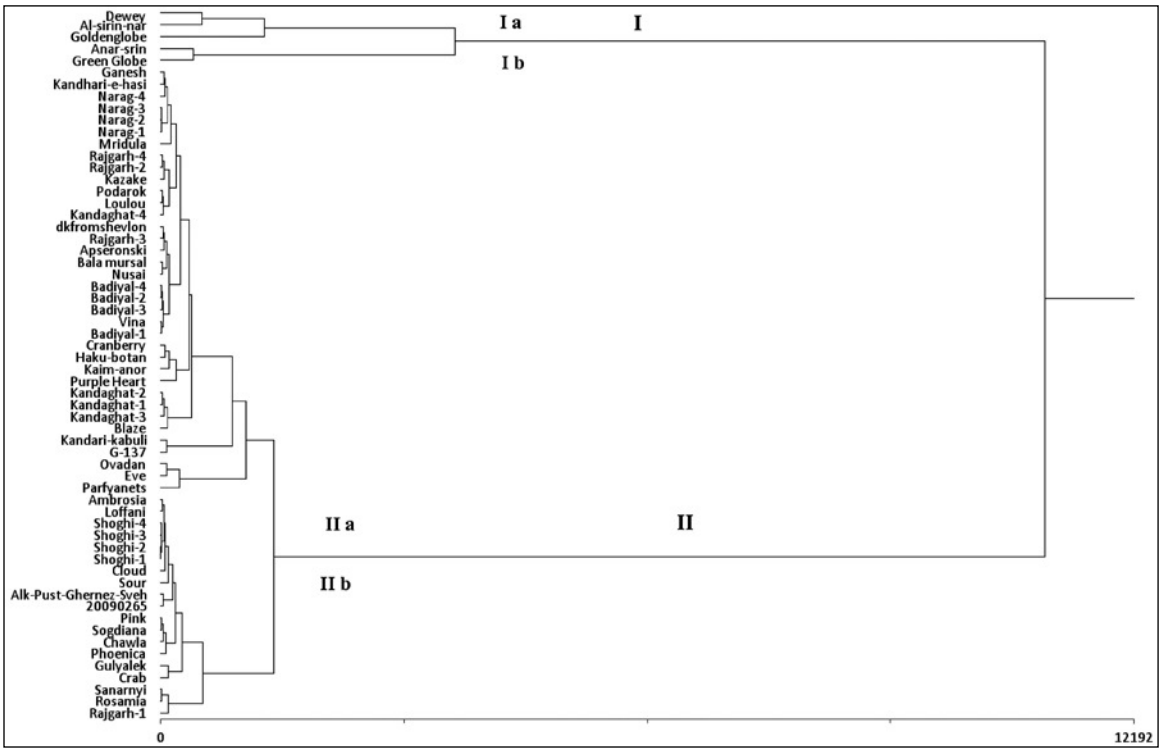

Fig. 2. Dendrogram showing the clustering pattern of pomegranate genotypes using morphological trait.

and preparation of manuscript (Dinesh Singh Thakur and Rajesh Kumar Dogra).

DECLARATION

The authors declare no conflict of interest.

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