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Evaluation of half and full sib progenies of wild pomegranate (*Punica granatum* L.) under nursery conditions

Jyoti Dhiman, Aman Deep Ranga and Mohit Kundal

Abstract
The study was carried out in 2013-2014 to evaluate growth characteristics of progeny under nursery conditions and for clustering of different breeding system applied in wild pomegranate genotypes at two locations. Phenotypic coefficient of variation (PCV) recorded higher than the genotypic coefficient of variation (GCV) for all characters and narrow difference between PCV and GCV indicated the negligible influence of environment. GCV and PCV values were observed maximum for the number of branches (136.708% and 136.78%). The highest heritability and genetic advance as a percent over mean reported for number of branches. The fruit length showed a highly significant and positive correlation with fruit diameter (r_g = 0.998, r_p = 0,988). The seedling height at 8 month showed highly significant and positive correlation with seedling height at 11-month, no. of branches, leaf area at 8-month, leaf area at 11-month, petiole length, internodal length and collar diameter. Path correlation coefficient results revealed highly significant relationship between collar diameter and other characters. The principal component analysis (PCA) indicated that first principal component (PC I) accounted for 77.059% of the total variation. The maximum inter-cluster distance was observed between crosses $T_4S_2 \times T_3S_1$ and $T_4S_1 \times T_2S_2$, whereas, the maximum intra-cluster distance was recorded between $T_4S_2 \times T_3S_1$ and $T_4S_2 \times T_5S_1$ in cluster I and S_1T_4 and $T_4S_1 \times T_2S_2$ in cluster II.

Keywords: Genetic divergence, crosses, variability, heritability, genetic advance

Introduction
The wild Pomegranate (*Punica granatum* L.) belongs to the order Myrtales and family punicaceae, is one of the ancient edible fruits natives to Iran and growing naturally in the foothills of Western Himalayas (Rana *et al*., 2007; Singh *et al*., 2015) [16, 20]. Wild pomegranate (*Punica granatum* L.), Vern. Daru can grow in a variety of agro-climatic conditions ranging from tropical to subtropical countries (Levin, 2006 and Jalikop, 2007) [10, 6]. There are two subspecies of granatum; *Punica granatum* ssp. *chlorocarpa* is native to the Transcaucasian region and *Punica granatum* ssp. *porphyrocarpa* is native to Central Asia. (Sharma *et al*., 2009) [17]. It is also spread to the Himalayas in Northern India. Mars (2000). The Western Himalayas show the availability of a very diverse collection of wild pomegranates (Rana *et al*. 2007) [16].
It is considered as a prototype of a cultivated plant and is similar to the cultivated pomegranate in terms of various morphological characteristics. In India, wild pomegranate only grows in three states: Jammu and Kashmir, Himachal Pradesh and Uttarakhand (Narzary *et al*. 2009; Mahajan *et al*. 2018) [14, 9]. There is a growing demand for good quality wild pomegranate fruit both for fresh use and for making anardana, which are the dried arils of wild pomegranate with a distinct sour taste and are mainly consumed in culinary preparations. (Murtaza and Ahmad 2017) [13]. Anardana is also used as a source of livelihood by the locals. The presence of secondary metabolites in different parts of wild pomegranate plant and the strong antioxidant activity are responsible for its health benefits and medicinal properties (Kaur *et al.* 2018) [9].
The wild pomegranate has resistance to the deadly fire blight, but not high yielding, while the cultivated varieties are high yielding but susceptible to bacterial blight which resulted in yield losses up to 60-80% (Sharma *et al*., 2015) [18]. The Indian Institute of Horticulture Research has found that not only the wild types but the hybrids of both cultivated and wild types are found to be resistant against the bacterial disease. Jalikop (2005) [7]. In addition, the commercial marketing of pomegranate is still limited by physiological disorders such as rind cracks, cold damage, skin burns and excessive weight loss (Caleb *et al*., 2012) [3].

The wild pomegranate has a thick fruit skin which makes it less susceptible to butterfly attacks and cracking, So the breeding for these traits becomes more important (Jalikop *et al.*, 2010) [10].

Present study was conducted to evaluate half and full sib progeny of wild pomegranate and the fruits of different genotypes with estimation of their variability, correlation between different growth traits, heritability and genetic advance. The study was also carried out to show genetic divergence between different breeding systems on the basis of analysis of different growth traits. The purpose of a large amount of parameter estimation is to allow the efficient prediction of breeding values, efficient selection procedures and to take assessment of crossibility pattern between different genotypes of this species to increase economic yield per unit area.

Materials and Methods

The present investigation was carried out during the period 2013-2014 in the Department of Tree Improvement and Genetic Resources, College of Forestry, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh. Two sites were selected i.e., Tatool (S_1) district Solan and Narag (S_2) district Sirmour to study different breeding systems in wild *Punica granatum.* On each site five morphologically best genotype/trees were selected and denoted as T_1S_1 i.e., tree 1 and site$_1$ (Tatool), T_2S_1 (tree 2 and site 1), T_3S_1 (tree 3 and site 1), T_4S_1 (tree 4 and site 1), T_5S_1 (tree 5 and site 1), and same for genotypes selected at site$_2$ i.e., T_1S_2; tree 1 site 2 (Narag), T_2S_2 (tree 2 site2), T_3S_2 (tree 3 site2), T_4S_2 (tree 4 site2), T_5S_2 (tree 5 site2) (Table 1). In each selected tree/genotype fifteen flowers were chosen to apply Self-pollination, Geitenogamy and Open pollination breeding systems and another twenty-five flowers were selected to apply controlled pollination between selected trees of both the locations (Table 1). Thus, a total of 80 different types of crosses were made i.e., 30 crosses made within both selected site and 50 controlled crosses made between genotypes of two sites. Fruit samples were collected separately for each cross/tree basis.

Table 1: List of genotypes under Study.

Sr. No.	Genotypes	Nature	Sr. No.	Genotypes	Nature	Sr. No.	Genotypes	Nature	Sr. No.	Genotypes	Nature
1	S_1T_1	SP	21	G_1T_1	G	41	$T_3S_1 \times T_1S_2$	CC	61	$T_2S_2 \times T_1S_1$	CC
2	S_1T_2	SP	22	G_1T_2	G	42	$T_3S_1 \times T_2S_2$	CC	62	$T_2S_2 \times T_2S_1$	CC
3	S_1T_3	SP	23	G_1T3	G	43	$T_3S_1 \times T_3S_2$	CC	63	$T_2S_2 \times T_3S_1$	CC
4	S_1T_4	SP	24	G_1T_4	G	44	$T_3S_1 \times T_4S_2$	CC	64	$T_2S_2 \times T_4S_1$	CC
5	S_1T_5	SP	25	G_1T_5	G	45	$T_3S_1 \times T_5S_2$	CC	65	$T_2S_2 \times T_5S_1$	CC
6	S_2T_1	SP	26	G_2T_1	G	46	$T_4S_1 \times T_1S_2$	CC	66	$T_3S_2 \times T_1S_1$	CC
7	S_2T_2	SP	27	G_2T_2	G	47	$T_4S_1 \times T_2S_2$	CC	67	$T_3S_2 \times T_2S_1$	CC
8	S_2T_3	SP	28	G_2T_3	G	48	$T_4S_1 \times T_3S_2$	CC	68	$T_3S_2 \times T_3S_1$	CC
9	S_2T_4	SP	29	G_2T_4	G	49	$T_4S_1 \times T_4S_2$	CC	69	$T_3S_2 \times T_4S_1$	CC
10	S_2T_5	SP	30	G_2T_5	G	50	$T_4S_1 \times T_5S_2$	CC	70	$T_3S_2 \times T_5S_1$	CC
11	O_1T_1	OP	31	$T_1S_1 \times T_1S_2$	CC	51	$T_5S_1 \times T_1S_2$	CC	71	$T_4S_2 \times T_1S_1$	CC
12	O_1T_2	OP	32	$T_1S_1 \times T_2S_2$	CC	52	$T_5S_1 \times T_2S_2$	CC	72	$T_4S_2 \times T_2S_1$	CC
13	O_1T_3	OP	33	$T_1S_1 \times T_3S_2$	CC	53	$T_5S_1 \times T_3S_2$	CC	73	$T_4S_2 \times T_3S_1$	CC
14	O_1T_4	OP	34	$T_1S_1 \times T_4S_2$	CC	54	$T_5S_1 \times T_4S_2$	CC	74	$T_4S_2 \times T_4S_1$	CC
15	O_1T_5	OP	35	$T_1S_1 \times T_5S_2$	CC	55	$T_5S_1 \times T_5S_2$	CC	75	$T_4S_2 \times T_5S_1$	CC
16	O_2T_1	OP	36	$T_2S_1 \times T_1S_2$	CC	56	$T_1S_2 \times T_1S_1$	CC	76	$T_5S_2 \times T_1S_1$	CC
17	O_2T_2	OP	37	$T_2S_1 \times T_2S_2$	CC	57	$T_1S_2 \times T_2S_1$	CC	77	$T_5S_2 \times T_2S_1$	CC
18	O_2T_3	OP	38	$T_2S_1 \times T_3S_2$	CC	58	$T_1S_2 \times T_3S_1$	CC	78	$T_5S_2 \times T_3S_1$	CC
19	O_2T_4	OP	39	$T_2S_1 \times T_4S_2$	CC	59	$T_1S_2 \times T_4S_1$	CC	79	$T_5S_2 \times T_4S_1$	CC
20	O_2T_5	OP	40	$T_2S_1 \times T_5S_2$	CC	60	$T_1S_2 \times T_5S_1$	CC	80	$T_5S_2 \times T_5S_1$	CC

Where, T_1S_1: Tree1site1, T_2S_1: Tree2site1, T_3S_1: Tree3site1, T_4S_1: Tree4site1, T_5S_1: Tree5site1, T_1S_2: Tree1site2, T_2S_2: Tree2site2, T_3S_2: Tree3site2, T_4S_2: Tree4site2, T_5S_2: Tree5site2, SP: Self-pollination, S1: self-crosses made in genotypes selected at site$_1$, S2: self-crosses made in genotypes selected at site$_2$, G: geitenogamy cross, G1: geitenogamy (pollen collected from one flower and applied on stigma of another flower of same tree) system applied in genotypes selected at site$_1$, G2: geitenogamy system applied in genotypes selected at site$_2$, OP: open pollination, O1: open pollination system applied in genotypes selected at site$_1$, O2: open pollination system applied in genotypes selected at site$_2$, CC: controlled crosses, $T_1S_1 \times T_1S_2$, $T_1S_2 \times T_1S_1$: controlled cross made between two sites.

To study growth performance of the progeny under Nursery conditions seeds were collected, processed and maintained separately on individual tree /cross basis. Seeds obtained from different methods of breeding system and controlled pollination were sown in the first week of October (2013) in poly bags (in three replication) under nursery conditions. Nursery is situated 30.8544° N, 77.1694°E at an altitude of 1300 m above mean sea level, with an average annual rainfall of 1262 mm. Seed were depulped before sowing and dried for 3-4 days and after that sowing was done. The germination of seeds takes place in third week of October.

Different growth characteristics of fruits i.e., fruit length [FL (mm)]and fruit diameter [FD (mm)] measured with the help of digital vernier calliper and of seedling/progeny *viz.*, seedling height [SH (cm)], and internodal length [IL (cm)], petiole length [PL (cm)] measured with scale, collar diameter [CD (cm)] with vernier calliper, number of branches [NB] visually counted and leaf area [LA (cm^2)] measured with the help of leaf area meter. Seedling height and leaf area was measured at age of 8th month and 11th month, whereas internodal length, petiole length, collar diameter, number of branches per seedling were recorded at age of 11th month.

The mean data of growth characteristics of fruits and progenies were subjected to ANOVA (Panse and Sukhatme 1954) [15], genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) analysis (Allard 1960) [1] and genetic advance and heritability as per Burton (1952) [2]. Genotypic correlation coefficients and principal

component analysis were calculated using OP-STAT (Sheoran *et al*., 1998) [19] and PAST (Hammer *et al*., 2001) [5]. Cluster analysis was performed on PAST (Ward, 1963) [22].

Results and Discussion

The analysis of variance (ANOVA) carried out for different fruit and seedling characteristics which showed positive and significant differences for all characteristics (Table 2). Highly significant differences, were found especially for characters *viz*; fruit dimeter, fruit length, seedling height at 8 month and for no. of branches.

Table 2: ANOVA for fruits and different characteristics of seedlings of wild pomegranate.

S.V.	df	FD (mm)	FL (mm)	SH8 (cm)	SH11 (cm)	NB	LA8 (cm^2)	LA11 (cm^2)	PL (cm)	IL (cm)	CD (cm)
Replication	2	0.332	1.702	1.622	2.888	0.167	0.006	0.002	0	0	0.038
Treatment	79	329.68**	330.00**	281.59**	460.17**	1,438.84**	2.55**	4.48**	0.02**	1.00**	3.70**
Error	158	1.507	1.473	1.456	1.904	0.534	0.01	0.017	0	0.002	0.015
SEM		1.002	0.991	0.985	1.127	0.597	0.083	0.107	0.007	0.04	0.101

**significant at 5% level

Where, FD: fruit diameter, FL: fruit length, SH: seedling height, NB: no. of branches, LA8: leaf area at 8 month, LA11: leaf area at 11 month, PL: petiole length, IL: Internodal length, CD: collar diameter, H^2: heritability, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation,

Genetic variability (Table 3) studies revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters under observations. Narrow difference existed between PCV and GCV in most characters showed that they were comparatively stable to environment pressure, which means environmental influence was very low and hence the phenotypic performance of traits can be used as a criterion for selection. GCV and PCV values were observed maximum for the number of branches (136.708% and 136.78%). GCV and PCV greater than 30% reported in internodal length (36.624 and 36.753), petiole length (31.753 and 31.865) whereas, less than 20% recorded in fruit diameter, fruit length, seedling height at 8-month, seedling height at 11-month, leaf area at 8-month, leaf area at 11 month and for collar diameter. Which indicated the presence of high magnitude of genetic variability in the genotypes. This supported by finding in genotype by environment interactions in forest tree breeding by Yongjun *et al*., 2017 [21]. Genetic divergence allows to identify the action nature of involved genes, as well as evaluating the efficiency of different selection methods and strategies, whether from endogamy, cross-breeding or selection **(**Cruz *et al.* 2014**)** [4]**.**

Table 3: Variability parameters for fruits and different characteristics of progeny of wild pomegranate.

Characters	Mean	Range	Coefficient of variation (%)		H^2 (%)	Genetic advance	Genetic advance as percent of mean
			Genotypic (GCV)	Phenotypic (PCV)			
FD (mm)	46.642	0.00-60.590	22.424	22.578	98.641	21.399	45.879
FL (mm)	47.112	0.00-61.250	22.218	22.367	98.673	21.414	45.465
SH8 (cm)	47.101	0.00-59.670	20.516	20.676	98.465	19.753	41.938
SH11(cm)	56.167	0.00-73.150	22.005	22.141	98.769	25.303	45.050
NB	16.017	0.00-59.390	136.708	136.784	99.889	45.081	281.462
LA8 (cm^2)	4.091	0.00-4.930	22.523	22.660	98.797	1.886	46.118
LA11(cm^2)	5.246	0.00-6.490	23.261	23.395	98.858	2.500	47.644
PL (cm)	0.303	0.00-0.390	31.753	31.865	99.295	0.199	65.180
IL (cm)	1.581	0.00-2.440	36.624	36.753	99.299	1.188	75.181
CD (cm)	4.965	0.00-6.590	22.340	22.479	98.773	2.271	45.738

Where, FD: fruit diameter, FL: fruit length, SH: seedling height, NB: no. of branches, LA: leaf area, PL: petiole length, IL: internodal length, CD: collar diameter, H^2: heritability, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation

All the characters displayed high heritability as well as high genetic advance as per cent over the mean. The highest heritability and genetic advance as per cent of mean were observed for no. of branches. While the low genetic advance was reported in leaf area, internodal length, petiole length and collar diameter. The association between heritability and genetic advance of a trait helps breeder to predict the performance of those traits in next generations and response to selection.

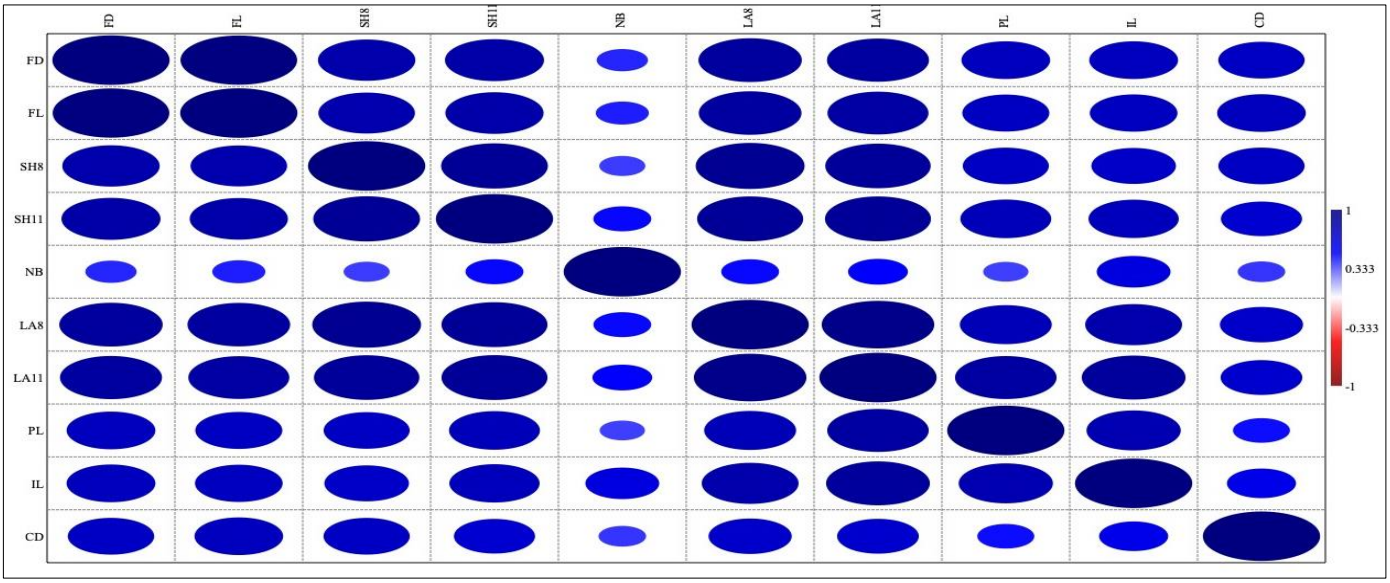
The Pearson genotypic and phenotypic correlation coefficient is presented in Table 4 and Fig 1. All the observed characters showed highly significant relationship with each other. The fruit length showed a highly significant and positive genotypic and phenotypic correlation with fruit diameter (0.998, 0.988), which depicts the very less effects of environmental factors.

Table 4: Pearson correlation coefficient between different characteristics of fruits and progeny of wild *Punica granatum.*

Characters		FD (mm)	FL (mm)	SH8 (cm)	SH11 (cm)	NB	LA8 (cm^2)	LA11 (cm^2)	PL (cm)	IL (cm)	CD (cm)
FD (mm)	rg	1.000									
	rp	1.000									
FL (mm)	rg	0.998**	1.000								
	rp	0.988**	1.000								
SH8 (cm)	rg	0.832**	0.824**	1.000							
	rp	0.819**	0.812**	1.000							
SH11 (cm)	rg	0.846**	0.838**	0.913**	1.000						

	rp	0.834**	0.827**	0.901**	1.000						
NB	rg	0.428**	0.444**	0.383**	0.486**	1.000					
	rp	0.425**	0.441**	0.379**	0.483**	1.000					
LA8 (cm^2)	rg	0.883**	0.877**	0.932**	0.906**	0.485**	1.000				
	rp	0.873**	0.868**	0.918**	0.896**	0.482**	1.000				
LA11 (cm^2)	rg	0.871**	0.863**	0.902**	0.906**	0.502**	0.963**	1.000			
	rp	0.861**	0.852**	0.888**	0.894**	0.499**	0.952**	1.000			
PL (cm)	rg	0.769**	0.755**	0.748**	0.783**	0.382**	0.794**	0.882**	1.000		
	rp	0.761**	0.747**	0.740**	0.776**	0.380**	0.786**	0.874**	1.000		
IL (cm)	rg	0.755**	0.746**	0.719**	0.768**	0.624**	0.826**	0.886**	0.815**	1.000	
	rp	0.747**	0.739**	0.711**	0.761**	0.621**	0.817**	0.877**	0.810**	1.000	
CD (cm)	rg	0.736**	0.756**	0.735**	0.689**	0.396**	0.707**	0.694**	0.511**	0.583**	1.000
	rp	0.726**	0.746**	0.722**	0.682**	0.393**	0.698**	0.686**	0.506**	0.578**	1.000

Where, FD: fruit diameter, FL: fruit length, SH8: seedling height at 8 month, SH11: seedling height at 11 month NB: no. of branches, LA8: leaf area at 8month, LA11: leaf area at 11 month PL: petiole length, IL: internodal length, CD: collar diameter, rg: genotypic correlation coefficient, rp: phenotypic correlation coefficient.



Where, FD: fruit diameter, FL: fruit length, SH8: seedling height at 8 month, SH11: seedling height at 11 month NB: no. of branches, LA8: leaf area at 8month, LA11: leaf area at 11 month PL: petiole length, IL: internodal length, CD: collar diameter.

Fig 1: Graph depicting genotypic correlation among different characteristics of fruits and progeny of wild pomegranate.

Similarly, Path coefficient analysis was estimated between collar diameter and other characters (Table 5). The result revealed highly significant relationship between collar diameter and all other characters. The significant positive correlations among characters gave positive results while making selection in the breeding programme. It also helps in understanding the basis of genetic linkage that is determined within and between the characters and crop improvement program can be designed to pyramid desirable genes and removing undesirable. Obtaining estimates of genetic and phenotypic parameters makes it possible to know the potential of segregating populations and study the association between target traits, allowing the use of selection indices to make the process more efficient.

Table 5: Genotypic and Phenotypic path coefficient analysis for quantitative characters of wild pomegranate fruits and progeny.

Characters		FD (mm)	FL (mm)	SH8 (cm)	SH11 (cm)	NB	LA8 (cm^2)	LA11 (cm^2)	PL (cm)	IL (cm)	Correlation coefficient of CD
FD (mm)	gp	-6.827	7.195	0.586	0.027	-0.071	-0.547	0.354	-0.244	0.262	0.736**
	pp	-0.604	1.135	0.436	-0.024	0.018	-0.404	0.417	-0.305	0.056	0.726**
FL (mm)	gp	-6.814	7.209	0.581	0.026	-0.074	-0.543	0.350	-0.239	0.259	0.756**
	pp	-0.597	1.149	0.432	-0.024	0.019	-0.402	0.413	-0.299	0.055	0.746**
SH8 (cm)	gp	-5.679	5.942	0.705	0.029	-0.064	-0.577	0.366	-0.237	0.250	0.735**
	pp	-0.495	0.932	0.532	-0.026	0.016	-0.425	0.430	-0.296	0.053	0.722**
SH11 (cm)	gp	-5.774	6.043	0.644	0.032	-0.081	-0.561	0.368	-0.248	0.267	0.689**
	pp	-0.503	0.950	0.479	-0.029	0.021	-0.415	0.433	-0.311	0.057	0.682**
NB	gp	-2.921	3.199	0.270	0.015	-0.167	-0.300	0.204	-0.121	0.217	0.396**
	pp	-0.257	0.506	0.201	-0.014	0.043	-0.223	0.242	-0.152	0.047	0.393**
LA8 (cm^2)	gp	-6.029	6.324	0.657	0.029	-0.081	-0.619	0.391	-0.251	0.287	0.707**
	pp	-0.527	0.997	0.488	-0.026	0.021	-0.463	0.462	-0.315	0.061	0.698**
LA11 (cm^2)	gp	-5.946	6.222	0.635	0.029	-0.084	-0.596	0.406	-0.279	0.308	0.694**
	pp	-0.520	0.979	0.472	-0.026	0.021	-0.441	0.485	-0.350	0.066	0.686**

PL (cm)	gp	-5.253	5.443	0.527	0.025	-0.064	-0.491	0.358	-0.316	0.283	0.511**
	pp	-0.459	0.858	0.393	-0.022	0.016	-0.364	0.424	-0.401	0.061	0.506**
IL (cm)	gp	-5.157	5.376	0.507	0.024	-0.104	-0.512	0.360	-0.258	0.347	0.583**
	pp	-0.451	0.849	0.378	-0.022	0.027	-0.378	0.425	-0.324	0.075	0.578**
GP Residual are 0.21632 PP Residual are 0.34994											

Where FD: fruit diameter, FL: fruit length, SH8: seedling height at 8 month, SH11: seedling height at 11 month NB: no. of branches, LA8: leaf area at 8month, LA11: leaf area at 11 month, PL: petiole length, IL: internodal length, CD: collar diameter, gp: genotypic path coefficient, pp: phenotypic path coefficient.

PCA (principal component analysis) (Table 6) results showed that the first principal components (PC I) gave eigenvalues >1.0 and accounted for 77.059% of the total variation. The variation in PC I explained 77.059% of the total variance and was associated with all the characters *viz*., fruit diameter, fruit length, seedling height at 8–month, seedling height at 11-month, no. of branches, leaf area at 8-month, leaf area at 11-month, petiole length, internodal length, collar diameter. Thus, the use of these characteristics will help in saving a considerable amount of time for the identification and selection of best genotypes of wild *Punica granatum.*

Table 6: Vector loading, Eigen value and percentage of variation explained by different characters.

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
FD (mm)	0.336	-0.164	0.104	-0.509	-0.269	0.064	0.037	-0.100	0.069	0.706
FL (mm)	0.335	-0.150	0.155	-0.523	-0.258	0.032	0.005	-0.058	0.018	-0.705
SH8 (cm)	0.331	-0.213	0.044	0.494	-0.190	0.015	-0.264	-0.693	0.111	-0.026
SH11(cm)	0.336	-0.062	-0.031	0.349	-0.299	-0.283	0.736	0.213	-0.064	-0.009
NB	0.200	0.884	0.238	0.011	-0.216	-0.211	-0.170	-0.031	0.020	0.022
LA8 (cm^2)	0.347	-0.066	-0.046	0.215	-0.154	0.351	-0.372	0.431	-0.596	0.029
LA11(cm^2)	0.350	-0.009	-0.175	0.139	0.104	0.156	-0.189	0.427	0.758	-0.021
PL(cm)	0.303	-0.026	-0.572	-0.165	0.297	-0.621	-0.208	-0.046	-0.181	0.007
IL(cm)	0.316	0.304	-0.254	-0.082	0.455	0.541	0.376	-0.289	-0.104	-0.027
CD(cm)	0.278	-0.152	0.693	0.056	0.599	-0.210	-0.004	0.085	-0.067	0.037
Eigenvalues	7.706	0.813	0.600	0.307	0.248	0.153	0.092	0.053	0.023	0.004
% Variance	77.059	8.131	6.000	3.075	2.483	1.532	0.918	0.535	0.226	0.042
Cumulative Variance (%)	77.059	85.190	91.190	94.265	96.748	98.280	99.198	99.733	99.959	100.001

Where, FD: fruit diameter, FL: fruit length, SH8: seedling height at 8 month, SH11: seedling height at 11 month NB: no. of branches, LA8: leaf area at 8 month, LA11: leaf area at 8 month, PL: petiole length, IL: internodal length, CD: collar diameter.

A biplot (Fig. 2) was also drawn using the values of PCA I and PCA II. The higher the coefficients of a particular characters, more it is related to the respective principal component axis. Two grouping of crosses was observed in Biplot and some overlapping occurred within groups demonstrating the relatedness of the growth performance of different crosses.

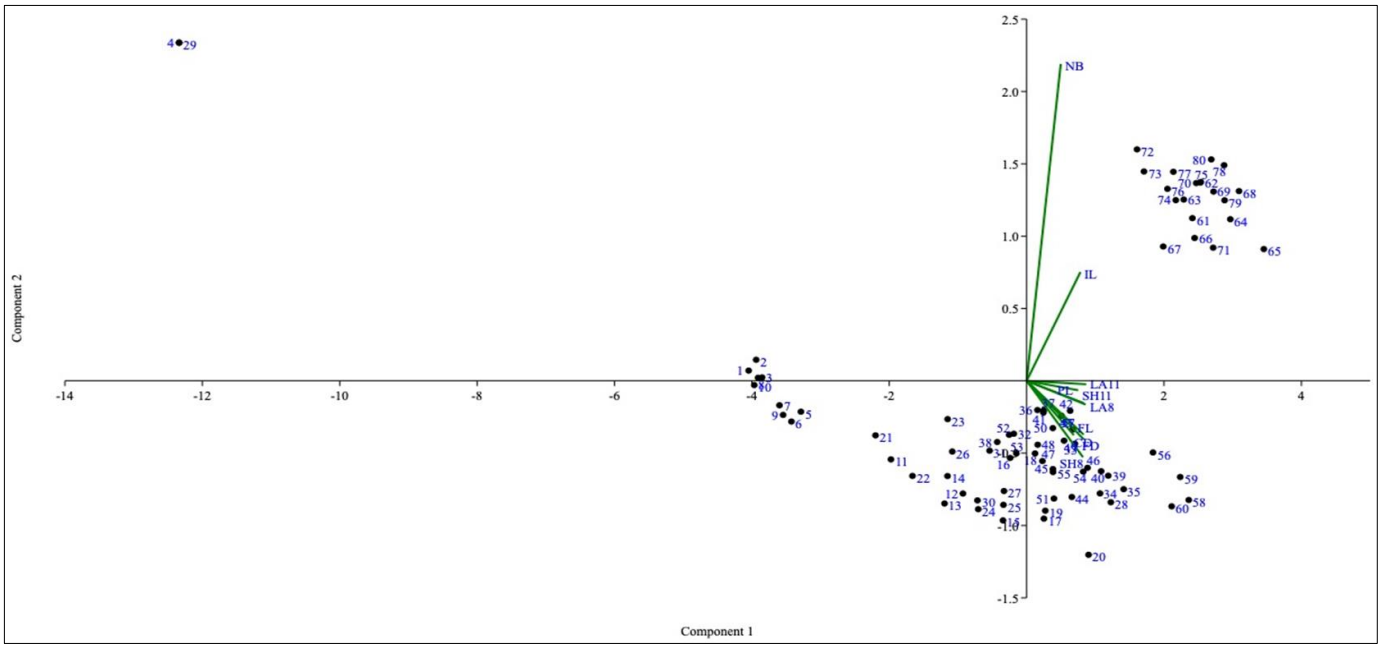


Fig 2: Bi plot between principal component 1 and 2.

In biplot graph of PCA, the quadrant I (+, +) consisting of 19 different crosses (Breeding systems) formed the cluster 1,

which were highly influenced by two growth characters *viz*., no. of branches (NB) and internodal length (IL). The cluster II corresponding to the quadrant II (-, +) contained 6 different crosses (Breeding systems). Similarly, the cluster III corresponding to quadrant III (-, -) consisted also of 25 different crosses (Breeding systems). The quadrant II and quadrant III least influenced by the growth characteristics under study. whereas, the cluster IV corresponding to quadrant IV (+, -) also consisted of 30 different crosses which were greatly influenced by leaf area at 11 month (LA11), petiole length (PL), leaf area at 8 month (LA8), seedling height at 11 month (SH11), fruit length (FL), fruit diameter (FD), seedling height at 8 month (SH8), and collar diameter (CD). (Fig. 2).

Genetic divergence analysis divided breeding system into two major clusters (Fig. 3) based on growth of different quantitative traits under consideration and presented through a dendrogram using Ward's method. Ward (1963) [22]. Cluster I and cluster II comprised of 20 and 60 different crosses respectively. Therefore, hybridization between the progenies of distant crosses may produce more hybrid vigour. The maximum inter-cluster distance was observed between $T_4S_2 \times T_3S_1$ and $T_4S_1 \times T_2S_2$, whereas, the maximum intra-cluster distance was observed between $T_4S_2 \times T_3S_1$ and $T_4S_2 \times T_5S_1$ in cluster I and S_1T_4 and $T_4S_1 \times T_2S_2$.

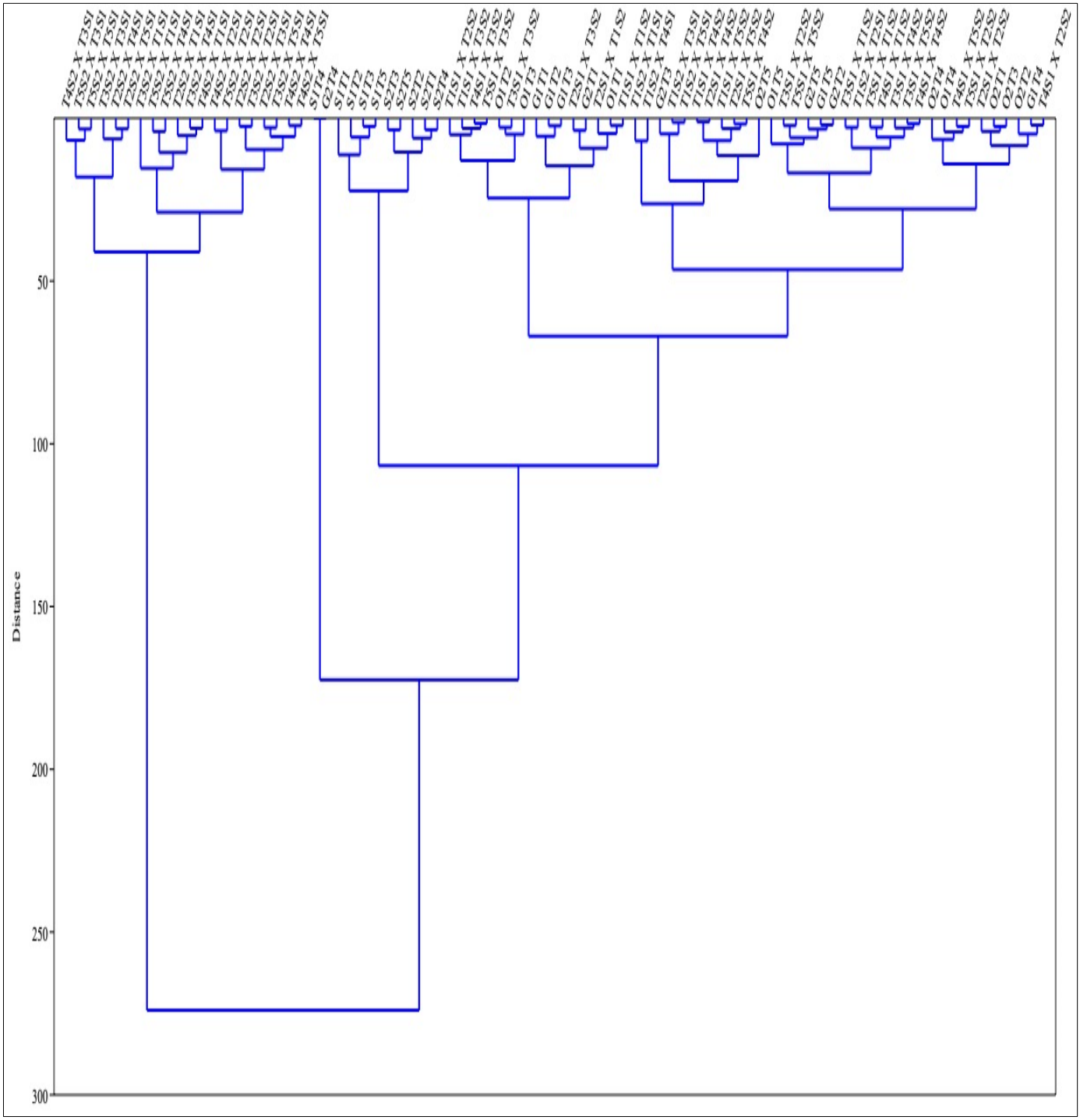


Fig 3: Dendrogram of 80 different crosses (breeding system) applied in wild pomegranate.

Conclusion

We conclude that in variance analysis highly significant

differences were found especially for characters *viz*; fruit dimeter, fruit length, seedling height at 8 month and for no. of branches. GCV and PCV values were observed maximum for the number of branches. The highest heritability and genetic advance as per cent of mean were observed for no. of branches. The fruit length showed a highly significant and positive genotypic and phenotypic correlation with fruit diameter. Path coefficient analysis showed significant relationship between collar diameter and all other characters. These growth characteristics of progeny can be used as a useful criterion for selection in further breeding programmes. The genetic divergence analysis divided eighty different crosses into two major cluster, these increases the selection efficiency of divergent genotypes and breeding between progeny of divergent crosses may lead to improved genetic gain.

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