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Heritability, genetic variability correlation and non-hierarchial euclidean cluster analysis of different almond (*Prunus dulcis*) genotypes

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ABSTRACT

Field trials were conducted during 2006–08 to study the genetic variability, heritability, correlation and cluster analysis of different almond [*Prunus dulcis* Miller (D.A.Webb)] genotypes. The study showed wide range of variation for various morphological, phenological and yield-contributing attributes. High co-efficient of variation was observed for tree height (27.15%), tree spread (45.61%) and yield/tree (43.85%) which indicate that a fair amount of variability exists for these traits. High heritability was recorded for kernel weight (93.08%), followed by kernel length (92.98%), tree spread (91.45%) and nut length (91.02%) shows that these characters can be improved upon by selection. Correlation studies significantly showed a positive correlation of yield with plant height, spread, nut length and kernel length. Thirteen almond genotypes under study were classified into 5 similar groups based on multivariate analysis of morphological traits. Maximum genotypes were placed in cluster IV and V and minimum in cluster I. Maximum intra-cluster distance was observed in cluster III and minimum in cluster I. Maximum inter-cluster distance was recorded between clusters II and V and minimum for II and IV.

Key words: Correlation, Genetic divergence, Heritability, *Prunus dulcis*, Variability

Almond [*Prunus dulcis* Miller (D.A.Webb)] is an important nut fruit with widespread popularity throughout the world. In the genus *Prunus*, almond is closely related to peach, but separated from it by evolution in the xerophytic environment of central and south-west Asia (Kester and Gradziel 1996). At present the USA is the world leading producer of almonds and contributed 82% to the total world production of 771.1 thousand tons in 2007 (Anonymous 2008a). India is a major importer of almonds from USA, after Spain and Germany. In India, almond cultivation is confined mainly to the northern parts including regions of Jammu and Kashmir and high hills of Himachal Pradesh. During 2006–07, the area under almond cultivation was 16 404 ha with annual production of 15 207 metric tonnes in Jammu and Kashmir (DOH 2008b), whereas in Himachal Pradesh the area was 5 766 ha and the production was 1 303 metric tonnes (DOH 2008c). Therefore in the present times evolving desirable varieties of almond is utmost important for this industry.

Selection of a desirable variety is important in establishing productive almond orchard. In varietal selection of almond, the main objective is the introduction of superior seedlings with desirable traits, like good growth habit, late bloom, frost and disease resistance, self fertility and high yield. Almond is heterozygous in its genetic constitution, which makes it most variable to adjust under diverse agro-climatic conditions that resulted in variation and modification in size, fruit colour and taste. In the past, propagation of almond was done using seeds, which resulted in the present day wide range of almond genotypes with different morphological and biological characteristics and it is well established fact that most of the commercial almond cultivars grown throughout the world have been selected by chance from the diverse gene pool of almond seedlings (Kester *et al*. 1990). The genetic variability in almond offers two distinct types, the genetic variability which is of the potential value of parent to give improved progenies and hybrids in the future. Therefore, the knowledge of genetic variability is of great importance in the improvement of those characters which are difficult to identify in the segregating generations. Yield is a complex trait in nut fruit crop like almond and is directly or indirectly affected by many other plant characters. Therefore, to breed for high yield, it becomes very important that correlation of

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those characters with yield is known. The measurement of correlation between characters is a matter of considerable influence in selection practice. The better understanding of the association is provided by the path analysis co-efficient in relation to direct and indirect effect of various component traits on yield. Hence, a study was conducted on genetic variability, heritability, correlation and cluster analysis of different almond genotypes.

MATERIALS AND METHODS

The present investigation was carried out during 2006–08 on 13 almond genotypes, viz 'IXL', 'Merced', 'Drake', 'Primorskij', 'Pranyaj', 'Nonpariel', 'Shalimar', 'Makhdoom', 'Waris', 'GP 10', 'GP 17', 'GP19', and 'GP 14'. The experiment was conducted at experimental farm of CITH, Srinagar situated at a latitude of 34°05' N and longitude of 74°50' E and at an altitude of 1 640 m above mean sea level. Randomized block design was used for testing the significant differences between different genotypes with respect to various characters. The statistical analysis for each character was carried out on mean values. The data were subjected to the analysis of variance (Panse and Sukhatme 1978). All the characters showed significant differences among genotypes and were further subjected to the analysis for different parameters. Co-efficients of variability were calculated at phenotypic, genotypic and environmental levels by the formula suggested by Burton and De Vane (1953). Heritability, genetic advance and genetic gain were calculated as per formulae given by Burton and De Vane (1953) and Johnson *et al.* (1955). The genotypic and phenotypic co-efficients were calculated by implying the techniques of statistical analysis in variance-covariance matrix in which total variability had been split into replications, genotypes and errors. All the components of variance were estimated from analysis of variance table and those of covariance from the analysis of covariance table. The phenotypic and genotypic co-efficients of correlation were computed by the method proposed by Al-Jibouri *et al.* (1958). Genetic divergence was calculated by using non-hierarchial euclidean cluster analysis (Beale 1969 and Spark 1973).

RESULTS AND DISCUSSION

The variability parameters, viz range, mean, heritability, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), genetic advance and genetic gain (genetic advance as per cent of mean) have been worked out and presented in Table 1.

Tree character

All the tree characters assessed in terms of tree height (m), tree spread (m), leaf area (cm^2) and yield (kg/tree) showed variability. The mean value of plant height for two years was found to be 2.35 m. The coefficient of variation at phenotypic and genotypic level was 29.20 and 27.15%, respectively, for plant height. Heritability value of 86.41% was assisted by genetic advance of 4.01 and genetic gain of 51.99% for the same character. Plant spread showed high heritability of 91.45% accompanied by low genetic advance (6.40) and high genetic gain (89.74%). Phenotypic and genotypic co-efficients of variation were 47.70 and 45.61%, respectively, for plant spread. The mean value of leaf area

Table 1 Estimates of various genetic parameters of almond

Character	Range	Mean	Co-efficient of variation (%)		Heritability (%)	Genetic advance	Genetic gain (%)
			Phenotypic	Genotypic			
Tree height (m)	1.67–3.33	2.35	29.20	27.15	86.41	4.01	51.99
Tree spread (m)	1.14–3.17	2.17	47.70	45.61	91.45	6.40	89.74
Leaf area (cm^2)	9.20–13.72	11.80	25.74	17.65	47.02	2.94	24.91
Yield (kg/tree)	0.64–1.84	1.14	50.29	43.85	76.03	0.89	78.77
Nut weight (g)	1.56–2.46	2.04	21.58	14.45	44.84	0.40	19.90
Nut length (mm)	26.22–40.18	32.56	21.84	20.84	91.02	13.33	40.93
Nut width (mm)	17.00–20.29	18.31	9.70	7.40	58.13	2.12	11.62
Nut thickness (mm)	10.87–13.67	12.65	10.72	5.96	30.97	0.86	6.88
Nut width/length	0.46–0.67	0.57	20.61	19.86	92.85	0.22	39.37
Percentage of sound kernels (%)	93.89–98.89	96.24	2.62	0.99	14.23	0.74	0.77
Percentage of double kernels (%)	6.11–26.67	12.52	53.38	33.55	39.51	5.43	43.37
Kernel weight (g)	0.77–1.22	0.94	20.43	19.71	93.08	0.37	39.09
Kernel length (mm)	18.08–28.38	23.24	22.28	21.48	92.98	9.91	42.64
Kernel width (mm)	10.69–12.39	11.31	7.98	5.10	40.98	0.76	6.71
Kernel width/length	0.38–0.62	0.49	23.62	22.84	93.52	0.22	45.49
Kernel (%)	36.23–59.48	47.68	25.68	23.38	82.91	20.91	43.85

was observed to be 11.80 cm^2 and the co-efficients of variation at phenotypic and genotypic level were found to be 25.74 and 17.65%, respectively. Heritability value was estimated as 47.02% assisted by genetic advance of 2.94 and genetic gain of 24.91% for leaf area. Damyar and Hassani (2006) have also reported significant differences between different almond cultivars for plant height, canopy and annual shoot growth. The mean yield/plant was observed to be 1.14 kg with a heritability value of 76.03% and genetic advance was estimated as 0.89, whereas genetic gain was recorded as 78.77%. Phenotypic and genotypic co-efficient of variation was recorded as 50.29 and 43.85%, respectively, for the character yield. Yield/plant in different genotypes ranged between 0.82 and 1.56 kg. Similar results were obtained by Dalal *et. al.* (2004) under Kashmir conditions. Under different ecological conditions variability in yield (0.33–5.56 kg/tree) was reported by Cordeiro *et al*. (2005) and the average yield was almost double than the present yield. This may be attributed to the different cultivars/genotypes used, orchards grown on fertile soils, efficient management practices and presence of pollinators in adequate amount. Whereas in the present study, the trees were densely spaced (4 m×4 m) and no additional pollinizing agents (bees) were supplied during flowering period. However the yield of 'Nonpariel' cultivar was in consonance with the reports of Kaska *et al*. (2005) under Turkey conditions. The estimates of genotypic co-efficient of variation was lower than phenotypic co-efficient of variation and both the phenotypic and genotypic co-efficients of variation in the present study were relatively high for tree height, tree spread and yield/tree indicating greater scope for improvement. High heritability coupled with high genetic advance was obtained in tree height and tree spread indicating additive gene action, thus selection for these characters would be effective.

Nut character

Heritability of 44.84% accompanied by genetic advance of 0.40 and genetic gain of 19.90% were recorded for the character nut weight. For the same character co-efficients of variation at phenotypic and genotypic level were 21.58 and 14.45%, respectively. Nut length showed a high heritability of 91.02%. Genetic advance estimate was 13.33, whereas genetic gain revealed a value of 40.93%. Phenotypic and genotypic co-efficients of variation were 21.84 and 20.84%, respectively. The mean nut width was observed to be 18.31 mm with a heritability of 58.13% and co-efficient of variation at phenotypic and genotypic level were observed as 9.70 and 7.40%, respectively. Estimates of genetic advance (2.12) and genetic gain (11.62%) were recorded for this trait. Nut thickness showed a heritability of 30.97% accompanied with low genetic advance (0.86) and genetic gain (6.88%). Phenotypic and genotypic co-efficients of variation were observed to be 10.72 and 5.96%, respectively. Nut width/length revealed a heritability of 92.85%, genetic advance of 0.22 and genetic gain of 39.37%. Co-efficient of variation at phenotypic level (20.61%) was greater than co-efficient of variation at genotypic level (19.86%) for nut width/length. Similarly, Thakur *et. al.* (2005) while studying 63 almond genotypes observed nut weight, nut width, nut length and nut thickness to vary between 0.65 and 2.68 g, 16.49 and 44.25 mm, 11.5 and 21.02 mm and 9.78 and 15.42 mm, respectively, with coefficients of variability as 30.34, 16.18, 14.01 and 10.73, respectively. Comparatively higher values of phenotypic and genotypic co-efficient of variability were recorded for the character nut length and higher heritability coupled with high genetic advance for the same character indicates additive gene action, thus selection would be effective for this character.

Kernel character

Kernel size, shape and weight are related both genetically and horticulturally. Kernel characters are extremely important marketing attributes in view of the fact that in the international market increasing quantities of produce is sold as kernel rather than in shell nut. Kernel characters have been reported to vary considerably in samples from trees of seedling populations. The phenotypic and genotypic co-efficients of variation for character double kernel were 2.62 and 0.99%, respectively. Same character showed heritability of 14.23% which was associated with low genetic advance (0.74) and genetic gain (0.77%). Heritability of 39.51%, genetic advance of 5.43 and genetic gain of 43.37% were recorded for percentage of double kernels. The co-efficient of variation at phenotypic level (53.38%) was found to be greater than the co-efficient of variation at genotypic level (33.55%) for same character. Double kernelled nuts results from the fertilization and development of both ovules originally present in the ovary. The relative tendency to produce double kernels among different individuals is apparently related to internal physiological conditions associated with genotype but affected by season, environment and age. Doubling is undesirable because resulting kernels are misshapen and difficult to screen for size prior to processing. (Kester and Asay 1975). In the present study, least double kernels were observed in 'GP10' (6.11%) and maximum in 'Primorskij' (26.67%). Sound kernels were in the range of 93.89–98.89%. The present findings are in accordance with the findings of Lovicu *et al*. (2002a) in which percentage of double kernels and sound kernels ranged from zero to 26.3 and 96.7 to 100, respectively. Further, Lovicu *et. al*. (2002b) reported sound kernels in the range of 96.5 to 100% while evaluating germplasm in Italy. Twin seeds (multiple embryos within the same seed coat) occur spontaneously in certain almond cultivars. The occurrence of these multiple embryos varies greatly and is strongly influenced by environmental conditions. In the present study no twin kernels were observed and this might be due to the rare occurrence of twin kernels as reported previously (Micke *et al.* 1996–99). Mean kernel weight was 0.94 g (Table 1). Phenotypic and genotypic co-efficients of variation were 20.43 and 19.71%, respectively. The heritability percentage was higher (93.08%) associated with a low genetic advance (0.37) and moderate genetic gain of 39.09%. In previous reports range of kernel weight extended from as high as 2.5 g to as low as 0.62 g (Dalal *et al.* 2004, Kaska *et al.* 2005). Kernel length showed a high heritability of 92.98% accompanied by genetic advance of 9.91 and genetic gain of 42.64%. Phenotypic co-efficients of variation were observed as 22.28 and 21.48%, respectively. For kernel width heritability of 40.98%, genetic advance of 0.76 and genetic gain of 6.71%, co-efficients of variation at phenotypic and genotypic level were 7.98 and 5.10%, respectively. In case of character kernel width/length phenotypic and genotypic co-efficients of variation were recorded as 23.62 and 22.84%, respectively. The trait showed high heritability of 93.52% accompanied by low genetic advance of 0.22 and moderate genetic gain of 45.49%. Heritability of 82.91%, genetic advance of 20.91 and genetic gain of 43.85% were recorded for kernel percentage and the co-efficients of variation at phenotypic and genotypic level were recorded as 25.68 and 23.38%, respectively. Kernel percentage in the present study ranged from 36.23 to 59.48%, and is in agreement with the findings of Dalal *et al.* (2004). Thakur *et al.* (2005) also observed kernel weight, kernel width, kernel weight, kernel thickness and kernel percentage to vary between 0.25 and 1.21 g, 11.06 and 30.56 mm, 7.43 and 14.43 mm, 5.04 and 8.08 mm and 27.02 and 73.04%, respectively with co-efficients of variability as 29.85, 18.24, 14.84, 9.81 and 26.73, respectively. Comparatively higher values of phenotypic and genotypic co-efficients of variability were recorded for the characters percentage of double kernels, kernel weight, kernel length, kernel width/length and kernel percentage, indicating greater scope for improvement. Higher heritability values coupled with higher genetic advance were recorded for kernel length and kernel percentage indicating additive gene action, thus selection would be effective for these characters.

Correlation

Simple correlation: The importance to asses the correlations present among the different traits to be improved has long been recognized by number of workers. Simple correlation co-efficients were calculated amongst various traits under study and are presented in Table 2. Plant height showed highly significant and positive correlation with plant spread (0.860), yield (0.843), nut length (0.623) and kernel length (0.684). Plant height was negatively correlated with leaf area (– 0.589), nut width/length (–0.586) and kernel width/length (– 0.717). Plant spread was significantly and positively associated with characters, like yield (0.722), nut length (0.605) and kernel length (0.646). It also showed significant and negative correlation with leaf area (– 0.625), nut width/length (0.549) and kernel width/length (0.633).

Table 2 Simple correlation

Genotype	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
X1	1.000																
X2	0.860**	1.000															
X3	–0.589*	–0.625*	1.000														
X4	0.106	0.099	–0.322	1.000													
X5	0.188	0.068	–0.068	–0.118	1.000												
X6	0.843**	0.722**	–0.616*	0.113	–0.142	1.000											
X7	–0.038	–0.017	0.210	–0.284	0.130	–0.108	1.000										
X8	0.623**	0.605*	–0.396	–0.160	0.030	0.674**	0.238	1.000									
X9	0.268	0.340	0.033	–0.362	–0.163	0.221	0.622**	0.295	1.000								
X10	–0.205	–0.170	–0.059	–0.260	0.015	–0.177	0.146	–0.137	0.224	1.000							
X11	–0.586*	–0.549*	0.458	–0.006	–0.111	–0.634**	0.035	–0.919**	0.087	0.265	1.000						
X12	0.513*	0.391	–0.344	–0.780	0.238	0.499*	0.071	0.729**	–0.592	–0.233	–0.765**	1.000					
X13	0.274	0.324	–0.192	–0.194	0.087	0.238	0.681**	0.726**	0.468	0.026	–0.550*	0.471	1.000				
X14	0.684**	0.646**	–0.388	–0.142	0.086	0.685**	0.203	0.966**	0.216	–0.244	–0.922**	0.761**	0.688**	1.000			
X15	–0.127	0.045	0.050	–0.202	–0.248	–0.067	0.399	–0.036	0.657**	0.262	0.321	–0.285	0.259	–0.143	1.000		
X16	–0.717**	–0.633**	0.346	0.086	–0.137	–0.664**	–0.092	–0.871**	–0.090	0.294	0.890**	–0.723**	–0.550*	–0.948**	0.393	1.000	
X17	0.393	0.422	–0.463	0.154	–0.072	0.435	–0.467	0.586*	–0.232	–0.211	–0.731**	0.439	0.315	0.586*	–0.234	–0.577	1.000

X1, Plant height (m); X2, plant spread (m); X3, leaf area (cm^2); X4, duration of flowering (days); X5, duration from full bloom to harvest (days); X6, yield (kg/tree); X7, nut weight (g); X8, nut length (cm); X9, nut width (mm); X10, nut thickness (mm); X11, nut width/length; X12, percentage of double kernels (%); X13, kernel weight (g); X14, kernel length (mm); X15, kernel width (mm); X16, kernel width/length; X17, kernel per cent (%)

$*P=0.05$ $**P=0.01$

Table 3 Genotypic and phenotypic correlation

Genotype		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
X1	P	1.000																
	G	1.000																
X2	P	0.874**	1.000															
	G	0.913**	1.000															
X3	P	–0.609	–0.628**	1.000														
	G	–0.844**	–0.831**	1.000														
X4	P	0.070	0.093	–0.346	1.000													
	G	0.119	0.095	–0.490*	1.000													
X5	P	0.188	0.067	–0.072	–0.127	1.000												
	G	0.174	0.063	–0.084	0.170	1.000												
X6	P	0.841**	0.722**	–0.628**	0.091	–0.149	1.000											
	G	0.857**	0.883**	–0.743**	0.148	–0.200	1.000											
X7	P	–0.062	–0.022	0.204	–0.313	0.127	–0.124	1.000										
	G	–0.111	–0.112	0.355	–0.438	0.147	–0.138	1.000										
X8	P	0.635**	0.604*	–0.396	–0.167	0.030	0.678**	0.240	1.000									
	G	0.743**	0.629**	–0.503*	–0.175	0.025	0.798**	0.195	1.000									
X9	P	0.237	0.337	0.028	–0.140	–0.172	0.200	0.618	0.296	1.000								
	G	0.238	0.368	0.132	–0.495	–0.219	0.222	0.563	0.255	1.000								
X10	P	–0.214	–0.171	–0.063	–0.107	0.015	–0.180	0.146	–0.137	0.227	1.000							
	G	–0.391	–0.214	0.070	–0.177	–0.069	–0.537*	0.438	–0.340	0.469	1.000							
X11	P	–0.622**	0.554*	0.457	–0.021	–0.114	–0.652**	0.027	–0.923**	0.077	0.265	1.000						
	G	–0.739**	–0.579**	0.579*	–0.020	–0.115	–0.763**	0.030	–0.938**	0.084	0.565*	1.000						
X12	P	0.501*	0.388	–0.317	–0.089	0.249	0.497*	0.078	0.748**	–0.078	–0.241	–0.795**	1.000					
	G	0.662**	0.492*	–0.579*	–0.059	0.312	0.679**	0.193	0.887**	–0.020	–0.393	–0.905**	1.000					
X13	P	0.278	0.323	–0.189	–0.198	0.088	0.238	0.688	0.726**	0.475	0.027	–0.551	0.481	1.000				
	G	0.537*	0.402	–0.248	–0.287	0.134	0.510*	0.639	0.899**	0.390	0.227	–0.767**	0.858**	1.000				
X14	P	0.688**	0.643**	–0.388	–0.157	0.085	0.682**	0.201	0.967**	0.208	–0.246	–0.932**	0.776**	0.689**	1.000			
	G	0.797**	0.667**	0.510*	–0.159	0.082	0.802**	0.125	0.978**	0.161	–0.490*	–0.961	0.930**	0.836**	1.000			
X15	P	–0.135**	0.048	0.039	–0.216	–0.251	–0.070	0.397	–0.035	0.663**	0.262	0.318	–0.284	0.262	–0.144	1.000		
	G	–0.054**	0.039	0.031	–0.364	–0.334	0.119	0.050	–0.218	0.742	0.844**	0.503	–0.369	–0.262	–0.394	1.000		
X16	P	–0.722	–0.631**	0.347	0.101	–0.136	–0.661	–0.088	–0.872**	–0.078	0.296	0.900**	–0.737**	–0.550**	–0.948**	0.369	1.000	
	G	–0.775	–0.661**	0.435	0.096	–0.123	–0.712**	–0.121	–0.908**	–0.080	0.627**	0.929**	–0.861**	–0.786**	–0.974**	0.535**	1.000	
X17	P	0.428	0.429	–0.461	0.177	–0.070	0.454	–0.461	0.590*	–0.220	–0.211	–0.730**	0.455	0.316	0.596*	–0.229	–0.587*	1.000
	G	0.717**	–0.564*	–0.630**	0.230	0.050	0.721**	–0.507	0.766**	–0.244	–0.392	–0.896**	0.694**	0.334	0.784**	–0.408	–0.749**	1.000

X1, Plant height (m); X2, plant spread (m); X3, leaf area (cm^2); X4, duration of flowering (days); X5, duration from full bloom to harvest (days); X6, yield (kg/tree); X7, nut weight (g); X8, nut length (mm); X9, nut width (mm); X10, nut thickness (mm); X11, nut width/length; X12, percentage of double kernels (%); X13, kernel weight (g); X14, kernel length (mm); X15, kernel width (mm); X16, kernel width/length and X17, kernel per cent (%)

*P=0.05

**P=0.01%

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Yield was significantly and positively correlated with nut length (0.674), percentage of double kernels (0.499) and kernel length (0.685). The data also showed significant and negative correlation with leaf area (– 0.616), nut width/length (– 0.634), and kernel width/length (– 0.664). Character nut weight was significantly and positively correlated with nut width (0.622) and kernel weight (0.681). Nut length was positively and significantly associated with kernel weight, kernel length, kernel per cent and percentage of double kernels. Highest value of correlation was recorded between nut length and kernel length (0.966).This trait had negative correlation with nut width/length and kernel width/length ratio. Percentage of double kernels recorded significant and positive correlation with kernel length (0.761). Kernel weight was positively and significantly linked with kernel length (0.688) and was negatively correlated with kernel width/ length. Kernel per cent was significantly and positively correlated with kernel length (0.586) and negatively with nut width/length and kernel width/length.

Multiple correlation: The existence of interrelation among the characters is of utmost significance which otherwise are very difficult and in some crops impossible to identify during the segregation. Therefore, the contribution of each component towards yield and their inter-relationship must be clearly studied. The results pertaining to correlation co-efficient (genotypic and phenotypic levels) among tree, flowering and nut characters of 13 genotypes are presented in Table 3. Genotypic correlation co-efficients for all the characters were higher than phenotypic correlation co-efficients. Plant height showed significant and positive correlation with plant spread, yield, nut length, percentage of double kernels, kernel weight, kernel length and kernel percent. Highest value was observed between plant height and plant spread (0.913) at genotypic level. Negative correlation was also observed with leaf area, kernel width/ length and nut width/length. Plant spread was significantly and positively associated with yield, nut length, kernel length both at genotypic and phenotypic levels and with kernel per cent (0.564) at genotypic level. Yield was significantly and positively correlated with nut length, percentage of double kernels and kernel length both at genotypic and phenotypic level and with kernel weight (0.510) and kernel per cent (0.721) at genotypic level. The data also showed significant and negative correlation with leaf area, nut width/length and kernel width/length. Nut weight depicted positive and significant correlation with nut width (0.618, 0.563) and kernel weight (0.688, 0.639) at both the levels. Nut length showed significant phenotypic and genotypic correlation with percentage of double kernels, kernel weight, kernel length and kernel per cent. Highest value was observed between nut length and kernel length (0.978) at genotypic level. Nut width was significantly and positively correlated with kernel width (0.663) at phenotypic level. Nut thickness showed positive and significant genotypic correlation with nut width/ length (0.565), kernel width (0.844), kernel width/ length (0.627) and was negatively correlated with kernel length (– 0.490). Percentage of double kernels depicted significant and positive correlation with kernel length (0.776, 0.930) at both the levels, whereas with kernel weight (0.858) and kernel per cent (0.694) at genotypic level. There was a significant and positive correlation of the kernel length with kernel weight (0.689, 0.836) and kernel% (0.596, 0.784) at both the levels.

In the present investigation fruit yield/plant was positively and significantly correlated with plant height, plant spread, leaf area, nut length, percentage of double kernels and kernel length. Among nut size parameters under study, there was a high positive correlation between nut weight and nut width, nut weight and kernel weight, kernel weight and kernel length. Thakur *et al.* (2005) also reported significant correlation of nut weight with nut width (0.395), nut length (0.634), nut thickness (0.617), kernel weight (0.537), kernel width (0.366), kernel length (0.544) and kernel thickness (0.283) in almond.

Non-hierarchical euclidean cluster analysis

The availability of statistical tool to quantitatively measure the genetic divergence between two or more populations and the contribution of individual character to the total divergence is essential in selection of genotypes for hybridization. Sharma (1998) pointed out that the genetically divergent parents used in hybridization under transgressive breeding programme are dependent upon categorization of breeding material on the basis of appropriate criteria. Clustering pattern of 13 genotypes of *Prunus amygdalus* on the basis of morphological attributes revealed that they could be classified into 5 clusters. Maximum number of genotypes (4) was accommodated in cluster IV (‘IXL’, ‘Mreced’, ‘Primorskij’ and ‘Pranyaj’) and cluster V (‘GP10’, ‘GP14’, ‘GP17’ and ‘GP19’) while cluster II had ‘Nonpariel and ‘Shalimar’ ‘and cluster III, ‘Makhdoom’ and ‘Waris’. Cluster I included cultivar ‘Drake’ only. The mean performance of each cluster for traits studied is presented in Table 4, which indicated appreciable difference for all the traits. From the 5 clusters, cluster I depicted the maximum mean values for the characters like duration of flowering (17.50 days), duration from full bloom to harvest (152.50 days), nut thickness (13.31 mm) and percentage of sound kernels (98.89). Contrary cluster II showed no highest entry for any of the traits studied. Cluster III revealed the maximum mean value for tree height (2.86 m), tree spread (2.96 m), yield (1.36 kg/tree), nut width (19.90 mm) and kernel width (11.73 mm). Likewise cluster IV recorded the highest entries for nut length (38.0 mm), percentage of double kernels (18.47), kernel weight (1.11 g), kernel length (27.04 mm) and kernel percentage (54.87%). Cluster V revealed maximum mean for leaf area (12.78 cm^2), nut weight (2.26 g), nut width/length (0.65) and kernel width/ length (0.60). Intra- and inter-cluster distances are given in

Table 4 Cluster mean and standard deviation of 5 clusters for different almond genotypes

Character	Parameter	Cluster				
		I	II	III	IV	V
Tree height (m)	Mean	2.39	2.76	2.86	2.39	1.86
	SD	0.00	1.02	2.18	0.49	0.47
Tree spread (m)	Mean	2.45	2.77	2.96	2.35	1.23
	SD	0.00	0.10	0.97	0.68	0.36
Leaf area (cm^2)	Mean	10.70	10.45	11.34	11.98	12.78
	SD	0.00	0.65	1.49	1.69	1.69
Duration of flowering (days)	Mean	17.50	15.50	11.50	12.62	13.12
	SD	0.00	1.41	1.41	1.55	1.60
Days from full bloom to harvest (days)	Mean	152.50	133.50	141.75	143.25	137.25
	SD	0.00	8.49	8.84	6.69	5.63
Yield (kg/tree)	Mean	0.64	1.33	1.36	1.32	0.82
	SD	0.00	0.33	0.69	0.23	0.10
Nut weight (g)	Mean	1.95	1.69	2.02	2.04	2.26
	SD	0.00	0.19	0.05	0.15	0.17
Nut length (mm)	Mean	29.01	35.06	31.74	38.00	27.15
	SD	0.00	0.13	1.35	2.00	1.05
Nut width (mm)	Mean	17.40	17.42	19.90	18.53	17.97
	SD	0.00	0.60	0.56	0.72	0.70
Nut thickness (mm)	Mean	13.31	11.10	13.17	12.86	12.78
	SD	0.00	0.33	0.10	0.64	0.60
Nut width/length	Mean	0.60	0.50	0.63	0.49	0.65
	SD	0.00	0.02	0.01	0.03	0.01
Percentage of sound kernels	Mean	98.89	95.56	95.28	95.14	97.50
	SD	0.00	0.78	1.97	0.95	0.56
Percentage of double kernels	Mean	13.33	13.34	8.05	18.47	8.19
	SD	0.00	3.93	1.97	6.21	2.15
Kernel weight (g)	Mean	0.94	0.91	0.91	1.11	0.82
	SD	0.00	0.01	0.06	0.09	0.05
Kernel length (mm)	Mean	22.06	25.41	22.53	27.04	19.01
	SD	0.00	0.82	0.65	1.36	1.03
Kernel width (mm)	Mean	10.92	10.93	11.73	11.39	11.30
	SD	0.00	0.34	0.94	0.40	0.05
Kernel width/length	Mean	0.50	0.43	0.52	0.43	0.60
	SD	0.00	0.03	0.02	0.03	0.03
Kernel (%)	Mean	48.49	54.56	45.04	54.87	38.00
	SD	0.00	6.95	4.30	0.49	1.48

Table 5. The intra-cluster distance ranged from 0.00 to 2.753. The intra-cluster distance was maximum (2.753) for cluster III. The inter-cluster distance ranged from 4.235 to 6.823. Highest value (6.823) for inter-cluster distance was recorded between clusters II and V while it was lowest (4.235) for clusters II and IV. The narrow range intra-cluster distance depicted the presence of narrow range of diversity within a cluster. Maximum cluster distance of 6.823 observed between clusters II and V indicated that genotypes falling in these clusters can be used in hybridization programme to get better recombinants in the segregating generations. Thakur *et al.* (2005) could accommodate 63 almond genotypes into 8 clusters with maximum intra- and inter-cluster distances of 2.02 (cluster 40 and 6.990 (between cluster 2 and cluster 7). Similarly, while investigating the genetic divergence of seedling trees of pecan in Himachal Pradesh, Kaushal and Sharma (2005) grouped 143 trees into 10 clusters with maximum intra- and inter-cluster distances of 2.68 (cluster 10) and 7.104 (between cluster 5 and cluster 10).

Table 5 Intra- and inter-cluster distance

Cluster	I	II	III	IV	V
I	0				
II	5.392	*1.752*			
III	5.635	5.490	*2.753*		
IV	5.491	4.235	4.399	*2.364*	
V	4.935	6.823	5.180	6.439	*1.641*

Italic figures represent intra-cluster distance

Table 6 Promising genotypes of almonds for different characters

Character	Highest	Lowest	Genotypes at par with highest
Plant height (m)	'Waris'	'GP 14'	
Plant spread (m)	'Waris'	'GP 14'	
Leaf area (cm^2)	'GP 14'	'Pranyaj'	'GP 10', 'Primorskij', 'IXL'
Number of primary branches	'Nonpareil'	'GP 17'	
Number of secondary branches	'Nonpareil'	'GP 17'	
Onset of flowering	'Drake'	'Makhdoom'	
Duration of flowering	'Drake'	'Makhdoom'	
Days from full bloom to harvest	'Nonpareil'	'Drake'	
Yield (kg/tree)	'Waris'	'GP 19'	'IXL', 'Primorskij', 'Pranyaj', 'Nonpareil'
Nut weight (g)	'GP 10'	'Nonpareil'	'GP 14'
Nut length (mm)	'Primorskij'	'GP 17'	
Nut width (mm)	'Waris'	Shalimar	
Nut thickness (mm)	'GP 10'	'Nonpareil'	'Drake', 'Merced', 'Primorskij', 'Pranyaj', 'Makhdoom', 'Waris'
Nut width/length	'GP 14'	'IXL'	'GP 10', 'GP 17'
Kernel length (mm)	'Primorskij'	'GP 17'	'IXL'
Kernel width/length	'GP 17'	'IXL'	
Kernel weight (g)	'Primorskij'	'GP 17'	'Pranyaj'
Kernel (%)	'Nonpareil'	'GP 14'	
Percentage of sound kernels (%)	'Drake'	'Pranyaj','Makhdoom'	
Percentage of double kernels (%)	'GP 10'	'Primorskij'	'GP 17', 'GP 19', 'GP 14'

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