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Oil content variability and genetic divergence in half-sib families of *Prunus armeniaca* L. in Kashmir Valley – India

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This research work is a part of NOVOD, Board sponsored project entitled "National Network on Integrated Development of Wild apricot (*Prunus armeniaca*)". The experiments were conducted to study the genetic variability-cum-diversity for seed and seedling characters among 25 half-sib families of *Prunus armeniaca* L. collected from different coordinates/locations of Jammu and Kashmir, India. Seeds of 25 candidate plus trees were collected and graded to constitute seed lots of different candidate plus trees (CPT). After the dimensional measurements for fruit, seed and kernel characters, part of the seeds from seed lots of each family/CPT were analyzed for oil content estimation. Part of the constituted seed lots of each family/CPT were sown in open field environmental conditions in the nursery following randomized block design (RBD), with a view to assess the expression of genetic diversity using non-hierarchical Euclidean cluster analysis. Intercrossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage. Candidate plus tree progenies were grouped into six clusters under open field environment. Inter-cluster distance was found to be highest between cluster II and VI, revealing their genetic closeness from high to medium. On the basis of inter and intra cluster distance cluster no. II and VI may be considered as diverse and can be utilized for hybridization when selecting genotypes for breeding purposes. Fruit length followed by fruit breadth and seedling height contributed maximum to the total divergence and played a prominent role in creating the genetic diversity.

Key words: Oil content, variability, cluster, genetic divergence, *Prunus armeniaca.*

INTRODUCTION

During the last few years, the domestic consumption of edible oils has increased substantially and has touched the level of 18.90 million tonnes in 2011 in India. By 2017 the per capita consumption of vegetable oils is expected to increase to 16 kg/person/year, thereby the demand is likely to touch 20.4 million tonnes (NMOOP, 2014). Due to ever increasing demand for edible oils in India, it was felt as the immediate need of the hour to go for alternate options for increasing production of edible oil seeds so as to cut shorts the import bill. Attention was paid to

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increase the production through tree borne oil seeds which are non-traditional oil crops. Wild apricot (*Prunus armeniaca* L.) is one amongst the many tree borne oil seed crops of India and very important in temperate regions of Himalaya. It has assumed greater significance in the recent past because of its being a potential source of edible oils. Kernels yield up to 53% of edible oil, however, little or negligible efforts have been taken for its genetic improvement.

P. armeniaca L. belongs to family "Rosaceae" and includes many varieties of cultivated and wild apricots which grow throughout north-western Himalaya between an elevation of 1,000 to 3,000 m. It's importance is well realized especially in temperate region as fuel, fodder, feed and small timber. It is one of the important multipurpose trees in the region under existing system of agroforestry (Singh and Chaudhary, 1993). The fruit of wild apricot is unfit for table purpose due to high acids and low sugars. The seed (stones) yields 27 to 33% of kernels and the kernels yield up to 53% of edible oil. Kernels are bitter in taste due to the presence of cyanogenic glycoside amygdalin (Montgomery, 1969). Oil has 94% unsaturated fatty acids (Gandhi et al*.,* 1997) and 75% oleic acid (Aggarwal et al., 1974). The oil is utilized for cooking, body massage and as raw material for cosmetic and pharmaceutical industry (Pamar and Sharma, 1992). Kernel weight which is directly related with oil yield is a complex character and it is dependent on a number of nut components. Having direct association and relationship among themselves, characters such as kernel length, breadth and weight are of paramount importance for making selections based on any of the three characters.

A characteristic feature of all living organisms is the immense natural variability present for various characters in most of the populations. In nature, widespread species variations are present between populations growing under different geographical conditions. Therefore the selection of appropriate plus tree/seed sources/genotype assumes the foremost importance in plantation. Selection of the superior tree is one of the major factor affecting establishment and productivity. For proper utilization of observed variation in a species, it is prerequisite to know the extent of variation and its cause, whether it is due to genetic (heritable) or due to the environmental factors (non-heritable). The proportion of total variation, which is heritable is termed as heritability in broad sense (Lush, 1937), knowledge of its magnitude gives an idea about scope of effecting/bringing genetic improvement in a species through selections**.**

Intercrossing of divergent groups would lead to greater opportunity for genetic material (gene) crossing over to release hidden variability by breaking linkage. Progeny derived from such diverse crosses are expected to show wide spectrum (scope) of genetic variability and provide a greater scope for isolating transgressive segregants in the advance generation. Hence, these genotypes might be used in multiple crossing programme to recover transgressive segregants (Thoday, 1960).

MATERIALS AND METHODS

The present experimental investigations were conducted in the valley of Kashmir in three districts of Kupwara, Srinagar and Budgam, enjoying both moist and dry temperate coniferous and deciduous forest types. This part of experimental work was carried out under the research project entitled "National Network on Integrated Development of Wild apricot (*P. armeniaca* L.)" sponsored by NOVOD, Board Project, Ministry of Agriculture, Govt. of India.

In the present study, candidate plus trees (genotypes) of a sample of (n = 25) of wild apricot based on tree check method were selected and marked. Table 1 gives the characteristics features of selected candidate plus trees in terms of their source of collection, approximate age in years (Information collected from the owner of the plus trees), height (m), diameter at breast height (cm), canopy (m^2), time of its flowering, fruiting and total fruit yield (kg). Selected trees were free from insect-pest incidence. From each individual plus tree (genotype) more than ten kilogram of fruits were collected soon after ripening. By using vernier caliper, dimensional morphological data was recorded on the following characters:

(1) Fruit, stone and kernel length (from base to apex)
(2) Fruit, stone and kernel breadth (edge-wise from the centre) and
(3) Thickness (from middle of the fruit, stone and kernel).

250 g of kernels in 5 replicates were used for oil percentage analysis. 300 seeds (number) from each plus tree were sown in open nursery beds at a depth of 1.0 cm in five replicates under open field environmental conditions using randomized block design (RBD) at Forest nursery, Faculty of Forestry, SKUAST-K Shalimar for further evaluation of their progenies. The nursery site is located at an altitude of 1,850 m amsl within the coordinates of 34°-05/N latitude and 74°-50/ E longitude, receiving a mean annual rainfall of about 660 mm and mean temperature of 13.3°C. Minimum temperature of the area may drop to -7°C in winter months while as maximum temperature may touch to 35°C in summer. Soil at the experimental site is neutral having available nitrogen of 100 kg/ha, phosphorus 10 kg/ha and potassium 200 kg/ha. A uniform pre-treatment was given to the seeds before sowing by soaking them in warm water, allowed to cool and kept soaked for 48 h. Regular watering was carried out as per requirements. Germination data was recorded soon after the emergence of plumule above soil for consecutive 21 days from the date of sowing. Observations on seedling height, collar diameter and number of branches per seedling were taken after one full-grown season for 20 seedlings/replication/plus tree.

To understand the significance of difference among 25 different plus trees, data was subjected to analysis of variance (ANOVA). Least significant difference (LSD) was calculated and plus trees were ranked for the variables studied using a computer software programme "SPSS". Coefficient of variation (CV %) among studied traits were calculated as described by (Panse and Sukhatme, 1967). Genotypic and phenotypic coefficient of variation, and heritability (broad sense) were calculated using the method of (Kempthorne, 1957). Genetic divergence and cluster information was assessed by non-hierarchical Euclidean Cluster Analysis (Spark, 1973).

Statistical analysis

The data was analyzed statistically for the assessment of analysis

Table 1. Passport details and morphological observations of 25 selected candidate plus trees of *P. armeniaca* L.

S/No	Accession No.	Source of collection	Approximate age (yrs)	Height (m)	Diameter (cm)	Canopy (m^2)	Total fruit yield (kg)	Time of flowering	Time of fruiting
01	CPT102	Kralpora (Kupwara)	53.33	25.33	46.0	14.06	55	Last week of April	Last week of June
02	CPT 103	Rawatpora (Kupwara)	62.66	28.00	28.0	12.25	50	-do-	-do-
03	CPT 104	Shimnagh (Kupwara)	58.00	33.33	32.0	12.25	60	-do-	1st week of July
04	CPT 105	Teetwal (Kupwara)	57.66	29.00	28.0	16.00	55	-do-	Last week of June
05	CPT 106	Teetwal (Kupwara)	68.33	46.00	48.0	36.00	65	-do-	-do-
06	CPT 107	Dildar (Kupwara)	70.00	35.66	30.0	9.00	50	-do-	-do-
07	CPT 108	Handwara (Kupwara)	65.33	31.33	42.0	25.00	60	-do-	1st week of July
08	CPT 109	Chowkibal (Kupwara)	64.00	30.00	36.0	12.25	55	-do-	-do-
09	CPT 110	Drugmulla (Kupwara)	69.66	34.33	38.0	30.25	60	-do-	-do-
10	CPT 111	Sempora (Srinagar)	59.00	26.00	27.0	9.00	50	2nd week of April	-do-
11	CPT 112	Sempora (Srinagar)	63.33	41.33	25.5	20.25	45	3rd week of April	2nd week of June
12	CPT 113	Khonmoh (Srinagar)	67.33	37.66	35.0	12.25	40	-do-	-do-
13	CPT 114	Yechhnambal (Srinagar)	70.66	30.33	24.0	6.25	50	3rd week of April	1st week of July
14	CPT 115	Zowur (Srinagar)	69.00	26.00	40.0	25.00	38	-do-	-do-
15	CPT 116	Chak (Srinagar)	64.33	38.66	35.0	16.00	40	-do-	-do-
16	CPT 117	SKUAST-K (Srinagar)	59.00	40.33	35.0	30.25	45	-do-	-do-
17	CPT 118	Shalimar (Srinagar)	64.66	38.33	28.0	9.00	35	-do-	-do-
18	CPT 119	Kurhama (Ganderbal)	57.00	34.00	35.0	16.00	30	-do-	-do-
19	CPT 120	Wakura (Ganderbal)	62.33	41.66	32.0	12.25	25	-do-	-do-
20	CPT 121	Aahan (Ganderbal)	58.00	29.00	38.0	9.00	40	-do-	-do-
21	CPT 122	Zazuna (Ganderbal)	62.66	37.33	45.0	42.25	35	-do-	-do-
22	CPT 123	Nunar (Ganderbal)	63.33	36.66	30.0	9.00	40	-do-	-do-
23	CPT 124	Dab (Ganderbal)	71.00	45.00	47.0	18.00	45	-do-	-do-
24	CPT 125	Kondbal (Ganderbal)	64.66	38.66	38.0	14.35	60	-do-	-do-
25	CPT 126	Choora (Ganderbal)	68.33	37.33	34.0	22.10	35	-do-	-do-

of variance, variance component, heritability, genetic gain, correlation and genetic divergence in completely randomized design (CRD) and randomized block design (RBD) for growth and biomass traits.

Critical difference (CD)

The critical difference (CD) was calculated as under:
CD = S.E x $t_{0.05}$ (error degree of freedom)

Where: S.E is the standard error of difference calculated as:

$$S.E. = \sqrt{\frac{2 \times MESS}{R \times T}}$$

MESS = Mean sum of square due to error, R = Number of replication, T= Number of treatments $t_{0.05}$ = Tabulated value of t at 5 per cent level of significance. Mean difference between any two families greater than calculated CD value was taken as significant difference.

Variability parameters

$$PCV(\%) = \sqrt{\frac{Vp}{\bar{X}}} \times 100 \qquad GCV(\%) = \sqrt{\frac{Vg}{\bar{X}}} \times 100$$

Where: Vp = Phenotypic variance, Vg= Genotypic variance, PCV (%)= Phenotypic coefficient of variation, GCV (%)= Genotypic coefficient of variation, $\overline{X}$ = Population mean of the character.

Coefficients of variation

Coefficients of variation were calculated as given by Pillai and Sinha (1968).

$$CV\ (\%) = (SD/\overline{X}) \times 100$$

Where: CV = Coefficient of variation, SD = Standard deviation, $\overline{X}$ = Population of mean.

Heritability (broad sense)

Heritability (borad sense) was calculated as suggested by Burton and Devane (1953) and Johnson et al. (1955).

$$h^2 = \frac{Vg}{Vp} \times 100$$

Where: h^2 = Broad sense heritability, Vg = Genotypic variance, Vp = Phenotypic variance.

Seedling height (cm)

Height was measured from collar region up to the apex of leading shoot at the end of growing season.

Collar diameter (mm)

Collar diameter was also measured at the end of growing season with the help of a digital Vernier caliper.

Germination percent

Germination percent was calculated as the number of seeds sown and the number of seeds germinated, expressed in percentage.

$$\text{Germination percent} = \frac{\text{Number of seeds germinated}}{\text{Total number of seed sown}} \times 100$$

RESULTS AND DISCUSSION

Fruit, stone and kernel characteristics

Table 2 presents data pertaining to 25 Candidate plus trees of wild apricot with variation in fruit, stone kernel and oil content characters. Analysis of variance indicated significant differences among 25 different candidate plus trees for all the studied characters. Oil content per cent recovered from kernels showed significant variations and ranged between 47.20% for CPT116 to 50.79% for CPT 110. Maximum value of 50.79% oil content recorded for CPT 110, was followed by CPT117 with 50.40% oil content, however both differed significantly. Six sources recorded above 50% of oil content. There is less than 4.00% oil content variation among all the CPTs, but most of the CPTs differ significantly from one another thereby implying that this character can be exploited for tree improvement programme. Morphometric characteristics of fruit, stone and kernels also recorded significant variations. Maximum fruit size was recorded in CPT 103 (length 31.76 x breadth 31.33 x thickness 29.90 mm). However, this had no relationship with stone and kernel size which was found different in different CPTs irrespective of their fruit size. Maximum seed length of 21.25 mm was recorded for CPT 119. Highest kernel length of 15.30 mm, breadth of 10.25 mm and thickness of 5.48 mm was recorded in CPT 118,103 and 104 respectively.

Germination, survival and seedling characteristics

Data presented in Table 3 revealed highly significant differences through analysis of variance among germination and all the morphological characters studied viz., germination percent, survival per cent, seedling height, seedling collar diameter and number of branches/seedling. The maximum value for germination percent (71.00), survival percent (46.00), seedling height (102.71 cm), seedling collar diameter (6.94 mm) and number of branches per seedling (4.66) were recorded in CPTs – 124, 106, 123, 106 and119 respectively. It has been demonstrated that seeds of a single species when collected from different coordinates (locations/altitudes) differ in viability, germination, growth and biomass performance, as reported by Isik (1986) in *Pinus brutia* , Todaria and Negi. (1995) in some Himalayan tree species and Chauhan et al. (1996) in *Alnus nepalensis.* Rapid genetic gain is the result of selection among CPTs which differ significantly in seed and seedling traits, similar findings were reported by Dangasuk et al. (1997) in *Faidherbia albida*.

Variations refer to observable differences in individual for a particular trait. These differences may partly be due to genetic factors and partly due to environmental effect. The observed value of a trait is the phenotypic value of that individual. The related magnitude of these components determines the genetic properties of any particular species. The extent of variation observed in germination per cent (CV-7.21%), survival per cent (CV-10.67%), seedling height (CV-5.78%), seedling collar diameter (CV-14.95%) and number of branches per seedling (CV-18.23%) was found to be moderately high (Table 3).

Table 2. Variation in fruit, seed, kernel characteristics and oil content (%) in different candidate plus trees of wild apricot (*P. armeniaca* L.)

S/No	CPT	Fruit length (mm)	Fruit breadth (mm)	Fruit thickness (mm)	Stone length (mm)	Stone breadth (mm)	Stone thickness (mm)	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Oil content (%)
01	CPT (WA)102	20.46	18.85	13.05	16.10	14.88	9.34	12.68	8.68	4.84	48.39
02	CPT (WA)103	31.76	31.31	29.90	20.25	15.60	10.29	13.02	10.25	5.34	49.40
03	CPT (WA)104	18.72	15.58	12.65	14.61	10.55	9.68	10.97	6.16	5.48	50.30
04	CPT (WA)105	23.12	22.84	20.20	20.33	15.82	10.04	13.60	8.88	5.37	47.50
05	CPT (WA)106	21.11	21.31	18.56	19.47	16.21	10.12	12.81	8.55	4.65	48.60
06	CPT (WA)107	22.44	25.65	22.46	19.84	15.03	9.79	12.94	8.65	5.16	47.80
07	CPT (WA)108	25.88	24.50	22.88	20.15	16.13	9.86	13.58	8.15	5.26	50.20
08	CPT (WA)109	24.65	24.03	21.79	21.22	15.77	9.74	12.95	6.49	4.47	49.20
09	CPT (WA)110	24.35	22.75	20.60	19.60	15.14	9.58	13.44	7.87	4.75	50.79
10	CPT (WA)111	23.24	24.15	20.04	18.93	15.00	9.89	14.55	9.11	4.77	48.60
11	CPT (WA)112	25.49	25.36	22.40	19.31	15.57	9.88	13.47	9.24	4.66	47.80
12	CPT (WA)113	22.93	20.52	17.67	19.94	15.31	10.41	13.14	9.37	5.40	49.20
13	CPT (WA)114	26.94	27.83	24.39	20.30	16.10	9.94	13.43	9.37	5.11	47.69
14	CPT (WA)115	24.72	23.62	21.14	21.01	15.37	9.58	12.17	8.67	4.98	50.10
15	CPT (WA)116	25.01	21.65	20.22	20.02	15.37	9.77	12.96	9.45	5.25	47.20
16	CPT (WA)117	27.67	25.74	24.94	20.81	16.05	9.91	12.98	8.80	4.90	50.40
17	CPT (WA)118	26.22	24.98	23.26	19.63	15.83	9.85	15.30	10.14	4.91	49.50
18	CPT (WA)119	26.35	25.26	23.32	21.25	16.23	10.22	13.72	9.83	5.12	49.00
19	CPT (WA)120	28.94	27.86	25.74	20.91	15.59	9.63	13.02	8.84	5.32	48.50
20	CPT (WA)121	28.29	26.69	25.16	19.90	16.22	9.59	12.33	8.46	4.51	47.80
21	CPT (WA)122	27.89	26.76	23.24	20.01	16.32	9.84	14.30	9.18	4.92	48.59
22	CPT (WA)123	27.37	27.46	23.46	20.92	15.88	9.84	14.60	9.47	4.85	48.99
23	CPT (WA)124	29.24	28.07	26.76	21.24	16.07	9.76	13.84	9.46	4.94	50.10
24	CPT (WA)125	30.49	28.26	25.43	20.38	15.64	9.91	13.28	9.31	4.96	48.70
25	CPT (WA)126	20.79	20.25	18.59	15.62	16.33	10.05	10.66	8.79	4.84	47.80
Mean		25.36	24.45	21.91	19.67	15.52	9.86	13.19	8.85	4.99	48.88
C.V.		3.44	3.43	3.73	3.65	3.60	2.96	5.63	6.24	7.36	0.30
S.E.		0.49	0.48	0.47	0.42	0.32	0.17	0.44	0.32	0.21	0.02
C.D. 5%		1.41	1.37	1.34	1.21	0.93	0.48	1.25	0.93	0.60	0.15
Range	Lowest	18.72	15.58	12.65	14.61	10.55	9.34	10.97	6.16	4.47	47.20
	Highest	31.76	31.31	29.90	21.25	16.33	10.41	15.30	10.25	5.48	50.79

Table 3. Germination and seedling characters of 25 CPTs of *P. armeniaca* L.

S/No.	Character	Germination (%)	Survival (%)	Seedling height (cm)	Seedling collar diameter (mm)	Number of branches/ seedling
01	CPT (WA)102	53.33	25.33	98.99	4.28	4.33
02	CPT (WA)103	62.66	28.00	85.83	5.20	3.33
03	CPT (WA)104	58.00	33.33	101.33	4.16	4.33
04	CPT (WA)105	57.33	29.00	94.42	4.57	3.66
05	CPT (WA)106	68.33	46.00	89.21	6.94	2.33
06	CPT (WA)107	68.00	35.66	79.79	5.96	3.33
07	CPT (WA)108	65.33	31.33	93.97	6.34	4.00
08	CPT (WA)109	64.00	30.00	89.38	6.73	2.66
09	CPT (WA)110	69.66	34.33	100.34	5.30	3.66
10	CPT (WA)111	59.33	26.33	94.03	4.28	3.33
11	CPT (WA)112	63.33	41.66	86.76	4.52	3.33
12	CPT (WA)113	67.33	37.66	82.17	5.84	2.66
13	CPT (WA)114	70.66	30.66	95.39	6.53	3.33
14	CPT (WA)115	69.33	25.66	87.04	4.59	4.33
15	CPT (WA)116	64.00	37.33	78.21	3.99	4.00
16	CPT (WA)117	59.33	39.00	83.91	4.79	2.33
17	CPT (WA)118	66.00	41.00	79.21	4.22	3.33
18	CPT (WA)119	57.00	35.00	99.79	5.50	4.66
19	CPT (WA)120	62.33	41.66	85.83	6.90	3.66
20	CPT (WA)121	58.33	29.66	94.81	5.55	4.66
21	CPT (WA)122	62.33	37.66	75.03	4.19	3.66
22	CPT (WA)123	63.33	36.66	102.71	4.75	2.33
23	CPT (WA)124	71.00	45.00	76.15	6.28	2.33
24	CPT (WA)125	64.33	38.00	81.53	5.03	3.66
25	CPT (WA)126	66.00	37.66	94.52	4.77	4.33
Mean		63.62	34.94	89.21	5.25	3.50
C.V.		7.21	10.67	5.78	14.95	18.23
S.E.±		2.65	2.15	2.97	0.45	0.36
C.D. 5%		7.53	6.12	8.47	1.28	1.04
Range	Lowest	53.33	25.33	75.03	3.99	2.33
	Highest	71.00	46.00	102.71	6.94	4.66

Cluster analysis and percent contribution of characters studied to total genetic gain

In measuring genetic distance between populations and differentiating population at early stages in variability studies, seed and seedling characters can be used as a quantitative character in defining a genotype. As tree characters measured in natural population are amenable to geographical and environmental interactions, seedling characters measured in different environment are more useful in differentiating population at preliminary stage (Hedge et al., 2004).

The analysis of variance revealed the existence of significant difference among 25 plus tree progenies for all the traits, indicating the existing of huge genetic variability. The cluster pattern of 25 candidate plus tree progenies/genotypes under open field environmental conditions is given in Table 4. Under open field environment they were grouped into six clusters. Cluster I recorded the highest number of 12 families (CPT-105, 126, 119, 111, 108, 114, 110, 115, 107, 116, 113 and CPT 120) followed by Cluster III with nine (9) families (CPT-117, 123, 122, 125, 118, 112, 124, 103 and CPT 109) under open field environment. Families of Candidate plus trees occupying same cluster numbers, indicate their genotypic stability with respect to the eco-geographical coordinates. Families of candidate plus tree formed same groups in different clusters indicating that even thought the genotypes (parents) were selected from different eco-geographical areas, the genetic make-up along with breeding system, heterogeneity, and unidirectional selection pressure may be the cause of genetic diversity among different families of candidate plus tree, besides geographical variation to some extent. The cluster pattern in *Bombex ceiba* and *Eucalyptus terreticornis* proved that geographical variation need not necessarily be related to

Table 4. Distribution of 25 CPTs in different clusters in open field environmental conditions.

Cluster	I	II	III	IV	V	VI
I	**0.00**	4.92	4.77	7.43	5.29	8.20
II		**0.00**	5.08	7.80	6.04	10.20
III			**0.00**	8.325	5.34	9.24
IV				**0.00**	7.96	7.23
V					**0.00**	9.22
VI						**0.00**

Table 5. Inter and Intra cluster distances of 25 CPT progenies of *Prunus armeniaca L.*

Cluster	Total No. of CPTs in each cluster	Notation of CPTs
I	12	CPT(WA)-105, 126, 119, 111, 108, 114, 110, 115, 107, 116, 113, 120
II	1	CPT(WA)-121
III	9	CPT(WA)-117, 123, 122, 125, 118, 112, 124, 103, 109
IV	1	CPT(WA)-102
V	1	CPT(WA)-106
VI	1	CPT(WA)-104

genetic diversity (Chaturvedi and Pandey, 2001; Surendran and Chandrasekharan, 1984). Intercrossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage. Progeny derived from such diverse crosses are expected to show wide spectrum of genetic variability providing a greater scope for isolating transgressive segregants in the advance generation. Hence, these genotypes might be used in multiple crossing programme to recover transgreesive segregants (Thoday, 1960). As revealed by Table 5 inter-cluster distance was found to be highest between cluster II and VI (10.20) under open field environmental conditions followed by 9.24 between cluster III and VI. Studies in linseed and maize have revealed that the material is vulnerable to the variable environmental conditions (Murthy et al., 1973; Prasad and Singh, 1990).

Mean performance of the clusters with respect to different character (Table 6) indicated that highest mean values for oil content (50.30%) and seedling height of 101.33 mm were recorded in cluster VI , whereas maximum mean values for kernel thickness (20.24 mm) kernel length (12.35 mm), kernel breadth (8.91 mm), kernel thickness (5.11 mm) and germination percent of 64.69 was recorded in cluster I. Cluster II recorded maximum values for fruit length, thickness and seed breadth and number of branches per seedling. Cluster V recorded maximum values for seed thickness (10.12 mm), survival 46% and seedling collar diameter of 6.94 mm. Cluster IV did not record highest mean even for a single parameter studied. The present results also get support from (Gupta and Patil, 1988) in *Leucaena latisiliqua* and (Manga and Sen, 2000) in *Prosopis cineraria*. Contribution of different characters to total divergence is illustrated in Figure 1. Fruit length contributed maximum (39.33%) followed by fruit breadth (11.00%) and seedling height (9.67%) under open field environmental conditions. Knowledge of percent contribution to total divergence gives us an idea about scope of effecting genetic improvement through selection of desired traits.

Conclusion

The cluster pattern proved that geographical variation need not necessarily be related to genetic diversity (Chaturvedi and Pandey, 2001; Surendran and Chandrasekharan, 1984). Intercrossing of divergent groups would lead to greater opportunity for genetic material (gene) crossing over, to release hidden variability by breaking linkage. Progeny derived from such diverse crosses are expected to show wide spectrum of genetic variability provided a greater scope for isolating transgressive segregants in the advance generation. Hence, these genotypes might be used in multiple crossing programme to recover transgreesive segregants (Thoday, 1960).

On the basis of inter and intra cluster distance cluster no. II and VI may be considered as diverse and can be utilized for hybridization when select genotypes for breeding purposes. Therefore for getting heterosis, the genotypes from cluster I, II, V and VI with high cluster means for majority of characters can be utilized for hybridization in the further tree improvement programme of this species.

Table 6. Mean and Grand Mean values for various characters in different clusters for 25 CPT progenies of *P. armeniaca* L.

Cluster/ characters	I	II	III	IV	V	VI	Grand mean
Oil content (%)	48.70	47.80	49.18	48.39	48.60	50.30	48.83
Fruit length (mm)	24.56	28.29	27.86	20.46	21.11	18.72	23.50
Fruit breadth (mm)	23.91	26.69	26.88	18.85	21.31	15.58	22.20
Fruit thickness (mm)	21.44	25.16	24.57	13.05	18.56	12.65	19.24
Seed length (mm)	20.24	19.90	20.42	16.10	19.47	14.61	18.46
Seed breadth (mm)	15.62	16.22	15.86	14.88	16.21	10.55	14.89
Seed thickness (mm)	9.90	9.59	9.89	9.34	10.12	9.68	09.75
Kernel length (mm)	13.35	12.33	13.75	12.68	12.81	10.97	12.65
Kernel breadth (mm)	8.91	8.46	9.15	8.68	8.55	6.16	08.32
Kernel thickness (mm)	5.11	4.51	4.88	4.84	4.65	5.48	04.91
Germination (%)	64.69	58.33	64.03	53.33	68.33	58.00	61.12
Survival (%)	33.52	29.66	37.44	25.33	46.00	33.33	34.21
Seedling height (cm)	90.46	94.87	84.50	98.99	89.21	101.33	93.23
Seedling collar diameter (mm)	5.38	5.55	5.08	4.28	6.94	4.16	5.23
Number of branches/ seedling	3.75	4.66	3.00	4.33	2.33	4.33	3.73

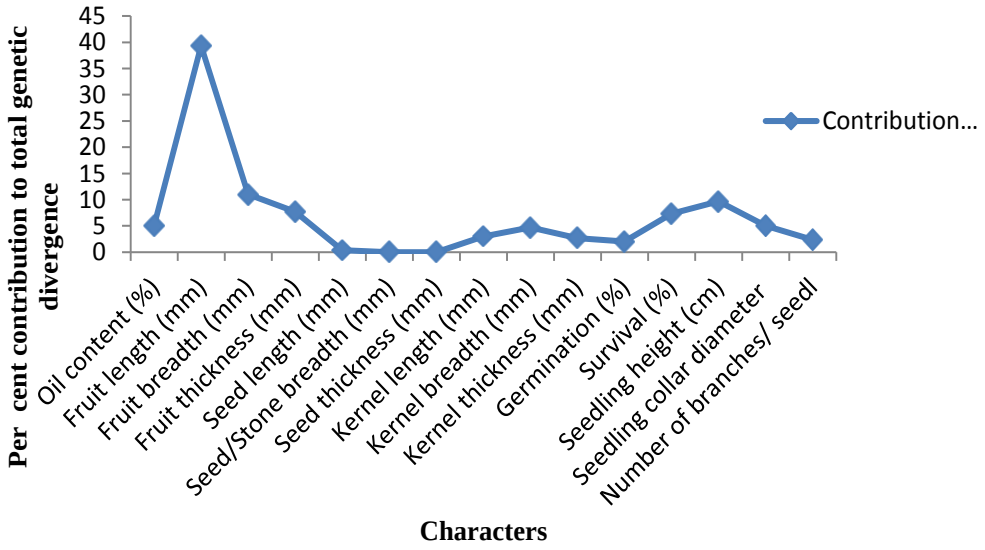

Figure 1. Percent contribution of each character to total divergence for 25 CPTs of *P. armeniaca* L.

Conflict of Interest

The authors have not declared any conflict of interest.

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