Studies on percentage oil content variability and genetic divergence analysis of *Prunus armeniaca* L. (Wild Apricot) in Kashmir and Ladakh regions of India.

Abstract

The study was undertaken to estimate the percentage oil content variability and genetic divergence for seed and seedling characters of 17 Candidate Plus Trees (CPTs)/half-sib families of Wild Apricot (*Prunus armeniaca* L) collected from different locations of Kashmir (temperate) and Laddakh (arid) regions in India. Seeds of 17 candidate plus trees were collected and graded to constitute seed lots of different CPTs. After the dimensional measurements for seed and kernel characters, part of the seeds from seed lots of each CPT/family 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 five clusters under open field environment. Inter-cluster distance was found to be highest between cluster III and IV, revealing their genetic closeness from high to low. On the basis of inter and intra cluster distance cluster no. III and IV may be considered as diverse and can be utilized for hybridization when selecting genotypes for breeding purposes. Seedling height followed by oil content (%) and number of branches/seedling respectively, contributed maximum to the total divergence and played a prominent role in creating the genetic diversity.

Keywords: Oil content per cent, genetic variability, cluster, genetic divergence, *Prunus armeniaca*

Introduction

As demanded in the present scenario of ever increasing human population, Indian NOVOD Board has been mandated to increase edible oil production through non-traditional oil seed crops. 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 tons (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 increase the production through tree borne oil seeds which are non-traditional oil crops. Wild apricot 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.

Wild apricot (*Prunus armeniaca* L.) belongs to family "Rosaceae" grows throughout north-western Himalaya between elevations of 1,000 to 3,000m. The importance of the plant is well realized especially in temperate region for 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 not edible as such due to high acids and low sugars. The seed (stones) yields 27-33% of kernels and the kernels yield up to 53% of edible oil.

(Anonymous 2009). Kernels are bitter in taste due to the presence of cyanogenic glycoside amygdalin (Montgomery 1969). Oil has 94% unsaturated fatty acids (Gandhi et al. 1974) and linoleic acids. The oil is utilized for cooking, body massage and as raw material for cosmetic and pharmaceutical industry (Parmar and Sharma 1992).

In wild apricot, kernel weight which is directly related with oil yield is a complex character and it is dependent on a number of nut components. Information on the association of different characters among themselves and their relationship with kernel weight is of paramount importance for making the selection. In nature widespread species variations are to be expected between populations growing under different geographical conditions, therefore the selection of appropriate plus tree/seed sources/genotype assumes the foremost importance in plantating. Selection of the superior tree is one of the major factor affecting establishment and productivity. 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 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 and Lal et al. 2005).

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 genetic improvement through selection**.**

Materials and Methods

The present experimental studies were conducted in Kashmir (temperate) and Laddakh (arid) regions of India, both the provinces fall within the extent of Himalaya belt with dimensional coordinates ranging between 73° 85´ – 79 ° 34´ E longitude and 33° 47´ – 35° 82´ N latitude This part of experimental work was carried out under the research project entitled "National Network on Integrated Development of Wild apricot (*Prunus armeniaca* L.)" sponsored by NOVOD, Board Project, Ministry of Agriculture, New Delhi, Govt. of India

In the present study, candidate plus trees (genotypes) of a sample of (n = 17) 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.

i. Stone and kernel weight, 100 by number and in 3 replicates (digital electronic balance)
ii. Stone and kernel length, 100 by number and in 3 replicates (from base to apex)

iii. Stone and kernel breadth, 100 by number and in 3 replicates (edge-wise from the centre)
iv. Width, 100 by number and in 3 replicates (from middle of the stone and kernel).

250 g of kernels in 5 replicates were used for oil analysis percentage (%). 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 1,850m amsl within the coordinates of 34^0-$05^/$N latitude and 74^0-$50^/$ E longitude, receiving a mean annual rainfall of about 660mm and mean temperature of 13.3 ^{0}C. Minimum temperature of the area may drop to -7 ^{0}C in winter months while as maximum temperature may touch to 35 ^{0}C in summer. Soil at the experimental site is neutral having available nitrogen of 100kg/ha, phosphorus 10kg/ha and potassium 200kg/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 hours. 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 17 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 Pillai and Sinha 1968. Genetic divergence and clustering information was assessed by non-hierarchical Euclidean Cluster Analysis (Spark 1973).

Statistical analysis

The data was analyzed statistically for the assessment of analysis of variance, variance component, heritability, genetic gain, correlation and genetic divergence in CRD and RBD design 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.

Coefficients of variation - CV (%)

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 end of growing season with the help of a digital Vernier caliper.

Germination (%)

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

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

. **Cluster analysis:** Genetic divergence and its per cent contribution of each character to total divergence was assessed by Non-hierarchical Euclidean Cluster Analysis (Spark 1973) using computer software SPSS.

K – Means clustering: Aimed to assign objects to a user defined number of clusters (K) in such a way that maximizes the separation of those clusters while minimizing intra-cluster distances relative to the clusters mean. Alternate distances or dissimilarities were transformed to be compatible with Euclidean representation.

Steps of K – Means clustering:

Algorithms did not allow a hierarchy and produced a single partition. Number of clusters (K) required were kept as five. In the first step initial cluster centres (the CPTs) were determined randomly for each of the clusters by SPSS software. Each iteration allocated clusters to each of the five clusters based on their distance from the cluster. Cluster centers were computed again and clusters were reallocated to the nearest cluster thereby stopped the process further

Table 1 Passport details and morphological observations of 17 selected Candidate plus trees (S_1-S_{17}) of *Prunus armeniaca* L. identified in Kashmir and Laddakh region of India.

CPT No.	CPT Notation.	Source of collection (Site Name)	Approximate Age (yrs)	Height (m)	Diameter (cm)	Canopy (m^2)	Total fruit yield (kg)	Time of flowering	Time of fruiting
01/100	S_1	Arwani (Anantnag)	20.00	7.50	28.63	12.00	42.00	1st weak of April	1st weak of July
02/100	S_2	Shopian (Pulwama)	18.00	9.00	23.86	7.20	29.00	2nd weak of April	Ending June
03/100	S_3	Malangpora (Pulwama)	10.00	5.50	15.11	3.00	60.00	Beginning of May	Mid August
04/100	S_4	Budgam (Budgam)	50.00	6.15	34.04	100.00	100.00	Beginning of May	Beginning of August
05/100	S_5	Ganderbal (Srinagar)	30.00	6.25	29.27	225.00	300.00	-do-	1st week of August
06/100	S_6	Manasbal (Baramulla)	100.00	9.23	39.13	100.00	200.00	-do-	-do-
07/100	S_7	Chitternar (Baramulla)	100.00	12.30	39.13	49.00	200.00	-do-	-do-
08/100	S_8	Onegam (Baramulla)	90.00	11.40	37.54	90.25	180.00	-do-	-do-
09/100	S_9	Kupwara (Kupwara)	20.00	6.50	20.68	12.00	50.00	April	Last week of June
10/100	S_{10}	Uri (Baramulla)	25.00	7.00	22.27	16.00	60.00	April	Last week of June
11/100	S_{11}	Poyen (Kargil)	27.00	7.20	22.59	15.00	62.00	April	Last week of June
12/100	S_{12}	Akchmal (Kargil)	35.00	10.50	46.00	14.06	55.00	Last week of April	Last week of June
13/100	S_{13}	Minjee (Kargil)	30.00	6.50	28.00	12.25	50.00	-do-	-do-
14/100	S_{14}	Saspool (Kargil)	30.00	9.50	32.00	12.25	60.00	-do-	1st week of July
15/100	S_{15}	Leh (Main city) (Leh)	40.00	8.50	28.00	16.00	55.00	-do-	Last week of June
16/100	S_{16}	Zangash (Leh)	45.00	9.00	48.00	36.00	65.00	-do-	-do-
17/100	S_{17}	Rambhirpora (Leh)	30.00	7.50	30.00	9.00	50.00	-do-	-do

. **Results and Discussion**

i) Stone and kernel characteristics

Table 2 presents data pertaining to 17 Candidate plus trees of wild apricot with variation in stone, kernel and oil content characters. Analysis of variance indicated significant differences among 17 different candidate plus trees for all the studied characters. Oil content per cent recovered from kernels showed significant variations and ranged between 40.35% for CPT08/100 (S_8) to 52.42% for CPT 04/100 (S_4). Maximum value of 52.42% oil content recorded for CPT04/100 (S_4) was followed by CPT16/100 (S_{16}) with 52.18% oil content. Out of 17 seed sources eight sources recorded above 50% oil content. There is more than12.00% oil content variation among all the 17 CPTs, but most of the CPTs differ significantly from one another as revealed by C.D 5% and C.V. % (Table 2) thereby implying that this character can be exploited for tree improvement programme.

Morphometric characteristics of stone and kernels also recorded significant variations. Maximum stone weight (147.54 g) was recorded for CPT13/100 (S_{13}) and the average stone weight recorded was (118.18 g). Average stone length recorded was (19.56 mm) and the highest value (21.67 mm) was recorded for CPT 06/100 (S_6). Average stone width recorded was (15.50 mm) and the highest value (17.72 mm) was recorded for CPT 05/100 (S_5). Average stone diameter recorded was (10.13 mm) and the maximum value (11.36 mm) was obtained for CPT 16 (S_{16}). Maximum kernel weight (49.91 g) was recorded for CPT 13/100 (S_{13}) and the average kernel weight recorded was (37.49 g). Average kernel length recorded was (13.28 mm) and the highest value (14.67mm) was recorded for CPT 13/100 (S_{13}). Average kernel width recorded was (9.78 mm) and the highest value (11.30 mm) was recorded for CPT 13/100 (S_{13}). Average kernel diameter recorded was (5.85 mm) and the maximum value (7.06 mm) was obtained for CPT 03/100 (S_3).

ii) Germination, survival and seedling characteristics

Data presented in (Table 2) revealed highly significant differences through analysis of variance among germination and all the morphological characters studied viz., germination per cent, survival per cent, seedling height, seedling collar diameter and number of branches/seedling. The maximum value for germination per cent (68.33), survival per cent (66.33), seedling height (160.10cm), seedling collar diameter (10.66mm) and number of branches per seedling (13.30) were recorded in CPTs – 06/100(S_6), 06/100(S_6), 08/100(S_8), 09/100(S_9) and01/100(S_1), 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 et al. 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- 3.67%), survival per cent (CV- 4.37%), seedling height (CV- 1.72%),

seedling collar diameter (CV-10.98%) and number of branches per seedling (CV-17.32%) was found to be moderately high (Table 2).

iii) Cluster analysis and percent contribution of characters studied to total genetic divergence and 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 17 plus tree progenies for all the traits, indicating the existing of huge genetic variability. The cluster pattern of 17 Candidate plus tree progenies/genotypes under open field environmental conditions is given in (Table 3). Under open field environment they were grouped into five (5) clusters. Cluster I recorded the highest number of 5 families (CPT- 02/100 (S_2), 03/100 (S_3), 04/100 (S_4), 05/100 (S_5) and 07/100 (S_7), followed by Cluster V with four (4) families (CPT-10/100 (S_{10}), 14/100 (S_{14}), 15/100 (S_{15}) and 16/100 (S_{16}) 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 though 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 *Eucalyptus terreticornis* and *Bombex ceiba* proved that geographical variation need not necessarily be related to genetic diversity (Surendran and Chandrasekharan 1984; Chaturvedi and Pandey 2001).

As revealed by Table 4, Inter-cluster distance was found to be highest between cluster I and III (2705.97) under open field environmental conditions followed by (1501.95) between cluster III and V. However, 17 families within a cluster showed low to medium (85.17 to 552.14) intra cluster distance under open field environmental conditions, revealing their genetic closeness from high to medium. Similar studies in Pigeon-pea, (Patel and Acharaya 2011), linseed (Murthy et al. 1973) and maize (Prasad and Singh 1990) have revealed that the material is vulnerable to the variable environmental conditions. The highest D^2 value (4082.72) and (3288.60) was observed between (S_9 & S_6) and (S_6 & S_1) respectively, (Table 5). 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 transgressive segregants (Thoday 1960 and Lal et al. 2005)

Mean performance of the clusters with respect to different character (Figure 1) indicated that highest cluster mean value for oil content (51.12%) was recorded in cluster V, maximum cluster mean values for kernel weight (41.99 g), kernel length (13.65 mm), kernel width (10.34 mm), stone weight (135.98 g), stone width (16.43 mm), stone diameter (10.82 mm), germination

percent (64.66) and survival percent (62.44) was recorded in cluster III. Cluster I recorded maximum values for seedling height (149.20 mm), collar diameter (9.10) and number of branches per seedling (11.23). Cluster II recorded maximum values for kernel diameter (6.23 mm), whereas Cluster IV recorded maximum mean value for stone length (20.58 mm). The present results also get support from Gupta and Patil 1988 in *Leucaena latisiliqua*, Manga and Sen 2000 in *Prosopis cineraria* and Konda et al. 2009 in *Vigma mungo*.

Contribution of different characters to total divergence is illustrated in (Figure 2). Seedling height contributed maximum (38.97 %) followed Oil content (33.09 %) and number of branches per seedling (15.44 %) under open field environmental conditions. Knowledge of per cent contribution to total divergence gives us an idea about scope of effecting genetic improvement through selection of desired traits.

Conclusion

From the present study it is revealed that considerable genetic differences exist in all the parameters i.e. oil content percent, seedling and morphometric characters among the 17 different genotypes of wild apricot (*Prunus armeniaca*). Out of 17 seed sources eight sources (S_3, S_4, S_{11}, S_{12}, S_{13}, S_{15}, S_{16} & S_{17}) recorded above 50% oil content in which four sources respectively (S_4, S_{13}, S_{16} & S_{12}) recorded more than 52% oil content and there is more than12.00% oil content variation among all the 17 CPTs, but most of the CPTs differ significantly from one another thereby implying that this character can be exploited for tree improvement programme. With respect to morphometric and seedling characters S_{13} and S_6 respectively out performed than rest of the sources. On the basis of inter and intra cluster distance cluster number. I and III may be considered as diverse and can be utilized for hybridization when selecting genotypes for breeding purposes. Therefore for getting heterosis, the genotypes from cluster III & I with high cluster means for majority of characters can be utilized for hybridization in the further tree improvement programme of this species. Similar results were substantiated in *Cajanas cajan* by Sreelakshmi et al. 2010. The cluster pattern proved that geographical variation need not necessarily be related to genetic diversity. 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 provided a greater scope for isolating transgressive segregants in the advance generation.

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Table 2 Variation in seed, kernel, seedling characteristics and oil content (%) in 17 different Candidate Plus Trees of Wild Apricot (*Prunus armeniaca* L.)

Character / CPT Notation	Stone Weight (g)	Kernel Weight (g)	Stone Length (mm)	Kernel Length (mm)	Stone Width (mm)	Kernel Width (mm)	Stone Diameter (mm)	Kernel Diameter (mm)	Germination (%)	Survival (%)	Seedling Height (cm)	Collar Diameter (mm)	No. of Branches/ Seedling	Oil Content (%)
S_1	117.76	37.42	20.41	13.39	15.89	9.60	10.56	6.12	47.66	37.66	146.80	7.78	13.30	43.63
S_2	125.22	36.55	20.62	13.29	16.34	9.76	10.59	5.51	48.66	45.68	149.70	8.36	9.80	49.32
S_3	116.00	36.16	20.39	12.40	15.00	9.12	10.34	7.06	54.00	49.33	142.20	8.05	11.20	50.90
S_4	116.50	37.00	20.21	12.86	15.62	9.33	10.82	6.10	55.33	50.11	132.80	7.10	8.10	52.42
S_5	114.14	36.90	20.42	13.36	17.72	9.32	10.74	5.69	50.33	49.33	131.20	7.20	9.60	48.12
S_6	138.08	42.30	21.67	12.88	16.89	9.97	11.29	5.63	68.33	66.33	139.10	8.04	9.10	49.01
S_7	113.80	39.40	18.22	13.52	14.38	9.57	9.63	6.11	58.66	55.00	146.70	8.55	11.00	48.11
S_8	114.42	33.47	19.91	12.96	15.04	9.32	10.18	5.44	48.66	37.33	160.10	8.86	10.80	40.35
S_9	105.40	34.63	14.25	13.22	10.42	9.69	5.14	5.55	53.33	52.00	140.70	10.66	9.60	48.13
S_{10}	116.18	38.80	20.92	14.02	14.87	9.49	9.74	5.74	56.66	52.33	129.40	7.12	10.76	45.57
S_{11}	73.37	34.11	18.43	12.94	15.82	9.79	9.51	5.57	59.33	57.33	125.50	7.72	9.13	50.23
S_{12}	95.01	33.88	18.38	13.02	14.96	9.93	10.01	5.48	62.11	60.00	128.10	7.86	10.75	52.01
S_{13}	147.54	49.91	20.60	14.67	16.85	11.30	10.92	6.09	59.33	57.00	123.70	7.12	8.76	50.25
S_{14}	122.35	33.76	18.55	13.41	15.56	9.77	10.27	5.65	66.33	64.00	129.80	8.00	10.70	47.51
S_{15}	114.70	34.98	20.78	13.61	15.35	9.98	9.89	5.25	58.33	53.33	127.80	7.61	9.96	50.61
S_{16}	135.48	38.90	19.21	12.86	16.31	10.11	11.36	6.08	60.33	55.66	139.53	7.62	7.13	52.18
S_{17}	143.12	39.22	19.51	13.31	16.42	10.26	11.23	6.43	55.66	52.00	151.10	8.35	11.63	51.89
Mean	118.18	37.49	19.56	13.28	15.50	9.78	10.13	5.85	56.65	52.61	137.90	8.00	10.08	48.84
C.V.	4.48	9.03	9.63	6.91	10.98	6.17	10.57	8.43	3.69	4.37	1.72	10.98	17.32	4.25
S.E.	3.06	1.95	1.09	0.53	0.98	0.35	0.62	0.28	1.21	1.33	1.37	0.51	1.01	1.20
C.D. 5%	8.80	5.63	3.13	1.53	2.83	1.00	1.78	0.82	3.48	3.82	3.95	1.46	2.90	3.45
Range Lowest	73.37	33.47	14.25	12.40	10.42	9.12	5.14	5.25	47.66	37.33	123.70	7.10	7.13	40.35
Range Highest	147.54	49.91	21.67	14.67	17.72	11.30	11.36	7.06	68.33	66.33	160.10	10.66	13.30	52.42

Table 3 Cluster distribution of 17 selected Candidate Plus Tree progenies (s_1-s_{17}) of *Prunus armeniaca* L.

Cluster No	No. of CPTs in each cluster	Notation of CPTs
I	5.00	S_2, S_3, S_4, S_5, S_7
II	3.00	S_6, S_{13}, S_{17}
III	3.00	S_1, S_8, S_9
IV	2.00	S_{11}, S_{12}
V	4.00	S_{10}, S_{14}, S_{15}, S_{16}

Table 4 Inter and Intra Cluster distances of 17 selected Candidate Plus Tree progenies (s_1-s_{17}) of *Prunus armeniaca* L.

Cluster No.	I	II	III	IV	V
I	249.992				
II	1108.327	229.217			
III	2705.979	790.181	552.14		
IV	1099.913	399.906	709.795	85.177	
V	1445.641	1048.825	1501.957	415.203	245.090

Table 5 D^2 value for 17 selected Candidate Plus Tree progenies (s_1-s_{17}) of *Prunus armaniaca* L.

Notation	S_1	S_2	S_3	S_4	S_5	S_6	S_7	S_8	S_9	S_{10}	S_{11}	S_{12}	S_{13}	S_{14}	S_{15}	S_{16}	S_{17}
S_1	0.00																
S_2	529.59	0.00															
S_3	609.58	162.15	0.00														
S_4	740.72	398.87	73.25	0.00													
S_5	654.89	410.63	152.85	75.83	0.00												
S_6	3288.60	1425.68	1306.32	1418.04	1442.53	0.00											
S_7	614.24	114.58	37.85	154.32	230.14	1252.34	0.00										
S_8	120.97	723.52	940.89	1173.85	1163.08	4014.56	882.76	0.00									
S_9	306.56	1039.75	872.53	890.90	987.68	4082.72	881.38	322.43	0.00								
S_{10}	833.20	546.93	248.55	144.43	48.66	1260.06	309.92	1430.64	1181.08	0.00							
S_{11}	1390.41	1517.5	821.31	487.46	601.47	2935.39	947.86	1823.79	1000.73	725.37	0.00						
S_{12}	1345.78	881.94	348.27	155.56	265.37	1505.15	423.91	1848.48	1264.62	310.77	245.08	0.00					
S_{13}	1538.32	827.28	695.73	698.09	554.56	755.90	717.72	2289.54	2243.81	351.44	1959.39	1063.44	0.00				
S_{14}	1934.92	954.08	545.31	438.74	424.64	493.86	585.88	2655.68	2305.60	296.16	1161.02	387.32	406.64	0.00			
S_{15}	1104.09	557.45	204.77	90.13	87.32	1008.87	272.28	1684.49	1354.27	64.67	626.20	149.38	455.90	168.46	0.00		
S_{16}	1112.54	270.54	137.99	220.25	304.59	664.26	139.40	1550.36	1522.44	296.60	1262.70	491.15	375.35	298.11	207.28	0.00	
S_{17}	1422.96	268.87	492.76	829.70	867.98	686.14	406.75	1739.71	2182.56	891.14	2458.79	1334.68	666.29	852.13	820.52	261.24	0.00

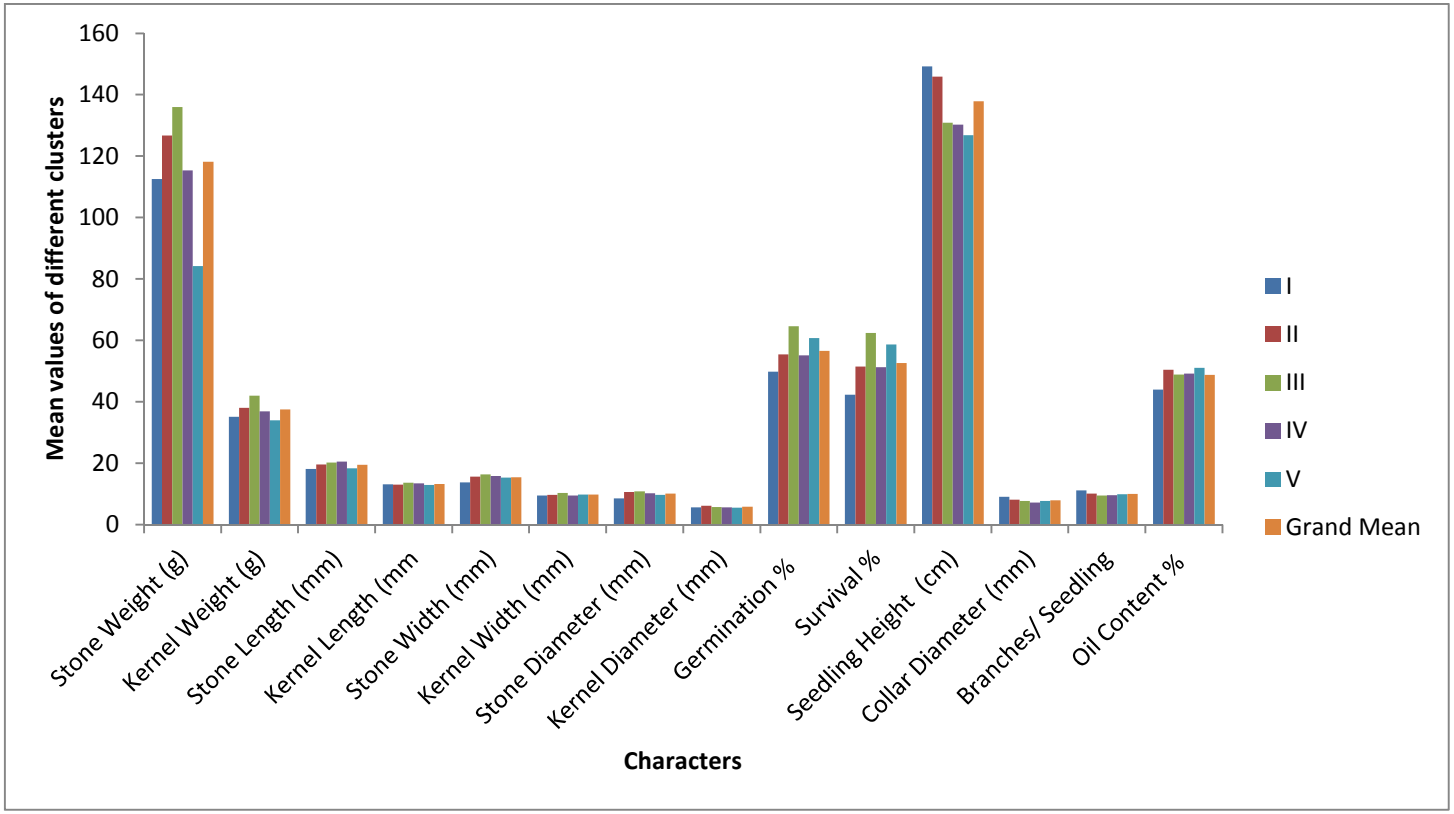

Figure 1 Mean values of various characters in different clusters for 17 candidate plus tree progenies (S_1-S_{17}) of *Prunus armeniaca* L.

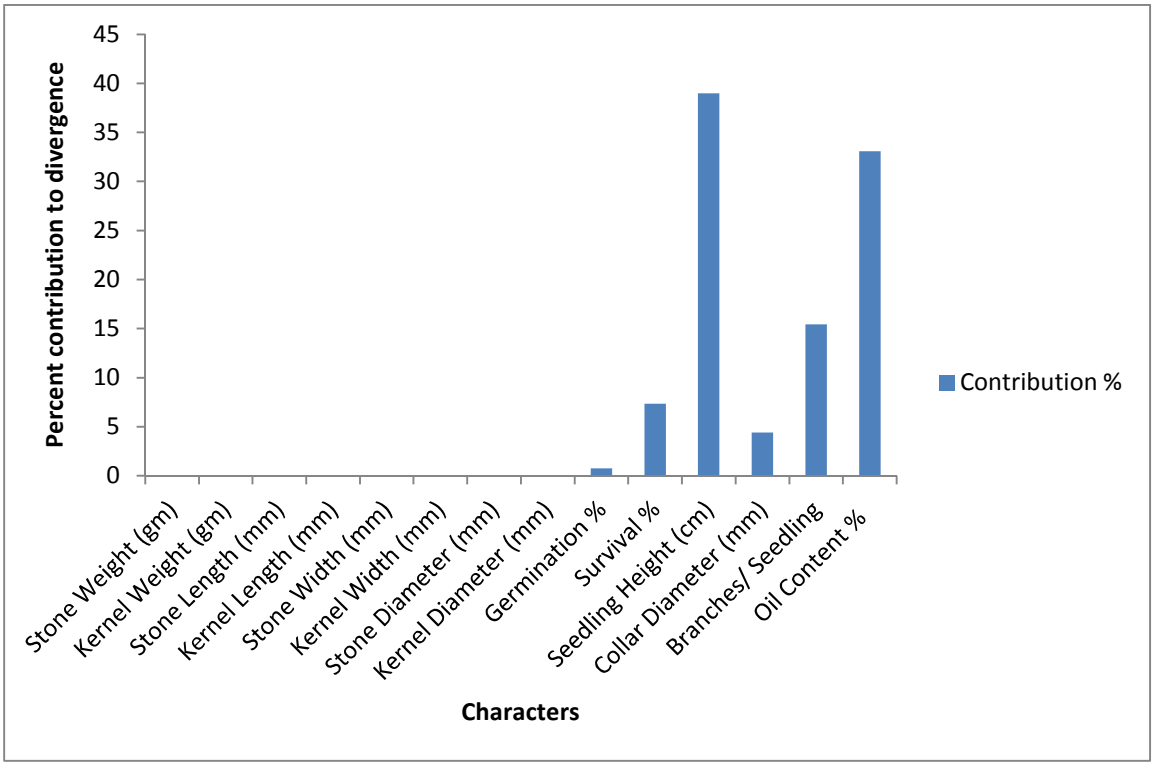

Figure 2 Percent contribution of each character to total genetic divergence for 17 different CPTs of *Prunus armeniaca L.*