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Oil Content Variation And Cluster Analysis Of Different Genotypes Of Wild Apricot Collected From Different Regions Of Jammu & Kashmir, India.

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***Abstract:* — The experimental investigation was undertaken at Faculty of Forestry, SKUAST-Kashmir, India, to estimate the percentage oil content variability and genetic divergence for seed and seedling characters of 22 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. Candidate Plus Trees (CPTs) of Wild Apricot (Prunus armeniaca L.) were selected, based on check tree method. Fresh and fully ripened open pollinated seeds of 22 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, with a view to assess the expression of genetic diversity using Non-hierarchical Euclidean cluster analysis. Analysis of variance indicated significant differences among 22 different candidate plus trees for all the studied characters. Oil content per cent recovered from kernels showed significant variations and ranged between 25.52% for CPT 15/075 (S5) to 54.64% for CPT 14/075 (S5). Candidate plus tree progenies were grouped into five clusters under open field environment. On the basis of inter and intra cluster distance cluster no. I and V may be considered as diverse and can be utilized for hybridization when selecting genotypes for breeding purposes. Seedling height followed by survival per cent, germination per cent, fruit diameter, fruit length and oil content per cent respectively contributed maximum to the total divergence and played a prominent role in creating the genetic diversity. Out of 22 seed sources four sources (S5, S8, S10, & S12) recorded above 50% oil content. With respect to morphometric and seedling characters S4, S5, S18 and S10 respectively out performed than rest of the sources. On the basis of inter and intra cluster distance cluster number. I and V may be considered as diverse and can be utilized for hybridization when selecting genotypes for breeding purposes.**

***Index Terms*— Oil content per cent, genetic variability, cluster, genetic divergence, Prunus armeniaca.**

I. INTRODUCTION

As demanded in the present scenario of ever increasing human population, in India 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 3,000 m. 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 unfit for table purpose 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).

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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 plantation. 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; 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. Therefore, the present study was undertaken to estimate the percentage oil content variability and genetic divergence for seed and seedling characters of 22 Candidate Plus Trees (CPTs)/half-sib families of Wild Apricot (Prunus armeniaca L)

II. 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, Govt. of India

In the present study, candidate plus trees (genotypes) of a sample of (n = 22) of wild apricot based on tree check method were selected and marked (Wani and Wani, 2013). 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 calliper, dimensional morphological data was recorded on the following characters (Wani *et al*., 2013)

i. Stone and kernel weight (digital electronic balance)
ii. Stone and kernel length (from base to apex)
iii. Stone and kernel breadth (edge-wise from the centre) and
iv. Width (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 (Mughal *et al.*, 2015).

To understand the significance of difference among 22 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,

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genetic gain, correlation and genetic divergence in CRD and RBD design for growth and biomass traits.

Critical difference (CD).

Critical difference (CD) was calculated as given by Fisher in 1935

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 / X) $\overline{x}$ 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).

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

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 was assessed by Non-hierarchical Euclidean Cluster Analysis (Spark, 1973) using computer software SPSS.

K – Means clustering: As suggested by MacQueen in 1967, 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:

1. Algorithms did not allowed a hierarchy and produced a single partition
2. Number of clusters (K) required were kept as five
3. In the first step initial cluster centres (the CPTs) were determined randomly for each of the clusters by SPSS software
4. Each iteration allocated clusters to each of the five clusters based on their distance from the cluster.
5. 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 22 selected Candidate plus trees (S1-S22) of Prunus armeniaca L. identified in Jammu and Kashmir, India.

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CPT Notation	CPT No.	Source of collection (Site Name)	Age Approx. (years)	Height of Tree (m)	Trunk Girth (cm)	Diameter	Canopy (m^2)	Total Yield (Kg)	Time of flowering	Time of fruiting
S_1	01/075	Zainger (Baramulla)	25.00	10.00	95.00	30.22	16.00	45.00	April	2nd weak of July
S_2	04/075	Baramulla	18.00	8.00	70.00	22.27	7.50	30.00	April	July
S_3	07/075	Upper Chakoora (Pulwama)	20.00	6.00	137.00	43.59	45.00	45.00	Ending April	July
S_4	10/075	Dusso (Pulwama)	18.00	9.00	75.00	23.86	7.20	29.00	2nd weak of April	Ending June
S_5	14/075	Poyen (Kargil)	100.00	9.23	123.00	39.13	100.00	200.00	Beginning of May	1st week of August
S_6	15/075	Achchmal (Kargil)	100.00	12.30	123.00	39.13	49.00	200.00	-do-	-do-
S_7	16/075	Khalsti (Leh)	90.00	11.40	118.00	37.54	90.25	180.00	-do-	-do-
S_8	20/075	Budgam (Budgam)	35.00	10.50	145.00	46.00	14.06	55.00	Last week of April	Last week of June
S_9	27/075	Chitru Dangerpora (Budgam)	35.00	9.00	113.00	36.00	12.25	55.00	-do-	1st week of July
S_{10}	32/075	Mugaam (Anantnag)	25.00	9.00	75.00	24.00	6.25	50.00	3rd week of April	1st week of July
S_{11}	41/075	Damhal (Anantnag)	35.00	9.00	94.00	30.00	9.00	40.00	3rd week of April	1st week of July
S_{12}	44/075	Arhama (Shopian)	28.00	10.00	68.00	21.64	16.00	70.00	April	1st week of July
S_{13}	50/075	Gagran (Shopian)	30.00	8.00	55.00	17.50	12.50	50.00	April	1st week of July
S_{14}	55/075	Nunmai (Kulgam)	25.00	10.00	80.00	25.46	25.00	40.00	April	2nd week of July
S_{15}	58/075	Hanjan (Kulgam)	20.00	6.00	75.00	23.87	25.00	70.00	April	1st week of July
S_{16}	61/075	Mughalpora (Kupwara)	25.00	8.00	72.00	22.91	9.00	45.00	April	3rd week of June
S_{17}	63/075	Dragmulla (Kupwara)	20.00	10.00	70.00	22.28	9.00	60.00	Beginning of May	Ending July
S_{18}	64/075	Nuchh (Bandipora)	25.00	15.00	68.00	21.64	25.00	70.00	April	3rd week of June
S_{19}	68/075	Sadrkoot Payeen (Bandipora)	30.00	9.00	65.00	20.69	9.00	45.00	April	Ending June
S_{20}	73/075	Doda	15.00	8.00	43.00	14.32	20.00	50.00	3rd week of March	Ending May
S_{21}	74/075	Batote	20.00	5.00	42.00	13.36	9.50	40.00	-do-	-do-
S_{22}	75/075	Ganpath Baderwah	30.00	6.00	48.00	15.27	22.00	60.00	-do-	-do-

3. RESULTS AND DISCUSSION

i) Stone and kernel characteristics

Table 2 presents data pertaining to 22 Candidate plus trees of wild apricot with variation in stone, kernel and oil content characters. Analysis of variance indicated significant differences among 22 different candidate plus trees for all the studied characters. Oil content per cent recovered from kernels showed significant variations and ranged between 25.52% for CPT 15/075 (S5) to 54.64% for CPT 14/075 (S5). Maximum value of 54.64% oil content recorded for CPT 15/075 (S5) was followed by CPT 20/075 (S8) with 53.00% oil content. Out of 22 seed sources four sources recorded above 50% oil content. There is more than 29.00% oil content variation among all the 22 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 stone and kernels also recorded significant variations. Maximum stone weight (278.12 g) was recorded for CPT 10/075 (S4) and the mean stone weight recorded was (186.04 g). Mean stone length recorded was (20.86 mm) and the highest value (25.46 mm) was recorded for CPT 32/075 (S10). Mean stone width recorded was (15.99 mm) and the highest value (18.90 mm) was recorded for CPT 41/075 (S11). Mean stone diameter recorded was (10.51 mm) and the maximum value (12.73 mm) was obtained for CPT 10/075 (S4). Maximum kernel weight (83.92 g) was recorded for CPT 41/075 (S11) and the mean kernel weight recorded was (51.17 g). Mean kernel length recorded was (13.94 mm) and the highest value (15.55 mm) was recorded for CPT 32/075 (S10). Mean kernel width recorded was (9.01 mm) and the highest value (11.35 mm) was recorded for CPT 14/075 (S5). Mean kernel diameter recorded was (5.58 mm) and the maximum value (7.33 mm) was obtained for CPT 10/075 (S4). Mean fruit length recorded was (26.36 mm) and the highest value (30.54 mm) was recorded for CPT 64/075 (S18). Mean fruit width recorded was (23.95 mm) and the highest value (32.88 mm) was recorded for CPT 64/075 (S18). Mean fruit diameter recorded was (21.35 mm) and the maximum value (29.06 mm) was obtained for CPT 64/075 (S18).

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 (60.33), survival per cent (40.33), seedling height (156.50 cm), seedling collar diameter (11.73 mm) and number of branches per seedling (14.50) were recorded in CPTs – 58/075(S15), 14/075(S5), 20/075(S8), 4/075(S2) and15/075(S6) 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 individuals 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- 7.15 %), survival per cent (CV- 7.82%), seedling height (CV- 4.12%), seedling collar diameter (CV-13.69 %) and number of branches per seedling (CV-15.63%) was found to be moderately high (Table 2).

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

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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 22 plus tree progenies for all the traits, indicating the existing of huge genetic variability. The cluster pattern of 22 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 II recorded the highest number of 8 families (CPT- 01/075 (S1), 04/075 (S2), 07/075 (S3), 15/075 (S6), 16/075 (S7), 20/075 (S8), 27/075 (S9) and 32/075 (S10) followed by Cluster IV with five (5) families (CPT- 44/075 (S12), 55/075 (S14), 61/075 (S16) and 63/075 (S17) and74/075 (S21) and Cluster V with five (5) families (CPT-50/075 (S13), 64/075 (S18), 68/075 (S19) and 73/075 (S20) and75/075 (S22) 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 V (3051.00) under open field environmental conditions followed by (1731.75) between cluster I and IV. However, 22 families within a cluster showed low to medium (153.95 to 554.16) intra cluster distance under open field environmental conditions, revealing their genetic closeness from high to medium. Similar studies in Pigeon-pea, linseed and maize have revealed that the material is vulnerable to the variable environmental conditions, Patel and Acharaya (2011), Murthy et al., (1973) and Prasad and Singh (1990). The highest D2 value (4037.58) and (3729.63) was observed between (S2 & S19) and (S9 & S19) 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; Lal et al., 2005)

Mean performance of the clusters with respect to different character (Fig. 1) indicated that highest cluster mean value for oil content (50.53%) was recorded in cluster II. Maximum cluster mean values for stone length (23.04 g), kernel length (15.30 mm), stone width (17.96 mm), stone diameter (11.96 g), kernel diameter (6.41 mm), germination percent (36.99) and survival percent (32.10) seedling height (135.96 mm), collar diameter (10.53) and fruit length (26.40 mm)was recorded in cluster II. Cluster V recorded maximum values for stone weight (243.69 g), kernel weight (67.24 g), kernel width (10.04 mm), fruit width (26.69 mm) and fruit diameter (24.53 mm). Cluster I recorded maximum values for branches/plant (9.88). The present results also get support from Gupta and Patil, (1988) in Leucaena latisiliqua , Manga and Sen, (2000) in Prosopis cineraria and Konda et a., (2009) in Vigma mungo.

Contribution of different characters to total divergence is illustrated in (Fig 2). Seedling height contributed maximum (28.57 %) followed Survival per cent (20.78 %), germination per cent (17.75 %), fruit diameter (12.55 %), fruit length (8.23 mm) and Oil content per cent (5.19 %) 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.

4. 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 22 different genotypes of wild apricot (Prunus armeniaca). Out of 22 seed sources four sources (S5, S8, S10, & S12) recorded above 50% oil content in which two sources respectively (S5, & S8) recorded more than 52.50 % oil content and there is more than29.00 % oil content variation among all the 22 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 S4, S5, S18 and S10 respectively out performed than rest of the sources. On the basis of inter and intra cluster distance cluster

number. I and V 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 II & V 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 (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 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; Lal et al., 2005).

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Table 2: Variation in seed, kernel, seedling characteristics and oil content (%) in 22 different Candidate Plus Trees of Wild Apricot (Prunus armeniaca L.)

Character / CPT Notation	Av. Stone Weight (g)/100 seeds	Av. Kernel Weight (g)/100 seeds	Av. Stone Length (mm)	Av. Kernel Length (mm)	Av. Stone Width (mm)	Av. Kernel Width (mm)	Av. Stone Diameter (mm)	Av. Kernel Diameter (mm)	Germination %	Survival %	Av. Height (cm)	Collar Dia (mm)	Branch/ Plant	Fruit length (mm)	Fruit width (mm)	Fruit diameter (mm)	Oil Content (%)
S_1	161.65	32.15	20.21	14.46	15.15	9.53	10.53	6.96	40.00	31.33	113.20	8.00	8.30	27.72	27.73	24.52	48.40
S_2	134.29	36.44	19.57	12.82	14.26	8.19	10.46	6.42	29.66	21.33	145.00	11.73	9.40	25.82	25.25	23.74	48.53
S_3	155.40	34.44	21.47	12.52	16.61	8.86	10.00	5.55	40.00	33.00	124.30	11.43	12.60	25.00	24.00	20.60	45.27
S_4	270.12	57.81	23.51	15.23	18.36	9.95	12.73	7.33	32.33	30.66	153.80	11.30	9.30	29.69	27.85	25.70	47.41
S_5	229.46	51.53	20.58	15.46	16.62	11.35	10.52	5.65	45.00	40.33	126.80	10.10	6.20	26.12	22.87	19.09	54.64
S_6	154.59	36.76	18.22	13.48	13.30	8.95	9.73	5.55	30.00	28.00	126.50	10.10	14.50	25.14	22.05	20.65	25.22
S_7	151.51	49.65	21.11	14.81	16.72	9.76	11.02	5.43	28.33	31.00	140.40	8.50	10.30	29.54	26.65	23.54	48.76
S_8	176.78	48.64	22.42	14.58	17.37	9.92	10.24	4.47	31.66	26.66	156.50	10.20	7.10	28.53	26.36	22.86	53.00
S_9	123.33	44.16	21.16	13.49	14.54	8.85	9.52	5.58	26.33	20.00	133.50	10.30	7.50	28.07	24.67	22.30	49.80
S_{10}	131.81	40.90	25.46	15.55	13.74	8.19	9.26	4.61	33.00	25.66	131.47	9.90	9.40	28.20	20.28	17.12	51.00
S_{11}	220.23	83.82	25.05	15.22	18.90	8.60	12.64	6.27	33.66	25.33	127.30	10.20	5.60	30.13	28.49	23.95	49.00
S_{12}	167.50	41.25	20.79	13.41	15.85	8.47	9.55	5.24	20.00	20.33	101.70	7.00	4.50	25.17	23.22	20.88	50.33
S_{13}	211.26	59.97	21.14	13.44	15.25	8.99	10.04	5.46	20.33	18.66	79.80	6.50	3.00	25.33	23.50	21.72	47.46
S_{14}	197.61	47.91	19.39	12.33	17.61	9.70	9.93	4.98	32.66	16.33	99.80	6.20	2.20	26.56	25.14	22.24	49.10
S_{15}	203.70	54.32	20.79	14.65	16.37	9.85	11.10	6.41	66.33	20.33	100.50	6.70	3.30	25.03	24.27	21.69	43.66
S_{16}	167.91	53.73	19.74	13.78	15.41	8.84	10.51	6.33	19.66	13.33	91.53	5.90	2.20	27.58	25.24	24.41	47.40
S_{17}	168.49	55.47	19.31	12.71	14.31	7.85	9.17	5.60	6.33	13.33	83.60	6.30	2.10	24.73	19.14	16.38	49.42
S_{18}	235.30	64.70	20.45	13.92	18.26	10.25	11.49	5.69	0.00	6.33	90.33	5.80	1.20	30.54	32.88	29.66	49.35
S_{19}	252.08	69.79	20.26	14.15	16.81	9.73	11.39	6.02	11.00	8.00	98.33	5.80	2.50	21.63	20.59	20.00	47.54
S_{20}	196.85	46.06	19.04	14.24	13.94	8.10	9.77	4.39	11.33	8.33	85.07	6.60	1.40	24.51	20.46	17.27	43.27
S_{21}	151.51	39.24	19.65	12.57	14.56	7.52	9.67	3.98	5.33	3.66	52.20	4.70	2.60	21.90	17.92	15.85	41.20
S_{22}	223.21	57.35	19.67	13.26	15.69	8.69	10.64	4.79	16.33	14.00	82.33	5.90	3.20	22.66	18.43	15.90	41.46
Mean	186.04	51.17	20.86	13.94	15.99	9.01	10.51	5.58	26.66	20.72	110.67	8.45	5.84	26.36	23.95	21.35	46.83
C.V.	3.55	6.67	6.17	6.59	10.49	11.70	11.15	13.44	7.15	7.82	4.12	13.69	15.63	9.00	7.17	7.17	5.24
S.E.	3.81	2.65	0.98	0.53	0.96	0.61	0.68	0.43	1.10	0.94	2.63	0.64	0.53	1.37	0.99	0.88	1.42
C.D. 5%	10.87	7.56	2.81	1.51	2.74	1.74	1.93	1.24	3.14	2.67	7.51	1.84	1.50	3.91	2.83	2.52	4.04
Range Lowest	123.33	34.44	18.22	12.33	13.74	8.10	9.17	3.98	5.33	3.66	52.20	4.70	1.20	21.63	17.92	15.85	25.22
Range Highest	270.12	83.82	25.46	15.55	18.90	11.35	12.73	7.33	66.33	40.33	155.50	11.73	14.50	30.54	32.88	29.66	54.64

Table 3: Cluster distribution of 22 selected Candidate Plus Tree progenies (S1-S22) of Prunus armeniaca L.

Cluster No	No. of CPTs in each cluster	Notation of CPTs
I	2.000	S_4 S_{11}
II	8.000	S_1 S_2 S_3 S_6 S_7 S_8 S_9 S_{10}
III	2.000	S_5 S_{15}
IV	5.000	S_{12} S_{14} S_{16} S_{17} S_{21}
V	5.000	S_{13} S_{18} S_{19} S_{20} S_{22}

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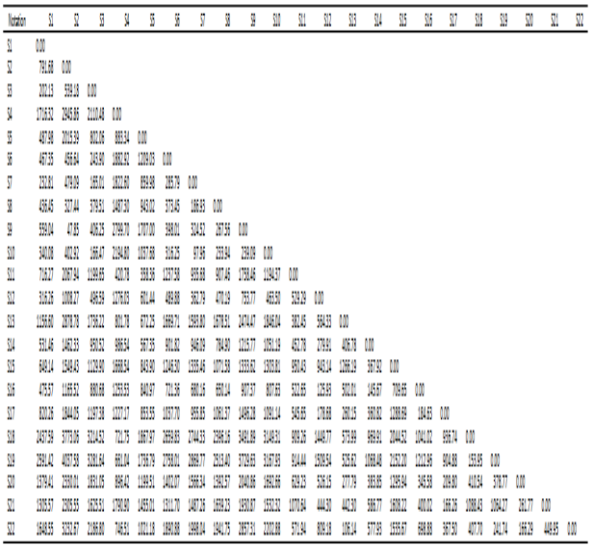
Table 4: Inter and Intra Cluster distances of 22 selected Candidate Plus Tree progenies (S1-S22) of Prunus armeniaca L

Cluster No	I	II	III	IV	V
I	334.551				
II	1501.652	554.166			
III	878.536	874.46	428.708		
IV	1731.755	924.284	698.235	270.801	
V	3051.008	1135.214	1431.055	653.273	153.954

Table 5: D2 value for 17 selected Candidate Plus Tree progenies (S1-S22) of Prunus armaniaca L.



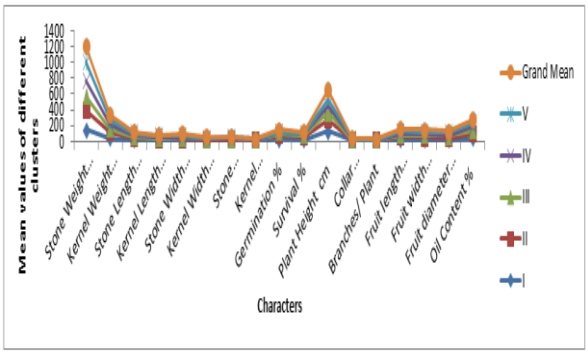


Figure 1: Mean values of various characters in different clusters for 22 candidate plus tree progenies (S1-S22) of Prunus armeniaca L.

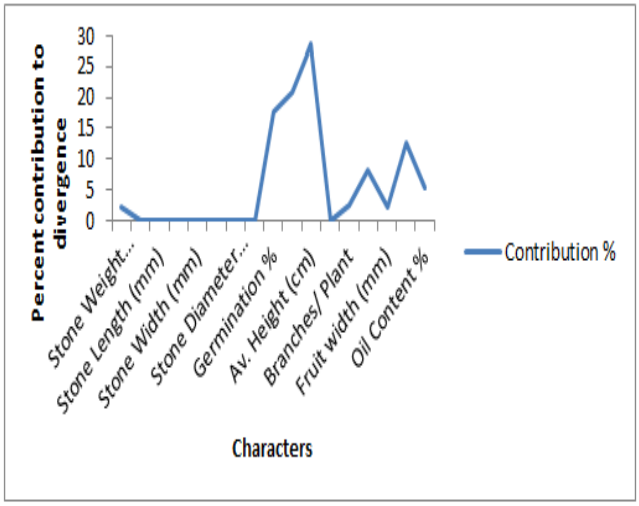


Figure 2: Percent contribution of each character to total divergence for 22 different CPTs of Prunus armeniaca L