



Variation Studies in Fruit Characteristics, Seed Germination and Seedling Growth of *Diospyros montana* (Roxb.) in Himachal Pradesh

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Abstract: The study was confined to 19 mother trees of *Diospyros montana* (Roxb.) distributed in Solan districts of Himachal Pradesh. Variation in fruit, seed and seedling traits were studied by collecting fruits and raising nursery of this species. There was large variation in fruit and seed traits. The maximum fruit weight, fruit length, fruit width and germination per cent was recorded for M₅ and M₇. Seedling parameters were recorded maximum for M₇. Repeatability coefficient was recorded maximum for seed length. GCV, PCV and heritability was recorded maximum for germination percent. This study revealed that fruit size and germination parameters could form a selection criterion for tree improvement in *D. montana*.

Keywords: Variation, Diospyros, Repeatability, PCA, Clusters, Correlation

India is blessed with all types of vegetation ranging from tropical to subtropical, temperate to subalpine and alpine because of diversified climatic and physiographic factors. In an ecosystem forest have both productive and protective role. Productive role of the forest is not only confined to timber production but also production of non-timber forest products. Non-timber forest products (NTFPs) are the biological products, other than timber, that are harvested by humans from wild biodiversity in natural and man-made environment (Sardesh Pande and Shackleton 2019). Non-timber forest products are mainly tans, dyes, medicinal plants, bamboo etc. According to an estimate 275 million people in India are dependent on these resources. There are many products which are not extracted fully, or which go to waste because of insufficient knowledge of their use. The biodiversity of most of the species is usually poorly studied. Even their identification and classification are often unsatisfactory, leading to considerable confusion when plants or their products are traded.

Among all, genus *Diospyros* is one of the potential NTFPs. The *Diospyros* largest genus of family Ebenaceae, around 700 species of deciduous and evergreen trees and shrubs (Akagiet al 2014). The majority are native to the tropics, with only a few extending into temperate regions. This plant is distributed all along the Western Ghats of India, Sri Lanka and Indo-China through Australia. In India its different species are distributed in the state of Kerala, Assam, Rajasthan, Uttar Pradesh, Maharashtra, Tamil Nadu and

Himachal Pradesh. Several species of *Diospyros* are commercially important for their edible fruits and timber. It is commonly known as ebony tree because of its hard, heavy and dark timber. *Diospyros* species have been ubiquitous to ethnic medication throughout the tropical regions. There are mainly six species of *Diospyros* (*D. kaki*, *D. embryopteris*, *D. tomentosa*, *D. melanoxylon*, *D. lotus* and *D. montana*) present in Himachal Pradesh (Kumar 2014, Bhardwaj and Seth 2017). Out of which *Diospyros montana*, commonly known as Bombay ebony found in some parts of Solan, Sirmour and Una district of Himachal Pradesh.

Diospyros Montana is a small deciduous tree up to 20 m high with spiny trunk and branches. Leaves are elliptic lance-shaped, somewhat heart shaped at the base and sharp or blunt at the tip. It is a dioecious tree species. Flowering takes place from March- April. The fruits are green turning orange when ripen and it mature in October. The green fruits are rich in tannin and thus avoided by most of herbivores. It is the one of the most important medicinal plant. It's almost all parts possess good therapeutic value in traditional system of medicines. Bark extract is anti-inflammatory, antipyretic and analgesic. It contributes to socio-economic livelihood of tribal people of India.

Wild populations of plant species exhibit the complex patterns of variation (Briggs and Walters 1997), making it crucial to select superior stands for breeding purposes (Gupta and Sehgal 2000). Variability in important traits is most crucial for tree improvement. Because the expression

of a character is the sum of many other genetically determined qualities so, screening and selection should be based on these factors. Variations are essential for adaptation and improvement of species through breeding program. If there is no variation, there is no possibility for tree breeding to improve the quality. Continuous development is possible if variation exists in a species. Understanding the diversity within and between tree populations is essential in order to set priorities for the conservation and enhancement of tree genetic resources. The species therefore provides an opportunity, for studying variation and also to select the superior seed sources for adaptability and growth. Due to longer rotation period of the tree, there is very less information available on its genetic improvement. Therefore, an effort was made to study the genetic differentiation in superior tree progenies to identify the diverse genotype to use further in hybridization programme.

MATERIAL AND METHODS

The experiment was conducted in the laboratory and experimental field of the Department of Tree Improvement and Genetic Resources, Dr YS Parmar UHF, Nauni, Solan (HP). Total 19 mother trees from Nalagarh area of district Solan of Himachal Pradesh were selected. The physical description of nineteen mother trees is given in Table 1.

Statistical analysis: The data of mother trees was analyzed statistically using Random Nested Model as follows,

$$Y_{ijkm} = \mu + p_i + M(p)j_{(i)} + e_{ijk}$$

Repeatability: We couldn't accurately measure genetic variance between and within populations because genetic effects can't be isolated from environmental effects in natural populations when parental origin and environmental influences aren't controlled. As a result, we are unable to calculate the heritability coefficient at the population or individual tree level. In this case, we use the repeatability coefficient, which may be considered as the top limit of the genetic-phenotypic variance relationship (Falconer and Mackey 1996). These coefficients also show the proportion of within-population variation that contributes to total variance and the proportion of between-tree variation that contributes to total population variation.

$$\text{More tree repeatability} = \sigma_m^2 = \frac{\sigma_m^2}{\sigma_m^2 + \sigma_w^2(m)}$$

Where, σ_m^2 = Mother tree variance

$\sigma_w^2(m)$ = Within mother tree variance

Heritability in percentage was calculated by formula suggested by Burton and De-Vane (1953) and Johnson et al (1955). The expected genetic advance at 5 per cent selection

intensity was calculated by the formula suggested by Lush (1940) and further used by Burton and De-Vane (1953) and Johnson et al (1955). Genetic gain was worked out following the method suggested by Johnson et al (1955). Principal component and cluster analysis were investigated by principal component analysis (PCA). PCA was performed using JMP pro 10 software. Cluster analysis was also performed to cluster genotypes into similarity groups using the method of UPGA (Unweighted Pair Group Average) using ward method (Ward 1963).

RESULTS AND DISCUSSION

Table 2 depicts the data pertaining to fruit and seed characters. Selected plant namely M_5 had maximum fruit weight (14.99g), while M_{19} had minimum fruit weight (7.28 g). Seed weight observed maximum (1.83 g) in M_3 , whereas, minimum (1.03 g) in M_{15} . Number of seeds recorded maximum (5.63) in M_1 , whereas minimum (3.33) in M_2 . Seed weight (100 seeds) was observed maximum (182.97g) in M_3 . The M_{15} plant depicted smallest seed weight (102.57g). Size of seed may vary due to external and internal environmental conditions (Roy et al 2004). Priya devi et al (2022) have found variation in fruit length, seed weight. etc. among different provenances.

Variance between mother trees for fruit and seed characteristics: Repeatability coefficient was found

Table 1. Physical description of mother trees

Mother trees	Altitude (feet)	Latitude (n)	Longitude (e)
M_1	1207	30°59'909"	76°44'713"
M_2	1202	30°59'915"	76°44'710"
M_3	1205	30°59'917"	76°44'712"
M_4	1201	30°59'867"	76°44'660"
M_5	1204	30°59'867"	76°44'655"
M_6	1200	30°59'881"	76°44'646"
M_7	1203	30°59'935"	76°44'742"
M_8	1202	30°59'984"	76°44'778"
M_9	1209	30°59'939"	76°44'762"
M_{10}	1597	30°59'694"	76°44'634"
M_{11}	1673	30°59'460"	76°44'625"
M_{12}	1719	30°59'472"	76°44'769"
M_{13}	1760	30°59'493"	76°44'965"
M_{14}	1764	30°59'505"	76°44'978"
M_{15}	1775	30°59'509"	76°44'019"
M_{16}	1859	30°59'668"	76°44'075"
M_{17}	1859	30°59'673"	76°44'076"
M_{18}	1862	30°59'675"	76°44'079"
M_{19}	1869	30°59'680"	76°44'085"

maximum (0.94) for seed length and was found minimum (0.19) for 100 seed weight. The magnitude of differences between PCV and GCV were more indicating the major role of environment in expression of various traits. In general, all characters studied in the magnitude of phenotypic coefficient of variation were greater over the respective genotypic coefficient of variation. The characters seed length (42.28 and 41.02) and fruit weight (23.82 and 17.75) shows higher estimates of both PCV and GCV, respectively (Table 3). Similar findings of genetic variability have been observed and reported earlier in *Pongamia pinnata* by Sunil et al (2009) and Rawale (2020) in Kaphal tree. Genetic gain was found maximum (81.97%) in seed length, whereas, maximum (19.35) genetic advance observed in 100 seed weight.

Estimation of correlation coefficients between different fruit, seed and leaf parameters: Correlation studies help in finding out the degree of inter-relationship among various characters and in evolving selection criterion for improvement of multiple characters and shorten the selection cycle. The Fruit weight is positively correlated with fruit length (0.67) and fruit width (0.83). Similarly, Fruit length is positively correlated with fruit width *i.e.* 0.83 (Selvan and Guleria 2012). Number of seeds was negatively correlated with seed width (-0.06).

Principal component analysis (PCA): PCA is used to explain pattern of variation among the populations. This technique helps in dividing the original variables in the dataset into smaller groups. The results from the PCA conducted in this study identified that PC1, PC2 and PC3 components accounted for 73.39% of the total variation in the studied variables for *D. montana* (Table 5). In PC1, the variables with the highest factor loadings were the fruit weight, the fruit length, seed length, 100 seed weight and number of seeds. Principal component analysis has been effectively used to evaluate and characterize the germplasm of many fruit trees (Hashemi and Khadivi 2020).

Cluster analysis: The diversity exists between the clusters I, II and III may result in substantial segregates. It is revealed that the existence of substantial variation and diversity can be utilized for genetic resource conservation and further tree improvement programmers of the species. Cluster I had highest mean value for 100 seed weight (152.63) (Table 6).

Nursery Performance of Half-sib Families

Variation between germination parameters: Seed germination behavior is an important factor in the distribution of species. There is a significant relationship between mean daily germination and germination percent. The maximum germination (33.83%) and mean daily germination (1.55)

Table 2. Variation for fruit and seed characters

Mother trees	Fruit length (cm)	Fruit width (cm)	Seed length (cm)	Seed width (cm)	Fruit weight (g)	Number of seeds per fruit	100 seed weight (g)
M ₁	2.98	3.24	1.55	0.79	14.47	5.63	155.34
M ₂	2.92	3.24	1.43	0.91	11.78	3.33	123.18
M ₃	2.90	3.22	1.41	0.84	13.33	4.43	182.97
M ₄	2.96	3.35	1.48	0.86	13.6	3.83	174.83
M ₅	3.09	3.46	1.41	0.79	14.99	4.90	141.94
M ₆	3.06	3.40	1.42	0.68	12.61	4.33	128.97
M ₇	3.08	3.42	1.39	0.8	14.47	4.90	151.60
M ₈	3.01	3.09	1.40	0.89	13.38	3.40	145.47
M ₉	2.85	2.94	1.41	0.83	10.67	4.73	156.37
M ₁₀	2.90	3.04	1.42	0.79	10.49	3.93	127.70
M ₁₁	2.95	3.23	1.32	0.73	11.66	4.77	140.40
M ₁₂	2.67	3.00	1.31	0.77	9.99	4.70	106.70
M ₁₃	2.78	3.07	1.32	0.78	10.2	4.37	106.37
M ₁₄	3.10	3.09	4.13	0.79	11.16	4.93	161.63
M ₁₅	2.85	3.10	1.27	0.69	10.36	3.97	102.57
M ₁₆	3.04	3.16	1.56	0.89	11.44	4.57	152.23
M ₁₇	2.85	2.94	1.22	0.63	8.96	4.23	126.77
M ₁₈	2.89	3.00	1.56	0.80	9.39	5.23	168.90
M ₁₉	2.87	3.00	1.31	0.68	7.28	3.33	135.33
CD (p=0.05)	0.08	0.10	0.08	0.04	0.93	0.64	22.53

was recorded for M_5 which was at par with M_4 (33.63%) and minimum values (14.95%) and (0.33) was recorded for M_{17} . However, maximum peak value (2.73) and germination value (3.74) was recorded for M_7 which was followed by M_5 , M_4 and minimum values (0.48) and (0.16) was recorded for M_{17} (Table 7). The premise behind germination energy is that only seeds that germinate quickly and vigorously under favourable conditions can produce vigorous seedlings in the field (Masoodi et al 2014).

Mother trees variation for seedling growth parameters (Six months): Maximum average seedling height was recorded in M_9 (60.13 cm) and minimum was recorded in M_{10} (33.33 cm). Maximum collar diameter was observed (2.04) in M_9 whereas, minimum (1.37 mm) in M_{11} . Number of branches were recorded maximum in M_2 (12.53) and minimum was recorded in M_3 (4.20). The maximum number of leaves (136.67) was recorded in M_{15} and minimum (52.60) was recorded in M_2 . Leaf width was recorded maximum for M_7 (2.6cm) and minimum (2.22 cm) was recorded for M_{17} . Maximum average leaf length was recorded in M_7 (7.55 cm) and minimum (6.41 cm) leaf length was recorded in M_{10} . Petiole length was observed maximum (0.27cm) and minimum (0.22 cm) was observed in M_6 , M_{13} , M_{17} and M_{18} . Maximum leaf area was recorded in M_7 (13.81cm²), which was followed by M_2 (11.84 cm²) and minimum (10.03 cm²)

was recorded in M_{17} (Table 8). Growth characters of seedlings were governed by genetic makeup and seed characters (Pathak et al 1984, Thakur 2013).

Variance component and heritability: Genetic variability (Table 9) studies revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters under observations. The maximum genotypic (31.89%) and phenotypic (43.82%) variability was observed in number of branches followed by number of leaves whereas, minimum GCV (3.61%) and PCV

Table 5. Principal component analysis of fruit and seed characters

Parameters	PC1	PC2	PC3
Fruit weight	0.64	0.56	0.01
Fruit length	0.7	0.36	-0.5
Fruit width	0.06	0.48	0.66
Number of seeds	0.62	0	0.3
Seed length	0.76	0.47	-0.32
Seed width	0.04	0.56	0.2
100 seed weight	0.47	0.42	0.5
Eigen value	4.05	2.75	1.27
Percent of variance	36.84	24.98	11.58
Cumulative percent	36.84	61.81	73.39

Table 3. Variance component and repeatability coefficient for fruit and seed characteristics

Parameters	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation	Repeatability	Genetic advance	Genetic gain (%)
Fruit weight	17.75	23.82	0.56	3.16	27.24
Fruit length	3.74	6.65	0.32	0.13	4.33
Fruit width	5.10	7.94	0.41	0.21	6.75
Number of seeds	13.60	31.73	0.18	0.53	12.01
Seed length	41.02	42.28	0.94	1.26	81.97
Seed width	9.81	13.28	0.52	0.11	14.92
100 seed weight	15.22	34.88	0.19	19.35	13.67

Table 4. Correlation between leaf, fruit and characters in *D. Montana*

Parameters	Fruit weight (g)	Fruit length (cm)	Fruit width (cm)	No. of seeds	Seed length (cm)	Seed width (cm)	100 seed weight (g)
Fruit weight	1						
Fruit length	0.67**	1					
Fruit width	0.83**	0.63**	1				
No. of seeds	0.14	0.18	0.28	1			
Seed length	-0.05	0.42	0.01	0.25	1		
Seed width	0.19	0.22	0.46*	-0.06	0.11	1	
100 seed weight	0.23	0.48*	0.4	0.32	0.3	0.44	1

(**) – Highly significant and correlation is significant at the 0.01 level

(*) - Significant and correlation is significant at the 0.05 level

(8.81%) was found for leaf width. Heritability may give useful indication about the relative gain from the selection (Ginwal and Gera 2000). Heritability was found maximum for germination percent (0.97) and minimum (0.04) for petiole length. Genetic advance was found maximum for number of leaves (33.07). Genetic gain was found maximum for number of branches (47.81%) and minimum (1.40%) for petiole length. Genetic gain was found maximum for all the characters as compared to genetic advance. Genetic gain was dependent on heritability of traits. These findings were supported by Kumari and Wani (2015) in *D. melanoxylan*.

They concluded that leaf area and seedling height performed better, indicating additive gene action on these two variables. As a result, these two qualities would yield better outcomes for improvement by simple selection. These results are in line with Thakur (2013) in *Melia azedarach*.

Estimation of correlation coefficients between different nursery parameters: All the observed characters showed significant relationship with each other. The seedling height showed a highly significant and positive correlation with collar diameter and number of leaves which depicts the less effect of environmental factors (Table 10). Significant and

Table 6. Mean value for leaf, fruit and seed characters for the cluster analysis

Cluster	1	2	3
No. of trees in cluster count	4	5	10
Notation of trees	M ₁ , M ₅ , M ₇ , M ₁₄	M ₂ , M ₄ , M ₆ , M ₈ , M ₁₆	M ₃ , M ₉ , M ₁₀ , M ₁₁ , M ₁₂ , M ₁₃ , M ₁₅ , M ₁₇ , M ₁₈ , M ₁₉
Fruit length	3.06	3.00	2.85
Fruit width	3.30	3.25	3.05
Fruit weight	2.12	1.46	1.36
Number of seeds per fruit	0.79	0.85	0.75
Seed length	13.77	12.56	10.23
Seed width	5.09	3.89	4.37
100 seed weight	152.63	144.94	135.41

Table 7. Variation between germination parameters

Mother trees	Germination percent (%)	Mean daily germination	Peak value	Germination value
M ₁	32.79	1.31	1.55	2.01
M ₂	30.44	1.28	1.33	1.71
M ₃	32.79	1.47	1.63	2.39
M ₄	33.63	1.53	1.92	2.94
M ₅	33.83	1.55	1.94	3.01
M ₆	33.00	1.48	1.65	2.45
M ₇	31.52	1.37	2.73	3.74
M ₈	24.83	0.88	1.82	1.58
M ₉	27.74	1.08	1.55	1.68
M ₁₀	24.35	0.85	0.94	0.80
M ₁₁	27.96	1.10	1.16	1.28
M ₁₂	25.10	0.90	0.90	0.81
M ₁₃	26.80	1.02	1.07	1.09
M ₁₄	27.96	1.10	1.10	1.22
M ₁₅	27.26	1.05	1.05	1.11
M ₁₆	25.10	0.90	1.13	1.01
M ₁₇	14.95	0.33	0.48	0.16
M ₁₈	26.08	0.97	1.02	0.98
M ₁₉	33.21	1.50	2.31	3.46
CD (p=0.05)	1.27	0.14	0.19	0.28

Table 8. Mother tree variation in seedling growth parameters (Six months)

Mother trees	Height (cm)	Collar diameter (mm)	Number of branches	Branch length per seedling (cm)	Number of leaves	Leaf width (cm)	Leaf Length (cm)	Petiole length (cm)	Leaf area (cm ²)
M ₁	40.33	1.66	6.33	17.1	61.53	2.53	6.57	0.24	11.48
M ₂	41.33	1.89	12.53	12.31	52.6	2.43	7.02	0.25	11.84
M ₃	44.4	1.63	4.2	18.62	67.73	2.36	6.56	0.23	10.77
M ₄	38.47	1.88	4.53	15.43	61.47	2.25	6.65	0.24	10.39
M ₅	39.27	1.47	4.87	14.48	58.07	2.42	6.47	0.25	10.85
M ₆	41.8	1.42	6	13.47	64.47	2.26	6.53	0.22	10.23
M ₇	37.67	1.46	4.53	15.13	65.4	2.63	7.55	0.27	13.81
M ₈	39.78	1.63	4.67	20.25	56.6	2.39	7.05	0.24	11.69
M ₉	60.13	2.04	9.13	18.44	123.33	2.33	6.92	0.24	11.17
M ₁₀	33.33	1.49	4.6	15.51	60.47	2.43	6.41	0.25	10.81
M ₁₁	32.31	1.37	5.67	14.89	60.6	2.39	7.02	0.24	11.64
M ₁₂	41.33	1.62	6.13	16.51	93.47	2.39	6.79	0.23	11.28
M ₁₃	40.53	1.56	7.8	15.99	97.6	2.23	6.63	0.22	10.23
M ₁₄	38.2	1.38	4.33	15.34	86.67	2.42	6.59	0.23	11.09
M ₁₅	42.93	1.94	7.47	19.64	136.67	2.41	7.01	0.24	11.77
M ₁₆	37.6	1.83	6.8	14.33	95.27	2.41	6.75	0.24	11.3
M ₁₇	35.96	1.79	5.53	15.91	82.2	2.22	6.5	0.22	10.03
M ₁₈	37.87	1.64	6.93	17.91	98.2	2.34	6.55	0.22	10.65
M ₁₉	41.47	2.04	8.07	18.53	104.33	2.38	6.77	0.23	11.2
CD (p=0.05)	5.64	0.24	1.35	3.25	17.78	0.14	0.41	0.04	1.16

Table 9. Variance component, heritability, genetic gain and genetic advance of growth parameters

Parameters	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability	Genetic advance	Genetic gain (%)
Germination percent	16.44	16.66	0.97	9.48	33.40
Height of seedlings	13.21	23.66	0.31	6.11	15.18
Collar diameter	11.99	22.80	0.28	0.22	12.99
Number of branches	31.89	43.82	0.53	3.02	47.81
Branch length	10.93	29.98	0.13	1.34	8.21
Number of leaves	29.14	42.50	0.47	33.07	41.16
Leaf width	3.61	8.81	0.17	0.07	3.05
Leaf length	3.54	9.33	0.14	0.19	2.76
Petiole length	3.53	18.34	0.04	0.00	1.40
Leaf area	6.55	15.86	0.17	0.62	5.58

Table 10. Correlation between different nursery traits

Parameters	Germination (%)	Height (cm)	Diameter (mm)	No. of branch	Branch length (cm)	No. of leaves	Leaf width (cm)	Leaf length (cm)	Petiole length (cm)	Leaf area (cm ²)
Germination percent	1									
Seedling height	0.19	1								
Collar diameter	-0.04	0.53*	1							
Number of branch	0.01	0.43	0.59**	1						
Branch length	-0.14	0.37	0.36	-0.14	1					
Number of leaves	-0.28	0.50*	0.53*	0.32	0.49*	1				
Leaf width	0.27	-0.14	-0.2	-0.08	-0.03	-0.2	1			
Leaf length	0.06	0.12	0.12	0.21	0.09	0.07	0.53*	1		
Petiole length	0.28	-0.07	-0.05	-0.04	-0.2	-0.33	0.77**	0.60**	1	
Leaf area	0.18	-0.02	-0.05	0.06	0.03	-0.07	0.86**	0.88**	0.78**	1

(**) – Highly significant and correlation is significant at the 0.01 level

(*) - Significant and correlation is significant at the 0.05 level

positive correlation was showed by branch length with number of leaf (0.49). Similar findings were obtained in *Bauhinia vahii* (Shweta 2020) and in Kaphal (Rawale 2020).

Principal component analysis: PCA (principal component analysis) (Table 11) results showed that the first principal components (PC I) gave eigen values >1.0 and accounted for 33.99% of the total variation for leaf parameters like leaf length (0.71), leaf width (0.89), petiole length (0.89) and leaf area (0.91). Thus, the use of these characteristics will help in saving a considerable amount of time for the identification and selection of best genotypes of *D. montana*. The third component explained 12.86% of total variation. The fourth component (Fig. 1) explained 10.35% of total variation followed by germination percent (0.71). Similar types of findings were also supported by Sharma et al (2019) in *Salix*

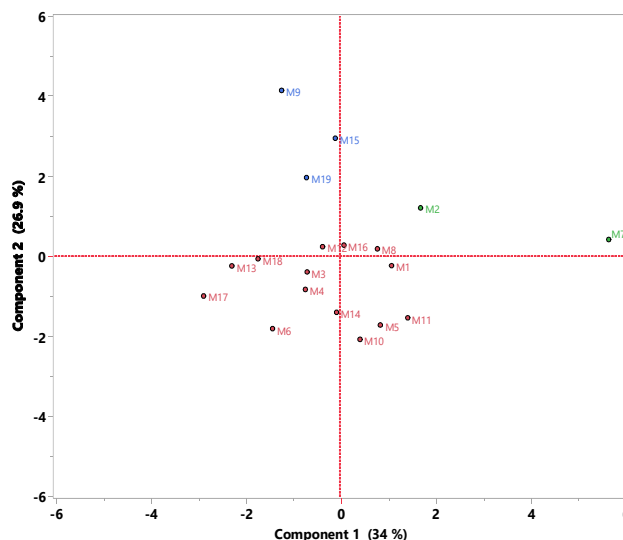


Fig. 1. Scatter plot diagram of PC1- PC2 for nursery traits

Table 11. Principal component analysis for seedling traits

Parameters	PC1	PC2	PC3	PC4
Germination percent	0.34	0.00	0.54	0.71
Height of seedlings	-0.22	0.74	0.2	0.36
Collar diameter	-0.28	0.79	0.19	-0.06
Number of branches	-0.11	0.62	0.58	-0.41
Branch length	-0.22	0.5	-0.65	0.41
Number of leaves	-0.42	0.7	-0.29	-0.07
Leaf width	0.89	0.11	-0.13	0.08
Leaf length	0.71	0.49	-0.14	-0.21
Petiole length	0.89	0.12	0.08	0
Leaf area	0.91	0.34	-0.17	-0.09
Eigen value	3.4	2.69	1.29	1.03
Percent of variance	33.99	26.86	12.86	10.35
Cumulative percent	33.99	60.84	73.71	84.06

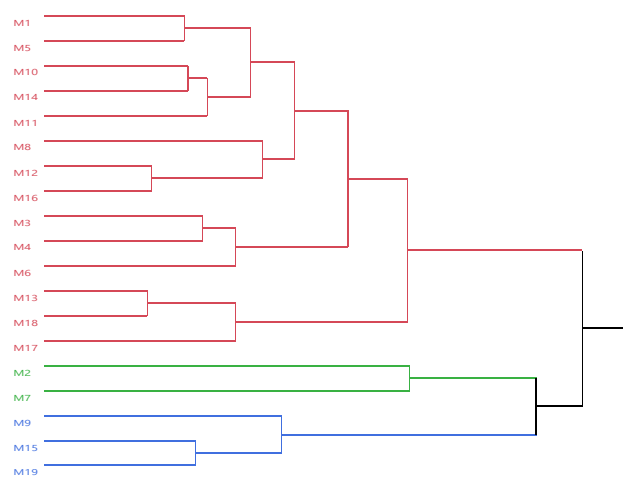


Fig. 2. Dendrogram showing clusters for seedling traits

Table 12. Mean value of seedling parameters for the clusters analysis

Cluster	1	2	3
No. of mother trees in cluster count	14	2	3
Notation of trees	M ₁₃ , M ₃ , M ₅ , M ₄ , M ₆ , M ₁₀ , M ₁₂ , M ₁₃ , M ₁₆ , M ₁₇ , M ₁₈ , M ₈ , M ₁₁ , M ₁₄	M ₂ , M ₇	M ₉ , M ₁₅ , M ₁₉
Germination percent	22.21	26.50	24.22
Seedlings height	38.66	39.50	48.18
Collar diameter	1.60	1.68	2.01
Number of branches	5.60	8.53	8.22
Branch length	16.12	13.72	18.87
Number of leaves	74.60	59.00	121.44
Leaf width	2.36	2.53	2.37
Leaf length	6.65	7.29	6.90
Petiole length	0.23	0.26	0.24
Leaf area	10.89	12.83	11.38

tetrasperma, where 82.84% of variation was showed by five principal components.

Cluster analysis: In cluster analysis cluster I and II (Fig. 2) contained desirable characters. Cluster II reported maximum values for germination percent (26.50), number of branches (8.53), leaf width (2.53), leaf length (7.29), petiole length (0.26) and leaf area (12.83). Cluster III reported maximum values for seedling height (48.18), branch length (18.87), collar diameter (2.01), number of leaves (121.44) In *Myrica esculanta* six clusters were observed for seedling parameters out of which cluster IV, V and VI contained maximum values for germination percent, leaf parameters and seedling height (Rawale 2020).

CONCLUSION

The maximum fruit weight, fruit length, fruit width and germination per cent was recorded for M_5 and M_7 . The higher values of PCV and GCV for germination percent indicated that further improvement can be achieved through selection based on these characters. High heritability with high genetic advance indicated that selection of this character would be more effective. Repeatability coefficient was recorded maximum for seed length. M_7 has better growth characters so further investigations should be conducted on M_7 .

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