

CLONAL EVALUATION AND GENETIC DIVERGENCE STUDIES IN MULBERRY GENOTYPES

Abstract:

This study evaluated 21 screened mulberry clones for various growth attributes through organized clonal evaluation tests, focusing on plant height, diameter at breast height (DBH), volume, and number of branches. Among these clones, only three (MI-0718, MI-0807, and MI-0845) consistently demonstrated superior growth across all periods. Volume exhibited high phenotypic and genotypic variance, followed by leaf area, leaf width, and plant height, which showed moderate values. Number of leaves, number of branches, leaf length, leaf petiole length, DBH, and basal diameter recorded low phenotypic and genotypic coefficients of variation. The study revealed higher phenotypic than genotypic coefficient of variance, suggesting environmental influence on the observed variability. Heritability was high for all traits, with volume showing the highest (98.57%) and basal diameter the lowest (75.69%). Genetic advance as a percentage of mean was highest for volume, indicating its potential for genetic improvement. Genotypic correlations were higher than phenotypic correlations for all traits, suggesting strong genetic control. Path coefficient analysis revealed that diameter at breast height had the highest positive direct effect on volume, followed by plant height and basal diameter. The study also clustered the clones, revealing genetic diversity not dependent on geographical locations. Cluster analysis showed high intra-cluster distance in clusters I and III, indicating diverse genotypes, whereas cluster II had similar genotypes. Volume contributed the most towards genetic divergence, followed by leaf area and plant height. This study provides valuable insights into mulberry clone selection for improvement programs, highlighting the importance of specific growth attributes in enhancing wood volume and genetic diversity.

Key words: Correlation, Growth Attributes, Genetic Diversity, Mulberry

Introduction

Mulberry (*Morus* spp.) is a crucial tree genus globally cultivated for its dual-purpose utility in sericulture and agroforestry systems. The leaves serve as the primary food source for silkworms (*Bombyx mori*), while the wood is valuable for various applications, including furniture, construction, and pulp production. The economic value of mulberry is significantly influenced by the quality of its wood and leaves, making genetic improvement through clonal selection essential for enhancing these traits.

Previous research has highlighted the genetic diversity and performance of mulberry genotypes, with studies by Das *et al.*, (2018) and Kumar *et al.*, (2020) emphasizing the

importance of wood and leaf quality traits. These studies have identified genetic variations among mulberry genotypes that could be exploited for improving wood and leaf quality.

Despite these advancements, there is still a need for comprehensive clonal evaluation and genetic divergence studies focusing on wood quality and leaf quality traits in mulberry genotypes. Understanding the genetic basis of these traits is crucial for selecting superior clones with improved wood and leaf characteristics for cultivation and breeding programs.

Therefore, this study aims to evaluate the wood quality and leaf quality traits of selected mulberry clones and assess the genetic divergence among them. The findings of this research will provide valuable insights into the genetic basis of wood and leaf quality traits in mulberry, contributing to the development of superior genotypes with enhanced economic value for the sericulture and agroforestry sectors.

Methodology

Twenty one genetic resources of mulberry were collected from all over India includes Karnataka, Tamil Nadu, Assam, West Bengal, Bihar, Nagaland, Uttarkhand, Telangana, Uttar Pradesh, Tripura and North West India. The seedlings were raised and systematic progeny test was carried out during 2018. Twenty one trees were selected based on comparison tree method (Pitcher and Dorn, 1966). These trees were felled, coppice shoots were induced and multiplied through mini clonal technology (Parthiban, 2017) and were designated as clones. The parental pedigree and the identified clonal selections are furnished in table 1.

These clones were evaluated through clonal test in a Row Column Design at an espacement of 2 m x 2 m with three replications for the assessment of analysis of variance as suggested by Panse and Sukhatme (1967). The clones were assessed periodically for various growth attributes such as basal diameter, diameter at breast height, height, number of branches, volume, leaf length, leaf width, leaf petiole length and leaf area.

The D2 statistics was adopted for the estimation of genetic divergence (Mahalanobis 1928). Using D2 statistical results, the clustering of clones was done. The D2 statistics was carried out using all the traits. The clones were grouped into different clusters using 'GENRES' statistical package on the basis of D2 values as suggested by Rao (1952). On completion of clustering, the intra and inter cluster relationship was studied and the mutual relationship between the clusters and their distances were represented.

Results and Discussion

1. Analysis of growth parameters of mulberry clones

The twenty one screened mulberry clones were evaluated through organized clonal evaluation test for 15 Month After Plantation (MAP) growth attributes, including plant height, diameter at breast height (DBH), volume, and number of branches. The mean values for these parameters across all clones were 4.32 m for plant height, 35.89 cm for DBH, 0.0022 m³ for volume, and 13.02 for the number of branches (Table 2) and leaf traits also evaluated through clonal evaluation for various clones of plants, including leaf length, leaf width, petiole length, number of leaves, and leaf area. The mean values for these parameters across all clones were 22.56 cm for leaf length, 13.29 cm for leaf width, 3.94 cm for petiole length, 143.4 for number of leaves, and 189.67 cm² for leaf area (Table 3).

Several clones exhibited significantly different values compared to the mean. Clones ME-0025, MI-0211, MI-0013, MI-0536, MI-0718, MI-0768, MI-0685, MI-0017, ME-0006, MI-0807, and MI-0845 showed significantly higher plant height and DBH. Additionally, clones ME-0025, MI-0211, MI-0013, MI-0536, MI-0718, MI-0768, MI-0685, MI-0006, MI-0807, and MI-0845 exhibited significantly higher volume, while clones ME-0025, MI-0211, MI-0013, MI-0718, MI-0768, MI-0685, and MI-0807 had significantly higher numbers of branches. In leaf trait aspects the clones MI-0349, MI-0536, MI-0718, MI-0807, and MI-0845 showed significantly higher leaf length, while clones MI-0211, ME-0109, MI-0013, MI-0536, MI-0718, MI-0768, MI-0663, MI-0685, MI-0807, and MI-0845 exhibited significantly higher leaf width. Additionally, clones ME-0001, MI-0349, MI-0536, MI-0615, MI-0718, MI-0807, and MI-0845 had significantly higher petiole length, and clones ME-0025, MI-0211, MI-0013, MI-0536, MI-0718, MI-0807, and MI-0845 showed significantly higher leaf area.

These findings are consistent with previous research by (Sharma *et al.*, 1994), who also observed similar trends in plant growth characteristics among different clones. The superior performance of these clones in terms of plant height, DBH, volume, number of branches, petiole length and leaf areahighlights their potential for selection in breeding and cultivation programs aimed at improving growth and productivity.

Table 1. Details of mulberry genetic resources

S.No	Morus species	genotypes number	Name	Origin
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1	<i>M. alba</i>	ME-0025	Shrim-8	RSRS, Kodathi
2		MI-0211	Rajasthan Local	North West India

Clones	plant height (m)	DBH (mm)	Volume (m ³)	No.of branches
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3	<i>M. australis</i>	ME-0001	<i>M. australis</i>	RSRS, Kodathi
4	<i>M. bombycis</i>	ME-0109	Artificial	CSR &TI, Berhampore
5	<i>M. indica</i>	MI-0013	S-36	CSR &TI, Mysore
6		MI-0349	Garobadha-2	North East India
7		MI-0395	Tingrai	North East India
8		MI-0536	Ananthagiri local	South India
9		MI-0615	Ukhimath	North West India
10		MI-0718	Chozhiakadu	South India
11		MI-0768	Mangari	North India
12		MI-0017	Sujanpur-5	CSR&TI, Mysore
13		MI-0663	Chauntra-2	North West India
14		MI-0034	Sujanpur-1	RSRS, Kodathi
15		MI-0685	Khakad-2	North India
16		MI-0308	Victory-1	RSRS, Kodathi
17		<i>M. latifolia</i>	ME-0006	<i>M. multicaulis</i>
18	MI-0807		JRH Jorhat	CISR, Jorhat
19	MI-0845		Rajapur-2	North East India
20	<i>M. macroura</i>	ME-0220	<i>M. macroura</i>	Karnataka
21	<i>M. rotundiloba</i>	ME-0095	<i>M. rotundiloba</i>	CSR&TI, Mysore

Table 2: Growth parameters of Mulberry clones at 15 MAP

ME-0025	5.67**	42.93**	0.0039**	16.28**
MI-0211	5.46**	38.26**	0.0029**	16.12**
ME-0001	2.98	33.24	0.0012	11.00
ME-0109	3.86	33.41	0.0016	10.00
MI-0013	5.01**	43.03**	0.0034**	13.00
MI-0349	3.79	31.78	0.0014	13.00
MI-0395	2.85	31.67	0.0011	10.00
MI-0536	4.20	36.28	0.0020	15.50**
MI-0615	4.89**	35.02	0.0022	12.76
MI-0718	4.95**	40.46**	0.0030**	12.84
MI-0768	5.20**	41.36**	0.0033**	13.00
MI-0034	3.79	32.31	0.0015	10.00
MI-0663	2.52	30.85	0.0009	15.98**
MI-0685	4.91**	42.34**	0.0032**	17.89**
MI-0017	3.75	32.72	0.0015	13.00
ME-0006	5.39**	33.16	0.0022	15.00**
MI-0807	5.42**	43.25**	0.0037**	12.00
MI-0845	5.51**	42.76**	0.0037**	11.00
ME-0220	4.38	32.97	0.0018	10.00
ME-0095	2.15	30.53	0.0007	13.00
MI-0308	4.14	27.61	0.0012	12.98
Mean	4.32	35.89	0.0022	13.02
SEd	0.13	0.74	0.0001	0.27
CD (0.05)	0.26	1.47	0.0002	0.54
CD (0.01)	0.34	2.25	0.0002	0.72

Table 3: Leaf traits of Mulberry clones at 15 MAP

Clones	leaf length (cm)	leaf width (cm)	petiole length (cm)	number of leaves	leaf area (cm ²)
ME-0025	21.20	11.10	3.02	165.00**	146.33
MI-0211	16.80	10.50	3.56	176.00**	110.28
ME-0001	20.90	10.80	4.41**	121.00	130.12
ME-0109	19.29	14.90**	4.13	110.00	170.47
MI-0013	22.60	11.20	4.77**	143.00	162.11
MI-0349	26.30**	12.50	4.12	142.91	220.69**
MI-0395	19.60	9.80	2.79	111.26	123.35
MI-0536	24.90**	12.90	5.17**	170.50**	210.56**
MI-0615	18.10	9.80	3.64	140.36	109.01
MI-0718	25.10**	19.30**	3.79	141.24	297.24**
MI-0768	22.40	13.70	3.72	146.67	167.66
MI-0034	21.90	13.00	3.03	110.00	173.39
MI-0663	22.90	12.50	3.44	175.78**	178.21
MI-0685	21.50	9.90	4.66**	196.79**	141.13
MI-0017	20.90	13.70	3.82	145.67	165.64
ME-0006	20.30	13.00	4.65**	165.00**	171.71
MI-0807	33.90**	22.10**	3.91	132.00	459.49**
MI-0845	26.70**	21.70**	4.24**	121.33	363.16**
ME-0220	23.10	11.90	4.00	110.00	167.26
ME-0095	21.40	11.20	3.89	143.53	131.97
MI-0308	23.99**	13.56	3.93	143.40	183.28
Mean	22.56	13.29	3.94	143.40	189.67
SEd	0.49	0.33	0.12	4.03	4.12
CD (0.05)	0.98	0.66	0.23	8.02	8.20
CD (0.01)	0.26	0.87	0.30	10.64	10.89

2. Determination of genetic evaluation and association studies

2.1 Variability and heritability studies

In the current investigation among the various growth attributes, volume recorded high phenotypic and genotypic variance followed by leaf area, leaf width and plant height exhibited moderate phenotypic coefficient of variation and genotypic coefficient of variance whereas number of leaves, number of branches, leaf length, leaf petiole length, DBH and basal diameter recorded low PCV and GCV. The success of tree improvement programme depends on the existence of variability among the genetic resources. In the current study there exist variability however, most of the traits registered higher PCV compared to their corresponding GCV (Figure.1). Similar research in mulberry also recorded Sushmitha *et al.*, (2021) where in the leaf yield parameters exhibited higher phenotypic coefficient of variance than genotypic coefficients of variance which corroborate the findings of current study. A plethora of workers have also reported similar higher values for PCV than GCV particularly in species like *Neolamarckiacadamba* (Parthiban *et al.*, 2019); *Jatropha curcus* (Gawaliet *al.*, 2016) and *Leucaena leucocephala* (Sangram and Keerthika, 2013) are lend support to the reports of current investigation. The higher values of PCV than GCV are expected when environmental variances are larger because phenotypic variances consist of genotypic and environmental variance. In other words, expression of traits has been affected by the influence of the environmental factors has reported earlier in Neem (Dhillon *et al.*, 2009); *Dalbergia* (Vakshasya *et al.*, 1992) and also in *Eucalyptus* (Vennila, 2009).

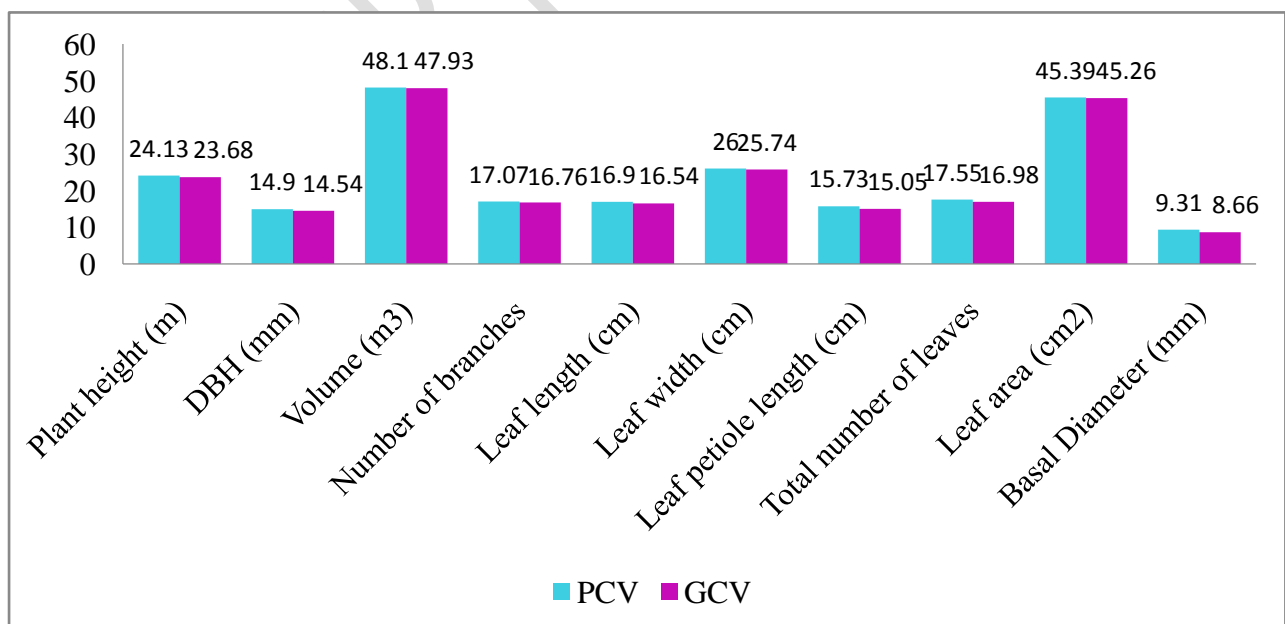


Figure. 1 PCV and GCV for Growth attributes

From these observations it is clearly evidenced that the higher PCV registered in the study would have influenced due to the environmental factors. In the current study, heritability was in higher range for all the characters under investigation. Among the traits, volume registered highest heritability (98.57%) and basal diameter registered lowest heritability (75.69 %). Such higher heritability for traits under investigation indicated that these traits are strongly under the control of additive gene action which influences the characters as reported in earlier in selected mulberry (Murthy *et al.*, 2010). Similarly higher heritability rate was also reported in leaf characterization of mulberry species (Rahman and Islam, 2020b and Doss *et al.*, 2006) which indicated the effect of additive action in expression of these characters. Several tree species *viz.*, *Ailanthus excels* (Kanna *et al.*, 2019); *Thespesia populnea* (Mahendran *et al.*, 2018); Eucalyptus (Vennila, 2009) and Willows (Choudhary *et al.*, 2016) also reported higher heritable value for most of the growth traits under the observation. These indicate that the higher heritability rate recorded in the current study for most characters particularly volume, would play vital role in selection and the associated mulberry improvement programme.

Table 4: Genetic estimation for growth attributes

Characters	Range		PCV	GCV	Heritability (%)	GA (%) of mean
	Minimum	Maximum				
Basal Diameter (mm)	41.04	53.46	9.31	8.66	75.69	16.60
DBH (mm)	23.72	42.50	14.90	14.54	90.25	29.23
Number of branches	10.00	15.98	17.07	16.76	92.16	33.89
Leaf length (cm)	16.80	33.90	16.90	16.54	92.16	33.32
Leaf width (cm)	8.90	20.50	26.00	25.74	96.04	52.50
Leaf petiole length (cm)	2.79	5.17	15.73	15.05	84.64	29.69
Total number of leaves	110	196.79	17.55	16.98	88.36	33.83
Leaf area (cm ²)	109.01	459.49	45.39	45.26	98.01	92.97
Plant height (m)	2.15	5.67	24.13	23.68	92.16	47.88

Volume (m ³)	0.0005	0.0037	48.10	47.93	98.57	98.38
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In the present study, the trend of genetic advance as per cent of mean was high in volume followed by leaf area and moderate in leaf width, plant height, number of branches, total number of leaves and leaf length whereas low in leaf petiole length, DBH and basal diameter indicated that improvement could be made in these biometric traits. The findings of current study are in line with those of Kanna *et al.* (2019) and Kaushik *et al.* (2017) in *Ailanthus excels*; Parthiban *et al.* (2019) in *Neolamarckiacadamba* and Behera *et al.* (2017) in *Eucalyptus* which lend support to the results of current investigation.

The best gains could be achieved for the characteristics that are strongly under genetic control and have wide range of variability. The characters with high heritability coupled with higher genetic gain could act as a reliable indicators as evidenced in *Prosopis juliflora* (Sundaram *et al.*, 2018) and also in *Leucaena leucocephala* (Sangram and Keerthika, 2013). Johnson *et al.*, (1955a) reported that heritability estimates along with expected genetic gain are more useful and realistic than the heritability alone in predicting the resultant effect for best genotypes. Hence the high heritability coupled with high genetic gain for volume recorded in the current study indicated that this character is strongly under genetic control and could act as a variable character for improvement programme in mulberry.

2.2 Association studies

2.2 (a) Correlation

In the present study the degree of correlations at genotypic level was higher than their corresponding phenotypic correlation coefficient in all the growth parameters indicating the genetic association among the characters. Similar results were observed by Selvan and Parthiban (2018) in *Neolamarckiacadamba*; Divakara (2017) in *Jatropha curcas* and Rao *et al.* (2011) in *Pongamia pinnata*. The current investigation the correlation matrix revealed that DBH, Plant height and Basal diameter have exhibited highly significant association with both at phenotypic and genotypic level. The results indicated that these characters are under strong association and could play a vital role in selection programme and the associated improvement programme in mulberry. It also exhibited a strong inherent genotypic relationship between characters studied as earlier reported by several authors Tasisa *et al.* (2012); Al- Aysh *et al.* (2012); De Souza *et al.* (2012); Dar *et al.* (2011); Islam *et al.*

(2010); Chikkalingaiah *et al.* (2009); and Harer *et al.* (2002) which extend greater support to the result of present investigation.

Similar positive and significant correlations have also been reported in species *Eucalyptus* (Behera *et al.*, 2017) and *Thespesia populnea* (Rajendran *et al.*, 2018). The correlated quantitative traits of major interest in an improvement programme as the improvement of one character may cause simultaneously and related changes in other associated characters (Meena *et al.*, 2014). The current study the genotypic and phenotypic correlation coefficient among the various traits revealed that the magnitude of correlation coefficient at genotypic level where higher than corresponding phenotypic correlation coefficient. Thus indicating that the minimum effect of the environment and true representation of genotypic through phenotypic selection (Saini *et al.*, 2018 and Parthiban, 2001).

2.2 (b) Path analysis

Selection is the most important activity in all breeding programmes. Tree yield, *i.e.* tree volume, is a complex and highly variable character that is influenced by many component characteristics. In the integrated structure of the plant, the overall correlation observed between two variables is a function of a series of direct and indirect relationship between different variables. Path analysis gives an insight into a complex relationship between different characteristics in a biological system (Pandey *et al.*, 1997). In current study, path co-efficient analysis indicated that among the nine traits, six traits exhibited positive direct effect on volume. The highest positive direct effect was exerted by diameter at breast height followed by plant height, basal diameter, leaf length, number of branches, leaf width and the other characters exhibited negative direct effect (Figure 2).

In the present investigation, basal diameter in addition to expressing direct effect on volume, also exhibited the highest indirect effect through diameter at breast height followed by plant height, leaf width, leaf length and other traits recorded negative indirect effect. The diameter at breast height also exhibited similar trend. Path analyses through direct and indirect effect of various characters are available only for leaf yield and not for wood volume (Sathyanarayana and Sangannavar, 2020 and Suresh *et al.*, 2017). Hence, the literature pertaining to other species are discussed.

Table 5: Phenotypic correlation coefficient of growth attributes

Effect of characters	Basal Diameter	DBH	Number of branches	Leaf length	Leaf width	Leaf petiole length	Total number of leaves	Leaf area	Plant height	Volume
Basal Diameter	1.00	0.678**	0.322	0.172	0.354	0.197	0.313	0.333	0.864**	0.829**
DBH		1.00	0.219	0.304	0.372*	0.145	0.232	0.395*	0.701**	0.936**
Number of branches			1.00	-0.124	-0.213	0.252	0.948**	-0.190	0.215	0.248
Leaf length				1.00	0.728**	0.177	-0.108	0.897**	0.207	0.322
Leaf width					1.00	0.128	-0.212	0.934**	0.389*	0.420*
Leaf petiole length						1.00	0.255	0.121	0.168	0.143
Total number of leaves							1.00	-0.184	0.223	0.252
Leaf area								1.00	0.353	0.433*
Plant height									1.00	0.872**
Volume										1.00

** Significant at 1% level
* Significant at 5% level

Table 6: Genotypic correlation coefficient of growth attributes

Effect of characters	Basal Diameter	DBH	Number of branches	Leaf length	Leaf width	Leaf petiole length	Total number of leaves	Leaf area	Plant height	Volume
Basal Diameter	1.00	0.762**	0.346	0.200	0.382*	0.196	0.356	0.357	0.926**	0.895**
DBH		1.00	0.238	0.332	0.375*	0.174	0.243	0.409*	0.730**	0.960**
Number of branches			1.00	-0.133	-0.218	0.260	1.008**	-0.195	0.219	0.254
Leaf length				1.00	0.756**	0.190	-0.129	0.915**	0.219	0.327
Leaf width					1.00	0.128	-0.219	0.945**	0.392*	0.422*
Leaf petiole length						1.00	0.276	0.130	0.174	0.149
Total number of leaves							1.00	-0.191	0.235	0.264
Leaf area								1.00	0.361*	0.436*
Plant height									1.00	0.889**
Volume										1.00

** Significant at 1% level

* Significant at 5% level

Table 7: Path coefficient analysis for growth attributes on volume

Effect of characters	Basal Diameter	DBH	Number of branches	Leaf length	Leaf width	Leaf petiole length	Total number of leaves	Leaf area	Plant height
Basal Diameter	0.141	0.482	0.024	0.019	0.021	-0.010	-0.023	-0.039	0.281
DBH	0.108	0.632	0.016	0.031	0.020	-0.009	-0.015	-0.045	0.221
Number of branches	0.049	0.151	0.069	-0.012	-0.012	-0.014	-0.064	-0.022	0.066
Leaf length	0.028	0.210	-0.009	0.093	0.041	-0.010	0.008	-0.101	0.067
Leaf width	0.054	0.237	-0.015	0.070	0.054	-0.007	0.014	-0.105	0.119
Leaf petiole length	0.028	0.110	0.018	0.018	0.007	-0.053	-0.017	-0.014	0.053
Total number of leaves	0.050	0.153	0.069	-0.012	-0.012	-0.015	-0.063	0.021	0.071
Leaf area	0.050	0.259	-0.013	0.085	0.051	-0.007	0.012	-0.111	0.109
Plant height	0.131	0.462	0.462	0.020	0.021	-0.009	-0.015	-0.041	0.304

Residual Value = 0.035

Diagonal values are direct effect

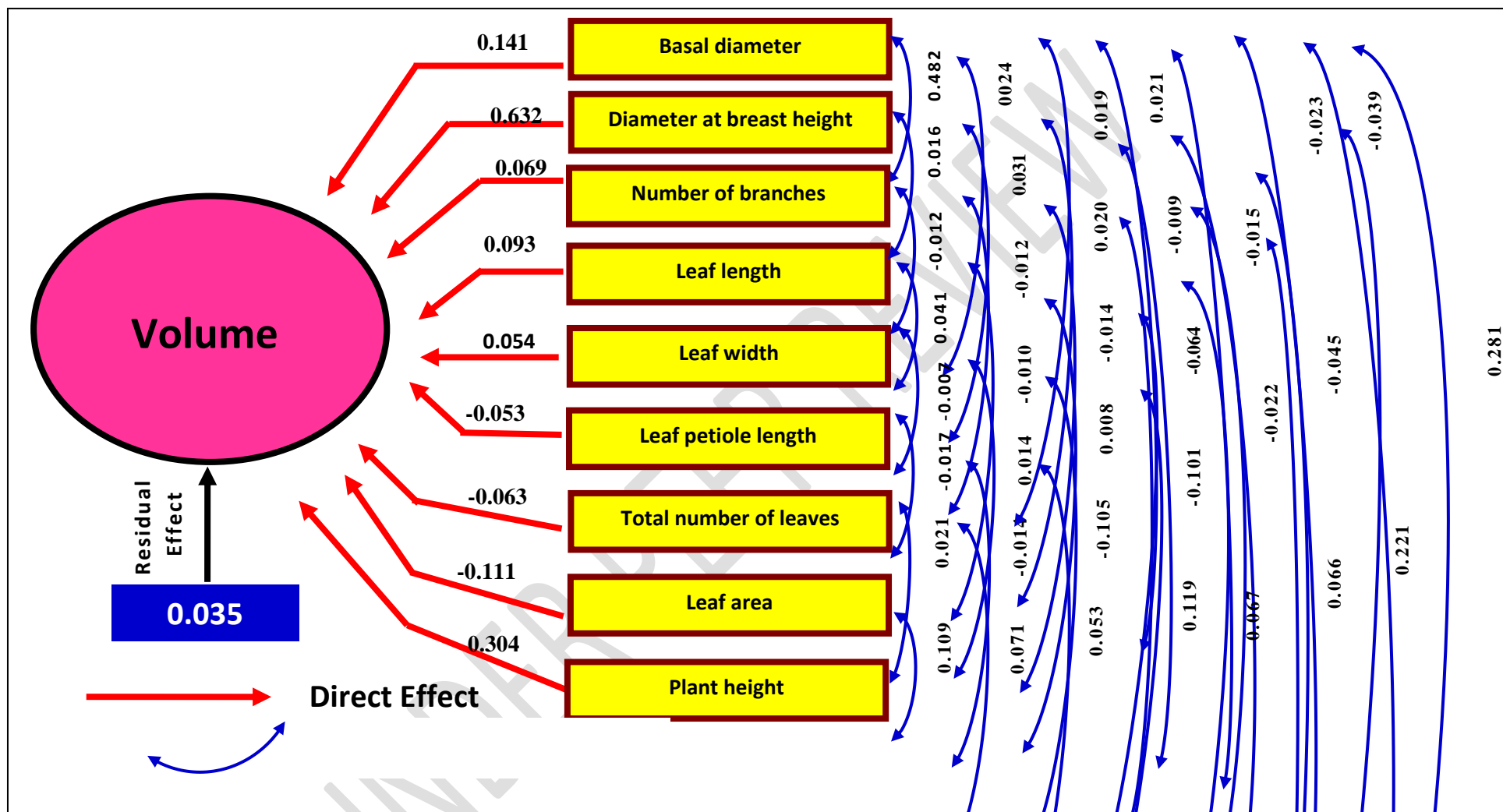


Figure 2: Path diagram showing relationship between volume and growth attributes (15 MAP)

UNDER PEER REVIEW

The path analysis provides a more resolution evidence of the interrelationship as if partition into direct as well as indirect effect *via* yield contributing factors. The current study volume was influenced through direct and indirect effects of basal diameter and DBH which revealed that these characters are under strong relationship towards influence in the total volume as evidence as in several species like *Leucaena leucocephala* (Sangaram and Keerthika, 2013); Pungam (Pavithra *et al.*, 2013) and Casuarina (Chavan *et al.*, 2012). Collar diameter and plant height had a direct effect on volume index in Eucalyptus (Ashok Kumar and Dhillon, 2016) attested the research of finds current study. Similarly, the previous study in Simarouba (Kumaran *et al.*, 2010) and Teak (Parthiban, 2001) also confirmed the findings of current study. Correlation and path analysis studies provide the relationship and dependency of one variable over the other. The present study envisaged that high and positive association coupled with intensive direct effect of diameter at breast height followed by plant height enhance the wood volume which could be used as selection criteria in mulberry improvement programme.

2.3 Genetic diversity studies

The nature and degree of genetic divergence in the seed sources is useful for classifying them into groups on the basis of their diversity, particularly when overlapping for one or more characters is frequent, the genetic divergence analysis also helps in identifying the desirable genotypes for improvement programme, presuming that genetic diversity would provide greater livelihood of promising genetic rearrangement (Parthiban *et al.*, 2019).

The current study resolved 21 clones into three clusters were in the clone in cluster I included genetic resources originated from different locations whereas the cluster II and III confined to North East India and Karnataka respectively, which indicated that the clone from different locations grouped together to form a single major cluster as evidence in cluster I. This pattern revealed that the pattern of genetic diversity was not dependent on geographical locations. These findings were agreement with results of Shree *et al.* (2018) in *Neolamarckiacadamba* and *Pinus roxburghii*(Sehgal *et al.*, 1995). Similarly, in *Pinus wallichiana* (Aslam *et al.*, 2011) and Teak (Prasad *et al.*, 1996) suggested that all the genotypes from given area may not necessarily form a single cluster. Hence, the pattern of divergence reported in the current study not dependent on the geographical nearness of the genotypes and such a pattern could be attributes to difference in the genetic makeup of the otherwise co-occurring genotypes (Chauhan and Sehgal, 2001).

Table 8: Clustering pattern of mulberry clones for growth attributes

Cluster No.	Number of clones	Members
I	17	ME-0025, MI-0211, ME-0001, ME-0109, MI-0013, MI-0349, MI-0395, MI-0536, MI-0615, MI-0718, MI-0768, MI-0034, MI-0663, MI-0685, MI-0017, MI-0308, ME-0006
II	2	MI-0807, MI-0845
III	2	ME-0220, ME-0095

In the current investigation, the high intra- cluster distance exhibited by cluster I followed by cluster III revealing the existence of diverse genotypes / clones in these cluster whereas the minimum intra cluster value showed by cluster II indicated that within the cluster the genotypes/ clones are similar. The intra cluster distance was much lower than inter cluster distance, indicating between the clusters were heterogeneous and also indicated wider genetic diversity among the clones of different cluster than those of same cluster. Such diversity between cluster were heterogeneous and homogenous within the clusters were also reported in *Neolamarckiacadamba* (Shree *et al.*, 2018) which lend support to the present findings.

The maximum inter cluster exhibited by cluster II and III which indicates extensive genetic differences between the clones in these cluster groups and selecting of parents from these clusters would prove useful in developing novel hybrids with traits like better diameter at breast height, plant height and volume. The minimum inter cluster observed between cluster I and cluster III indicating the clones belonging to these clusters were genetically closer and also selection of tree as parents from these clusters should be avoided. The results of present study are in line with the findings of other workers in different tree species *viz.*, *Ailanthus excels* (Kanna *et al.*, 2019); *Neolamarckiacadamba* (Parthiban *et al.*, 2019 and Shree *et al.*, 2018); *Bixa orellana* (Kala and Kumaran, 2012); *Pongamia pinnata* (Rao *et al.*, 2011) and *Bombax ceiba* (Chaturvedi and Pandey, 2001).

Table 9: Intra (diagonal) and Inter cluster D²& D (Parentheses) values for growth attributes

Effect of characters	I	II	III
I	684.28 (26.16)	2534.64 (50.35)	642.48 (25.35)
II		290.29 (17.04)	3198.91 (56.56)
III			447.24 (21.15)

2.4 Contribution of growth attributes to genetic divergence

The contribution of growth attributes towards genetic divergence shall guide the breeder towards deploying the contributory traits for further breeding and improvement programme. In the current study, among the growth attributes, volume contributed maximum (72.38 %) towards genetic divergence followed by leaf area and plant height (Figure 3). Hence, the present findings indicated that the trees with higher volume production in this species could play a vital role towards existence of genetic diversity. Similar results were earlier recorded in *Neolamarckiacadamba* (Parthiban *et al.*, 2019); *Eucalyptus* (Vennila 2009) and *T. grandis* (Bagchi, 2000) which corroborate the findings of current study.

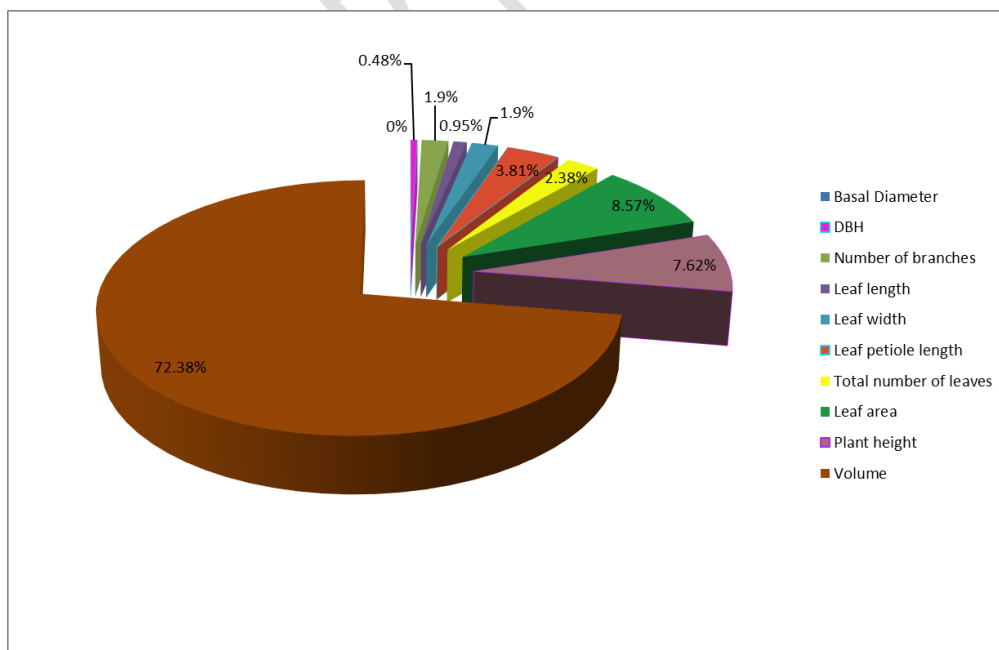


Figure 3: Percentage contribution of growth attributes to genetic divergence

Conclusion

The evaluation of 21 mulberry clones for growth attributes revealed that clones MI-0718, MI-0807, and MI-0845 consistently exhibited superior growth performance for the period of 15 months after plantation. Volume, leaf area, and plant height were identified as key attributes contributing to genetic divergence among the clones. These findings suggest that these clones could be prioritized for further breeding and improvement programs aimed at enhancing wood volume and overall productivity. The study also highlighted the importance of considering both phenotypic and genotypic variance, as well as heritability, in selecting traits for improvement. The high heritability observed for most traits indicates that they are strongly controlled by additive gene action, making them suitable targets for selection in breeding programs. Furthermore, the clustering analysis revealed that genetic diversity among mulberry clones is not solely dependent on geographical origin, suggesting that selection of parents for hybridization should be based on genetic rather than geographical considerations. Clones from different locations grouped together, indicating the potential for creating novel hybrids with desirable traits by selecting parents from diverse clusters. In conclusion, this study provides valuable insights into the genetic variability and potential for improvement in mulberry clones, emphasizing the importance of selecting superior clones for breeding programs to enhance wood volume and overall productivity in mulberry cultivation.

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