Received: 26 Mar 2021 | Revised: 08 Jun 2021 | Accepted: 09 Jun 2021

Electronic Journal of Plant Breeding

Research Article

Genetic analysis for growth and wood fiber properties in second generation clones of *Acacia auriculiformis*

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Abstract
Genetic variability of growth, wood density and fibre characters was determined in twenty second-generation clones of Acacia auriculiformis grown at IFGTB- Field Research Station, Neyvli, Tamil Nadu, India. Total volume revealed high phenotypic (29.10 %) and genotypic coefficient of variation (31.30%). Moderate PCV and GCV values were observed for height, fibre lumen diameter, Runkel ratio, slenderness ratio and wood density. The volume and fibre lumen diameter had high heritability 86 and 76 per cent, respectively. Fibre length, Runkel ratio, slenderness ratio and rigidity coefficient showed high heritability coupled with high to moderate genetic advance. Twenty clones was formed into four clusters by D2 analysis. Maximum inter-cluster distance was recorded between cluster II and cluster IV (7.396) and minimum inter-cluster distance was recorded between clusters II and IV (3.364). Higher intra-cluster values were observed in clusters I (4.171) and lower values in cluster III (3.179). Selection of clones based on clusters provides an opportunity for further improvement of growth and wood quality.

Key words
Acacia auriculiformis, Genetic Variability, Diversity, Heritability and Genetic advance

INTRODUCTION

Acacia auriculiformis is a fast-growing, multipurpose tree species belonging to the family Mimosoideae. The species grows in natural stands up to 30 m in height and 60 cm in diameter (Phi, 2009; Ismail *et al*., 2012). It is native to Australia, Papua New Guinea, Indonesia (Pinyopusarerk *et al*., 1991) and the species is widely planted in Malaysia, Vietnam, India, Zaire, Tanzania, and Nigeria (Shukla *et al*., 2007; Phi, 2009). In India, it has been planted in West Bengal, Bihar and Andhra Pradesh, Karnataka, Orissa, Uttar Pradesh and Maharashtra (Barari, 1993). It has a maximum percentage of straight-grained heartwood with fine to medium texture. Wood density ranged between 0.500 and 0.800 g cm^{-3} and it is heavy, durable, light brown to dark red. It is widely used for making round wood, building poles, light construction, flooring, industrial and domestic woodware, wood carvings, turnery, furniture, composite boards, wood cement, fuelwood charcoal (Pinyopusarerk,1990; Anup *et al*., 2017). The wood is also used for making wood chips, pulp, paper, plywood and fibre board (Pinso and Nasi,1991). The bark contains tannins that have great scope for utilizing as a natural dye in textile industries. *A. auriculiformis* is used to check soil erosion, soil improvement, restoration of degraded land and host plant for lac cultivation. (Pinyopusarerk,1990; Orwa *et al*., 2009) .

The main objective of a tree improvement program is the selection of genotypes with a wide adaptability, higher

wood volume with desirable stem form and wood quality (Doede and Adams, 1998; Zobel and Talbert, 1984). Wood-based industries emphasise on improving the wood quality to fit the industrial requirement of sawlog, pulp and paper industries (Lepoittevin *et al*., 2011). The tree improvement programs require knowledge on variability, genetic control and their relationship with growth and wood traits (Stackpole *et al*., 2010, 2011; Ma *et al*., 2015). The presence and maintenance of genetic variation in tree population plays a significant role in forest ecosystem long-term stability (Libby *et al*., 1997). The exploitation of variations is an important step in the genetic improvement of any tree species. Variation in growth traits were recorded in various provenances of *Albizia lebbeck* (Thakur *et al*., 2014) and seed sources of *Acacia catechu* (Prakash, 2011). The clonal variation and genetic divergence were recorded in species of Eucalyptus (Vennila, 2009), Dalbergia (Dhixya Deve and Parthiban, 2014) Casuarina (Parthiban *et al*., 2018) and Cadamba (Thirunirai Selvan and Parthiban, 2018).

Acacia is a cross-pollinated tree with a wide genetic variation present in nature as well as planted forests. Clonal propagation of Acacia plays an important role in capturing immediate genetic gains in wood yield. High levels of genetic variation in the breeding material provides good opportunities to the breeder for the selection of genotypes with desirable traits. The information and estimation of genetic variability is desirable and prerequisite for any tree improvement program (Zobel, 1971; Johnson *et al*., 1955). The presence of variability in anatomical characteristics has a profound influence on the wood properties (Dadswell, 1957; Burley and Palmer, 1979). Studies on wood properties in *A. auriculiformis* have been studied in different ages by Varghese *et al*. (1999), Ishiguri *et al*. (2004) and Shukla *et al*. (2007). However, in India, a few studies were available on genetic variability on growth, density and fibre property in *A. auriculiformis*. The assessment of genetic variation of growth and wood traits among the genotypes and clones are very much essential tree improvement programs. Hence, the present study was conducted to estimate genetic variability of growth, wood density and fibre characters in 20 second-generation clones of *A. auriculiformis* grown in Tamil Nadu, India.

MATERIALS AND METHODS

Early introduction of *A. auriculiformis* in India resulted in a land race of poor form and growth. It produced multiple and crooked stems and reduced the utility of species only to fuel wood. Systematic tree improvement program of *A. auriculiformis* was initiated in Institute of Forest Genetics and Tree Breeding (IFGTB), Coimbatore during 1996 with the collaboration of Australian Tree Seed Centre, CSIRO for improving stem form and wood productivity. Unpedigreed breeding populations were established with a bulk seed lot drawn from 1030 trees selected in seed orchards in Australia, PNG, Fiji and Thailand. Substantial

Table 1. Details on origin of the second generation *A.auriculiformis* clones

S. No.	Clone Code	Pedigree	Source	Geographical coordinates	
				Latitude	Longitude
1	IFGTBAA 1	RI-90/3(R5 C8)	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
2	IFGTBAA 2	RI-90/1	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
3	IFGTBAA 4	RI-37/3(C15)	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
4	IFGTBAA 7	RV-87/1(R1 C4)	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
5	IFGTBAA 18	RVI-119/1	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
6	IFGTBAA 19	RII-129/4	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
7	IFGTBAA 20	RI-113/3	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
8	IFGTBAA 23	RIII-95/3	SGPANAMPALLY	10°47’15.5”N	76°45’46.4”E
9	IFGTBAA 26	2	SGNILAMBUR	11° 16’ 40.2096”N	76° 14’ 34.2744”E
10	IFGTBAA 27	3	SGNILAMBUR	11° 16’ 40.2096”N	76° 14’ 34.2744”E
11	IFGTBAA 28	4	SGNILAMBUR	11° 16’ 40.2096”N	76° 14’ 34.2744”E
12	IFGTBAA 30	6	SGNILAMBUR	11° 16’ 40.2096”N	76° 14’ 34.2744”E
13	IFGTBAA 34	10	SGNILAMBUR	11° 16’ 40.2096”N	76° 14’ 34.2744”E
14	IFGTBAA 42	RI-111/1	SGPALLODE	8° 44’ 6.3924”N	77° 3’ 18.3996”E
15	IFGTBAA 46	RI-46/3	SGPALLODE	8° 44’ 6.3924”N	77° 3’ 18.3996”E
16	IFGTBAA 51	RIV-58/3	SGPALLODE	8° 44’ 6.3924”N	77° 3’ 18.3996”E
17	IFGTBAA 54	RII-52/3	SGWADAKANCHERY	10° 39’ 28.2276”N	76° 14’ 29.9544”E
18	IFGTBAA 59	RIII-4/2	SGWADAKANCHERY	10° 39’ 28.2276”N	76° 14’ 29.9544”E
19	IFGTBAA 60	RII-83/4	SGWADAKANCHERY	10° 39’ 28.2276”N	76° 14’ 29.9544”E
20	IFGTBAA 62	RIII-118/4	SGWADAKANCHERY	10° 39’ 28.2276”N	76° 14’ 29.9544”E

improvement in growth and stem was observed in the introduced seed lot compared to the local germplasm. After two successive thinning to remove inferior trees, the breeding populations were converted into seedling seed orchards. During 2005, superior trees were selected from the first generation seed orchards based on stem form and wood volume and the open-pollinated seeds collected from them were used to establish half-sib progeny trials in Panampally, Nilambur, Palode and Wadakancherry, Kerala. Evaluated second-generation progeny trials of *A. auriculiformis* and many families showed significantly better tree form and productivity over the local seed lots. About 20 outstanding trees were selected based on superiority in stem form, volume, wood quality and propagated through rooting of coppice shoot cuttings (Mayavel *et al*., 2018). The details on the origin of the clones are presented in **Table 1.**

The clonal evaluation trial of *A. auriculiformis* was established with 20 clones at IFGTB-Field Research Station, Neyveli, Cuddalore, Tamil Nadu (11°54'32" N, 79°47'60" E, 87 MSL) India during 2014. The area receives an annual rainfall of about 980.44 mm, the mean maximum summer temperature (April–June) of 37.62°C and the mean minimum temperature (December–February) of 28.75°C . The clones were planted at an espacement of 3 × 3 m in Row Column Design with four replications and each replication consisted of four ramets. The topography is almost flat, with red sandy loam soil. The clonal trial of *A. auriculiformis* was evaluated for growth parameters and wood traits during 2018, at the age of four. Data on tree height was measured using height measuring pole, diameter at breast height (DBH), was taken with the help of measuring tape at the age of harvesting.

The volume was calculated as per the method suggested by Huong (2020).

Standing volumes were calculated as:

$$V = \pi(D/200)^2*H*F$$

Where, V is the stem volume in m^3, D is DBH in cm, H is total height in m and F is a form factor (0.475).

The wood core samples were extracted 1.37 m height from the base in the north-south direction using increment borer. Samples were considered for anatomical studies *viz.,* fibre length, fibre diameter, wall thickness and wood density. These samples were cut into small pieces with a razor blade and placed in test tubes containing Hydrogen peroxide (H_2O_2), water and glacial acetic acid in the ratio of 1:4:5 followed by maceration (Peterson *et al*., 2008). After that the 20 (µm) transverse sections of the core samples put into a test tube and kept in a hot water bath at 70ºC in 12-18 hours, the samples turn into white colour macerated form from yellow colour. Macerated samples were prepared with sliding and then stained with safranin, dehydrated in a graded ethanol series and mounted on glass slides. Photomicrographs taken with a digital live camera (Nikon eclipse Ci) mounted on a microscope were used for measuring fibre length, fibre diameter and fibre wall thickness measured for 30 fibres at each clone using NIS elements software. The pulp and paper quality can be estimated using the following indices: Runkel ratio (Runkel, 1949), Luce's shape factor (Luce, 1970), flexibility coefficient (Malan and Gerischer, 1987), slenderness ratio (Malan and Gerischer, 1987), solids factor (Barefoot *et al*., 1964) and wall coverage ratio (Hudson *et al*., 1998).

The analysis of variance for testing the variance among treatments was carried out as per the method suggested by Panse and Sukhatme (1967). Phenotypic Co-efficient of Variation (PCV) was arrived at by using the formula as described by Burton (1952). Broad sense heritability (h^2) was calculated according to Lush (1940). The genetic advance was worked out based on the method of Johnson *et al*. (1955). The values of Phenotypic and genotypic variance heritability and genetic advance as per cent of mean (GAM) were classified (Johnson *et al*., 1955). Mahalanobis D^2 statistics were used for the calculation of genetic divergence between clones using R version 3.1.2. Grouping of the clones into various clusters were done based on growth, wood density, and fiber parameters using Mahalanobis D^2 statistics.

RESULTS AND DISCUSSION

The genetic parameters can be used to estimate the amount of benefit that can be expected from various provenances/populations. The variance between populations is widely used to measure the degree of genetic control for a specific trait and as an indicator of overall genetic variation (Foster and Shaw, 1988). Variability in anatomical characteristics has a big impact on wood properties including cell size, proportion and arrangement of different components, and basic gravity (Burley and Palmer, 1979). The overall variability of different growth and wood characters does not include details about how to identify the characters with the most variability.Therefore the estimates of GCV and PCV are needed for quantifying the extent of variability in different characters.

The general statics for 20 clones are presented for different wood density and growth parameters. The extent of variability present in the 20 clones of *A. auriculiformis* were measured in terms of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAM) are presented in **Table 2**. The wide range of variation was recorded for total height (7.29–12.21 m), DBH (9.05–12.63 cm), wood density (0.410-0.580 gcm^{-3}), total volume (0.02 - 0.07 m^3), fibre length (785.39 - 1140.59 µm), fibre diameter (18.20- 24.30 µm), lumen diameter (9.40 - 14.10µm), cell wall thickness (8.40 - 10.70 µm), runkel ratio (0.69 - 1.13), flexibility coefficient (47.90-59.90), slenderness ratio (38.20 - 59.90), rigidity

Table 2. Genetic parameters of growth traits and wood characteristics

Traits	General mean	Range	GCV (%)	PCV (%)	ECV (%)	h^2 (%)	GA(%) of Mean
Height (m)	8.65	7.29 - 12.21	10.89	15.31	10.76	51.00	15.95
Diameter at breast height (cm)	10.91	9.05 - 12.63	7.01	9.74	6.77	52.00	10.38
Fibre Length (µm)	941.52	785.39- 1140.59	8.69	11.03	6.79	62.00	14.12
Fibre width (µm)	20.65	18.20 - 24.30	7.20	9.92	6.83	53.00	10.76
Fibre Lumen Diameter (µm)	11.13	9.40 - 14.10	12.18	14.00	6.90	76.00	21.83
Double wall Thickness	9.52	8.40 - 10.70	4.51	8.16	6.80	31.00	5.14
Runkel Ratio	0.91	0.69 - 1.13	11.09	13.00	6.79	73.00	19.49
Luce Shape Factor	0.56	0.47 - 0.63	5.47	8.95	7.08	37.00	6.89
Flexibility Coefficient	53.42	47.90 - 59.90	3.98	7.87	6.79	26.00	4.15
Slenderness Ratio	46.96	38.20 - 59.90	10.94	12.86	6.77	72.00	19.16
Rigidity Coefficient	0.48	0.40 - 0.50	8.59	10.72	6.43	64.00	14.16
Wall Fraction	46.60	40.30 - 52.10	5.00	8.40	6.75	35.00	6.12
Volume (m^3)	0.04	0.02 - 0.07	29.10	31.30	11.52	86.00	55.74
Wood density (gcm^{-3})	0.47	0.41 - 0.58	10.05	11.50	6.93	52.00	10.85

coefficient (0.40 - 0.50), wall fraction (40.30 - 52.10), luce's shape factor (0.47 - 0.63). The presence of variability among the clones of *A. auriculiformis* will help in selecting outstanding clones in the existing clonal assemblage

Burton (1952) proposed that combining the genetic coefficient of variation with heritability estimates could provide an accurate estimate of the genetic benefit expected from selection. It has been stated that having a high heritability combined with a high GCV is beneficial for practising selection (Hanson *et al*., 1956). Higher magnitude of the phenotypic coefficient of variation over the genotypic coefficient of variation was observed for all the growth, wood density and fiber characters of *A. auriculiformis* clones. The results indicated the influence of the environment on the expression of the characters. The PCV ranged from 7.87 to 31.30 and GCV ranged from 3.98 to 29.10 per cent among all the growth and fiber traits of acacia clones. Higher estimates of phenotypic and genotypic coefficient of variation were obtained for total volume (31.30 and 29.10 %). The moderate PCV and GCV were recorded in height (15.31 and 10.89 %), lumen diameter (14.00 and 12.18%), runkel ratio (13.00 and 11.09 %), slenderness ratio (12.86 and 10.94%) and wood density (11.50 and 10.05%). The traits registered high and moderate values of PCV and GCV have the scope for selection of parents for the breeding program. Whereas the lower values PCV and GCV were recorded on DBH (9.74 and 7.01 %), fiber diameter (9.92 and 7.20 %), double wall thickness (8.16 and 4.50 %), flexibility coefficient (7.87 and 3.98 %) and wall fraction (5.00 and 4.80 %). High genotypic coefficient of variation and phenotypic coefficient of variation was recorded in volume and the moderate height, lumen diameter, runkel ratio slenderness ratio and wood density. The variability parameter estimates in the current investigation are in close conformity with the findings of genetic parameters in Teak (Arun Prasad, 1996) *Azadirachta indica* (Dhillon *et al*., 2003), *Pongamia pinnata* (Kumaran, 1991), and *Dalbergia sissoo* (Dogra *et al*., 2005).

GCV does not give the entire variation present in the population and the variation in the population is the total of heritable and non-heritable components. Higher heritability estimates indicate that the phenotype of the traits is strongly influenced by the genotype. The heritability value ranged from 26 (Flexibility Coefficient) to 86 per cent (Volume). In the present investigation, high heritability was recorded in volume (86%), fibre lumen diameter (76 %), runkel ratio (73 %), slenderness ratio (72%), rigidity coefficient (64%) and fibre length (62 %). Moderate heritability values in height (51%), diameter at breast height (52 %), fiber width (53 %), double wall thickness (31%), luce shape factor (37 %), wall fraction (35 %) and wood density (52 %) whereas flexibility coefficient (26 %) registered the lower heritability values. Similarly, the high heritability estimates for volume index were earlier reported in Eucalyptus (Balaji, 2000), Casuarina (Ashok Kumar and Paramathma, 2005), Meliadubia (Kumar, 2011 and Saravanan, 2012) and *Leucaena leucocephala* (Chavan and Keerthika, 2013).

Genetic advance indicates the amount of genetic advantage that can be achieved by selection, while heritability indicates how much of phenotypic variability is heritable. The genetic advance percentage of mean ranged from 4.15 to 55.74 per cent and higher values were recorded in volume (55.74%) and fiber lumen diameter (21.83 %) whereas moderate value in height (15.95 %), diameter at breast height (10.38 %), fiber length (14.12 %), fiberwidth (10.76), runkel ratio (19.46 %), slenderness ratio (19.16%), rigidity coefficient (14.16%) and wood

density (10.85 %). The lower GA values were registered in double wall thickness(5.14%), luce shape factor (6.89 %), flexibility coefficient (4.15 %) and wall fraction (6.12).

Estimates of heritability in a wide sense could be accurate if they are followed by a high level of genetic progress (Burton and Devane, 1953). In volume and lumen diameter, high heritability estimates were observed, as well as high genetic advance as a percentage of the mean. It indicates additive gene action, making selection based on these characteristics more effective. The fiber length, runkel ratio, slenderness ratio, and rigidity coefficient showed a high heritability with moderate genetic advance and the presence of a moderate amount of heritable additive genetic component that can be exploited for further selection and improvement of this species. Low heritability with the low genetic advance was registered in double wall thickness, luce shape factor, flexibility coefficient and wall fraction, indicates the presence of non-additive gene action. The present finding confirms the finding of Subramanian *et al*. (1995) reported that height, clear bole height, girth, diameter and basal area showed a moderate heritability and genetic advance in *Eucalyptus grandis*. Pande *et al*. (2013) also found a high heritability coupled with a moderate level of genetic advance and genetic gain for girth at breast height, specific gravity and height in *L. leucocephala*.

In any tree breeding programme, genetic diversity is important. Hybrids from different parents display more heterosis or hybrid vigour than closely related individuals. The current investigation was carried out to understand the genetic diversity among 20 clones of *A.auriculiformis* grown in Tamil Nadu, South India. Data collected for wood variables and growth traits for 20 clones were subjected to Mahalanobis' D2 analysis and Tocher' clustering to study the genetic divergence. On the basis of Euclidean distances, 20 clones were grouped into four clusters (**Table 3**). The maximum number of clones (11) was included in cluster II and other clusters I, II and cluster IV had 3 clones. The clones developed from different second-generation orchards located in different geographical regions were grouped to form a larger cluster and it may be due to the growth, wood and fiber similarity pattern of clones. The clustering pattern in the present study supports the findings in *C. equisetifolia* by Vishnu *et al.* (2018) grouped 46 clones into 7 clusters, and Kumar and Gurumurthi (2000) grouped 42 clones into 12 clusters based on genetic divergence. Pande *et al.* (2013) grouped 28 populations of *Leucaena leucocephala* into six clusters based on growth and wood traits.

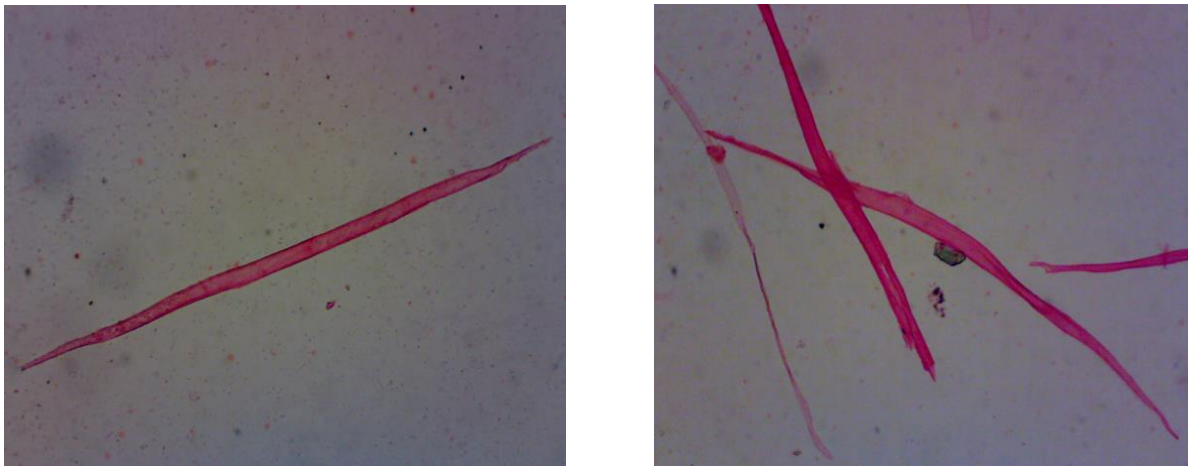
The inter-cluster values ranged from 4.061 (C II and C IV) to 7.396 (cluster III and IV) (**Table 4**). The maximum inter-cluster distance was recorded between cluster II and cluster IV (7.396) followed by clusters I and IV (6.620), and clusters II and III (6.120) whereas the minimum inter-cluster distance was recorded between clusters II and IV (3.364). Intra-cluster distance ranged from 3.179 to 4.171 and the maximum values were observed in clusters I (4.171) followed by cluster III (3.948) and the minimum values were recorded in cluster III (3.179). It indicates the presence of significant diversity within the cluster and the clones in cluster I and III could be selected for improving growth and wood traits through hybridization. Pande *et al*. (2013) reported hybridization between the populations selected from diverse clusters is expected to express higher heterosis and produce desirable recombinants.

Table 3. Composition of clusters for growth and wood traits among *A .auriculiformis* clones

Cluster	Height (m)	Diameter at breast height (cm)	Fibre Length (µm)	Fibre width (µm)	Fibre Lumen Diameter (µm)	Double wall Thickness	Runkel Ratio	Luce Shape Factor	Flexibility Coefficient	Slenderness Ratio	Rigidity Coefficient	Wall Fraction	Volume (m^3)	Wood density (gcm^{-3})
I	8.98	11.31	965.19	23.48	13.27	10.21	0.83	0.52	56.03	42.16	0.43	44.02	0.042	0.521
II	8.05	10.35	923.64	19.88	10.52	9.35	0.94	0.56	52.56	47.72	0.50	47.44	0.032	0.465
111	10.22	12.21	909.69	21.63	12.53	9.13	0.76	0.50	57.63	43.37	0.40	42.43	0.058	0.438
1V	8.92	11.30	1015.25	19.67	9.83	9.83	1.05	0.60	49.73	52.60	0.50	50.26	0.043	0.489

Table 4. Intra- and inter-distances of clusters classified based on parameters of *A .auriculiformis* clones

Cluster number	Number of clones	Details of clones
I	3	IFGTBAA - 1, IFGTBAA- 4, IFGTBAA -18
II	11	IFGTBAA- 2, IFGTBAA -19, IFGTBAA -26, IFGTBAA- 28, IFGTBAA- 42, IFGTBAA- 46, IFGTBAA 51, IFGTBAA -54, IFGTBAA- 59, IFGTBAA- 60,IFGTBAA- 62
III	3	IFGTBAA-7, IFGTBAA - 27, IFGTBAA - 34
IV	3	IFGTBAA -20, IFGTBAA -23,IFGTBAA -30



(A) (B)

Fig. 1. Fibre anatomy of *A. auriculiformis* clone IFGTBAA - 4

The mean values for different characters were calculated cluster-wise reveal considerable genetic differences among the clones (**Table 5**). Cluster III had the highest mean values height (10.22 m), diameter at breast height (12.21 cm), volume (0.058 cm) and flexibility coefficient (57.63). Similarly, cluster IV had the maximum mean values for fiber length (1051.25 µm), luce shape factor (0.60), slenderness ratio (52.60) and runkel ratio (1.05). The higher mean values of fiber width (23.48 µm) and wood basic density (0.521 gcm^{-3}) were shown in cluster I (**Fig. 1**). However, the minimum mean values for growth traits were observed in cluster II and wood properties in Custer III. The mean cluster values showed significant variations among the clusters. Cluster III showed a higher height, diameter at breast heights and tree volume. Cluster I showed a higher values of wood density, fiber length, fiber width double wall thickness and flexibility coefficient. The dendrogram (**Fig. 2**) for 20 clones was prepared using Tocher Method to reveal a similar pattern of information.

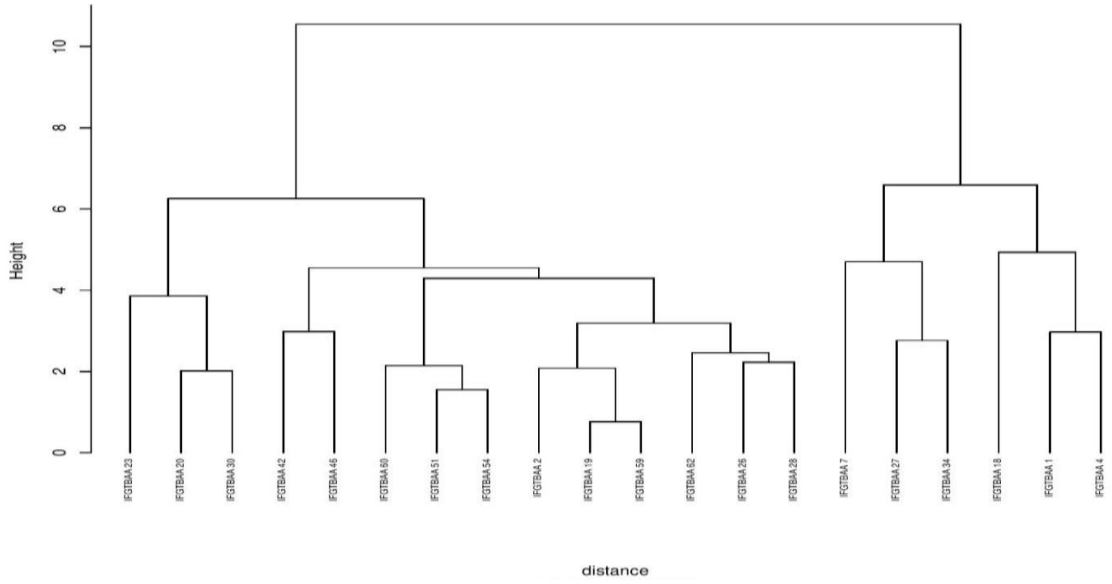


Fig. 2. Dendrogram developed through Tocher Method for different clones of *A. auriculiformis*

Table 5. Cluster mean value for growth and wood traits among *A .auriculiformis* clones

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	4.17	5.77	4.97	6.62
Cluster II		3.17	6.12	4.06
Cluster III			3.94	7.39
Cluster IV				3.23

Table 6. Per cent contribution of each character towards divergence of *A. auriculiformis*

Character	% contribution
Height (m)	0.00
Diameter at breast height (cm)	0.00
Fibre Length (µm)	11.57
Fibre width (µm)	9.47
Fibre Lumen Diameter (µm)	8.42
Double wall Thickness	0.52
Runkel Ratio	0.00
Luce Shape Factor	0.00
Flexibility Coefficient	17.89
Slenderness Ratio	18.42
Rigidity Coefficient	0.52
Wall Fraction	1.05
Volume (m^3)	13.68
Wood density (gcm^{-3})	18.42
Total	100

The degree of diversification and relative contribution of each character to the total divergence was presented in **Table 6**.The present study, stem volume and slenderness ratio contributed maximum (18.42 %) towards divergence followed by flexibility co efficient (17.89 %), and wood density (13.68 %). Since these parameters contributed substantially towards total divergence and it could well be used as desirable traits for selection. The variation in the contributing factors for genetic divergence could be attributed to differences between clones and it might be due to environmental conditions at the locations of the clones and their associated interaction.

The pattern of variability in *A.auriculiformis* within and between the clones will not only have an effect on higher growth for production of more wood but will also affect the product of wood. For development, wood, and fibre characters, there is a lot of genetic diversity among the clones, which indicates that they have a lot of room for improvement. The heritability of volume and lumen diameter was high, as was the genetic advance, and volume is a combined effect of tree height and DBH. Characters like height, DBH, volume, fibre length, lumen diameter, runkel ratio, slenderness ratio, and rigidity coefficient display a lot of genetic divergence and have a high heritability with a high genetic progress. These characteristics may be used to help choose a parent for the species' improvement. Hybridization between populations selected from various clusters is expected to generate desirable recombinants and transgressive segregants with higher heterosis. Acacia clones found in clusters with a high mean values for tree height, DBH, volume, wood density, and fibre length may be used in future tree improvement efforts. Genetic divergence studies are an important tool for developing seed orchards with diverse parents so that improved seed can be harvested in the most cost-effective manner, as diverse parents would have equal opportunities for hybridization and seed development.

ACKNOWLEDGEMENT

The authors are thankful to Director General, Indian Council of Forestry Research and Education, Dehradun and Director, Institute of Forest Genetics and Tree Breeding, Coimbatore for carrying research work on long term Tree Improvement program of *A. auriculiformis*.

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