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Provenance variation in growth and genetic potential of *Aquilaria malaccensis* under nursery condition

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Aquilaria malaccensis **Lam. is commonly known as Agarwood which is distributed in the Indo-malesian genus Aquilaria of family Thymelaeaceae known to produce resin-impregnated heartwood that is fragrant and highly valuable. Agarwood is reputed to be the most expensive wood in the world. Twenty two open pollinated families in *A. malaccensis* were selected and evaluated for growth attributes and genetic divergence. The experiment was conducted at Forest College and Research Institute, Tamil Nadu Agricultural University; Mettupalayam situated at 11° 19' N longitude, 76° 56' E latitude at 300 MSL during January - December 2010. The study indicates significant differences among the selected families for various growth attributes. Among the twenty two progenies evaluated, three progenies viz., NHJA, KHOW-1 and CHEK-1 exhibited consistent superiority over growth periods for shoot length, collar diameter and number of branches. Genetic divergence studies resulted in grouping of the selected families into six clusters which indicated the existence of adequate genetic divergence. Among the clusters, cluster VI was the largest with 9 progenies while the maximum intra clusters distance was recorded in cluster V. The intra and inter cluster distance revealed that maximum inter cluster distance was recorded between cluster IV and V which indicated the presence of wide genetic distance between *A. malaccensis* progenies. Among the various growth attributes, number of branches contributed maximum towards genetic divergence followed by shoot length. These two characters could act as a reliable indicator for future improvement programme in this economically important species. Genetic analysis of the progenies indicated adequate variability in the population. The phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) estimates exhibited superiority of number of branches followed by shoot length and collar diameter. In case of shoot length, collar diameter and number of branches exhibited moderate heritability. The genetic advance was high for shoot length followed by number of branches which indicated the reliability of these two parameters for inclusion in future improvement programme.**

Key words: *Aquilaria malaccensis,* provenances, variability, heritability, genetic divergence, intra and inter cluster distance.

INTRODUCTION

Aquilaria malaccensis Lam. is one of the 15 tree species in the Indomalesian genus Aquilaria of family Thymelaeaceae and eight are known to produce resin-impregnated heartwood that is fragrant and highly valuable (Ng et al., 1997). There are many names for this resinous wood, including agar, agarwood, aloe(s) wood, eaglewood, gaharu and kalamabak. This wood is in high demand for medicine, incense and perfume across Asia

and the Middle East. The tree grows in natural forests at an altitude of a few meters above sea level to about 1000 m, and it grows best around 500 m in locations with average daily temperatures of 20 to 22°C (Afifi, 1995; Keller and Sidiyasa, 1994; Wiriadinata, 1995). *Aquilaria* sp. has adapted to live in various habitats, including those that are rocky, sandy or calcareous, well-drained slopes and ridges and land near swamps. It is a large evergreen tree, growing over 15 to 40 m tall and 0.6 to 2.5 m in diameter, and has white flowers (Chakrabarty et al., 1994; Sumadiwangsa, 1997). The 2002 IUCN Red List classifies this species as vulnerable. *A. malaccensis* occurs mostly in the foothills of the North-eastern region (Assam, Meghalaya, Nagaland, Mizoram, Manipur, Arunachal Pradesh and Tripura) and West Bengal up to an altitude of 1000 m. In Assam and Meghalaya, it occurs sporadically in the district of Sibsagar, Sadiya, Nowgong, Darrang, Goalpara, Garo Hills and Cachar (Atal and Kapoor, 1982). A report by Chakrabarty et al. (1994) documenting India's trade in agarwood concluded that *A. malaccensis* is highly threatened in that country due to exploitation of the species for commercial purposes. *A. malaccensis* is threatened in its natural habitat because of overexploitation.

Demand for agarwood has resulted in the unsustainable harvesting of the species, leading to local extinctions. Wild agarwood was heavily extracted from Arunachal Pradesh between the late 1950s and the early 1980s, virtually exhausting the natural stock. Wild *A. malaccensis* is now considered almost extinct in Assam. Surveys undertaken by the Regional CITES Management Authority in Tripura indicate that the natural stock is almost exhausted in that State as well. In Mizoram, the lack of agarwood plantations in Mizoram and Meghalaya has resulted in much illegal harvesting from natural forests. *A. malaccensis* in Nagaland and Manipur is so depleted that a large proportion of the raw agarwood used by processing units in these two States is sourced from neighbouring countries. Because of its vast natural distribution and the diversity of ecological conditions where the species occurs, *A. malaccensis* would be expected to have considerable genetic variation (Shivkumar and Banerjee, 1986). Knowledge of variability within a species is a prerequisite for developing effective tree improvement / breeding strategies (Vakshasya et al., 1992). The significance of genetic variation studies and provenance testing in forest tree improvement is well realized.

Success in the establishment and productivity of forest tree plantations is governed largely by the species used and the source of seed within species (Larsen, 1954; Lacaze, 1978). No matter how sophisticated the breeding techniques, the largest, cheapest and fastest gains in most forest tree improvement programs will accrue if use of suitable species and seed sources within species is assured (Zobel and Talbert, 1984). Provenance research is therefore of paramount importance. Provenance is defined as a subdivision of species consisting of genetically similar individuals, related by common descent and occupying a particular territory to which it has become adapted through natural selection.

Therefore, present investigation has been carried out to estimate genetic variation present in *A. malaccensis* populations and survival percentage of species at Forest college and Research institute, Mettupalayam, Tamil Nadu.

MATERIALS AND METHODS

Selection of superior genetic resource

The survey has been conducted in predominant *A. malaccansis* growing areas of India and twenty two different provenances from North-Eastern states of Assam (6), Tripura (10) and Nagaland (6) were selected. Based on morphological characters such as diameter, height, number of branches and clear bole height of superior Agar wood, genetic resources were selected and measurement were recorded as given in the Table 1.

Geographical location of the population

Six provenances from Assam (MDLY, UDLY-1, UDLY-2, NHJA, NHSU, and HAKH), Ten Provenances from the state of Tripura (KHOW-1, KHOW-2, AMBS, CENT-1, CENT-2, KUMA-R, KUMA, FUKO, KUMA-RO, ROWA) and six provenances (DI-FC, DI-TY, DIPU, CHEK-1, CHEK-2, CHEK-3) from Nagaland were used for this study. Geographic locations, altitude, locations of twenty two different provenances were seeds are collected for study are cited in Table 2.

Experimental site description

The experiment was conducted at Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam situated at 11^{o} 19'N longitude and 76 ^{o}56'E latitude at 300 msL during January to July 2013. The experimental site receives an annual rainfall of 800 mm/annum with the maximum and minimum temperature of 33.8 and 21.2°C, respectively. The soil is predominantly red lateritic with a pH of 7.1.

Nursery technique and seedling establishment of each provenance

Pretreated seeds were directly sown in polythene bags (20 × 40 cm size) containing potting mixture of sand, soil and farmyard manure in the ratio of 2:1:1 and watered regularly as and when required.

Experimental design and treatment

The nursery experimental trail was laid out using a Completely

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Table 1. Morphological characters of superior genetic resources of Agar wood.

S/N	Provenance name	Location	GBH (cm)	Height (m)	Clear bole Height (m)	Number of Branches
1	MDLY	Modhertally	52.20	7.50	4.50	16
2	UDLI-1	Udali-1	68.00	16.5	4.00	20
3	UDLI-2	Udali-2	70.00	14.0	5.00	20
4	NHJA	Nahaurani-Jangoan village	89.00	19.5	9.00	21
5	NHSU	Nahaurani- Sumoni	81.00	19.0	5.00	17
6	HAKH	Hatiekhowa village	79.00	17.5	6.50	18
7	KHOW-1	Khowai-1	103.0	18.5	7.00	22
8	KHOW-2	Khowai-2	100.0	19.0	7.50	20
9	AMBS	Ambassa	390.0	27.0	7.00	52
10	CENT-1	Central nursery-1	110.0	18.0	12.0	10
11	CENT-2	Central nursery-2	127.0	22.0	11.0	17
12	KUMA-R	Kumargath-RFO house	147.0	25.0	10.0	18
13	KUMA	Kumargath	88.00	18.0	7.00	22
14	FUKO	Fukirkohi	87.00	16.0	2.00	18
15	KUMA-RO	Kumargath-range office	230.0	28.0	3.80	96
16	ROWA	Rowa	81.00	13.0	3.00	15
17	DI-FC	Dimapur-Forest colony	72.00	16.5	4.00	16
18	DI-TY	Dimapur- Tykho village	58.00	12.0	6.00	18
19	DIPU	Diphupur	72.00	17.5	7.50	16
20	CHEK-1	Chekieye village-1	87.00	18.0	6.50	24
21	CHEK-2	Chekiye village-2	75.00	17.0	7.00	17
22	CHEK-3	Chekiye village-2	83.00	16.5	7.00	18

Table 2. Details of location, latitude, longitude, elevation (m) of superior genetic resources of Agar wood provenance.

S/N	Provenance name	Location	State	Latitude	Longitude	Elevation (m)
1	MDLY	Modhertally	Assam	$26^0$08.100	$92^0$49.771	123
2	UDLI-1	Udali-1	Assam	$25^0$53.304	$93^0$00.604	89
3	UDLI-2	Udali-2	Assam	$25^0$53.303	$93^0$00.600	90
4	NHJA	Nahaurani-Jangoan village	Assam	$26^0$38.856	$94^0$03.318	80
5	NHSU	Nahaurani- Sumoni	Assam	$26^0$38844	$94^0$03.348	78
6	HAKH	Hatiekhowa village	Assam	$26^0$36.476	$94^0$01.826	82
7	KHOW-1	Khowai-1	Tripura	$24^0$04.186	$91^0$36.868	40
8	KHOW-2	Khowai-2	Tripura	$24^0$06.170	$91^0$36.840	47
9	AMBS	Ambassa	Tripura	$23^0$55.138	$91^0$50.522	74
10	CENT-1	Central nursery-1	Tripura	$23^0$54.891	$91^0$53.144	115
11	CENT-2	Central nursery-2	Tripura	$23^0$54.927	$91^0$53.175	126
12	KUMA-R	Kumargath-RFO house	Tripura	$24^0$10.501	$92^0$01.922	38
13	KUMA	Kumargath	Tripura	$22^0$09.695	$92^0$02.661	39
14	FUKO	Fukirkohi	Tripura	$24^0$10.700	$92^0$01.288	32
15	KUMA-RO	Kumargath-range office	Tripura	$24^0$10717	$92^0$01.923	61
16	ROWA	Rowa	Tripura	$24^0$22.084	$98^0$49.328	97
17	DI-FC	Dimapur-Forest colony	Nagaland	$25^0$54.733	$93^0$42.825	152
18	DI-TY	Dimapur- Tykho village	Nagaland	$25^0$53.189	$93^0$43.271	158
19	DIPU	Diphupur	Nagaland	$25^0$51.294	$93^0$45.493	160
20	CHEK-1	Chekieye village-1	Nagaland	$25^0$51.856	$93^0$45.049	162
21	CHEK-2	Chekiye village-2	Nagaland	$25^0$51.863	$93^0$45.479	164
22	CHEK-3	Chekiye village-2	Nagaland	$25^0$51.871	$93^0$45.488	165

Randomized Block Design with 22 provenances for 3 replications. Observation with respect to survival percentage, shoot, collar diameter and numbers of branches were taken at every one month interval till the end of experiment (6 months) in order to, assess the suitable provenances and their survival percentage before planting in main field.

Biometrical observation

Mean performance of progenies

Survival percentage: Survival of seedlings was calculated and expressed as percentage.

$$\text{Survival percentage (\%)} = \frac{\text{No. of survival seedling}}{\text{No. of seedlings planted in nursery}} \text{ X } 100$$

Measurements: Shoot length, Collar diameter of individual seedlings was measured and numbers of branches was counted at an interval of one month and observation was recorded.

Variability studies: These parameters were estimated as per the method described by Johnson et al. (1955).

Phenotypic co-efficient of variability: Phenotypic Co-efficient of Variation (PCV) was arrived by using the formula as described by Burton (1952).

$$\text{PCV (\%)} = \frac{(\text{Phenotypic Variance})^{1/2}}{\text{General Mean}} \times 100$$

Genotypic co-efficient of variability: Genotypic Co-efficient of Variation (GCV) was arrived by using the Burton's (1952) formula.

$$\text{GCV(\%)} = \frac{(\text{Genotypic Variance})^{1/2}}{\text{General Mean}} \times 100$$

Heritability (h^2): Broad sense heritability (h^2) was calculated according to Lush (1940)

$$h^2 = (\sigma^2 g / \sigma^2 p)$$

Heritability percentage = h^2 x 100

Genetic advance: Genetic advance was worked out after Johnson et al. (1955a).

$$\text{Genetic Advance (GA)} = [(\text{Genotypic Variance} / \text{Phenotypic Variance})^{1/2} \times K$$

Where, K = 2.06, a selection differential at 5% selection intensity

$$\text{GA(\%)} = \frac{\text{GA}}{\text{Grand Mean}} \times 100$$

Data analysis

Biometric data for shoot length, collar diameter and number of branches were subjected to analysis of variance (Panse and Sukhatme,1978) and genetic divergence of the open pollinated families was studied following Mahalanobis D^2 (Mahalanobis, 1928) statistics. Grouping of the superior open pollinated families into various clusters was made by Tocher's method (Rao, 1952). On completion of clustering, the *intra* and *inter* cluster relationships were studied and the mutual relationship between clusters and their distances were represented. The average *intra* cluster distance was measured using the formula. $D^2 = D_1^2 / n$ where D^2 was the sum of the distances between all possible combinations of the open pollinated families included in a cluster whereas the average *inter* cluster divergence was arrived at by taking into consideration all the component D^2 values possible among the numbers of the two clusters. The genetic distance D between the clusters was obtained from the square root of the average D^2 values. Estimation of genetic parameters *viz*., variability, PCV and GCV were computed (Burton, 1952). Heritability and genetic advance were computed (Lush, 1940; Johnson et al., 1955).

RESULTS AND DISCUSSION

Mean performance of *A. malacansis* genotypes

Success in the establishment and the productivity of forestry plantation is governed largely by the species used and the source of seed within species (Larson, 1954; Lacaze, 1978). No matter how sophisticated the breeding techniques, the largest, cheapest and fastest gains in most forestry improvement programmes will accrue if use of suitable species and seed sources within species is assured (Zobel and Talbert, 1984). Seeds were much influenced by their place of origin (Heydecker, 1972) especially due to environmental variation in latitude, altitude, rainfall, temperature, moisture, soil and the external factors (Holzer, 1965). The seed source variations were reported on many tree species (Shivakumar and Banerjee, 1986; Murthy, 1989; Masilamani and Dharmalingam, 1999) and were dictated by environmental and edaphic factors. This might also be due to altitudinal variation (Barnett and Farmer, 1978) or region of collection (Bonner, 1984). Significant differences among provenances were detected for survival percentage. The survival rate showed a decreasing trend with decreasing latitude of provenance The survival percentage of provenance ranged from 21 (AMBS) to 42% (NHJA and CHEK-1). The highest mean survival (42%) was recorded in NHJA and CHEK-1 followed by UDLI-2 AND KHOW-1 (41.66%). The provenance from AMBS-1 (21%) followed by UDLI-1, HAKH, DI-FC and CHEK-2 (23.66%) had lowest survival percentage (Table 3). In the present investigation, significant variation was observed for all the attributes viz., shoot length, collar diameter and number of branches at nursery level for 22 progenies of *A. malacancis*. Among the progenies, the superiority of three progenies viz., NHJA, KHOW-1 and CHEK-1 was evident for most of the growth characteristic investigated (Table 4). The shoot length of Agarwood provenances were observed to increase in shoot length with increase in number of days of observation.

Table 3. Survival percentage of 22 provenance of Agar wood.

Provenance number	Provenance name	Survival percentage (%)
1	MDLY	34.33
2	UDLI-1	23.66
3	UDLI-2	41.66
4	NHJA	42.00
5	NHSU	33.00
6	HAKH	23.66
7	KHOW-1	42.00
8	KHOW-2	35.33
9	AMBS	21.00
10	CENT-1	24.33
11	CENT-2	33.33
12	KUMA-R	33.66
13	KUMA	20.66
14	FUKO	25.33
15	KUMA-RO	31.33
16	ROWA	32.00
17	DI-FC	23.33
18	DI-TY	27.33
19	DIPU	25.00
20	CHEK-1	41.66
21	CHEK-2	23.66
22	CHEK-3	34.33
	Mean	30.98
	SE.d	1.483
	CD (0.05)	2.99 0

Table 4. Morphological characters of superior genetic resources of Agarwood.

Provenance number	Provenance name	Shoot length (cm)		Collar diameter (mm)		Number of branches	
		120 DAP	180 DAP	120 DAP	180 DAP	120 DAP	180 DAP
1	MDLY	18.83	40.26	5.533	11.12	1.000	3.000
2	UDLI-1	21.83	37.93	5.816	10.70	1.000	2.000
3	UDLI-2	19.73	41.16	5.666	11.10	1.333	2.000
4	NHJA	23.26	48.16	4.383	11.16	1.000	2.000
5	NHSU	19.70	32.66	5.950	11.06	1.000	4.000
6	HAKH	18.70	39.33	5.350	11.05	0.000	1.000
7	KHOW-1	24.50	45.00	5.833	11.12	0.666	2.000
8	KHOW-2	18.56	27.50	4.190	10.90	1.000	2.666
9	AMBS	18.56	27.50	4.190	11.01	1.000	2.000
10	CENT-1	18.40	36.93	4.926	11.02	0.666	3.000
11	CENT-2	17.10	32.00	3.983	10.93	1.333	3.000
12	KUMA-R	18.53	37.26	4.136	11.18	1.000	2.000
13	KUMA	16.40	28.40	5.566	10.80	0.666	3.000
14	FUKO	18.50	30.83	5.466	11.01	0.666	4.000
15	KUMA-RO	16.56	24.00	6.133	11.03	0.666	4.000
16	ROWA	17.90	30.16	5.433	11.09	1.333	3.000
17	DI-FC	18.86	31.00	5.333	11.14	1.000	2.000
18	DI-TY	20.43	33.56	5.216	11.10	0.666	4.000
19	DIPU	15.73	25.00	5.600	11.14	0.666	3.000

Table 4. Contd

20	CHEK-1	18.46	36.66	5.766	11.16	1.000	3.000
21	CHEK-2	17.13	39.23	5.766	11.26	0.666	3.000
22	CHEK-3	14.53	25.50	4.766	11.14	1.333	3.000
	Mean	18.68	34.47	5.163	11.05	0.924	3.030
	SE.d	1.259	6.117	0.606	0.158	0.471	0.864
	CD (0.05)	2.537	12.32	1.222	0.318	0.950	1.742

Table 5. Clustering pattern in *Aquilaria malaccansis* for morphometric attributes.

Cluster number	Number of family	Members
I	3	MDLY, NHJA, KUMA-R
II	2	NHSU, FUKO
III	2	UDLI-2 , KHOW-1
IV	2	DIPU , CHEK-3
V	4	UDLI-1, HAKH, KHOW-2, CENT-1
VI	9	AMBS, CENT-2, KUMA, KUMA-RO, ROWA, DI-FC, DI-TY, CHEK-1, CHEK-2

Provenances only differed significantly in mean shoot length. At 120 DAP, the length of shoot varied and ranged from KHOW-1 (24.50 cm) to KUMA (16.40 cm). At 180 DAP, the provenance exhibited significant variation in shoot length ranged between NHJA (48.16 cm) and FUKO (30.83 cm). NHJA (48.16 cm) and KHOW-1 (47 cm) were recorded significantly higher shoot length compared to general mean (Table 4). All other provenances were on par with general mean for this parameter.

At 120 DAP, the collar diameter ranged between NHJA (6.133 cm) and CENT-1 (3.983 cm). Other than NHJA provenance, all provenances were on par with general mean for the collar diameter. At 180 DAP, two provenance viz., NHJA (48.16 cm) and CHEK-1 (11.36 cm) were recorded significantly higher value and UDLY-1 (10.70 cm) had significantly lower value compared to general mean (Table 4). The provenance HAKH (0.000) had not produced any branches and all other provenances were on par with general mean for numbers of branches at 120 DAP. At 180 DAP, number of branches varied between NHJA, KHOW-1, CHEK-1, DI-TY (4.000) and HAKH (1.000). HAKH (1.000) were recorded significantly lower value compared general mean (Table 4). Similarly in teak variations in several growth characters, stem and morphological characters were evident due to provenance (Rawat et al., 1998). A plethora of workers reported on the existence of variations in morphometric traits of various tree species like *Dalbergia sissoo* (Tewari et al., 1996), *Eucalyptus tereticornis* (Otegbeye, 1990), *Santalum album* (Bagchi and Sindu Veerendra, 1991), *Tecomella undulata* (Jindal et al., 1991) *Lagerstroemia* spp. (Jamaludheen et al., 1995) and *Terminalia arjuna* (Srivastava et al., 1993).

Cluster composition

Clustering methods have the goal of separating a pool of observations in many subgroups to obtain homogeneity within and between the formed subgroups. D^2 statistics is an important tool in plant breeding for estimating genetic divergence (Aslam Mohd et al., 2011). D^2 statistics is an important tool in plant breeding for estimating genetic divergence. The application of D^2 clustering technique in *A. malacancis* genetic resources resolved the twenty two genotypes into six clusters. Among the six clusters, the clusters VI and V were the biggest with 9 and 4 members, respectively. The Cluster I contains 3 members and remaining cluster constitutes two progeny each (Table 5). In *Tectona grandis* using D^2 clustering technique 80 batches of teak had been grouped into eight clusters, of which group A formed the largest cluster containing 46 batches (Bagchi, 2000). And also, *Melia dubia* has been grouped into six clusters in that cluster I formed biggest group (Kumar et al., 2013). In the present investigation it was observed that the families from different locations got clubbed together to form a single major cluster as evident in cluster I and therefore the pattern of divergence was not dependent upon the geographic locations. Inclusion of geographically divergent provenances of teak in the same cluster may be attributed to the fact that the factors other than geographic distribution might be responsible for their genetic similarity (Subramanian et al., 1994).

Intra and inter cluster average distance

The *intra* and *inter* cluster analysis indicated that this may be due to introduction and demonstration during past

Table 6. Inter and intra cluster distances for morphometric attributes.

Cluster	1	2	3	4	5	6
I	0.48437	3.01125	0.43116	3.70187	3.29812	3.03829
II		0.12625	4.17527	1.97394	5.21623	1.69394
III			0.19793	4.90531	2.65486	3.87403
IV				0.22385	7.96942	2.2769
V					3.47435	5.64495
VI						2.86515

Table 7. Inter (diagonal) and intra cluster D2 values for morphometric attributes.

Cluster	1	2	3	4	5	6
I	0.69597	1.73529	0.65663	1.92402	1.81607	1.74307
II		0.35532	2.04335	1.40497	2.28391	1.30151
III			0.44489	2.21479	1.62937	1.96825
IV				0.47313	2.82302	1.50894
V					1.86396	2.37591
VI						1.69268

Table 8. Percentage contributions of morphometric traits to genetic divergence at -180 DAP.

Characters	Number of first rank	% contribution
Shoot length	85	36.79
Collar diameter	15	6.493
Number of branches	131	56.71
Total	231	100

years as evidenced in *Bombax ceiba* (Chaturvedi and Pandey, 2001). The maximum *intra* cluster distance was shown by the cluster II (1.803). The average intra and inter cluster D^2 and D values among the six clusters are presented in Table 6 and 7. The maximum intra cluster distance was shown by the cluster V (3.474) followed by cluster VI (1.692). From the inter cluster distance, it is inferred that the cluster I and III (0.484) were the closest while the maximum inter cluster distance was recorded between Cluster IV and V (7.969) which indicated the presence of wider genetic distance between *A. malaccansis* families. Such inter and intra cluster distance among *Pinus gerardiana* (Anilkant et al., 2006) and *M. dubia* reported which lend support to the current findings (Kumar et al., 2013).

Contribution of traits towards genetic divergence

Number of branches contributed the maximum towards genetic divergence (56.71%) followed by shoot length(36.79%) and the least by Collar diameter (6.493%) (Table 8).

Variability parameters

The assessment of genetic variability is a key to progress in tree improvement (Zobel, 1981) and is a useful tool in determining the strategies for tree improvement and breeding of any species. To understand the causes of variation, apportioning of total phenotypic variation is having more utility. The genetic variation which is heritable can be exploited for further improvement programme. In this study, number of branches registered high PCV (38.02) and GCV (15.04). Shoot length recorded moderate PCV (25.37) and GCV (14.27) followed by collar diameter PCV (1.805) and GCV (0.616) (Table 9) Higher GCV for number of branches in *E. tereticornis* and low GCV for height in the same species were earlier reported (Paramathama,1992). Similarly, low GCV and PCV for height and collar diameter were also reported in *Bambusa pallida* (Singh and Beniwal, 1993). The exhibition of low to moderate PCV and GCV for

Table 9. Genetic estimates for growth attributes at 180 DAP.

Traits	GCV	PCV	ECV	Heritability	Genetic advance (%)
Shoot length	14.27	25.37	20.98	0.316	16.54
Collar diameter	0.616	1.805	1.697	0.116	0.433
Number of branches	15.04	38.02	34.92	0.156	12.25

collar diameter and shoot length in the present study is in conformity with the above assertions. The genotypic and phenotypic coefficient of variation for shoot length, collar diameter and number of branches recorded in the current study provided evidences for existence of adequate genotypic variations (Kumar et al., 2010) and thus extend the scope for exploitation of genetic variability for further improvement in this multiple utility species. The relative values of PCV and GCV give an idea about the magnitude of variability present in a genetic population. In the current study, the estimates of GCV were less than PCV for many traits indicating the role of environment in the expression of the traits. The variability parameter estimates in the study are in close approximation with the findings of genetic parameters in *Azadirachta indica* (Dhillon et al., 2003), *Pongamia pinnata* (Kumaran, 1991) and also in progenies of *Dalbergia sissoo* (Dogra et al., 2005) which lend support to the findings of current investigation.

Heritability and genetic advances

Heritability has an important place in tree improvement programme as it provides an index of relative strength of heredity versus environment. Dorman (1976) reported that heritability is very important in tree improvement programme. Heritability expresses the degree to which a character is influenced by heredity as compared to the environment (Kumar et al., 2010). Estimation of broad sense heritability for various characters showed low to moderate heritability for shoot length (0.31), number of branches (0.15) and collar diameter (0.11) (Table 9). The results are in agreement with the studies carried out in *Eucalyptus globulus* who reported low heritability for DBH during field evaluation of 8 sub races (Apiolaza et al., 2005). Similarly, low to moderate heritability was also recorded in *E. globulus* and in *Eucalyptus nitens* (Raymond, 2002) for different genetic parameters and low to moderate heritability for height and tree volume in *Eucalyptus grandis* (Osorio et al., 2001). The authors also reported that the heritability varied with changing environment and age. Though heritability in broad sense may give useful indication about the related value of selection, heritability along with associated genetic gain should be considered together for valid, reliable and useful conclusion. In the current study, the trend of genetic advance as percent of mean was maximum in Shoot length (16.54) followed by number of branches (12.25) and collar diameter (0.433) (Table 9) indicating a wide scope for genetic improvement in the species. The findings of current study are in line with those of *Heracleum candicans* (Devagiri et al., 1997). In a holistic view, the existence of adequate variability for different growth attributes coupled with low to moderate heritability indicates the possibility for identification of the best family suitable for commercial utilization.

Conflict of interests

The authors did not declare any conflict of interest.

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