Electronic Journal of Plant Breeding, 9 (2) : 692-704 (June 2018) DOI: 10.5958/0975-928X.2018.00083.2
ISSN 0975-928X

Research Article

Clonal evaluation and genetic divergence studies in *Neolamarckia cadamba* roxb.

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(Received: 19 Apr 2018; Revised: 17 Jun 2018; Accepted:17 Jun 2018)

Abstract

Twenty five *Neolamarckia cadamba* clones were evaluated for growth attributes and genetic divergence. The clonal evaluation test conducted for a period of 15 months indicated that the clones differed significantly for various growth and leaf attributes. Among twenty five clones evaluated, two clones *viz.*, AC17 and AC15 reigned supreme in terms of all growth attributes and they are under sharp focus for immediate adoption and incorporation in future breeding programme. The clones were characterized for the existence of genetic divergence through Mahalanobis D^2 analysis. The study resolved twenty five clones into ten major clusters. In which Cluster II was maximum with nine clones. Five clusters *viz.*, VI, VII, VIII, IX and X registered only one clone each indicating their clonal genetic divergence. The intra-cluster distance was ranged between 0.00 and 15.03 and the inter cluster distance was ranged between 8.75 and 64.77. The highest inter cluster distance was registered between cluster VIII and X indicating wider genetic variation and extends scope for further improvement. Among the growth attributes, volume contributed maximum genetic divergence which could be incorporated in selection and improvement programme of *Neolamarckia cadmaba*. This study examines, the variability pattern and growth attributes and recommends two clones for immediate adoption.

Keyword
Neolamarckia cadamba, Diversity, Intra and Inter cluster distance, Growth performance, Leaf attributes

Introduction

Neolamarckia cadamba is a tropical multipurpose tree species and exhibits a wide range of natural distribution from South Asia to South East Asia including India, Jawa, Sumatra, China, Indonesia, Malaysia, Bangladesh, Sri Lanka, Cambodia, Papua New Guinea, Philippines and Singapore. In India, it occurs in the sub Himalayan tract from Nepal to west Bengal and Assam. It is also found in interior states of India particularly in Bihar, Madhya Pradesh, Andra Pradesh and evergreen forests of Karnataka and Kerala (Anon, 1985). This species has large tropical trees with characteristics of straight cylindrical bole and reaches a height upto 15 m. (Ghosh, 1977)

This species has profound attraction in India due to its fast growth and multiple industrial utility. The wood of this species would used in pulpwood, light construction material, flooring, beams and rafters, tea-chests, packing cases, match splints, bobbins and pencil (Soerianegara and lemmans, 1993). The pulp of the species is mixed with long fibre material to produce medium quality paper (Parthiban and Seenivasan, 2017). The leaves of this species are found to have an excellent feed quality (Zayed *et al.,* 2014). Such a multiple utility species received only little research attention and demanded systematic research programme. Traditional tree improvement programme have been conducted sequentially with successive species, provenance and progeny tests. However, in practice there is a strong economic pressure to reduce the testing interval between these stages.

The use of combined provenance and progeny test has been advocated to reduce the testing interval between provenance and progeny stage (Zheng *et al.*, 1994; Sebbenn *et al.*, 2003; Finkeldey, 2005). Accordingly, tree improvement program in *Neolamarckia cadamba* was reported in combined provenance and progeny tests experimental in Indonesia (Sudrajat *et al*., 2016). Barring this study, there is no systematic tree improvement programme on this multiple utility species which demanded a systematic approach to improve this species. Accordingly, a systematic progeny test was carried out to deploying 30 progenies selected from different parts of India and evaluated during the period between 2013 and 2015 (Prakash, 2017). Based on the early superiority, twenty five clones were selected based on the progeny test and was evaluated for screening short rotation clone. This study examines the growth and diversity pattern of *Neolamarckia cadamba* clonal genetic resources.

Materials and Methods

Thirty open pollinated genetic resources of *Neolamarckia cadamaba* were collected from 11 natural ranges distributed in India includes Tamil Nadu, Assam, Bihar, Nagaland, Uttarkhand, Telangana, Uttar Pradesh, Maharastra, Karnataka, Kerala and Tripura. The seedlings were raised and systematic progeny test was carried out during 2013. Twenty five plus 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 esplacement 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, total number of leaves and leaf area.

The D^2 statistics was adopted for the estimation of genetic divergence (Mahalanobis 1928). Using D^2 statistical results, the clustering of clones was done. The D^2 statistics was carried out using all the traits. The clones were grouped into different clusters using ‘GENRES’ statistical package on the basis of D^2 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

The clonal evaluation test exhibited significant variation among the clones due to growth attributes and the results are furnished in table 2. The basal diameter differs significantly due to clones. Compared to the average basal diameter two clones *viz.*, AC17 (86.31 mm) has exhibited significantly higher basal diameter followed by AC15 (74.13 mm). Two clones *viz.*, AC20 and AC24 recorded significantly lower basal diameter compared to the average basal diameter of all clones. This indicated superiority of few clones which may be suitable for deployment as short rotation clone. Similarly, the diameter at breast height also exhibited variation due to clones. The same two clones *viz.*, AC17 (56.92 mm) and AC15 (52.69 mm) exhibited significantly higher diameter at breast height compared to average diameter at breast height.

The variation is a prerequisite for genetic improvement of any crop species (Sharma *et al.*, 1994). The desired genetic improvement can be achieved only through exploitation of variation. Hence, the variation recorded in the current investigation extends the scope for deployment of clones with increased values for growth attributes. Such variation in growth attributes were recorded earlier in various provenances of *Albizia lebbeck* (Thakur *et al.*, 2014) and seed sources of *Acacia catechu* (Prakash, 2011). The variation due to clone was also recorded in Eucalyptus (Vennila, 2009), Casuarina (Parthiban *et al.*, 2018) which lend support to the current investigation.

Height is one of the important factors which decide the performance of a clone in a specific site quality. The clones differed significantly due to height which varied between 1.93 m (AC 20) and 5.77 m (AC 17) with overall average height of 3.90 m. Compared to the average height, three clones *viz.*, AC 17 (5.77 m) followed by AC 15 (5.37 m) and AC 16 (4.93 m) registered significantly higher plant height. Barring five clones *viz.*, AC 10, AC 12, AC 20, AC 21 and AC 24, other clones exhibited parity with the average height of the clones.

The number of branches also exhibited variation due to the clone and it ranged between 6.67 (AC 20) and 17.33 (AC 17). The average number of branches recorded was 12.04. Compared to average number of branches only one clone *viz.*, AC 17 (17.33) reigned supreme. Volume of the clones also exhibited variation and it ranged between 0.0002 m^3 (AC 20) and 0.0074 m^3 (AC 15). The average volume recorded was 0.0026 m^3. Compared to the average volume, four clones *viz.*, AC 17 (0.0074 m^3), AC 15 (0.0057 m^3), AC 16 (0.0043 m^3) and AC 23 (0.0043 m^3) recorded significantly higher volume.

Considering all the growth attributes into account, out of twenty five clones’ evaluated, only two clones *viz.*, AC 17 and AC 15 came into lame light. Such superiority of selected provenances, progenies and clones have earlier been recorded in several species like *Melia dubia* (Kumar *et al.*, 2013), Casuarina (Parthiban *et al.*, 2018), Teak (Parthiban, 2001), *Melia azadirach* (Meena *et al.*, 2014), *Acacia catechu* (Tej Prakash, 2011) and *Albizia lebbeck* (Thakur *et al.*, 2014)

The significant variation among clones for all growth attributes recorded in the current investigation may be attributable to their genetic constitution as reported earlier in poplar clones (Toky *et al.*, 1996; Sidhu and Dhillon, 2007).

Leaf traits

The growth and productivity of tree species depends on the leaf traits and hence, the clones deployed in the clonal test were characterized for leaf traits *viz.*, leaf length, leaf width, leaf petiole length, total number of leaves and leaf area and the results are furnished in Table 3.

The leaf length differed significantly due to clones. The higher leaf length was recorded by the clone AC 15 (42.63 cm) followed by AC 14 (40.13 cm) and AC7 (39.07 cm). The average leaf length recorded was 30.49 cm. Compared to average leaf length, two clones *viz.*, AC 15 (42.63 cm) and AC 14 (40.13 cm) recorded significantly higher leaf length. Similarly, the clones exhibited variations for leaf width which varied between 10.80cm (AC 10) and 21.37 cm (AC 15).

The leaf petiole length also exhibited variation due to clones and it ranged between 3.07 cm (AC 9) and 5.83 cm (AC5). The total number of leaves also exhibited variations due to clones and it was ranged between 60.67 (AC 5) and 224.11 (AC 17). The average value for this parameter recorded was 124.43. Compared to average number of leaves, only one clone *viz.,* AC 17 (224.11) registered significantly higher value. The leaf area differed due to clones and it varied from AC 10 (0.0233 m^2) to AC 15 (0.0744 m^2). The average leaf area recorded was 0.0430 m^2. Compared to the average leaf area, only one clone *viz.,* AC 15 (0.0744 m^2) registered significantly higher leaf area.

The studies on leaf trait characterization indicated wide variations among the clones and extends greater scope for selection using leaf traits. Such variation in leaf traits and its correlation with productivity has earlier reported in poplar (Monclus *et al.,* 2005)

Among the leaf traits, the leaf area and the leaf number play a vital role in biomass production. These two traits exhibited larger clonal variability but were negatively correlated with each other as recorded in Poplar (Monclus *et al,* 2005). Similar results are recorded in the current investigation wherein, the clone AC15 recorded the highest leaf area but lower leaf number and the clone AC 17 recorded higher leaf number but comparatively lower leaf area. These two parameters are directly related to biomass production which attested the results of current study wherein, the clones' AC 17, AC 15 and AC 16 registered higher values for all growth attributes.

Considering both growth and leaf attributes, these two clones *viz.,* AC 17, AC 15 and AC16 came into lame light and are focused for immediate adoption and deployment in future breeding program.

Assessment of genetic divergence in the population of *Neolamarckia cadamba* is of great significance in all breeding programs. The genetic divergence may help in inter-mating of divergent groups and increase the variability which may be useful in developing genetically superior planting material (Chaturvedi and Pandey, 2011). Hence, genetic divergence studies were carried out using the growth and leaf attributes of twenty five clones deployed in the current evaluation.

The genetic divergence studies indicated that the twenty five *Neolamarckia cadamba* clones were resolved into ten different clusters and the results are furnished in Table 4. Among the clusters, the cluster II consisted of nine clones followed by cluster IV with four clones, Cluster I with three clones, Cluster II and V with two clones. The clusters VI, VII, VIII, IX and X had only single clone each. Similar studies earlier registered in various species like Neem (Kumaran, 1991), Teak (Arun Prasad *et al.,* 2009) and *Pinus wallichiana* (Aslam *et al.,* 2011). The clustering revealed in the current study indicated that, there exists a large range of variability among the tested clones. Some clusters, for example cluster II included clones from all locations but other clusters included only a clone from particular location. Such results were earlier reported by several authors and indicated that all the genotypes from a given area may not necessarily be from a single cluster (Sagwal, 1982; Khosla *et al.,* 1994; sehgal *et al.,* 1994). This indicated that the pattern of genetic divergence is not depend on the geographical nearness of the genotype and such a variation could be attributable due to the genetic makeup of the genotypes (Bhaumik *et al.,* 1971; Chauhan and sehgal, 2001).

Intra and inter cluster average distance

Intra cluster distance ranged from 0.00 to 15.131. The highest intra - cluster D^2 was registered in cluster IV (15.131) and minimum was recorded in cluster VI, VII, VIII, IX and X (0.00). The D values also registered the same pattern as D^2 values (Table 5).

Inter – cluster D^2 values ranged from 8.759 to 64.772 and the corresponding the D values varies from 2.960 to 8.048. Highest inter cluster distance was recorded between cluster VIII and X (64.772), followed by cluster VI and VIII (61.127) suggesting that there is a wide genetic diversity between these groups. The minimum inter-cluster distance was between cluster I and V (8.759).

Similar results genetic distances were obtained by Aslam *et al.* (2011) in *Pinus wallichiana* wherein the highest intra-cluster value (1.635) was obtained for cluster VIII followed by cluster IX (1.423) and the inter-cluster distances varied from 1.479 to 9.901. The lowest inter-cluster distance of 1.479 was observed between cluster X and III and the highest inter-cluster distance of 9.901 was observed between cluster IX and VII, indicating a high degree of genetic divergence among the plus tree progenies.

In the current study inter and intra cluster distance was higher and it helps in high heterotic effect during hybridization drawn from genetically diverse clusters (Aslam *et al.,* 2011). Such inter and intra cluster distance among *Pinus gerardiana* (Kant *et al.,* 2006) was also reported which supports the results of the current study.

Cluster mean expressed significant variation among the clusters for growth parameters and leaf attributes. The members in cluster VIII showed the highest performance of for basal diameter (86.31 mm) followed by cluster III (66.06 mm) while, the minimum was observed for the cluster VI (28.98

mm). The maximum cluster mean for diameter at breast height was observed in cluster VIII (56.92 mm) whereas, the least cluster mean was exhibited by the cluster VI (14.77 mm). The maximum cluster mean for height was observed in cluster VIII (5.77 m) whereas the least cluster mean was exhibited by the cluster VI (1.93 m). The members of I, V, VII and X clusters have registered higher mean performance for number of branches (14.00) while the minimum was registered in the cluster VI (6.67).The members of cluster III showed higher performance for leaf length (41.38 cm) and minimum performance was registered by cluster VII (24.80 cm). The maximum cluster mean for leaf width was observed in cluster III (20.83 cm) whereas the least cluster mean was exhibited by the cluster IV (12.90 cm). The maximum cluster mean for leaf petiole length was observed in cluster V (5.03 cm) whereas, the least cluster mean was exhibited by the cluster IX (3.47 cm). The maximum cluster mean for the total number of leaves was observed in cluster VIII (224.11) whereas, the least cluster mean was exhibited by the cluster VI (42.00). While computing cluster mean for leaf area, the higher cluster mean was recorded by cluster III (0.070 m^2) and least was observed in cluster VI (0.023 m^2). In case of volume, the cluster mean was higher in cluster VIII (0.007 m^3) and the lowest was observed in cluster VI (0.000 m^3). In general, the cluster VIII and cluster VI had the highest and the lowest mean values for most of the traits respectively. Considering all the cluster mean values, the cluster VIII representing clone AC17 has recorded increased cluster mean values for basal diameter (86.31 mm), diameter at breast height (56.92 mm), height (5.77 m), number of branches (17.33), total number of leaves (224.11) and volume (0.007 m^3). This indicated that this clone is genetically divergent and also a superior performer which may be exploited for immediate adoption. Such superiority of few genetic resources representing different clusters have been recorded in *Prosopis cineraria* (Manga and Sen, 2000), *Bahunia varigata* (Anand *et al.*, 2005), *Pongamia pinnata* (Panravada *et al.*, 2006) and *Azadirachta indica* (kaushik *et al.*, 2007). The Existence of similar results in *Bixa orellana* progenies (Kala and kumaran, 2012) also extends support to the findings of current investigation.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 various growth attributes investigated, Volume contributed maximum divergence (32.67%) followed by leaf area (14.00%), leaf length (12.67%), leaf petiole length (12.33%), height (12.00%), basal diameter (6.33%), diameter at breast height (5.67%), total number of leaves (2.00%), leaf width (1.33%) and number of branches (1.00%). The study clearly indicated that volume contributes maximum towards genetic divergence and hence, the trees with higher volume production in this species could play a vital role towards existence of genetic diversity. Similar results were earlier reported in *Neolamarckia cadamba* (Prakash, 2017) also extends support to the findings of the current investigation.

The clonal evaluation test was identified, two clones *viz.,* AC 17 and AC 15 as superior performers which would be recommended for immediate adoption and for further improvement. The clones were characterized for their genetic divergence using growth and leaf attributes which resolved twenty five clones into ten clusters. Among the clusters, Cluster II was dominant representing nine clones and the cluster VI, VII, VIII, IX and X represented one clone each indicating their genetic difference. The *inter* and *intra* cluster distance was also higher indicating, higher genetic divergence among the clones. The inter cluster distance was maximum between cluster VIII and X and least between I and V. Among the clusters, Cluster VIII registered higher cluster mean value for maximum growth attributes which indicated that the presence of only one clone *viz.,* AC 17 in cluster VIII could be superior performer and this clone is under sharp focus for immediate adoption. Among the various growth attributes, volume contributed maximum to genetic divergence whereas Number of branches contributed least to the genetic divergence. The higher genetic distance among the Cluster VIII and Cluster X shows that AC 17 and AC 21 can be further utilized for future hybridization program for the improvement of *Neolamarckia cadamba* genetic resources.

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Table 1. Location details of *Neolamarckia cadamba* clones.

Sr. No.	Original Seed Source	State	Latitude	Longitude	Altitude (m)	Screened Clone
1	Patna	Bihar	25°33’N	84°40’E	063	AC 01
2	Thahekhu	Nagaland	25°53'N	93°43'E	161	AC 02
3	Jorhat	Assam	26°45'N	94°11'E	064	AC 03
4	Pantnagar	Uttarakhand	29°01’N	79°28’E	237	AC 04
5	Rangapahar I	Nagaland	25°50'N	93°43'E	159	AC 05
6	Allahabad	Uttar Pradesh	25°24’N	81°50’E	093	AC 06
7	Chandrapur	Maharashtra	19°59’N	79°21'E	219	AC 07
8	Rangapahar II	Nagaland	25°51'N	93°43'E	160	AC 08
9	Thekampatty	Tamil Nadu	11°14’N	76°52’E	355	AC 09
10	Lankajan	Assam	25°55'N	92°57'E	127	AC 10
11	Nahorani	Assam	26°41'N	94°00'E	067	AC 11
12	Thrissur	Kerala	10°32’N	76°16’E	030	AC 12
13	Gkvk	Karnataka	13°04’N	77 °34’E	919	AC 13
14	Anandvan	Maharashtra	20°15’N	79°01’E	214	AC 14
15	Mettupalayam	Tamil Nadu	11º32′ N	76º93′ E	330	AC 15
16	Mettupalayam	Tamil Nadu	11º32′ N	76º93′ E	330	AC 16
17	Khowai	Tripura	24º04′ N	91º36′ E	46	AC 17
18	Mettupalayam	Tamil Nadu	11º17′ N	76º56′ E	330	AC 18
19	Coimbatore	Tamil Nadu	11º17′ N	76º56′ E	330	AC 19
20	Coimbatore	Tamil Nadu	11º17′ N	76º56′ E	330	AC 20
21	Haryana	Haryana	29º41′ N	76º59′ E	251	AC 21
22	Tripura	Tripura	23º49′ N	91º17′ E	78	AC 22
23	Coimbatore	Tamil Nadu	11º17′ N	76º56′ E	330	AC 23
24	Karnal	Haryana	29º41′ N	76º59′ E	251	AC 24
25	Haryana	Haryana	29º41′ N	76º59′ E	251	AC 25

Table 2. Growth parameters of *Neolamarckia cadamba* clones at 15 MAP

Clone	Basal Diameter (mm)	DBH (mm)	Height (m)	No. of Branches	Volume (m^3)
AC 1	55.42	42.77	3.83	14.00	0.0028
AC 2	66.10	38.69	3.72	13.67	0.0021
AC 3	60.19	38.37	3.43	11.00	0.0021
AC 4	60.11	40.19	3.68	12.67	0.0027
AC 5	50.57	28.83	3.33	9.33	0.0011
AC 6	61.46	40.93	4.07	9.67	0.0029
AC 7	66.32	45.23	4.57	10.67	0.0035
AC 8	54.79	34.59	4.12	10.67	0.0019
AC 9	38.67	24.52	3.33	9.67	0.0008
AC 10	41.70	22.99	2.87	10.67	0.0006
AC 11	67.13	43.44	4.78	12.67	0.0033
AC 12	45.62	30.13	2.90	10.33	0.0010
AC 13	70.65	46.00	4.50	13.33	0.0035
AC 14	57.99	39.31	4.53	10.33	0.0029
AC 15	74.13	52.69	5.37	13.00	0.0057
AC 16	71.41	47.94	4.93	15.33	0.0043
AC 17	86.31	56.92	5.77	17.33	0.0074
AC 18	59.37	45.56	4.10	12.33	0.0033
AC 19	51.12	27.65	3.25	9.00	0.0010
AC 20	28.98	14.77	1.93	6.67	0.0002
AC 21	50.65	28.44	2.35	14.00	0.0007
AC 22	54.85	36.18	4.25	14.00	0.0024
AC 23	65.53	46.30	4.60	14.00	0.0043
AC 24	36.41	21.71	2.65	14.00	0.0005
AC 25	71.06	47.68	4.63	12.67	0.0043
Mean	**57.86**	**37.67**	**3.90**	**12.04**	**0.0026**
Minimum	**36.41**	**14.77**	**1.93**	**6.67**	**0.0002**
Maximum	**86.31**	**56.92**	**5.77**	**17.33**	**0.0074**
CV	**17.13**	**22.63**	**15.36**	**22.50**	**59.77**
SEd	8.09	6.96	0.49	2.21	0.0013
CD (0.05)	16.27	14.00	0.98	4.45	0.0026

* 5% significance

Table 3. Leaf traits of *Neolamarckia cadamba* clones at 15 MAP

Clone	Leaf Length (cm)	Leaf Width (cm)	Leaf Petiole Length (cm)	Total No of Leaves	Leaf Area (m^2)
AC 1	34.63	17.73	4.57	140.83	0.0478
AC 2	30.30	17.40	4.67	120.88	0.0441
AC 3	34.83	19.91	4.65	106.17	0.0562
AC 4	27.33	17.70	5.03	121.20	0.0422
AC 5	28.10	16.17	5.83	60.67	0.0315
AC 6	36.60	19.97	4.37	111.68	0.0590
AC 7	39.07	20.24	4.27	95.33	0.0674
AC 8	27.97	13.83	4.37	98.11	0.0332
AC 9	21.50	11.27	3.07	81.93	0.0206
AC 10	24.20	10.80	3.87	109.73	0.0233
AC 11	33.63	19.43	4.73	141.37	0.0540
AC 12	29.17	16.57	5.13	103.56	0.0377
AC 13	27.07	16.63	4.33	172.33	0.0358
AC 14	40.13	20.30	4.93	112.13	0.0662
AC 15	42.63	21.37	4.67	167.60	0.0744
AC 16	31.10	18.30	5.07	182.13	0.0472
AC 17	32.23	18.40	3.60	224.11	0.0459
AC 18	27.83	14.83	3.47	133.44	0.0322
AC 19	25.57	12.97	3.67	75.89	0.0260
AC 20	27.10	13.40	4.70	42.00	0.0230
AC 21	25.03	14.20	4.53	132.80	0.0290
AC 22	31.67	19.87	4.63	154.27	0.0523
AC 23	28.33	16.67	5.43	149.67	0.0384
AC 24	24.80	18.83	4.50	113.53	0.0349
AC 25	31.50	19.17	3.73	159.33	0.0520
Mean	**30.49**	**17.04**	**4.47**	**124.43**	**0.0430**
Minimum	**21.50**	**10.80**	**3.07**	**42.00**	**0.0206**
Maximum	**42.63**	**21.37**	**5.83**	**224.11**	**0.0744**
CV	**19.20**	**16.98**	**18.55**	**34.84**	**37.47**
SEd	4.78	2.36	0.68	35.40	0.0131
CD (0.05)	9.61	4.75	1.36	71.17	0.0264

* 5% significance

Table 4. Composition of clusters for growth traits among *Neolamarckia cadamba* clones

Cluster No.	No. of Clones	Members
I	3	AC1, AC11, AC16
II	9	AC2, AC3, AC4, AC5, AC6, AC7, AC8, AC13, AC25
III	2	AC14, AC15
IV	4	AC9, AC10, AC12, AC19
V	2	AC22,AC23
VI	1	AC20
VII	1	AC24
VIII	1	AC17
IX	1	AC18
X	1	AC21

Table 5. Estimates of inter and intra cluster distances for growth traits in *Neolamarckia cadamba* clones

	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**
I	13.819 (3.717)	14.029 (3.746)	11.554 (3.399)	19.941 (4.466)	8.759 (2.960)	49.993 (7.071)	31.068 (5.574)	25.689 (5.068)	13.551 (3.681)	43.271 (6.578)
II		13.592 (3.687)	18.078 (4.252)	18.092 (4.254)	14.619 (3.824)	44.023 (6.635)	33.152 (5.758)	31.647 (5.626)	18.882 (4.345)	30.813 (5.551)
III			3.855 (1.963)	24.547 (4.955)	10.606 (3.257)	45.081 (6.714)	36.989 (6.082)	20.472 (4.525)	18.768 (4.332)	60.094 (7.752)
IV				15.131 (3.890)	17.811 (4.220)	35.470 (5.956)	29.633 (5.444)	38.733 (6.224)	19.612 (4.429)	30.393 (5.513)
V					9.185 (3.031)	44.254 (6.652)	22.226 (4.714)	21.222 (4.607)	16.976 (4.120)	43.027 (6.559)
VI						0.000 (0.000)	25.173 (5.017)	61.127 (7.818)	57.220 (7.564)	37.172 (6.097)
VII							0.000 (0.000)	44.619 (6.680)	43.095 (6.565)	32.025 (5.659)
VIII								0.000 (0.000)	41.378 (6.433)	64.772 (8.048)
IX									0.000 (0.000)	50.288 (7.091)
X										0.000 (0.000)

Table 6. Cluster mean value for growth traits among *Neolamarckia cadamba* clones

Cluster	Basal Diameter (cm)	DBH (cm)	Height (m)	Number of branches	Leaf Length (cm)	Leaf Width (cm)	Leaf Petiole Length (cm)	Total Number of Leaves	Leaf Area (m^2)	Volume (m^3)
I	64.66	44.72	4.52	14.00	33.12	18.49	4.79	154.78	0.050	0.003
II	62.36	40.06	4.01	11.52	31.42	17.89	4.58	116.19	0.047	0.003
III	66.06	46.00	4.95	11.67	41.38	20.83	4.80	139.87	0.070	0.004
IV	44.28	26.32	3.09	9.92	25.11	12.90	3.93	92.78	0.027	0.001
V	60.19	41.24	4.43	14.00	30.00	18.27	5.03	151.97	0.045	0.003
VI	28.98	14.77	1.93	6.67	27.10	13.40	4.70	42.00	0.023	0.000
VII	36.41	21.71	2.65	14.00	24.80	18.83	4.50	113.53	0.035	0.001
VIII	86.31	56.92	5.77	17.33	32.23	18.40	3.60	224.11	0.046	0.007
IX	59.37	45.56	4.10	12.33	27.83	14.83	3.47	133.44	0.032	0.003
X	50.65	28.44	2.35	14.00	25.03	14.20	4.53	132.80	0.029	0.007

Table 7. Contribution of different growth traits to total divergence among *Neolamarckia cadamba* Clones

Character	**No. of First Rank**	**% Contribution**
Basal Diameter	19	6.33
DBH	17	5.67
Height	36	12.00
Number of branches	3	1.00
Leaf Length	38	12.67
Leaf Width	4	1.33
Leaf Petiole Length	37	12.33
Total Number of Leaves	6	2.00
Leaf Area	42	14.00
Volume	98	32.67
Total	**300**	**100.00**