

Original Research Article

Variability Study Analysis for half-sib families under control environmental conditions in *Neolamarckia cadamba* (Kadamb)

ABSTRACT

Neolamarckia cadamba is a widespread medium-sized deciduous forest tree over most of India, Bangladesh, and Sri Lanka. Twenty-half-sib progenies of kadamb (*Neolamarckia cadamba*) from various regions in Bihar, Rajasthan, and Uttar Pradesh were sown in a glasshouse in 2022 in order to assess the genetic diversity using non-hierarchical Euclidean cluster analysis. Significant variation was seen in the biomass and morphological traits of a few plus trees. Under greenhouse conditions, significant differences were seen in the growth parameters of plus tree progenies. Six clusters were formed from the twenty NPTs, according to the genetic divergence analysis. Clusters V and VI were found to have the greatest inter-cluster distance (5.530). The cluster (4.258) displayed the highest intra-cluster distance. As a result, there was a genetic divergence between clusters. Therefore, in order to obtain high-yielding genotypes in *Neolamarckia cadamba*, hybridization involving trees of clusters VI and V is advised. Collar diameter was a major factor in the creation of genetic diversity and contributed the most to the overall divergence. The superior plus trees of cluster V (NPT₄, NPT₅, NPT₁₁, NPT₁₂, NPT₁₃, NPT₁₇) and cluster VI (NPT₁₈, NPT₁₉, NPT₂₀) may be taken into consideration as possible parents for a future tree improvement program in *Neolamarckia cadamba* due to their high cluster mean and large genetic distance.

Keywords: *Neolamarckia* Plus Tree (NPTs), Genetic divergence, Euclidean cluster, D² statistics

INTRODUCTION

Neolamarckia cadamba Syn. *A. indicus*, *A. chinensis* (Lam.), *Anthocephalus cadamba* (Family-Rubiaceae), also known as kadamba, has a prestigious place in Ayurveda, an Indian indigenous system of healing. It is also known as the burflower tree. The Kadamb tree is revered in India as a sacred tree to Lord Krishna and is incorporated in Indian faiths and traditions. This tree is endemic to India, Sri Lanka, Bangladesh, China, Indonesia, Malaysia, Jawa, Sumatra, Cambodia, Singapore, Philippines, Papua New Guinea, and the Indo-Malayan area (**Bijalwan et al., 2014**). It grows in secondary north Indian tropical wet deciduous forests, tropical freshwater swamp forests, and southern tropical semi-evergreen forests. Except in the desert part of Rajasthan, it is found in semi-evergreen to evergreen woods throughout much of India (**Champion and Seth, 1968**).

Kadamb (*Neolamarckia cadamba*) is a valuable and rapidly growing tree in South Asia. Kadamb is a medium to big deciduous tree that may grow to be 45 m tall. The bole is straight and cylindrical, frequently branchless for more than 25 m, up to 100-160 cm in diameter but usually less, occasionally with tiny buttresses up to 2 m high and reaching up to 60 cm from the stem (**Luna, 1996**). Kadamb grows quickly and is ideal for regeneration in watersheds and degraded regions, as well as windbreaks in agroforestry systems. It's also a great shade tree for dipterocarp line planting. It is a lightweight hardwood with a short lifespan. It is mostly used to make pulp for low- and medium-quality paper. Because it is perishable when in touch with the earth, the wood may only be utilized for minor building work indoors (**Pandey et al., 2016**). The bark is used to treat fevers, while the leaf extract is used to gargle (**Kapil et al., 1995**). According to research, practically all components of the kadam plant are useful in the treatment of numerous ailments. A decoction of the leaves is used to treat aphthae or stomatitis, ulcers, and wounds (**Dubey et al., 2011**).

The species is widely distributed in India, growing on the slopes of evergreen forests up to 500 meters in height. Its growth, morphology, vigor, fruit output, and seed yield vary greatly. The species' broad geographic distribution indicates that *Neolamarckia cadamba* should exhibit a wide range of genetic variability, which requires identification and investigation. Therefore, by identifying and selecting plus trees with favorable features, a considerable genetic gain can be obtained. Understanding the genetic divergence among tree species is critical to any breeding program. For trees to get better, genetic diversity evaluation is essential (**Zobel, 1971**). Sorting

diverse populations into comparable groupings for conservation purposes or to be utilized in upcoming breeding and enhancement initiatives is the main objective of genetic variation research. The best statistical method for statistically evaluating the genetic divergence of biological groups is D^2 analysis. Using D^2 analysis, the current study aimed to determine the level of genetic diversity among the plus tree species of *Neolamarckia cadamba* and to identify stable and varied genotypes for the program for improving *Neolamarckia cadamba* trees.

MATERIALS AND METHODS

The study was conducted in the College of Forestry Nursery at SHUATS, Prayagraj, U.P. during 2021-22 in greenhouse condition. Based on morphological characteristics, over fifty fully developed fruits were extracted from various sections of a single tree's crown, and trees were chosen from twenty distinct locales in Bihar, Rajasthan, and Uttar Pradesh. Observations on fruit characters were taken and after taking observations, seeds were extracted from fruit and kept plus tree and replication wise for taking observations on seed characters in the month of December-January, 2021. Table 1 provides the details of plus trees.

Under greenhouse conditions, the seeds were planted in three replications of a completely randomized design using 15 x 25 cm poly bags that were filled to the brim with a mixture of sand, soil, and FYM (1:1:1). The seeds were sown two centimeters deep. Regular irrigation, weeding and hoeing was done as and when required. The data was recorded immediately after the seeds emerged outside the soil i.e., after germination. The morphological and biomass data was recorded. The following traits were noted when fifteen seedlings of each plus tree progenies were randomly chosen, tagged, and recorded.

Table 1: Details of twenty plus trees of *Neolamarckia cadamba* collected from twenty different locations.

Seed source	Locality	State	Latitude	Longitude	Tree height (m)	Tree girth DBH (m)	Fruit size (mm)	100- Seed weight (mg)
NPT ₁	Chajjubagh, Patna,	Bihar	25.6160 ⁰ N	85.1371 ⁰ E	17.38	1.02	38.72	17
NPT ₂	Sohsarai, Bihar Sharif	Bihar	25.2271 ⁰ N	85.5161 ⁰ E	10.50	0.40	38.27	15
NPT ₃	Kalyanbigah	Bihar	25.3831 ⁰ N	85.5070 ⁰ E	6.70	0.50	38.61	11
NPT ₄	Bedhna road, Barh	Bihar	25.4619 ⁰ N	85.7097 ⁰ E	12.92	0.31	37.56	12
NPT ₅	Near Nursery, Chandi	Bihar	25.3192 ⁰ N	85.4070 ⁰ E	18.28	1.19	42.71	23
NPT ₆	Narauli, Karauta	Bihar	25.4651 ⁰ N	85.4410 ⁰ E	11.86	0.63	39.16	17
NPT ₇	Mohmadpur, Samastipur	Bihar	25.9839 ⁰ N	85.6656 ⁰ E	6.09	0.76	39.67	20
NPT ₈	Dumri, Begusarai	Bihar	25.4057 ⁰ N	86.1202 ⁰ E	17.00	0.83	38.34	18
NPT ₉	Patna (Fatuhmarg)	Bihar	25.5712 ⁰ N	85.2451 ⁰ E	12.00	0.64	38.27	17
NPT ₁₀	Sharifganj, Katihar	Bihar	25.5224 ⁰ N	87.5646 ⁰ E	5.53	0.584	37.07	11
NPT ₁₁	Sudari	Bihar	25.3920 ⁰ N	85.4419 ⁰ E	14.32	0.45	38.72	22
NPT ₁₂	NayatolaMadhopur, Bakhtiarapur	Bihar	25.4559 ⁰ N	85.5361 ⁰ E	18.00	0.82	34.12	16
NPT ₁₃	Rahui, Nalanda	Bihar	25.1304 ⁰ N	85.4475 ⁰ E	15.24	0.14	40.28	10
NPT ₁₄	Chandi mod, Harnaut	Bihar	25.3653 ⁰ N	85.5294 ⁰ E	16.55	0.74	43.88	21
NPT ₁₅	Hanuman temple, Sangam	Prayagraj	25.4313 ⁰ N	81.8813 ⁰ E	16.76	0.14	41.52	19
NPT ₁₆	Khan chauraha, Naini	Prayagraj	25.4087 ⁰ N	81.8405 ⁰ E	18.93	0.12	36.52	13
NPT ₁₇	GTB Nagar, Kareli	Prayagraj	25.4255 ⁰ N	81.8186 ⁰ E	19.00	1.20	42.55	16
NPT ₁₈	Subhashchauraha, Civil lines	Prayagraj	25.4500 ⁰ N	81.8345 ⁰ E	20.11	0.424	32.19	23
NPT ₁₉	Saipau road, Dholpur,	Rajasthan	26.7015 ⁰ N	77.8698 ⁰ E	13.65	0.96	28.01	19
NPT ₂₀	Chadi, Jodhpur	Rajasthan	25.3426 ⁰ N	75.9606 ⁰ E	5.79	0.58	30.90	21

In last week of June, fifteen seedlings from each family of plus trees (replication), excluding the border ones, were chosen at random and tagged after three months of growth. Eight morphological and biomass traits—seedling height, collar diameter, fresh weight, dry weight, shoot/root ratio, and biomass—were the subjects of the data collection. Non-hierarchical Euclidean cluster analysis (**Spark, 1973**) was used to compute genetic divergence, and genotypes were sorted into distinct clusters using Tocher's approach, as detailed by **Rao (1952)**.

RESULTS AND DISCUSSION

The use of statistical techniques that can quantify genetic divergence across multiple populations and the proportion of each type of individual character to total divergence has allowed for the monitoring of evolutionary patterns in some annual species such as rice and tobacco in particular when selecting parents for hybridization and in general for numerous agricultural crops and a few forest tree species (**Rao, 1952; Burley and Burrows, 1972**). Furthermore, the fundamental theory of genetic divergence is to group a significant amount of selected phenotypically superior batches into several small homogeneous groups, so that representative plants from each group can be included thereby decreasing the overall number of entries in a provenance/progeny trial and seed orchard and to estimate the extent of divergence among groups, so that groups with greater genetic variance can be hybridized (crossed) to produce greater genetic diversity at a later period for selection.

The statistical evaluation of variability found a substantial variation in all variables across 20 plus tree progenies, demonstrating the presence of significant genetic diversity. Under greenhouse conditions in 2021-22, twenty-plus tree progenies were divided into six groups based on morphological and biomass parameters (Table 2). Cluster V and III exhibited the highest number of 6 and 5 plus trees (NPT₄, NPT₅, NPT₁₁, NPT₁₂, NPT₁₃, NPT₁₇) and (NPT₁, NPT₃, NPT₉, NPT₁₀, NPT₁₅) respectively. Cluster VI comprehended three (NPT₁₈, NPT₁₉, NPT₂₀). Cluster IV exhibited two plus trees (NPT₇, NPT₁₄). Cluster I exhibited two plus trees (NPT₆, NPT₁₅) and Cluster II exhibited two plus trees (NPT₈, NPT₁₆).

Table 2: Distribution of twenty plus trees in different clusters (Greenhouse condition)

Cluster	No. of seed sources	Notation of Cluster
I	2	6, 15
II	2	8,16
III	5	1, 3, 9 , 10, 15
IV	2	7, 14
V	6	4, 5, 11, 12, 13, 17
VI	3	18, 19, 20

Table 3: Inter and intra cluster distance of twenty plus tree progenies of *Neolamarckia cadamba* (Greenhouse condition)

Cluster	I	II	III	IV	V	VI
I	0.762	1.079	3.462	2.010	4.096	3.592
II		0.967	3.706	1.663	4.339	3.729
III			4.042	3.918	4.412	4.865
IV				1.775	4.085	4.405
V					4.258	5.530
VI						3.386

Table 4: Mean cluster for various traits in different cluster for twenty plus tree progenies of *Neolamarckia cadamba* (Greenhouse condition)

Traits Clusters	Seedling height	Collar Diameter	Shoot fresh Weight	Root fresh Weight	Shoot Dry Weight	Root Dry Weight	Shoot Root ratio	Seedling Biomass
I	24.94	2.66	1.05	0.76	0.56	0.40	1.37	0.96
II	23.35	2.70	0.96	0.52	0.47	0.28	1.67	0.75
III	42.30	3.09	2.65	1.35	1.29	0.82	1.69	2.10
IV	30.99	3.32	1.51	0.71	0.56	0.35	1.67	0.91
V	32.45	3.33	2.64	1.49	1.00	0.79	1.39	1.79
VI	16.10	1.16	0.88	0.53	0.21	0.17	1.68	0.38
Percent contribution	8.95	23.68	14.74	7.37	11.05	21.05	10.00	3.16

The distribution of progenies in different clusters implies that, even though the genotypes have been chosen across various eco-geographic areas, genetic composition, breeding system heterogeneity, genetic drift, natural and unilateral selection pressure, and other factors must be contributing factors of genetic diversity among different progenies, in addition to geographic variations. To some extent, the cluster pattern demonstrated that geographical diversity does not always have to be related to genetic diversity. As a result, rather than geographic diversity, genotypes for hybridization might be chosen based on genetic diversity. Geographic diversity, on the other hand, must be given adequate consideration in order to ensure adequate genetic diversity in the germplasm. The present result supports the findings of **Yadav and Murthy (2022)** in *Balanites roxburghii*, **Paw et al., (2020)** in *Curcuma caesia*, **Wani and Chauhan (2007)** in *Bauhinia variagata*, **Anand (2003)** in *Bauhinia variegata* and **Parthiban et al., (2019)** in *Neolamarckia cadamba* half-sib progeny, **Gupta, et. al.,(2020)** in *Acacia nilotica*.

Table 3 revealed that generalized inter-cluster distance (5.530) was observed highest between cluster VI and V which was followed by cluster VI and III (4.865). The minimum inter-cluster distance was observed between cluster II and I (1.079). The maximum intra cluster was found in cluster V and V (4.258) and minimum was found in cluster I and I (0.762). The inter-cluster distance was as high as 5.530 (between cluster VI and V) which indicated presence of higher order of divergence among the progeny of plus trees. The variation under greenhouse conditions for total number of clusters and various clusters having different features might be attributed mostly to environmental variables owing to the vast spectrum of day as well as night temperature and humidity. Mean values for morphological and biomass traits under greenhouse condition revealed that maximum was observed by cluster III for six traits, followed by cluster V for two traits (Table 4). Highest mean values for different traits under greenhouse condition was shown by cluster III for seedling height (42.30), shoot fresh weight (2.65), shoot dry weight (1.29), root dry weight (0.82), shoot root ratio (1.69) and seedling biomass (2.10) (Table 4) whereas, collar diameter (3.33) and root fresh weight (1.49) were observed in maximum in cluster V. Contribution of different characters to total divergence is illustrated in Table 4. Collar diameter (23.68%) was the main contribution for genetic divergence followed by root dry weight (21.05%) and shoot fresh weight (14.74%). Minimum contribution was observed for seedling biomass (3.16%) under greenhouse conditions. Further, the result of this study suggests that classification of a number of plus tree progeny using D^2 statistics provide not only a set of groups

from which parent can be chosen for further breeding programme but also indicates that such grouping remains unstable over environments that means the material is vulnerable to the variable environmental conditions. The present study result substantiates, the findings of **Hooda, et al., (2009)** in *Pongamia pinnata* and **Kumar and Gurumurthi (2000)** in *Casuarina equisetifolia*.

CONCLUSION

We may conclude from the current analysis that, the selection of genotypes from the cluster VI (NPT₁₈, NPT₁₉, NPT₂₀), cluster V (NPT₄, NPT₅, NPT₁₁, NPT₁₂, NPT₁₃, NPT₁₇) exhibit maximum inter cluster distance and can be utilized as potential parents and crossing between these genotypes resulting in high heterotic expression for yield and its components. Mean values for morphological and biomass traits under greenhouse condition revealed that maximum was observed by cluster III for six traits, followed by cluster V for two traits. Collar diameter was the main contribution for genetic divergence. The genotypes from above clusters may be included in hybridization programme for obtaining superior and desirable recombinants in tree improvement programs.

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