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Genetic studies in *Neolamarckia cadamba* (Kadam) tree species

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Abstract
Neolamarckia cadamba (Kadam) large straight tree, deciduous evergreen or semi-evergreen. The Kadamba is one of the important medicinal plants belonging to the *Rubiaceae* family. Studies were carried out in *Neolamarckia cadamba* to draw out information on the variability and heritability studies. In order to carry out populations study in Kadam, a population of 30 sources was surveyed and variation present within a population was estimated Morphological traits taken for the study were height, girth at breast height, basal diameter, clear bole length and volume. The variability registered highest phenotypic coefficient of variance (PCV) (45.32) and genotypic coefficient of variance (GCV) (28.86) followed by clear bole length (PCV 28.65 (GCV 19.09), tree girth PCV20 51) (GCV 15.39), basal diameter (PCV 19.32) (GCV 15/71), tree height (PCV 15.93) (GCV 724) to find out amount of variation in the population The above results can be utilized for selection of wood volume. Heritability was recorded by bole height and low heritability by tree height while volume registered moderate heritability. The trend of genetic advance as percent of mean was maximum in volume (36.73) followed by clear bole height (35 11), basal diameter (26.33), tree girth (23.78), tree height 6.79) indicating a wide scope of genetic improvement in the species. In a holistic perspective, findings shows exists a wide value of variation in Kadam genotypes which could play a significant and vital role in enhancing productivity This study also laid foundation in order to tree improvement studies in future.

Keywords: Genotypic variation, Genetic advance, Heritability, Kadam, Phenotypic variation

Introduction
One such underexplored plant is a tropical evergreen tree *Neolamarckia cadamba* (Roxb.) Bosser (Rubiaceae), which grows mainly in South Asia and South East Asia. The demands extend not only to various goods and services produced by forest but are intertwined with the forest ecosystem as a whole. The diverse demands on forest are quite often mutually compatible. The world's total forest area is just over 4 billion hectares which covers 31 percent of land area. The average per capita of the world forest works out to be 0.6 ha. In south Asian region, three countries namely Bhutan, Sri Lanka and Nepal have higher percentage of land area under forest than India. With less than 2 percent of the world's population. Not only is the forest wealth of the country is poor but its productivity in terms of MAI is also one of the lowest. The MAI of Indian Forest is a meagre of 05-07 m'ha compared to the global average of 21 m'ha (Srivastava, 2005) [11] and the annual productivity of India's forests is only 3.175 m' ha yr, which is too low, compared to other developed countries 8.20 m ha' yr.

Neolamarckia cadamba (Kadam) is a evergreen or semi-evergreen tree, grows with horizontal branch. It grows to a height of 20m with a clean hole of about 9 m and a girth of 1.5 to 2.0 m. This evergreen, tropical tree can rise upto a height of 20 feet and has a moderately thick trunk. The beauty of the tree lies in its sweet-scented orange flowers. The flowers are round in shape and also have dense, white globe-shaped clusters. The *Neolamarckia cadamba* grows in alluvial and fertile river soil that is found under 1000 m of elevation. It draws a lot of nourishment from this rich fertile soil. However, they can also survive on other types of soil as long as you fertilise them from time to time. The tree can also tolerate flooding but not on a regular basis.

The Kadam tree or *Neolamarckia cadamba* needs plenty of sunlight to thrive. Although the tree doesn't have much demand from the soil, it does require adequate sunlight for growth. When planting a Kadam tree, always make sure to plant them in a place where the sunlight stays at least for 5-6 hours a day. Avoid planting young trees in damp and under the shade of other tall trees. The ideal temperature required for the Neolamarckia cadamba is between 25-30 °C. The tree is highly intolerant to cold weather temperatures, which is why they are found in plains and low-lying areas. Brown wrapping paper can also be prepared by sulphate process. Fruits are edible Bark and leaves are used for medicinal purposes.

Compared with the other types of wood species, it is a fast growing tropical tree species which is also known as Kadam. It has been planted on a large scale in Indonesia since 1930s. The wood has a density of 290-560 kg/m at 15% moisture content, a fine to medium texture, straight grain, low luster and has no characteristic odour of taste. However, the wood is rated as non-durable, graveyard tests in Indonesia show an average life in contact with the ground of less than 15 years

Recently there is a growing awareness on the promotion and utilization of Kadam a species with multipurpose utility amenable for plantation forestry and their integration in Agroforestry system. For any tree improvement programme, determination of the species, or geographic source within species, amount, kind and cause of variation within the species are very important initial steps. Abundant variation is available in trees in the nature, which the foresters can tap and use it to get the maximum improvement in a short span of time. Intensive studios on variation within species are necessary for the improvement programmes to be successful. Study of morphometric traits in field traits was valid way of assessing genetic variation.

The heritability of selected traits and the biology of a species contribute to developing appropriate plus tree selection procedures and breeding plans based on economic importance. Estimation of heritability helps in assessing the heritable portion of variation and would help in selection. Knowledge on association among components of economic importance can help in improving the efficiency of selection. Tree yield *i.e.,* tree volume is a complex and highly variable character which is influenced by many component characters (Pandey *et al*., 1997). The genetic diversity existing in the population will help to generate a rich base population for initiating proper selection. Determination of genetic diversity in Kadam has not been attempted so far and thus underscores investigation. Against this backdrop, the current study was designed to elicit information on the following in respect of *Neolamarckia cadamba* genetic resources. Hence this project is focused on following objectives, to determine the Variation, Heritability and genetic advance for morphometric traits.

Materials and Methods
A study was undertaken to evaluate the base population and different genotypes *Neolamarckia cadamba* for morphological characterization. Accordingly, genetic resources field survey was carried out in the Forest College and Research Institute, Mettupalayam. A total of thirty various sources of *Neolamarckia cadamha* were taken and average was computed for the height (m) and girth (cm) characters. Complete populations were identified based on the morphometric and quantitative traits during the study.

Statistical analysis
The data collected were analyzed statistically wherein Mean, Standard Deviation, Variance, Skewness, Kurtosis and Range were calculated. (Snedecor and Cohran, 1968; Tuma and Guney, 2009). Mean is the arithmetic average of the values in the set, obtained by summing the values and dividing by the number of values. The standard deviation is the square root of the variance. The mean data of quantitative traits were subjected to the analysis of variance using AGRISTAT (V.1.2004) package.

Skewness
Skewness is a statistical measure that assesses the asymmetry of a probability distribution. It quantifies the extent to which the data is skewed or shifted to one side.
For univariate data Y1, Y2, ..., YN, the formula for kurtosis is:

$$g = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^3}{(n-1)s^3}$$

- $\bar{x}$ is the sample mean
- x_i is the ith sample, while n is the total number of observations
- s is the standard deviation
- g sample skewnes

Kurtosis
It is measure of whether the data are peaked or flat relative to a normal distribution. This data sets with high kurtosis tend to have a distinct peak near the mean, decline rather rapidly, and have heavy tails. Data sets with low kurtosis tend to have a flat top near the mean rather than a sharp peak. A uniform distribution would be the extreme case.
For univariate data X1,X2, XN, the formula for kurtosis is given below

$$K = n \frac{\sum_{i=1}^{n}(X_i - X_{avg})^4}{(\sum_{i=1}^{n}(X_i - X_{avg})^2)^2} - 3$$

Where x is the mean
n is the number of data points

Estimation of genetic parameters
Phenotypic and genotypic variances
The estimates of variability parameters were worked out according to the method suggested by Lush (1940) [22] utilizing the mean sum of square values from the variance table.

- Genotypic Variance $(\sigma^2 g) = \dfrac{M_g - M_e}{r}$
- Phenotypic Variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Phenotypic and genotypic coefficients of variation (%)
Phenotypic and genotypic coefficients of variation were calculated based on the method advocated by Burton (1952).

(i) Phenotypic co-efficient of variation (PCV) (%)

$$= \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100 = \frac{\sigma_p}{\text{Grand mean}} \times 100$$

(ii) Genotypic co-efficient of variation (GCV) (%)

$$= \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100 = \frac{\sigma_g}{\text{Grand mean}} \times 100$$

Categorisation of the range of variation was followed as proposed by Sivasubramanian and Menon (1973) [12].
Less than 10 percent - Low
10-20 percent - Medium
More than 20 percent - High

Heritability in broad sense [h²(BS)] (%)
Heritability in broad sense was estimated as per (Allard, 1960) [23] and expressed in percentage

$$\text{Heritability in broad sense [h}^2\text{(BS)]} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Range of heritability was categorized as suggested by Johnson *et al*. (1955) [13]
Less than 30 percent - Low
30 to 60 percent - Moderate
More than 60 percent- High

Genetic advance as percent of mean (%)
Genetic advance was estimated by the method suggested by Johnson *et al*. (1955) [13].

$$\text{Genetic advance} = \frac{\sigma^2_g}{\sigma^2_p} \times k \times \sqrt{\sigma^2_p}$$

Where,
k = Selection differential which is equal to 2.06 at 5 percent level of selection intensity
σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Genetic advance was expressed as percentage of mean by using the following formula as given by Johnson *et al*. (1955) [13].

$$\text{Genetic advance as percent of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance was categorised as suggested by Johnson *et al*. (1955) [13]

Low	-	Less than 10 percent
Medium	-	10-20 percent
High	-	More than 20 percent

Results and Discussion
The present study aimed at assessing the morphological variations presenting *Neolamarckia cadamba* population and finding the significant relationship between the morphological traits. The results obtained from the investigation of 30 progenies of *Neolamarckia cadamba* for identifying superior progeny for higher productivity based on variability, heritability and genetic diversity of different biometric traits. The variation in the selected population was studied in terms of height, girth, basal diameter, clear bole height and volume. The mean, maximum range, minimum range standard deviation, skewness, kurtosis were calculated and explained in Table 1. The mean value for height was 6.87 m, girth was 33.35 cm basal diameter was 15.67, clear bole height was 3.77 and volume was 0.0653. The standard deviation value for height was 1.18. girth was 5.57, basal diameter 2.02, clear bole height was 1.06 and volume was 0.03. The skewness for a normal distribution is zero, and any symmetric data should have skewness near zero. By skewed left, it explains about the left tail had long relative to the right tail. Similarly, skewed right means that the right tail was long relative to the left tail. Others skewed right means that these characters have longer tail on right hand side. Positive kurtosis indicated a "peaked" distribution and negative kurtosis indicated flat distribution. The kurtosis value of height, girth, basal diameter, clear bole height and volume are listed in the Table 1

Table 1: Analysis of population baseline characters

Static	Tree height (m)	Tree girth(cm)	Basal diameter(cm)	Clear bole (m)	Volume(m³)
Mean	6.87	33.35	15.67	3.77	0.0653
Maximum	30.5	46.8	19.73	6.5	0.128
Minimum	3.5	18	9.23	0.2	0.01
Standard deviation	1.18	5.57	2.02	1.06	0.03
Error	0.7958	3.7	1.43	0.6582	0.0186
Kurtosis	0.5347	0.2076	0.06955	2.729	8.1475
Skewness	0.0884	-0.1085	-0.06409	-0.5203	1.91

Variation and Heritability study in morphometric traits
All trees were statistically analyzed for coefficient of variation like genotypic coefficient of variation, phenotypic coefficient of variation and also heritability studies like heritability % and genetic advance for their height, girth, basal diameter, clear bole height and volume. Results are presented in Table 2. Variability analysis revealed that the height has showed low genotypic coefficient of variation (7.24%) and phenotypic coefficient of variation (15.93%). Heritability (21 %) and genetic advance (6.79) also too low when compared to all traits (Table 2). Variability analysis revealed that the girth has showed genotypic coefficient of varition (15.39%) and phenotypic coefficient of

variation (20.51%). Heritability (56%) and genetic advance (23.78) has showed moderato effect (Table 2). Variability analysis revealed that the basal diameter has showed genotypic coefficient of a variation (15.71%) and phenotypic coefficient of variation (19.32%). Heritability (66%) and genetic advance (26.33) has showed moderate effect like tree girth (Table 2). Variability analysis revealed that the clear bole height has showed genotypic coefficient of variation (19.09%) and phenotypic coefficient of variation (28.65%). Heritability (79%) and genetic advance (35.11) has showed good effect next to volume (Table 2). Variability analysis revealed that the volume has showed high genotypic coefficient of variation (28.86%) and

phenotypic coefficient of variation (45.32%). Heritability (41%) and genetic advance (36.73) also high when compared to all traits (Table 2).

The progeny evaluation trial was conducted in the field showed significant differences, among 30 progenies of *Neolamarckia cadamba* for growth characteristics tree height, tree girth, basal diameter, bole height, and volume at 60 MAP. Considering all the 30 progenies, FCRI NC 9 showed consistently superior performance. Current study was supported by plethora of workers also reported the existence of significant differences and superiority of few seed sources. progenies and provenances in various trees like *Azadirachta indica* (Syed *et al.* 2013) [14] *Populus deltoides* (Jha, 2012) [15] *Gmelina arborea* (Kumar *et al.*, 2005) [16] *Eucalyptus tereticornis* (Ginwal *et al.* 2004) [17], *Dalbergia sissoo* (Tewaric *et al.*, 1996) [18].

Table 2: Variation and Heritability values for morphometric traits

Traits	PCV%	GCV %	Heritability	GA % of mean
Tree height (m)	15.93	7.24	21	6.79
Tree girth(cm)	20.51	15.39	56	23.78
Basal diameter(cm)	19.32	15.71	66	26.33
Clear bole (m)	28.65	19.09	79	35.11
Volume (m^3)	45.32	28.86	41	36.73

Success of the tree improvement program depends on the variability present in material. *Neolamarckia cadamba* can be considered a more exploitable tree crop and therefore, to the improvement work in this tree crop, the assessment of genetic variability in the under study becomes imperative. Significant differences that existed different progenies could be evinced due to the considerable range of variability to almost all the characters under study. The maximum range of obtained for volume followed by clear bole height and tree girth in study. The coefficient of variations being independent of the scale of the unit of measurement for different mean values, *etc,* can be conveniently used for comparison between different populations. In the present study, volume recorded highest phenotypic coefficient of variation and highest genotypic coefficient of variation. Characters like tree height, girth (GBH), basal diameter, clear bole length exhibited low to intermediate genotypic and phenotypic coefficient of variation. Current findings are similar to studies in teak which showed higher GCV for volume index (Arun Prasad *et al.,* 1996) [1].

Heritability has an important place in tree improvement programme as it provides an index of relative strength of heredity versus environment. Dorman *et al* (1976) [19] reported that heritability is very important in tree improvement programme. It is also useful for ranking importance of each trait in cross breeding programme. Heritability expresses the degree to which a character influenced by heredity as compared to the environment. Estimation of broad sense heritability for various characters showed moderate heritability for Girth at breast height (0.56), and volume (0.33) tree height (0.21), while high for Bole Height (0,79) and basal diameter (0.66), and low for tree height (0.21). The results are in agreement with the studies carried out by Apiolaza *et al.* (2005) [20] on *Eucalyptus globulus* which reported low for height during field evaluation of 8 sub races. Similarly low to moderate heritability also recorded in *Eucalyptus globulus* and the *Eucalyptus nitens* (Raymond *et al.,* 2002) [19] for different genetic parameters: Low to moderate heritability was for height and tree volume in *E. grandis* (Osorio *et al.,* 2001) [20] and for clean stem collar diameter in *Eucalyptus tereticornis* (Ginwal, 2004) [17]. The authors also reported that the heritability varies with changing environment and age.

This study essentially provides the direction to genetic improvement of the crop in future. These sources will be utilized for developing synchronized tree with higher yield.

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