

Genetic variability, correlation and path analysis in *Neolamarckia cadamba* (Roxb.) Bosser

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ABSTRACT: Twenty-five *Neolamarckia cadamba* clones were evaluated for variability, heritability and genetic advance studies based on the growth attributes viz., basal diameter, diameter at breast height (DBH), height, number of branches, volume, leaf length, leaf width, leaf petiole length, total number of leaves, leaf area and volume. Genotypic co-efficient of variation was lower than the phenotypic co-efficient of variation for all the growth traits. Among the genotypic co-efficient of variation, volume recorded higher GCV (57.46%), followed by leaf area (26.55%), total number of leaves (25.33%), DBH (24.61%) and height (22.42%). Heritability was relatively higher for four growth attributes viz., height (68.35%), basal diameter (59.00%), DBH (54.18%) and volume (47.93%), and lower for leaf petiole length (20.46%). Higher genetic gain was attributed to volume (81.95%), followed by height (38.16%) and DBH (37.32%). Genotypic correlations were higher than the phenotypic correlation for all the growth traits which indicated the use of variability of these attributes for further tree improvement program. These relationships will help in selecting one or other traits for tree improvement. Among growth traits, leaf area (0.971) registered highest direct positive effect on volume, followed by total number of leaves (0.767), height (0.351), DBH (0.175) and basal diameter (0.121), and maximum indirect effect on volume registered by leaf length (0.970) and leaf width (0.958) through leaf area. Hence, for the selection of better clone to maximize the volume, the characters viz., DBH, height, leaf area, total number of leaves, leaf length and leaf width could be used as selection criteria in this multipurpose species.

Key words: Broad sense heritability, genetic advance and variability.

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1. INTRODUCTION

Neolamarckia cadamba (Roxb.) Bosser belongs to the family Rubiaceae and commonly called as kadam. It is medium to large sized deciduous species attaining height of 20-40 m and girth about 2-2.5 m with clean cylindrical branches and rounded crown with the distribution in all over India on the slopes of evergreen forests up to 500 m (Dubey *et al.*, 2011). The wood of this species is used in pulpwood, light construction material, flooring, beams and rafters, tea-chests, packing cases, match splints, bobbins and pencil. Apart from this, many communities and tribal across India use its bark, leaf and flower against various ailments such as sour throat, cough, fever, infections and inflammation.

Traditional tree improvement programmes 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 (Sebbenn *et al.*, 2003). Accordingly, tree improvement program in *N. cadamba* was reported in combined provenance and progeny tests experimental in Indonesia (Sudrajat, 2016). Barring this study, there is no adequate tree improvement programme on this species, which

demanded a systematic approach to improve this species.

Among different growth attributes, volume is a complex and highly variable character, which influences by many component characters (Jha, 2012). In integrated structure of the plant, the overall correlation observed between two variables is a function of a series of direct and indirect relationships between different variables. To understand the specific forces in building up the total correlation, it is essential to resort through path co-efficient (Wright, 1921). Genetic correlations between commercially important traits are critical to understand the effects of selection for one trait on another (Callister and Collins, 2008). Such correlations were lacking in the *N. cadamba* clonal genetic material. Against this backdrop, this study aims to assess the phenotypic and genotypic correlation between the growth traits and direct and indirect effect of each growth traits to the volume of *N. cadamba*. Components of variance and genetic parameters were estimated from data, obtained from 15 months old clonal genetic materials.

2. MATERIALS AND METHODS

Thirty open pollinated families of *N. cadamba* were collected from 11 natural ranges distributed in the states of Tamil Nadu, Assam, Bihar, Nagaland, Uttarakhand, Telangana, Uttar Pradesh, Maharashtra,

Karnataka, Kerala and Tripura of India. The seedlings were raised and systematic progeny trial was established in the year 2013. From this progeny trial, 25 plus trees were selected based on comparison tree method. These selected trees were cut to induce coppice shoots, which were multiplied through mini clonal technology (Parthiban, 2017) and designated as clones. These clones were evaluated through clonal test in a row coloumn design at spacing of 2m × 2m with three replications in the year 2016-2018. The clones were evaluated for various growth attributes viz., basal diameter, diameter at breast height (DBH), height, number of branches, volume, leaf length, leaf width, leaf petiole length, total number of leaves, leaf area at 15 months after planting (MAP).

Statistical analysis

The variability, phenotypic, genotypic and environment coefficient of variance, broad sense heritability and genetic advance were determined according to Burton (1952) and Johnson *et al.* (1955). The correlation coefficients were calculated according to the method suggested by Goulden (1952). Path coefficient analysis was done as suggested by Dewey and Lu (1959), to study the direct and indirect effects.

3. RESULTS AND DISCUSSION

The genotypic and phenotypic co-efficient of variations indicated that all the growth and leaf attributes exhibited higher phenotypic values compared to the genotypic values. Among growth attributes, volume registered high phenotypic co-efficient of variation (83.00%), followed by leaf area (45.71%), total number of leaves (43.08%), DBH (33.44%), height (27.10%), number of branches (26.88%), basal diameter (26.67%), leaf length (23.35%), leaf width (22.18%), leaf petiole length

(20.80%), and the corresponding genotypic co-efficient of variation also exhibited similar trends of higher PCV with volume and lowest GCV with leaf petiole length. This indicated that the environmental variances are larger due to the variation of genotypic environmental variable present in the phenotype. It also indicates that the expressed characters were influenced by action of environment as reported in *Populus* (Jha, 2012). In the current study, volume exhibited higher co-efficient of variation compared to other parameters. Such higher variability in volume attributes as earlier been documented in several species by Farmer *et al.* (1988), Bentzer *et al.* (1989), Burdon *et al.* (1992), Gera *et al.* (1993) and Singh *et al.* (2001) supports to the findings of current study. Burton (1952) reported that the GCV together with heritability estimate would give a better picture of the amount of advance to be expected by selection. Hence, heritability estimation was carried out for all growth attributes and the results are furnished in Table 1. Among the growth attributes, height registered maximum heritability of 68.35% and leaf petiole length registered the lowest heritability value of 20.46%.

The basal diameter and DBH registered higher heritability values of 59.00 and 54.18%, respectively. Heritability in a broader sense is the ratio of total genetic variation to the phenotypic variation. This broad sense is very useful to transfer both additive and non-additive variations particularly when clonal propagation is deployed (Zobel and Talbert, 1984). In current study, *N. cadamba* is exploited through clonal technology and hence, higher heritable value recorded for height, basal diameter and DBH is attributable to the combined action of both additive and non-additive variations. Such high estimates of heritability were also recorded for various growth

Table 1. Variability parameters for different growth traits among different clones of *Neolamarckia cadamba*

Character	GCV* (%)	PCV (%)	ECV (%)	Heritability (%)	Genetic advance as percent of mean
Basal diameter	20.49	26.67	17.08	59.00	32.42
DBH	24.61	33.44	22.63	54.18	37.32
Height	22.41	27.10	15.25	68.35	38.16
Number of branches	14.69	26.88	22.50	29.89	16.55
Leaf length	13.29	23.35	19.20	32.40	15.59
Leaf width	14.27	22.18	16.98	41.40	18.92
Leaf petiole length	9.41	20.80	18.55	20.46	8.77
Total number of leaves	25.33	43.08	34.84	34.58	30.69
Leaf area	26.55	45.71	37.21	33.74	31.77
Volume	57.46	83.00	59.90	47.93	81.95

*GCV - Genotypic Coefficient of Variation, PCV - Phenotypic Coefficient of Variation, ECV - Environmental Coefficient of Variation

genotypic level but positive and non-significant correlation at phenotypic level (0.014). The height also exhibited similar trend whereas the number of branches exhibited positive and highly significant correlation with total number of leaves (0.900) and volume (0.553) in phenotypic correlation. Leaf length exhibited positive and highly significant correlation with leaf width and leaf area at genotypic level and at phenotypic levels. Leaf width had positive and highly significant correlation with leaf petiole length (0.535), total number of leaves (0.620), leaf area (0.982) and volume (0.746) at genotypic level, and leaf area (0.862) and volume (0.437) at phenotypic level. Leaf petiole length exhibited negative correlation with total number of leaves and volume at genotypic level and volume at phenotypic level while non-significant positive correlation registered with leaf area at genotypic and phenotypic levels. The total number of leaves exhibited highly significant and positive correlation with volume at both genotypic and phenotypic levels.

The leaf area recorded highly significant and positive correlation with volume both at genotypic and phenotypic levels. The analysis indicated that most of the traits had a positive and significant correlation with other traits, except leaf petiole length. The genotypic correlation is an estimated value whereas phenotypic correlation is derived value from the genotype and environmental interaction. Hence, genotypic correlation is more reliable estimate for defining the degree of relationship between the traits. Hence, the significant and positive genotypic correlation in the current study is a more reliable estimate and indicated the relationship between the traits (Chaturvedi and Pandey, 2004).

The correlation measures speak only about interrelationships between characters whereas the

path analysis apportions the total correlation through direct and indirect effect of other character. In the current study, the path analysis reveals (Table 3) that basal diameter exerted positive direct effect and indirectly through all the traits barring number of branches and leaf length where it registered negative indirect effect. In case of DBH, the direct effect was positive (0.175) and through height, leaf width, total number of leaves and leaf area, it exerted positive effect indirectly, barring number of branches (-0.473), leaf length (-0.704) and leaf petiole length (-0.004). The height exerted positive and indirect effect with basal diameter (0.108), DBH (0.164), leaf width (0.011), total number of leaves (0.623) and leaf area (0.802) but had indirect and negative effect with other traits. The number of branches also exhibited similar trend. The leaf length and leaf width exhibited negative indirect effect through number of branches, leaf length and positive indirect effect with other traits. The leaf petiole length executed indirect negative effects through DBH (-0.007), height (-0.048), leaf length (-0.210), total number of leaves (-0.229) but executed indirect positive effect with other traits. The total number of leaves exerted negative indirect effect with three traits and the leaf area exerted negative indirect effect with number of branches (-0.249) and leaf length (-0.880).

The perusal of results indicated that basal diameter, DBH, height, total number of leaves and leaf area had highly contributed direct effect on volume. However, the basal diameter, DBH, height, number of branches indirectly through total number of leaves contributed maximum to volume. The leaf length, leaf width and leaf petiole length through leaf area contributed maximum towards volume. Total number of leaves and leaf area also exhibited similar trend. This indicates that increase in values of basal diameter,

Table 3. Path analysis showing direct and indirect effects on volume

Effect of characters	Basal diameter	DBH	Height	Number of branches	Leaf length	Leaf width	Leaf petiole length	Total number of leaves	Leaf area
Basal diameter	0.121	0.169	0.315	-0.488	-0.608	0.011	0.000	0.674	0.742
DBH	0.117	0.175	0.328	-0.473	-0.704	0.012	-0.004	0.673	0.827
Height	0.108	0.164	0.351	-0.404	-0.676	0.011	-0.015	0.623	0.802
Number of branches	0.088	0.123	0.211	-0.672	-0.056	0.009	-0.011	0.688	0.360
Leaf length	0.083	0.140	0.270	-0.043	-0.880	0.015	0.027	0.241	0.970
Leaf width	0.082	0.132	0.246	-0.381	-0.843	0.016	0.060	0.476	0.958
Leaf petiole length	0.001	-0.007	-0.048	0.064	-0.210	0.009	0.112	-0.229	0.222
Total number of leaves	0.106	0.154	0.286	-0.603	-0.276	0.010	-0.034	0.767	0.530
Leaf area	0.092	0.149	0.290	-0.249	-0.880	0.016	0.026	0.418	0.971

Residual effect = 0.269

DBH, height and total number of leaves will enhance the wood volume. Such results are earlier reported by many authors such as Joshi and Singh (1996a,b) which lend support to the findings of current investigation. The residual effect of 0.269 indicated the contribution of factors other than those studied in the present investigation.

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