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Growth Performance and Variability in Different Clones of *Gmelina arborea* (ROXB.)

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Abstract

A clonal trial of *Gmelina arborea* consisting of seventy clones selected from ten geographical locations in four

states of northeast India was evaluated for height, diameter at ground level (DGL) and diameter at breast height (DBH) at the Experimental Station, Rain Forest Research Institute, Jorhat, Assam, India. The performance of all the traits at the age of 24 months showed significant variations between the clones. Broad sense heritability for height, DGL and DBH was 0.31, 0.44

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and 0.37 with a genetic gain of 18.1, 24.6 and 30.1%, respectively. Diameter at breast height (DBH) was determined to be an important trait with maximum genotypic and phenotypic coefficients of variation of 18.6 and 30.4%, respectively.

Clones selected from the geographical location of Lanka (Assam) were better performers over other locations. Clone 106 attained the greatest height (517 cm) and DGL (119 mm), whereas Clone 108 performed poorly for all the traits studied. Clone 106 maintained its superiority from an early age of 12 months. Clones 009, 017 and 079 showed an increasing trend for height, and markedly changed rankings from 13th, 15th and 20th positions at the age of 12 months to 2nd, 4th and 15th positions at 24 months of age. The interim assessment of different clones indicated large genetic improvement possibilities in *G. arborea*.

Key words: *Gmelina arborea*, clones, heritability, genetic advance, genetic gain.

Introduction

The demand for wood and wood based products has continuously been on the increase, and is likely to further increase with continuous growing rate of literacy, liberalization of economic policies and advancement of utilization technology. The requirement of various woods in India by 2010 has been projected to 344 million m³ of fuel wood and charcoal, 37 million m³ industrial wood, 33 million m³ sawn timber, 5.7 million m³ pulp and paper wood and 1.3 million m³ wood based panels (ANON, 1993). However, the problem is extremely serious due to low productivity of Indian forests of 0.5 to 0.7 m³ha⁻¹yr⁻¹ against world average of 2.5 m³ha⁻¹yr⁻¹ (LAL, 2000).

Significant improvement in yield has been achieved in many forest species through application of selection and breeding coupled with clonal forestry. Capture of non-additive variation is possible only by adopting clonal approach. The approach is also particularly attractive in

capturing gains for characters that have low heritabilities (ZOBEL, 1981) and in the exploitation of hybrids. The productivity of *Populus* and *Eucalyptus* plantations has been appreciably increased through the clonal approach. Clonal multiplication of trees with desired traits could become commercially acceptable in *Gmelina arborea* as well.

Gmelina arborea (ROXB.) belongs to the family Verbenaceae, and is distributed eastwards from Pakistan, throughout India, Bangladesh and Myanmar to parts of Sri Lanka, Thailand, Laos, Cambodia, Vietnam, China and Yunnan. In India, it is found in the eastern sub-Himalayan tract, the Indo-gangetic plains, the Aravalai Hills, central India, the western peninsula and the western Himalayas (Fig. 1). It contributes substantially in timber, industrial wood and fodder production and is grown extensively both on government and private lands of northeastern India. Application of clonal forestry in *Gmelina arborea* could immensely increase the productivity and contribute substantially in narrowing the gap between demand and supply. Clonal forestry however is only successful with genetically superior clones and therefore present paper is a start towards testing and selection of elite clones.

Material and Methods

A total of seventy clones (Figure 2 and Table 1) were randomly selected from 119 clones established in a clone/gene bank and multiplied vegetatively through chip budding. The clonal trial was established at the Experimental Station, RFRI, Nahorani about 30 km from Jorhat during 2000 in a completely randomised block design with three replication and five ramets of each clone planted in a row. Measurements were taken every 6 months for height, diameter at ground level (DGL) and diameter at breast height (DBH). Following analysis was carried out using statistical package for social studies (SPSS).

Figure 1. – Map for geographical distribution of *Gmelina arborea*.

Figure 2. – Location map for the plus trees of *Gmelina arborea*.

Analysis of variance

The observation taken in the month of July 2002 was analysed for analysis of variance (ANOVA) as per SUKHATME and AMBLE (1989).

Variance

The genotypic and phenotypic components of variance were calculated from the ANOVA as described by BURTON (1952).

- Genotypic variance
 $(\sigma^2g) = (\sigma^2e + R\sigma^2c) - \sigma^2e)/r$ (Where r represents number of replications)
- Phenotypic variance
 $(\sigma^2p) = \sigma^2g + \sigma^2e$
- Genotypic Coefficient of variance
 $GCV = (\sqrt{\sigma^2g}/\text{mean}) \times 100$
- Phenotypic coefficient of variance
 $PCV = (\sqrt{\sigma^2p}/\text{mean}) \times 100.$

Heritability

Broad sense heritability was calculated as per LUSH (1949).

$$h^2 = \sigma^2g/\sigma^2p \times 100.$$

Genetic Advance

The genetic advance was calculated as described by JOHNSON *et al.* (1955).

$$(Gs) = K. h^2. \sqrt{\sigma^2p} \text{ (Where, } K = 2.66).$$

Genetic gain

The expected genetic gain, in per cent of mean, was calculated following BURTON and DEVANE (1953).

$$\text{Genetic gain} = (Gs/\text{mean}) \times 100.$$

Results and Discussion

The genetic parameters are useful tools in predicting the amount of gain to be expected from clonal material. The variation between clones is commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait (FOSTER and SHAW, 1988). Though the selection of superior trees was carried out using index method of selection with intensive selection criteria (KUMAR *et al.*, 2003), genetic superiority *per se* had to be demonstrated. Using analytical tools, variance (both genotypic and phenotypic), broad sense heritability, genetic advance and genetic gain for height, DGL and DBH were calculated and are presented in Tables 2 and 3. Although all 70 clones were planted under uniform conditions, significant differences were found in growth behaviour for all the traits in various clones. Height ranged from 233 (clone 108) to 518 cm (clone 106) with a variation of 122%. DGL ranged from 57 (clone 108) to 119 mm (clone 106) and DBH ranged from 24 (clone 108) to 72 mm (clone 17) to

Table 1. – Details of *Gmelina arborea* clones and their source selected for clonal trial.

Geographical location	State	No. of clones
Medo	Arunachal Pradesh	8
Chowkham	Arunachal Pradesh	1
Lanka	Assam	17
Langting	Assam	8
Lumding	Assam	2
Bilkhawthlir	Mizoram	7
Kolasib	Mizoram	3
Cooch Behar	West Bengal	15
Kurseong	West Bengal	8
Buxa Tiger Reserve	West Bengal	1
Total		70

Table 2. – Analysis of variance for different traits.

Source of variation	Degrees of freedom	Mean sum of squares		
		Height	DGL	DBH
Clones	69	10555.47**	633.59**	373.62**
Replications	2	58404.64	3598.29	1020.27
Residual	138	4469.52	187.83	134.04

** Significant at 1 per cent level of significance

Table 3. – Different genetic parameters estimated for 70 clones of *Gmelina arborea*.

Genetic parameter	Height	DGL	DBH
Genetic variance (σ^2_g)	2028.7	148.6	79.9
Phenotypic variance (σ^2_p)	6498.2	336.4	213.9
Broad sense heritability (h^2)	0.31	0.44	0.37
Genetic advance (Gs)	66.9	21.5	14.5
Genetic gain (%)	18.1	24.6	30.1
Genotypic Coefficient of variance (GCV)	12.2	13.9	18.6
Phenotypic coefficient of variance (PCV)	21.9	20.9	30.4

with a variation of 109 and 200% for both the characters, respectively. Amongst 70 clones, clone 106 was found to be an exceptional clone by achieving maximum values for both height and DGL.

The data presented in the analysis of variance table (Table 2) showed that values for all the traits were highly significant. The genotypic and phenotypic coefficient of variation for all the characters provided evidence for the existence of adequate genotypic variations. The data presented in Table 3 showed that DBH was the most important trait with maximum genotypic and phenotypic coefficient of variation of 18.55 and 30.37%, respectively. The results showed that considerable inter clonal variation exists for further genetic improvement.

The heritability expresses the degree to which a character is influenced by genes as compared to the environment. Estimation of broad sense heritabilities for various characters (Table 3) showed moderate heritability for height (0.31), DGL (0.44) and DBH (0.37), and are in conformity with the results of NELSON and TAUER (1987) in poplars. They reported moderate to high broad sense

heritabilities for juvenile traits such as height, diameter, growth and leaf size. Nonetheless, there is a need to estimate narrow-sense heritabilities for individual growth components so that additive genetic variance associated with individual growth components can be calculated, because these estimates facilitate selection on those traits from which a positive genetic response can be expected at reasonable selection intensity. In the present study greatest genetic advance was observed for height (66.94) followed by DGL (24.60) and DBH (14.52). However, maximum genetic gain (30.2%) was reported for DBH and was moderate for DGL (24.6%) and height (18.2%). Genetic gain for all the traits has been positive, particularly for the most important trait of DBH.

The described heritabilities, genetic advance and genetic gain were estimated at relatively early stage of 24 months after planting. The growth rate generally enters the log phase in third or fourth year of age, thus heritability estimates carried out at that age would be more accurate. The present results, however, can serve as an indicator to be compared with the results to be obtained at later stages and also to establish the corre-

Table 4. – Change in the ranking for height in different clones of *Gmelina arborea*.

Ranks	Clone No.	AGE OF PLANTS		
		12 Months	18 Months	24 Months
1	106	178 (106)	306 (106)	517 (106)
2	101	167 (101)	278 (009)	491 (009)
3	37	164 (037)	277 (099)	491 (086)
4	3	162 (003)	268 (101)	485 (017)
5	39	161 (039)	263 (017)	475 (099)
6	8	158 (008)	262 (039)	461 (008)
7	16	157 (016)	259 (003)	449 (037)
8	38	156 (038)	254 (038)	448 (039)
9	7	155 (007)	254 (016)	440 (003)
10	11	153 (011)	252 (008)	435 (038)
11	4	152 (004)	242 (037)	431 (016)
12	99	152 (099)	241 (011)	430 (101)
13	9	150 (009)	239 (007)	420 (004)
14	86	148 (086)	239 (102)	417 (011)
15	17	147 (017)	238 (112)	410 (079)
16	27	143 (027)	235 (086)	403 (102)
17	116	140 (116)	229 (027)	400 (116)
18	102	132 (102)	227 (079)	398 (007)
19	112	132 (112)	225 (004)	395 (112)
20	79	120 (079)	218 (116)	394 (027)
Average		151.4	250.3	439.5
S.D.		13.4	21.5	36.9

Figures in parenthesis indicate clone number

lations. Assessment at 3 to 4 years would determine whether genetic analysis at early stage is reliable.

If found reliable, genetic assessment for other populations could also be carried out with suitable correlation factors or the extent of the relationship can be determined. In the present study, clones 8, 9, 16, 17, 37, 39 and 106 were the best performers for all traits. Their superiority, however, needs to be tested over period of time to make suitable recommendations. On the basis of mean height at the age of 24 months, thirty-two of seventy clones were taller than the mean height (369 cm). A total of 38% of the clones from geographical locations in Lanka were found to be above average mean height followed by Cooch Behar (22%) and Medo (13%). This reflects superiority of selections from Lanka over other geographical locations.

The top twenty clones in terms of mean height were assessed for their ranking at the age of 12 (May 2001), 18 (December 2001) and 24 (August 2002) months (Table 4). Clone 106 maintained 1st rank over the period. Clones 9, 17 and 79 showed an upward trend whereas clones 3, 7, 11, 16, 27, 39 and 101 showed a decreasing trend. Though average increment for these 20 selected clones from May 2001 to August 2002 was 190%, clones 79, 17 and 9 showed an increment of 242, 230 and 227%, respectively. The results are clear indications that testing of clones needs to be carried out for longer durations so that elite genotypes are identified and deployed thorough plantations programmes. It is also necessary to examine the trend of all the clones over the years and to group different clones for various end uses. The rapid growing clones may well be used to establish biomass plantations for paper industry whereas slower growing clones may be recommended for timber and furniture industry. However, individual clones needs to be analysed for different wood properties before recommending their deployment through plantations programmes. Nonetheless, described results indicate clonal behaviour only for height at one single location and needs to be tested for real superiority *per se* at different locations.

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A Study of Population Variation and Inheritance in Sitka Spruce

IV: Correlated response in the progeny population based on selection in the parental population

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Summary

This study investigated the potential benefits to a tree breeding programme of selection based on height in the original ortet population, and on diameter and wood density of grafted-ramets representing the same ortets growing in a clone bank. The trees studied were a large, randomly selected same-aged population of Sitka spruce