

## Preliminary Analysis of Quantitative Characters in Teak

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The genetic architecture of quantitative characters in teak (*Tectona grandis*) was studied using 27 half-sib families. The results indicated the presence of considerable genetic variation in the material. Preponderance of additive gene action was noticed for height as evidenced by both high heritability and genetic gain values. Diameter and basal area were found to be under the control of non-additive gene action. Highly significant and positive genetic correlation were found among all the characters. Clones ORPUB-8, 18 and 23 were found to be best general combiners for height, diameter and basal area.

**Key Words :** Half-sib, Heritability, Genetic gain, Additive gene action, Combining ability

### Introduction

Teak (*Tectona grandis*) is widely known because of its high grade even density wood suitable for use as veneer, particle board, structural products including furniture and cabinet making. Teak is indigenous to India and south-east Asian region with maximum variability found in India. Genetic variation of teak in India is assumed to relate directly to variation in geographical conditions in which it grows.

An extensive programme was undertaken during 70s to collect the variability by selecting phenotypically superior trees (plus trees) from all the teak growing states. In Orissa alone 75 plus trees were selected. A tree improvement programme involving provenance trials, establishment of seed or-

chards with untested plus trees was undertaken almost two decades back. Also, a programme for genetically improving growth, form and quality traits has been undertaken with a number of first generation progeny tests being established over the past one decade. However, such tests are not yet evaluated and as a result there is lack of reliable genetic information required for the efficient operation of a breeding programme. Also, there is no published report on the magnitude of genetic variation in teak and associations between economically important traits and on the selection of "elite" trees based on general combining ability estimates.

In this study we examined genetic variation in 12 year growth traits for 27 selected families of teak. The specific objective of

the study were to: (i) assess the extent of genetic variation (ii) estimate narrow sense heritabilities and genetic gain, and (iii) identified best general combiners.

### Materials and Methods

Material for the present study came from the orchard established with 27 clones. Open pollinated seeds were collected from all the ramets of each clones. Seeds were kept separately by ramets and seeds from all the ramets of each clone were mixed to form a bulk seed sample. Finally equal quantities of seeds were taken from all the clones to raise seedlings. During the year seed collection all the ramets were in flowering stage and therefore half-sib relationship among the progeny were assumed, though the presence of negligible percentage of full-sibs and selfs were not ruled out.

One year old seedlings (root-shoot) were planted in the field at Dhandatopa, Orissa in 1982. Twenty five seedlings (stump) of each clone were planted in family blocks following a randomized complete block design with three replications at a spacing of 2.5 × 2.5m. Survival of field planted seedlings were to the tune of 98%. Casualty replacement was done with in six months of field planting. Due care was provided so as to raise a good crop.

Data on morphological characters were recorded every year. However, data recorded in 1984 on height and diameter forms the basis of this report : Statistical analysis of data and estimation of different genetic parameters was done following the methods and formulae given in Zobel and Talbert (1984).

### Results and Discussion

Analysis of variance indicated highly significant differences among all families

(table 1). Family alone accounted for 35-50% of total variation in different characters. Family x replication interaction variations were not significant suggesting that characters studied are not susceptible to environmental variation.

**Table 1** Analysis of variance for growth characters

Source of variation	d.f.	Mean squares		
		Height	Diameter	Basal area
Replication	2	19.48	11.35	5394.75
Family	26	35.45*	28.71*	8724.86*
Fam. × Rep.	52	13.23	11.22	3438.09
Tree within plot (error)	648	3.82	8.94	2745.55

\*Significant at 1% level

**Table 2** Estimates of heritability and expected genetic advance

Character	Heritability (%)	Genetic gain	Genetic gain in percent of mean
Height	58.0 (76.0)	3.68 (2.10)	34.46 (19.66)
Diameter	26.0 (64.0)	2.17 (1.71)	20.97 (16.52)
Basal area	26.0 (53.0)	2.85 (2.78)	4.19 (3.03)

Values within the parenthesis indicate values for family heritability and genetic gain

Individual and family heritability values ranged from 26.0 to 58.0 and 53.0 to 76.0%, respectively (table 2). Height recorded moderately high values of heritability, while diameter and basal area registered low values of heritability. Moderately high heritability values for height both at the individual tree and family level indicate that height is less likely to be influenced by environmental changes.

The variation measured in terms of mean values and range is high and also most of the variation for height was observed between individuals thereby raising the heritability values to moderate intensity.

As expected height recorded highest (34.46%) and diameter and basal area recorded low genetic gain (table 2). The genetic gain values were calculated assuming 10% selection intensity. High heritability values coupled with high genetic gain indicate the predominant role of additive gene action for height.

Highly significant and positive genetic correlations among height, diameter and basal area (table 3) suggest that the relationship

Table 3 Genetic correlation coefficient among different characters

	Diameter	Basal area
Height	0.7739**	0.9794**
Diameter		0.7293**

\*\*Significant at 1% level

at the genetic level is very strong. It means that simultaneous improvement can be achieved by selecting one or the other character. Since height is controlled by additive gene action and also genetically strongly correlated with basal area and diameter, a selection programme using height as a primary parameter for selection is recommended for teak improvement work.

More than 50% of the total clones included in the study were found to have positive gca values for atleast one characters (table 4). ORPUB-23 recorded highest gca values for all the traits. ORPUB-30 is the poorest parent among all. Eleven clones namely, ORPUB 1, 5, 7, 8, 9, 18, 19, 20, 23, 26 and 29 were found to be good

combiners for all characters. However, in order of merit ORPUB 8, 18 and 23 considered to be best general combining parents.

Table 4 General combining ability (gca) for height, diameter and basal area

Clone	Height	Diameter	Basal area
ORPUB - 02	- 0.38	- 0.41	- 8.00
ORPUB - 19	0.99	0.72	8.92
ORPUB - 20	0.76	0.38	10.00
ORPUB - 21	- 1.00	- 0.54	- 9.11
ORPUB - 22	- 1.03	- 0.58	- 14.98
ORPUB - 18	1.48	1.24	22.56
ORPUB - 12	- 0.54	- 1.06	- 16.60
ORPUB - 06	1.68	0.61	- 6.10
ORPUB - 01	0.68	1.17	25.70
ORPUB - 27	- 1.53	- 1.42	- 24.37
ORPUB - 31	- 0.81	- 0.59	- 12.03
ORPUB - 05	0.70	0.88	17.48
ORPUB - 26	0.26	1.02	22.33
ORPUB - 23	2.50	2.15	35.70
ORPUB - 07	0.92	0.50	6.59
ORPUB - 03	- 1.80	- 1.22	- 18.52
ORPUB - 30	- 2.34	- 1.98	- 32.40
ORPUB - 10	- 0.03	- 0.91	- 16.19
ORPUB - 17	- 1.33	- 1.26	- 20.28
ORPUB - 24	- 0.78	- 0.55	- 9.38
ORPUB - 29	0.28	0.60	10.22
ORPUB - 13	0.23	0.26	1.21
ORPUB - 09	0.32	0.91	14.45
ORPUB - 28	- 0.96	- 0.92	- 0.92
ORPUB - 15	0.30	0.70	- 16.07
ORPUB - 08	1.35	1.09	12.75
ORPUB - 25	0.03	- 0.92	- 14.13

This report on the genetic analysis of quantitative characters in teak is based on limited number of materials, and therefore the results of this study should be used with caution for generalization purpose.

#### **Reference**

Zobel B and Talbert J 1984 *Applied Forest Tree Improvement* (New York : Wiley)