

Genetic Variation for Quantitative Traits among Teak (*Tectona grandis* L) clones

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Abstract: Present study was carried out on genetic variability in different teak clones during 2013-14 at the Department of Forestry, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra and the observations were taken from Teak Clonal Orchard established at the same campus. The study was undertaken on fifteen clones of teak (*Tectona grandis* L) using randomized block design with three replications. The teak plantation was established in the year 1992 at a spacing of 5 x 5 m. The observations for quantitative characters were recorded from three randomly selected trees for each clone. Clone APT 4 exhibited maximum DBH (34 cm), height (15 m), and basal area (963 cm²). A dendrogram was created based on the quantitative observations and grouped the clones into seven major clusters. But the dispersion plot defined by the first two principal components did not show any significant grouping. The phenological characters for all fifteen clones like month of flowering, month of leaf shedding, month of leaf initiation and month of fruiting were recorded. No significant difference was observed in their phenological behaviour. Clone APT 4 is a superior genotype and thus can be recommended for vegetative multiplication and *ex-situ* mass planting in reforestation programmes.

Keywords: Teak, quantitative traits, cluster analysis, principle component analysis

Introduction

Teak (*Tectona grandis* Linn. F.; Verbenaceae) is one of the most valuable and widely planted tropical timber species; growing naturally in forests of India, Myanmar, Northern Thailand, Laos and Indonesia and in India it occurs naturally from 8° to 24°N latitudes. Within the well-marked distribution boundary, teak grows in diverse climatic and edaphic conditions resulting in distinct populations. Major teak areas occur in two distinct geographic regions: the Deccan Plateau which lies between 16° and 24°N latitude covering most of the Central India and the mountainous Western Ghats region, mostly below 16°N latitude (Troup, 1921).

The natural teak forests in India are the largest in the world, occupying an area of 8.9 million ha (Tewari, 1992).

The mounting global demand of products from teak and diminishing availability of teak from natural forest; plantations become the important source for timber. About 94 per cent of global teak plantations are in tropical Asia, with India (44%) and Indonesia (31%) accounting for the bulk of the resource. In India and Myanmar the first systematic efforts to establish teak plantations were made more than 150 years ago (FAO, 1993). The first teak plantation in India was established in 1842 at Nilambur, Kerala with the purpose of enriching the teak forests (Katwal, 2005). At the moment, teak plantations exist around 1.5 million hectare in India and around 50,000 hectare of teak plantations are propagated annually (Subramanian *et al.*, 2000). To preserve the genetic resources and ensure the supply of genetically superior quality germplasm for improvement and plantations, a core collection of superior genotypes with large genetic diversity is a prerequisite. Genetic improvement of teak in India was started in the year 1954 and it has focused on identifying phenotypically superior trees from diverse regions and deploying them in seed orchards.

Seed orchards form an important connection between ongoing tree improvement programme and profitable planting. One objective of tree improvement programme is mass production of genetically superior seed. Seed orchards are indented to supply superior seeds in ample quantity (Zobel and Talbert, 1984). CSOs are the main focus of genetic improvement of teak in India; they are planned and established for raising the production of high quality seeds for growing superior plantations. But the output from these orchards has been far from satisfactory. Poor flowering, asynchrony in flowering phenology, low fruit and seed set were the major problems faced (Vasudeva *et al.*, 2001; Mathew and Vasudeva, 2003; Gunaga and Vasudeva, 2005). Since teak is a highly cross pollinated species, one of the reasons for low fruit and seed set and poor seed viability could be the low genetic variability between the clones which are assembled in clonal orchards. The natural crossing between genetically similar or related genotypes may be causing poor seed set because of self-incompatibility and inbreeding depression. These clones are to be tested for genetic variability in order to avoid planting of genetically related clones for avoiding inbreeding in the clonal seed orchard.

Teak resources of the world need instant attention for their sustainable management and conservation of diverse gene pool. The bottlenecks in tree improvement and seed production have to be removed through improved basic research; the potential of leading edge areas like biotechnology must be used for speedy improvement. How to manage, which and how many materials we should manipulate and where we should establish or protect the gene resources, depends on whether we really know the genetic background of particular species which we wants to conserve.

Genetic analysis and information about quantitative traits would allow the comprehensive conservation and improvement programs such as population sampling, seed orchard design and management, controlled pollination methods, and clonal forestry programs.

Material and Methods

Experimental site

The study was conducted in an experimental farm and the observations were taken from Teak Clonal Orchard established at College of Forestry, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola.

Details of layout of Clonal Orchard

- 1) Date of Planting : 7-7-1992
- 2) Date of Grafting : 8-8-1993
- 3) Design of Planting : Quincunx
- 4) Spacing : 5m x 5m

Basic plant material

The materials under present study constituted by fifteen clones of teak (*Tectona grandis* Linn. F.). the clones under study has been listed along with their sources in Table 1.

Table 1: Details of the clones under study

<i>Sr. No.</i>	<i>Name of clones</i>	<i>Source</i>
1.	APJNB -1	Andhra Pradesh
2.	APMN-4	
3.	APT-4	
4.	APT-17	
5.	APT-20	
6.	MHAL-A4	Maharashtra
7.	MHAL-A8	
8.	MHAL-P6	
9.	MHSC-J2	
10.	ORPB-15	Orissa
11.	ORANP-7	
12.	TNT-6	Tamil Nadu
13.	TNT-11	
14.	TNT-17	
15.	TNT-18	

Quantitative characters selected

The observations for quantitative characters were recorded from three randomly selected tree for each clone.

Plant height (m): Plant height of randomly selected clone per replication was recorded in meter by using the altimeter.

Diameter at Breast Height (cm): Diameter of each clone was recorded from 1.37 m above the ground level by using the tree caliper along the major and minor axis.

Diameter at Stump Height (cm): Diameter at stump height of each clone was recorded at 30 cm above the ground level by using the tree caliper along the major and minor axis.

Basal Area (cm²): Basal area is the cross-sectional area at breast height of the tree and calculated by the formula;

$$\text{Basal Area} = G^2 / 4 \pi, \text{ where } G = \text{Girth.}$$

Number of branches: Number of primary branches of each clone was counted manually for each clone.

Results and Discussion

The quantitative and phenological observations were recorded on randomly selected plants from each clone.

Table 2: Quantitative characteristics of fifteen teak clone samples

Sr. No.	State	Clone Name	Height (m)			DBH (cm)			Stump Diameter (cm)			Basal Area (cm ²)			No. of Branches			
1	Andhra Pradesh	APJNB	1	13	13	12	29.5	25.5	27	35	27.5	30	719	460	562	24	26	24
2		APMN 4	8	7	9	24	24	25	30	29	31	484	460	510	10	10	9	
3		APT 4	14	15	14	25.5	34	32	31	37	34	510	963	704	15	17	16	
4		APT 17	8	8	8	22	24.5	22	28	34	27	347	484	390	9	14	12	
5		APT 20	9	8	8	30	22.5	26	33	24.5	27	674	401	548	10	11	11	
6	Maharashtra	MHAL A4	9	8	8	26	21	24	30.5	22	27	535	347	448	11	10	10	
7		MHAL A8	7	6	7	22.5	22	22	26	25	26	448	390	424	16	13	15	
8		MHAL P6	8	7	6	16.5	16	16	17.5	16	17	224	191	199	5	6	5	
9		MHSC J2	7	6	7	18	21	18	21	25	22	241	326	250	9	8	9	
10	Orissa	ORANP 7	6	6	6	16	16	16	17	16.5	16.5	224	199	215	11	9	10	
11		ORPB 15	10	7	8	29	17	24	30	19	25	674	215	448	13	10	13	
12	Tamil Nadu	TNT 6	11	10	10	27	26	26	27	27	27	522	497	497	15	14	15	
13		TNT 11	8	9	8	23	24	23	24.5	25	25	413	448	424	10	9	10	
14		TNT 17	9	8	8	26.5	25	25	29	26	26	522	448	497	8	15	14	
15		TNT 18	12	12	12	28.5	26	27	30	30.5	29	617	497	535	17	19	19	

Cluster analysis based on quantitative traits

The clustering of fifteen teak clones based on quantitative characters was done and the detailed information is furnished diagrammatically (Table 3; Fig. 1). The generated information revealed that there were seven major clusters – 1, 2, 3, 4, 5, 6 and 7.

Cluster 1 comprised the majority and was found with two sub-clusters A and B. Sub-cluster A consists of seven clones namely, MHAL A4, TNT 11, APT 20, ORPB 15, TNT 17, APMN 4 and MHSC J2 while sub-cluster b contain only one viz., APT 17.

Cluster 2 is made of two sub-clusters A and B comprising one clone each viz., MHAL P6 and ORANP 7 respectively.

Cluster 3, 4, 5, 6 and 7 contains one clone each namely TNT 6, MHAL A8, TNT 18, APJNB 1 and APT 4 respectively.

Table 3: Cluster analysis based on quantitative data

Particulars	Cluster	Sub-cluster	Sub-sub-cluster	No. of clones	Teak clone
	1	A	A1	5	MHAL A4, TNT 11, APT 20, ORPB 15, TNT 17
			A2	1	APMN 4
			A3	1	MHSC J2
		B		1	APT 17
	2	A		1	MHAL P6
		B		1	ORANP 7
	3			1	TNT 6
	4			1	MHAL A8
	5			1	TNT 18
	6			1	APJNB 1
	7			1	APT 4
Total	7	-	-	15	-

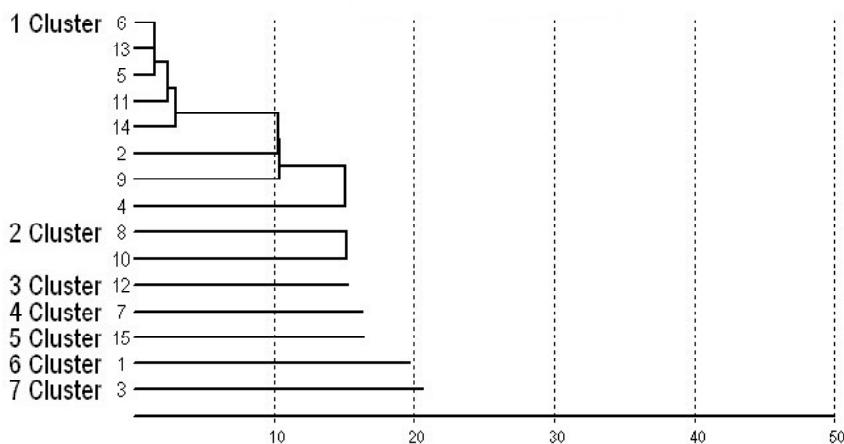


Figure 1: Dendrogram depicting the cluster of fifteen teak clones based on quantitative parameters

Principal Component Analysis

Principal component analysis showed that the first two components (PCs), which had Eigenvalue, explained a total of 94.21 per cent of the whole phenotypic variability (Table 4). In the first PC (84.4%), all the five traits were approximately equally important. In the second PC (9.7%), however, height and number of branches were the predominant trait (Table 5). A dispersion plot defined by the first two principal components did not show any significant grouping (Fig. 2).

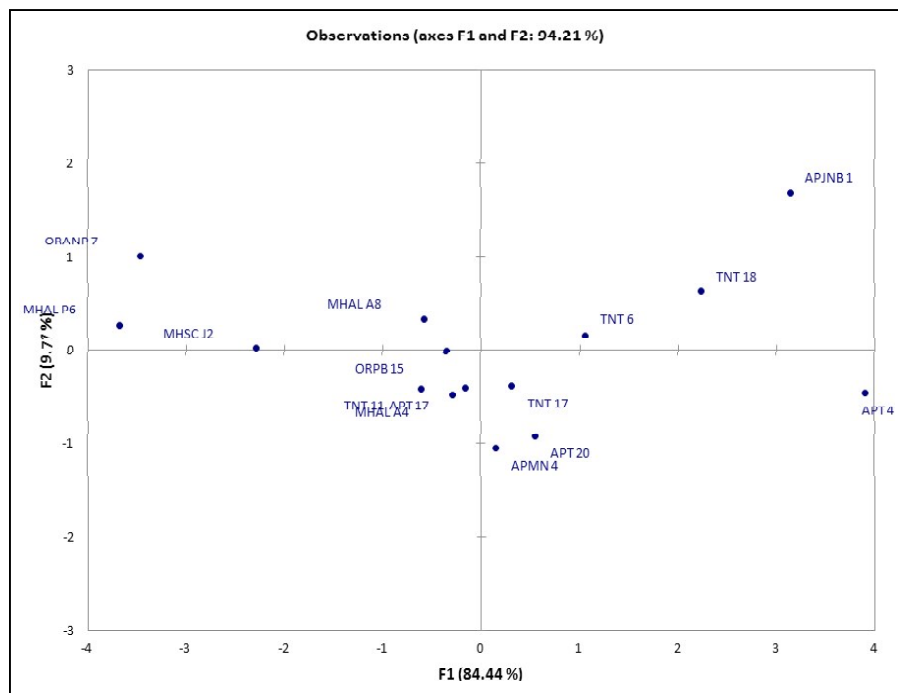


Figure 2: Two-dimensional graph of *Tectona grandis* clones derived from principal component analysis of quantitative trait values.

Table 4: Eigen value and Variability

Principal Component	Eigen value	Variability (%)
1	4.222	84.437
2	0.489	9.772
3	0.206	4.124
4	0.0702	1.444
5	0.011	0.223

Table 5: Coefficients of each quantitative variable for the first two significant principal components

Variable	Component	
	Component 1	Component 2
Height	0.444	0.257
DBH	0.472	-0.277
Stump Diameter	0.451	-0.378
Basal Area	0.473	-0.267
No. of Branches	0.391	0.802

Table 6: Phenological characters of fifteen teak clones

Sr. No.	Name of genotypes	Month of leaf shedding	Month of leaf initiation	Month of flowering	Month of fruiting
1	APJNB 1	December	June	August	January
2	APMN 4	December	June	August	January
3	APT 4	December	May	August	January
4	APT 17	December	May	August	January
5	APT 20	December	May	August	January
6	MHAL A-4	November	June	August	December
7	MHAL A-8	November	June	August	December
8	MHAL P-6	November	June	August	December
9	MHSC J-2	November	June	August	December
10	ORANP 7	December	May	August	January
11	ORPB 15	December	May	August	January
12	TNT 6	December	May	August	January
13	TNT 11	December	May	August	January
14	TNT 17	December	May	August	January
15	TNT 18	December	May	August	January

Low overall seed productivity remains a serious handicap for seed orchards. The production is less than the quantity of seeds produced from natural stands and might be due to the fact that the clones are issued from “Plus” tree selection only, then established in different regions where environmental conditions are not optimal for seed formation (Kaosaard, 1996). Other major factor affecting the final fruit set in teak is the asynchronous flowering phenology among the clones selected from different areas (Gunaga and Vasudeva, 2005). Hence it is essential to study the phenology and match the flowering phenology of clones before deploying clones in the seed orchards.

Appendix 1. ANOVA analyses for the five quantitative traits (design Nested ANOVA)

Source	d.f.	Height		DBH		Diameter at stump height		Basal Area		No. of branches	
		MS	F	MS	F	MS	F	MS	F	MS	F
Within State	3	30.254	61.883***	126.237	21.236***	201.865	26.197***	136934.582	12.549***	61.581	27.992***
Within Clone	11	13.729	28.082***	28.145	4.735***	32.953	4.277***	35776.485	3.279**	65.294	29.679***
Error	30	489									

*** P < 0.001

** P < 0.01

Conclusion

The quantitative traits namely, height, DBH, stump diameter, basal area and number of branches were measured and then subjected to nested ANOVA analysis which revealed significant differences in all the traits within and among the clones Clone APT 4 is a superior genotype and thus can be recommended for vegetative multiplication and *ex-situ* mass planting in reforestation programmes. The result of clustering coefficient analysis showed the variations between the clones and this might be due to the source of the clones from where they are procured. The principal component analysis estimated using genetic distance values mostly supported the UPGMA cluster analysis and also provided resolution of teak populations according to their geographical locations from where they are obtained.

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