Genetic Diversity Assessment of Teak (Tectona grandis Linn. F.) in a Clonal Seed Orchard

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Abstract

The investigation was carried out to find out the inter-clonal variation in terms of growth performance and genetic variability of 25 Teak clones at 30 and 31-years age, planted at a spacing of 6m x 6m in the Clonal Seed Orchard of Silvicultural Research Station, Angul, Orissa, India, located at $21^{0}01'17.8''$ N longitude and $84^{0}55'19.6''$ E latitude. The experiment was laid out in Latin Square Design with 25 replications with 25 numbers of Teak clones as treatments. Maximum DBH (29.46 cm) was observed for ORANP-17 and in next year, nearly 8% increase in DBH was observed for many Teak clones. Tree height of Teak clones varied from 17.02 m to 21.16 m and 17.34 m to 21.90 m at 30 and 31 years of age and at 31st year, tree height seems to be saturated and only 3 to 4% increase was noticed. Both at 30th and 31st year, maximum volume of stem was recorded for ORANP-17 (100.62 m^3 and 118.10 m^3 respectively), which varied significantly with rest of the 24 Teak clones. Nearly 18% increase in volume of stem was observed between 30th and 31st year for most of the clones. Maximum value of CAI of volume of stem was recorded for ORANP-17 (17.48 m^3) followed and *at par* with only one clone *i.e.* ORANP-16 (15.50 m^3). Nearly three times difference was noticed between top and least performed clones. The range of MAI of stem volume at 30th year was 2.05 m^3, while at 31st year, it was 2.33 m^3 *i.e.* maximum 3.81 m^3 for ORANP-17. Percentage increase in MAI of stem volume between both the years was varied between 13 to 14%. In case of DBH, higher value of genotypic coefficient of variation (6.73) was noticed than phenotypic coefficient of variation (6.67), which showed that DBH of Teak clones are more influenced by genetic characters. Higher impact of environmental factor was noticed on the traits like CAI in DBH, CAI in height, CAI of stem volume and MAI of stem volume. Maximum intra cluster divergence was noticed for cluster II (13.21), followed by I (11.48), cluster III (7.50) and cluster VI (7.22). Maximum inter-cluster divergence was noticed between cluster II and VIII (72.83), followed by cluster II and VII (72.86) and cluster VI and VIII (72.83). Clustering pattern indicated that maximum number of 10 germplasm came in cluster I. Cluster VIII consist of most superior close of Teak, because it gave maximum value for all the growth parameters. Maximum percentage contribution in divergence of Teak clones was noticed by tree height (67.67%) followed by length of straight stem (29.33%). Cluster VIII consists of most superior close of Teak (ORANP-17), because it gave maximum value for almost all the growth parameters. Next to cluster VIII, best performing cluster is VII (ORANP-16). From this study, it is recommended for the vegetative multiplication of clone ORANP-17 which manifested highest stem volume of 118.10m^3/ha and MAI of 2.63m^3/ha at the age of 31 years. It is also inferred that appropriate improvement is possible in MAI as well as CAI in stem volume of different Teak clones by providing adequate silvicultural and cultural practices.

Introduction

Natural variation is essential for conservation and utilization of different tree species, so it is important to collect, evaluate and conserve the genetic variation within a species and genus (Namkoong, 1984). Knowledge of the genetic stock and of natural genetic diversity is indispensable for genetic improvement work for Teak since it is essential for the estimation of heritability and genetic gain, and also for its genetic resources management. Genetic variability study aims at quantify the genetic and environmental components of phenotypic variability between trees from different geographic origin. The knowledge of variability within species is a prerequisite for developing effective tree improvement strategy. The success of a tree improvement program depends highly upon the determination of amount, type and causes of genetic variability within a species. During last few decades, wide concern was emerged to solve the problem of the erosion of genetic resources. The only realistic solution of the continuing loss of plant germplasm is to collect and maintain in gene resources centers (Thakur and Thakur, 2015). Teak is known to have a great genetic variability in India, with its natural distribution spreading over 8.9 M ha of forests ranging from very dry to very moist conditions. In fact, Indian subcontinent is considered as center of diversity for Teak because of huge genetic variation for economically important traits such as bole form and timber quality (Kumar et al., 1997).

Teak (*Tectona grandis* Linn. f.) is one of the most valuable tree species of the world and considered as king of Indian timbers. It is widely planted tree species in South Asia and indigenous of peninsular India. For the first time, Teak plantations were raised in India in 1842 in Nilambur. It is the principal timber tree of India, Myanmar, Indonesia & Thailand and one of the most important timbers of the world. The natural habitat of Teak lies between 10^{0}N and 25^{0}N in Indian subcontinent and South East Asia, especially in India, Myanmar, Thailand, Laos, Cambodia, Vietnam and Indonesia. In India, it has a discontinuous distribution from its western limit at 24°42'N latitude, northern limit to 25° 33'N from where it extends to Mahanadi river in the east (Brandis, 1906). The Teak forests in India are classified into five major types, based on the rainfall: very dry, dry, semi-moist, moist and very moist types. In the south, Teak bearing forests found up to Travancore and Tinnevelly. In Kerala, it is found in the Wynaad and Annamalai hills and in Tamil Nadu, it is confined to lower slopes of Nilgiri hills. In Andhra Pradesh, it is distributed in the river basins of Godavari and Krishna and in Karnataka in the Western Ghat forests. Teak is distributed throughout the Maharashtra state in deciduous forests; the richest forests are in Chandrapur district. Gujarat has good Teak forests in southern parts of the state particularly in Surat and Dangs districts. In Madhya Pradesh, Teak forests are found in Hoshangabad, Betul, Nimar, Chhindwara, Seoni and parts of Mandla and Bastar. In Rajasthan, it is mainly confined into the southern parts namely Banswara. In Odisha, Teak was introduced in few places, out of all Barbara Teak plantation established in 1910 find a special identity for research and development in the state. Teak is probably the most thoroughly studied species both from managerial and silvicultural angle. Distinct genetic variations are found in Teak of different forest types, which is important for its improvement program. About 1000 ha of Clonal Seed Orchards (CSOs) has been established in different states (Andhra Pradesh, Arunachal Pradesh, Karnataka, Kerala, Madhya Pradesh, Maharashtra, Orissa, Tamil Nadu) (Katwal, 2005). Nevertheless, the major constraint in CSOs is low seed production and similar trend has been reported in Thailand also by Kaosaard et al., 1998. Success in establishment and enhancement of productivity of forest tree plantations can only be achieved when genetically best trees are grown under intensive management. All tree improvement programs must include determination of the amount, kind and causes of variability, desired qualities in trees, mass production of superior clones and maintaining a genetic base population, broad enough for needs in advanced generations (Gera, 2000).

Due to low productivity of Indian forests of 0.5 to 0.7 m^3 ha^{-1} yr^{-1} against world average of 2.5 m^3 ha^{-1} yr^{-1} (Lal, 2000), it is essential to increase the productivity of plantations. Mathew (1961) in his report to the Government of India, emphasized that top priority should be given to the genetic improvement of Teak. Following the recommendations of Kedarnath and Mathews (1962), Teak tree improvement gained momentum in all the Teak growing states of the country. During the past four decades, considerable progress has been made in improving planting stock of Teak. Besides India's participation in the IUFRO-DANIDA International series of Teak Provenance trials, there has been considerable progress within the country for improving the planting stock of Teak through the establishment of Seed Production Areas (SPAs) and Clonal Seed Orchards (CSOs).

Teak improvement program like enhancement of its productivity becomes the most important research field with focus on seeking new provenances and clones that can provide higher yields on shorter rotation (Keshwani, 2001). Teak covers about 14% of the total tropical plantations. Every year about 50000 hectares are planted with Teak in India (Subramanian et al., 2000). However, the productivity of Teak in India is very low. It has been reported that the average productivity of Teak in Kerala is 2.85 m^3/ha/year over a 53-year rotation, which is very low in comparison with other Teak growing countries. Teak timber provides a long-term prospect for storage of carbon due long rotation (Bhat, 2003: Keogh, 2003). Understanding heritability in traits attributable to yield is helpful for efficient selection. High heritability indicated that the variation of traits is mostly due to genotypic effect. Since quantitative traits are complex, genotypic variance, heritability and genetic advance of the breeding materials is important to choose the parents used for improving the traits. Research shown that clonal plantations play an important role to increase productivity (Palanisamy et al., 2010). Clonal seed orchards (CSOs), established through grafts of genetically superior trees are considered to be channels of genetically improved seed and starting point for domestication. The judicious use of suitable Teak clones can bridge up the visible demand supply gap of Teak timber and also helps to improve the socioeconomic condition of small holder tree growers. In view of the importance of clonal testing in Teak for the identification of suitable clones to ensure establishment of genetically uniform and superior plantations, the present study was conducted to evaluate the growth performance and genetic diversity among 25 different Teak clones in Orissa.

Materials and Methods

Study site

The experiment was conducted at Clonal Seed Orchards (CSOs) of Teak established inside Koshala Research Station, Angul (Silviculture Division, Bhubaneswar), Orissa State Forest Department, which is located at $21^0$01'17.8" N longitude and $84^0$55'19.6" E latitude. The CSOs was established in 1983 under Latin square design (LSD). The Koshala Research Station, Angul is situated in the central part of Orissa about 165 km away from headquarter of Orissa University of Agriculture and Technology (OUAT), Bhubaneswar and is the main silvicultural research station carrying out silvicultural trials on Teak in Orissa. The site is about 440m above msl. The mean annual rainfall is about 1250 mm. The forest type found in the area is dry deciduous. The land is gently sloppy and soil is sandy loam with poor humus. The soil of the experimental site is acidic in nature which is lateritic and generally poor in organic carbon. Available nitrogen, phosphorus and potassium were of medium status. The textural characteristic is sandy loam, well drained and low water holding capacity.

Table 1
Initial soil properties of the experimental site

Sl. No.	Parameters	Values	Status
1	pH	5.80	Slightly acidic
2	Organic Carbon (%)	0.55	Medium
3	Available Nitrogen (kg ha^{-1})	276.00	Medium
4	Available Phosphorus (kg ha^{-1})	30.00	Medium
5	Available Potassium (kg ha^{-1})	180.00	Medium
6	Texture	Sandy loam	

Experimental site

The experiment was laid out in Latin Square Design with 25 replications. There were 25 numbers of clones of Teak as treatments. The clones were planted at a spacing of 6.0 m x 6.0 m in 1983. The clones of CSOs have been derived from 25 plus trees located at Purunakote, Berbera, Rayagada and Angul provenances of Orissa. In total, there were 625 numbers of trees in the experiment.

Tree observations/measurements

The parameters taken to enumerate different growth and yield parameters for CSOs were diameter at breast height, tree height, length of straight stem from the ground, length of clean bole from the ground, current annual increment in DBH, mean annual increment in DBH, current annual increment in height, mean annual increment in height, current annual increment of volume of stem, mean annual increment of stem volume and leaf area of different Teak clones. The data was collected for two consecutive years and statistically analyzed for the validation of the results. DBH was measured with the help of caliper in two directions following the established guidelines and average was computed and expressed in cm. Height of trees was measured from ground level to the top of the main shoot with the help of altimeter and expressed in meter. Then, the average stem volume per tree was calculated by the formula given by Forest Survey of India (FSI, 1996) for Orissa i.e.

VUB (m^3) = $-0.0645 + 0.2322D^2H$

Where, VUB = Volume under bark; D = DBH over bark; H = Height of the tree
The volume of stem per hectare was calculated by multiplying the average volume of stem per tree with plant population per ha. It was expressed in m^3/ha. The CAI in DBH, height and volume was from the difference of parameters recorded in two consecutive years and expressed in cm, m and m^3/ha respectively. The MAI of stem volume/ha was calculated by dividing the total volume/ha by the age of trees, which was expressed in m^3/ha/year. The data on these observations were analyzed as per the procedure described for LSD and DMRT (Duncan Multiple Range Test).

Genetic Studies:

The phenotypic coefficient of variation (PCV) was calculated by dividing the square root of phenotypic variance by the population mean and multiplying by 100 (Burton, 1952).

$$\text{P.C.V.} = \frac{\sqrt{6^2 p}}{x} \times 100$$

Where, 6^2p = phenotypic variance, x = population mean of the particular character

The Genotypic coefficient of variation (GCV) was calculated by dividing the square root of genotypic variance by the population mean and multiplying by 100 (Burton, 1952).

$$\text{G.C.V.} = \frac{\sqrt{6^2 g}}{x} \times 100$$

Where, 6^2g = genotypic variance, x = population mean of a particular character.

Heritability in the broad sense (H^2) was estimated according to the formula suggested by Johnson et al., (1955).

$$h^2 = \frac{6^2 g}{6^2 p} \times 100$$

Where, 6^2g = genotypic variance, 6^2p = phenotypic variance
Genetic advance was estimated by the formula suggested by Johnson et al., (1955).

Genetic advance = K× бp×h^2

Where, h = heritability in broad sense, бp = Phenotypic standard deviation

K = Standardized selection differential expressed in terms of standard deviation units and its value varies with the intensity of selection. In the present study K = 2.06, which is the value at 5% selection intensity (Miller et al., 1958).

Results and Discussion

At CSOs, the DBH of Teak clones varied from 22.75 cm to 29.46 cm at the age of 30 years (Table-2). Among all, maximum DBH (29.46 cm) was observed for ORANP-17 whereas lowest DBH (22.75 cm) was found for ORAN-2. Clones like ORANP-16 also performed *at par* with ORANP-17 (28.42 cm). The clones which performed significantly superior at 30th years than other clones were ORANP-17 (29.46 cm), ORANP-16 (28.42 cm). Other superior clones which performed superior were ORANP-3 (27.61 cm), ORANR-6 (27.57 cm) and ORAN-1 (26.94 cm). At 31st year, nearly 8% increase in DBH was observed in many Teak clones and maximum DBH was recorded in case of ORANP-17 (31.02 cm), ORANP-16 (29.94 cm) and lowest in ORAN-2 (23.77 cm). There was the range of 7.25 cm in DBH of 31 years old Teak clones of Clonal Seed Orchards and five Teak clones which were top performed as regards to DBH production were ORANP-17, ORANR-3, ORANR-6, ORPUB-23 and ORAN-1. In Kerala, Palanisamy et al., (2009) reported about GBH (girth at breast height) of some selected Teak clones of aged 51–64 years in the range of 151–220 cm (48–70 cm DBH). Prachim et al., (1975) found significant difference for diameter at breast height and height for different Teak clones and found that diameter at breast height was strongly correlated with height. The comparison of growth of Teak clones with the empirical study findings indicates a similar growth trend though the location of the site differs. The relatively higher DBH growth in ORANP-17 may be due to better genetic character of the clone and the inferior performance of ORAN-2 may be due to poor genetic makeup of the clone. Provenance variation and tree to tree variation accounts for as much as 90% of the within species variation, leading to the fastest gains in most tree improvement program being obtained by selection from the best seed source within the appropriate species (Zobel and Talbert, 1984). Hence, provenance variation was also very less which was mainly due to location of provenances within a small geographical region (district). Similar observations were recorded for tree height which varied from 17.02 m to 21.16 m and 17.34 m to 21.90 m at 30 and 31 years of age, respectively (Table – 2). Both at 30 and 31 years, significant differences were observed in tree height of different Teak clones of Clonal Seed Orchards. Three top clones which gave maximum tree height were ORANP-17 (21.16 m), ORANP-16 (20.69 m) and ORANR-3 (20.12 m). At 31st year, tree height seems to be saturated and only 3 to 4% increase in tree height was noticed. At 31st year, top performing Teak clones were ORANP-17 (21.90 m), ORANP-16 (21.32 m) and ORANR-3 (20.74 m) and the range between top and least performing Teak clones was calculated as 4.56 m *i.e.* 21.90 m for ORANP-17 and 17.34 m for ORAN-2. So, in Clonal Seed Orchards, clones like ORANP-17, ORPUB-23, ORANP-16, ORANR-3 and ORANR-6 can be screened out as top performing clones. Similar height growth has been reported by Rao et al., (2001) in Andhra Pradesh and Palanisamy et al., (2009) in Kerala. The closeness in height growth among different clones may be attributed to less variation in their genetic characters. The data pertaining to stem volume/ha manifested significant difference among different clones of Teak at the age of 30 and 31 years. Both at 30th and 31st year, maximum volume of stem was recorded for ORANP-17 (100.62 m^3 and 118.10 m^3 respectively), which varied significantly with rest of the 24 Teak clones. Large differences were found between top and least performing Teak clones. Clone ORANP-17 gave nearly triple times volume of stem than ORAN-2. At 30th year, the range in volume of stem was calculated as 61.69 m^3, while at 31st tear, it was 72.79 m^3 *i.e.* 118.10 m^3 for ORAN-17 and 45.31 m^3 for ORAN-2. Large differences were observed in volume of stem between different Teak clones and there was nearly two and half-time difference between best and least performing Teak clones. Nearly 18% increase in volume of stem was observed between 30th and 31st year for most of the clones. Bhudimitra (1962) found basal area increment annually is 59.74 sq.cm. per year per tree in Teak. The range of stem volume production is in line with the report of Saxena et al., (1971) and Kharche (1974). The higher accumulation of stem volume in ORANP-17 may be ascribed for the presence of better genetic characters as well as more DBH and height growth.

Table 2
DBH, height and volume production of different Teak clones in CSO-1983

Treatments	Clone No.	DBH (cm)		Tree height (m)		Stem volume (m^3 /ha)	
		30-years old	31-years old	30-years old	31-years old	30-years old	31-years old
T_1	ORANP-8	25.64 ^{cd}	27.08 ^{cd}	18.62 ^{bc}	19.06 ^{bc}	61.09 ^{e}	72.29 ^{de}
T_2	ORANP-9	23.78 ^{de}	25.14 ^{cd}	17.38 ^{cd}	17.76 ^{cd}	45.51 ^{fg}	54.53 ^{ef}
T_3	ORANP-10	26.38 ^{bc}	27.81 ^{bc}	18.94 ^{bc}	19.40 ^{bc}	67.15 ^{de}	78.92 ^{de}
T_4	ORANP-12	26.34 ^{bc}	27.75 ^{bc}	18.92 ^{bc}	19.38 ^{bc}	66.80 ^{de}	78.40 ^{de}
T_5	ORANP-13	24.21 ^{de}	25.63 ^{cd}	18.16 ^{bc}	18.52 ^{c}	50.78 ^{fg}	60.60 ^{ef}
T_6	ORANP-14	26.79 ^{bc}	28.21 ^{bc}	19.18 ^{b}	19.70 ^{bc}	70.93 ^{de}	83.27 ^{cd}
T_7	ORANP-15	26.31 ^{bc}	27.72 ^{bc}	18.88 ^{bc}	19.34 ^{bc}	66.43 ^{de}	78.00 ^{de}
T_8	ORANP-16	28.42 ^{ab}	29.94 ^{ab}	20.69 ^{ab}	21.32 ^{ab}	89.94 ^{b}	105.44 ^{b}
T_9	ORANP-17	29.46 ^{a}	31.02 ^{a}	21.16 ^{a}	21.90 ^{a}	100.62 ^{a}	118.10 ^{a}
T_{10}	ORANP-18	26.25 ^{bc}	27.68 ^{bc}	19.02 ^{bc}	19.48 ^{bc}	66.67 ^{de}	78.41 ^{de}
T_{11}	ORANP-21	26.18 ^{c}	27.60 ^{bc}	18.68 ^{bc}	19.12 ^{bc}	64.72 ^{de}	76.09 ^{de}
T_{12}	ORPUB-15	23.62 ^{de}	24.87 ^{cd}	17.56 ^{c}	17.92 ^{cd}	45.31 ^{fg}	53.62 ^{ef}
T_{13}	ORPUB-17	26.61 ^{bc}	28.04 ^{bc}	19.14 ^{bc}	19.62 ^{bc}	69.56 ^{de}	81.65 ^{d}
T_{14}	ORPUB-19	23.03 ^{e}	24.21 ^{d}	17.12 ^{cd}	17.46 ^{cd}	40.68 ^{gh}	48.13 ^{f}
T_{15}	ORPUB-22	26.78 ^{bc}	28.02 ^{bc}	19.14 ^{bc}	19.56 ^{bc}	70.68 ^{de}	8a1.20 ^{de}
T_{16}	ORPUB-23	27.44 ^{bc}	28.89 ^{bc}	19.64 ^{ab}	20.18 ^{b}	77.53 ^{cd}	90.79 ^{cd}
T_{17}	ORPUB-24	26.22 ^{bc}	27.59 ^{bc}	18.98 ^{bc}	19.42 ^{bc}	65.30 ^{de}	77.47 ^{de}
T_{18}	ORPUB-26	26.23 ^{bc}	27.48 ^{c}	18.88 ^{bc}	19.32 ^{bc}	65.86 ^{de}	76.25 ^{de}
T_{19}	ORPUB-30	24.46 ^{d}	25.83 ^{cd}	17.96 ^{bc}	18.32 ^{cd}	51.43 ^{fg}	60.97 ^{e}
T_{20}	ORANR-2	23.70 ^{de}	24.85 ^{cd}	17.34 ^{cd}	17.70 ^{cd}	43.94 ^{g}	52.62 ^{ef}
T_{21}	ORANR-3	27.61 ^{b}	29.10 ^{b}	20.12 ^{ab}	20.74 ^{ab}	81.08 ^{c}	95.44 ^{bc}
T_{22}	ORANR-4	24.32 ^{de}	25.50 ^{cd}	18.32 ^{bc}	18.70 ^{bc}	52.01 ^{f}	60.56 ^{ef}
T_{23}	ORANR-6	27.57 ^{bc}	29.02 ^{bc}	19.72 ^{ab}	20.32 ^{ab}	78.83 ^{cd}	92.53 ^{c}
T_{24}	ORAN-1	26.94 ^{bc}	28.37 ^{bc}	19.04 ^{bc}	19.56 ^{bc}	71.27 ^{d}	83.69 ^{cd}
T_{25}	ORAN-2	22.75 ^{ef}	23.77 ^{d}	17.02 ^{d}	17.34 ^{d}	38.93 ^{h}	45.31 ^{g}
S.E. $_{(m)}$		**0.52**	**0.57**	**0.63**	**0.58**	**2.53**	**3.66**
C.D. $_{5\%}$		**1.43**	**1.61**	**1.72**	**1.65**	**7.24**	**10.45**
CV $_{(\%)}$		**24.03**	**25.51**	**18.08**	**17.86**	**27.01**	**28.36**

Significant difference was observed in CAI of volume of stem of different Teak clones between 30 and 31 years (Table 3). Maximum value of CAI of volume of stem was recorded for ORANP-17 (17.48 m^3) followed and *at par* with only one clone *i.e.* ORANP-16 (15.50 m^3). Nearly three times difference was noticed between top and least performed clones. Many of the Teak clones gave moderate value of CAI of stem volume. The range of stem volume production is in line with the report of Saxena et al., (1971) and Kharche (1974). Chen et al., (1983) reported that dry matter production largely depends on leaf area index development.

Significant difference was observed in CAI of volume of stem of different Teak clones between 30 and 31 years. Maximum value of CAI of volume of stem was recorded for ORANP-17 (17.48 m^3) followed and *at par* with only one clone *i.e.* ORANP-16 (15.50 m^3). Nearly three times difference was noticed between top and least performed clones. Many of the Teak clones gave moderate value of CAI of stem volume. Both at 30th and 31st year, significant differences were observed in MAI of stem volume of different Teak clones. At 30th year, maximum MAI of stem volume was recorded for ORANP-17 (3.35 m^3), followed and *at par* with ORANP-16 (3.00 m^3). At 31th year, maximum MAI of stem volume was recorded for ORANP-17 (3.81 m^3), followed and *at par* with ORANP-16 (3.40 m^3). The range of MAI of stem volume at 30th year was 2.05 m^3, while at 31st year, it was 2.33 m^3 *i.e.* maximum 3.81 m^3 for ORANP-17 and minimum 1.46 m^3. Percentage increase in MAI of stem volume between both the years was varied between 13 to 14%. Similar CAI in volume has been reported by Rao (1973) in Andhra Pradesh, Indira and Bhat (1997) in Dadra and Nagar Haveli, India. The quantity of stem volume is in line with the volume reported by Rao (1973) in Kerala, Indira and Mohanadas (2002) in Kerala, India. Murugesh et al., (1997) recorded the volume at 20-year Teak tree as 7.00 ft^3/tree.

Table 3
Annual growth increments in different clones of Teak

Treatments	Clone No.	CAI $_{30-31yrs}$ of DBH (cm)	CAI $_{30-31yrs}$ of Height(cm)	CAI $_{30-31yrs}$ of stem volume (m^3)	MAI volume of stem (m^3) (30 years)	MAI volume of stem (m^3) (31 years)
T_1	ORANP-8	1.44 ^{ab}	0.44 ^{cd}	11.20 ^{bc}	2.04 ^{cd}	2.33 ^{cd}
T_2	ORANP-9	1.36 ^{ab}	0.38 ^{cd}	9.02 ^{e}	1.52 ^{dc}	1.76 ^{de}
T_3	ORANP-10	1.42 ^{ab}	0.46 ^{cd}	11.77 ^{bc}	2.24 ^{c}	2.55 ^{cd}
T_4	ORANP-12	1.40 ^{ab}	0.46 ^{cd}	11.60 ^{bc}	2.23 ^{cd}	2.53 ^{cd}
T_5	ORANP-13	1.41 ^{ab}	0.36 ^{d}	9.82 ^{cd}	1.69 ^{de}	1.95 ^{de}
T_6	ORANP-14	1.43 ^{ab}	0.52 ^{bc}	12.34 ^{bc}	2.36 ^{bc}	2.69 ^{bc}
T_7	ORANP-15	1.41 ^{ab}	0.46 ^{cd}	11.58 ^{c}	2.21 ^{cd}	2.52 ^{cd}
T_8	ORANP-16	1.52 ^{ab}	0.64 ^{ab}	15.50 ^{ab}	3.00 ^{ab}	3.40 ^{ab}
T_9	ORANP-17	1.56 ^{a}	0.74 ^{a}	17.48 ^{a}	3.35 ^{a}	3.81 ^{a}
T_{10}	ORANP-18	1.42 ^{ab}	0.46 ^{cd}	11.74 ^{bc}	2.22 ^{cd}	2.53 ^{cd}
T_{11}	ORANP-21	1.42 ^{ab}	0.44 ^{cd}	11.37 ^{cd}	2.16 ^{cd}	2.45 ^{cd}
T_{12}	ORPUB-15	1.25 ^{bc}	0.36 ^{d}	8.31 ^{cd}	1.51 ^{de}	1.73 ^{de}
T_{13}	ORPUB-17	1.42 ^{ab}	0.48 ^{c}	12.09 ^{bc}	2.32 ^{bc}	2.63 ^{c}
T_{14}	ORPUB-19	1.18 ^{bc}	0.34 ^{de}	7.45 ^{ef}	1.36 ^{de}	1.55 ^{de}
T_{15}	ORPUB-22	1.23 ^{bc}	0.42 ^{cd}	10.52 ^{cd}	2.36 ^{bc}	2.62 ^{cd}
T_{16}	ORPUB-23	1.45 ^{ab}	0.54 ^{bc}	13.26 ^{bc}	2.58 ^{bc}	2.93 ^{bc}
T_{17}	ORPUB-24	1.37 ^{ab}	0.44 ^{cd}	11.19 ^{cd}	2.21 ^{cd}	2.50 ^{cd}
T_{18}	ORPUB-26	1.26 ^{b}	0.44 ^{cd}	10.39 ^{cd}	2.20 ^{cd}	2.46 ^{cd}
T_{19}	ORPUB-30	1.38 ^{ab}	0.36 ^{d}	9.54 ^{cd}	1.71 ^{de}	1.97 ^{d}
T_{20}	ORANR-2	1.15 ^{bc}	0.36 ^{d}	7.68 ^{ef}	1.50 ^{de}	1.70 ^{de}
T_{21}	ORANR-3	1.49 ^{ab}	0.62 ^{b}	13.36 ^{bc}	2.70 ^{b}	3.08 ^{b}
T_{22}	ORANR-4	1.17 ^{bc}	0.38 ^{cd}	8.55 ^{ef}	1.74 ^{d}	1.95 ^{de}

Treatments	Clone No.	CAI $_{30-31yrs}$ of DBH (cm)	CAI $_{30-31yrs}$ of Height(cm)	CAI $_{30-31yrs}$ of stem volume (m^3)	MAI volume of stem (m^3) (30 years)	MAI volume of stem (m^3) (31 years)
T_{23}	ORANR-6	1.44 ^{ab}	0.60 ^{bc}	13.70 ^{b}	2.63 ^{bc}	2.98 ^{bc}
T_{24}	ORAN-1	1.43 ^{ab}	0.52 ^{bc}	12.42 ^{bc}	2.38 ^{bc}	2.70 ^{bc}
T_{25}	ORAN-2	1.02 ^{c}	0.32 ^{e}	6.38 ^{f}	1.30 ^{e}	1.46 ^{e}
S.E. $_{(m)}$		**0.08**	**0.04**	**0.74**	**0.04**	**0.14**
C.D. $_{5\%}$		**0.21**	**0.12**	**2.11**	**0.12**	**0.41**
CV $_{(\%)}$		**34.21**	**27.21**	**31.80**	**27.21**	**31.79**

Table 4 represents components of genetic variability of growth characters of Teak clones in Clonal Seed Orchards – 1983. Growth characters like tree height, CAI in DBH, MAI in DBH, CAI in height, CAI in height, CAI of stem volume, MAI of stem volume and leaf area showed higher value of phenotypic coefficient of variation than genotypic coefficient of variation, which showed that these characters were more influenced by external factors rather than internal factors. However, in case of DBH, higher value of genotypic coefficient of variation (6.73) was noticed than phenotypic coefficient of variation (6.67), which showed that DBH of Teak clones are more influenced by genetic characters. Higher impact of environmental character was noticed on the traits like CAI in DBH, CAI in height, CAI of stem volume and MAI of stem volume. Growth character like tree height showed highest heritability (99.27%), followed by DBH (98.81%). Parameters like CAI and MAI in stem volume also showed higher value of heritability (more than 90%). However minimum heritability was observed for CAI in DBH (21.68%).

Highest value of genetic advance was observed for MAI of stem volume (47.84 and 61.31% at 5% and 1% respectively), which was followed by volume of stem, CAI of stem volume and CAI in height. Parameters like DBH, tree height, and CAI in DBH showed minimum genetic advance which varied between 4.42 to 13.79% at 5% level. So, it can be inferred that appropriate improvement is possible in MAI as well as CAI in stem volume of different Teak clones by providing adequate silvicultural and cultural practices, however little improvement can be achieved in tree height and DBH of Teak clones.

Table 4
Components of genetic variability of growth characters of *Tectona grandis* in Clonal Seed Orchards – 1983

Parameters	Variance			PCV	GCV	ECV	Heritability (%)	GA% of means (at 5%)	GA% of means (at 1%)
	Phenotypic	Genotypic	Environment						
DBH	3.61	3.57	0.04	6.67	6.73	1.28	98.81	13.79	17.67
Tree height	1.29	1.28	0.009	5.71	5.69	0.084	99.27	11.68	14.97
CAI in DBH	0.01	0.003	0.01	9.91	4.61	15.19	21.68	4.42	5.67
CAI in Height	0.01	0.009	0.001	21.72	20.42	12.83	88.36	39.54	50.67
Volume of stem	300.97	289.29	11.67	23.08	22.63	7.87	96.12	45.71	58.59
CAI of stem volume	7.07	6.47	0.60	23.60	22.57	11.93	91.48	44.47	57.00
MAI of stem volume	0.35	0.33	0.02	24.88	24.04	11.14	93.32	47.84	61.31

Average intra and inter-cluster D^2 values among Teak clones of Clonal Seed Orchards 1983 - High inter and intra-cluster divergence was observed in Teak clones of Clonal Seed Orchards, which indicate high divergence among the different clones (Table 5). Maximum intra cluster divergence was noticed for cluster II (13.21), followed by I (11.48), cluster III (7.50) and cluster VI (7.22). No intra cluster divergence was noticed for cluster IV, cluster V, cluster VII and cluster VIII because in these four clusters, only one Teak clones was recorded.

Maximum inter-cluster divergence was noticed between cluster II and VIII (72.83), followed by cluster II and VII (72.86) and cluster VI and VIII (72.83). It indicates that parents may be selected from this cluster for further improvement through hybridization program. In the analysis of genetic diversity of Shisham, Gera (2000) found highest inter cluster distance between cluster IX and III (48.43) followed by cluster IX and IV (46.09). The lowest inter cluster distance was observed between cluster IX and VIII (23.85). Higher value of inter-cluster divergence was also recorded between cluster VI and VII (65.98), cluster II and V (59.02), cluster II and IV (54.00) and cluster V and VI (53.60). Lowest inter-cluster divergence was recorded for cluster V and VII (14.74), followed by cluster VII and VIII (17.24) and cluster I and IV (17.61). Moderate inter-cluster divergence was noticed between rest of the cluster combinations.

The intra cluster distance ranged from 0.00 to 20.37. It may be inferred from the data of inter-cluster divergence, that clones like ORANP-13, ORANR-4, ORANP-16, ORANP-17 may be selected as male parent, because they are distinct from rest of the clones. Teak clones like ORANP-9, ORPUB-15, ORANR-2, ORPUB-19, ORPUB-30 and ORAN-2 may be selected as female parents for crop improvement of Teak through hybridization program. Singh and Choudhary (1985) also suggested that choice of a particular cluster from which a clone is to be selected as parent, selection of clones from a particular cluster and relative contribution of characters to the total divergence.

Table 5
Average intra and inter-cluster divergence among *Tectona grandis* of Clonal Seed Orchards

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**11.48**	40.52	30.29	17.61	22.33	43.18	35.34	49.59
II		**13.21**	43.48	54.00	59.02	32.80	72.86	85.30
III			**7.50**	30.89	33.49	23.55	44.41	50.33
IV				**0.00**	5.58	49.95	19.86	33.99
V					**0.00**	53.60	14.74	28.92
VI						**7.22**	65.98	72.83
VII							**0.00**	17.24
VIII								**0.00**

Clustering pattern of Tectona grandis of Clonal Seed Orchards 1983 based on genetic divergence among growth parameters - Clustering pattern of Teak clones based upon genetic divergence among growth parameters indicated that maximum number of 10 germplasm (ORANP-21, ORPUB-26, ORANP-8, ORPUB-24, ORANP-12, ORPUB-17, ORPUB-22, ORANP-14, ORAN-1 and ORPUB-23) came in cluster I (Table 6). Cluster II consists of 6 clones (ORANP-9, ORPUB-15, ORANR-2, ORPUB-19, ORPUB-30, ORAN-2). Cluster III consists of 3 Teak clones namely ORANP-15, ORANP-18 and ORANP-10. Cluster VI consists of 2 Teak clones namely ORANP-13 and ORANR-4. Cluster IV, V, VII and VIII consists of one Teak clones only namely ORANR-6, ORANR-3 ORANP-16 and ORANP-17 respectively. Cluster VIII consist of most superior close of Teak, because it gave maximum value for all the growth parameters.

From the data of clustering pattern, it can be inferred that the cluster IV, V, VII and VIII are totally distinct of each other. So, the Teak clones ORANR-6, ORANR-3, ORANP-16 and ORANP-17 should be used for crop improvement program.

Table 6
Clustering pattern of *Tectona grandis* of Clonal Seed Orchard based on genetic divergence among growth parameters

Sl. No.	Clusters	No. of genotypes	Genotypes
1.	I	10	ORANP-21, ORPUB-26, ORANP-8, ORPUB-24, ORANP-12, ORPUB-17, ORPUB-22, ORANP-14, ORAN-1, ORPUB-23
2.	II	6	ORANP-9, ORPUB-15, ORANR-2, ORPUB-19, ORPUB-30, ORAN-2
3.	III	3	ORANP-15, ORANP-18, ORANP-10
4.	IV	1	ORANR-6
5.	V	1	ORANR-3
6.	VI	2	ORANP-13, ORANR-4
7.	VII	1	ORANP-16
8.	VIII	1	ORANP-17

Clustering pattern (Fig-1) also indicated large diversity among Teak clones of Clonal Seed Orchards based upon variability among growth characters. Large diversity is indicated by presence of clusters and out of 8 clusters, cluster IV, V, VII and VIII consist of one member only and each of them are quite distinct from each other. This graph is useful to select the parents for crop improvement activities through hybridization program based upon genetic distances of different clusters formed. Fofana et al., (2009) studied the genetic variability and structures of 166 Teak trees distributed over its natural area and inferred that two clusters of India could be considered as main centers of genetic diversity. Inza et al., (2009) analyzed genetic diversity of Teak and found four main centers of variability, two clusters in India were the main centers, while third cluster of Thailand and Laos and fourth one was from Central Laos. Godwin et al., (2010) found five clusters by cluster analysis with similarity ranging from 54–96% in *Moringa oleifera*. Seethalakshmi et al., (2011) through cluster analysis of RAPD data found five distinct clusters in different Teak clones of Kerala.

Sources and contribution of different characters towards genetic divergence in different Teak clones of Clonal Seed Orchards 1983 – Out of the 12 growth parameters, which crated divergence in Teak clones of Clonal Seed Orchards, maximum percentage contribution was noticed by tree height (67.67%) followed by length of straight stem (29.33%). Rest of the traits showed minimum contribution towards divergence in Teak clones. CAI in height (0.67%), volume of stem (0.33%) and MAI of stem volume (0.67%) contributed very little part in divergence of Teak clones of Clonal Seed Orchards. No contribution towards genetic divergence was observed by parameters like DBH, CAI in DBH and CAI of stem volume.

Table 7
Components of genetic divergence of growth parameters in *Tectona grandis* of Clonal Seed Orchard with their percentage contribution

Sl. No.	Growth parameters	Percentage contribution
1.	DBH	0.00
2.	Tree height	67.67
3.	Length of clear bole	1.00
4.	Length of straight stem	29.33
5.	CAI in DBH	0.00
6.	MAI in DBH	0.00
7.	CAI in Height	0.67
8.	MAI in Height	0.00
9.	Volume of stem	0.33
10.	CAI of stem volume	0.00
11.	MAI of stem volume	0.67
12.	Leaf area	0.33

Mean performance of clusters for growth parameters in Tectona grandis of Clonal Seed Orchards 1983 - Cluster mean of DBH was recorded maximum for cluster VIII (32.09 cm) followed by cluster VII (31.03 cm), while its minimum value was recorded for cluster II (25.49 cm) (Table 8). In case of tree height, maximum value was recorded for again cluster VIII (22.50 m), followed by cluster VII (21.92 m) and least in cluster II (18.43 m). Maximum value of length of clear bole was recorded for cluster VIII (9.64 m), followed by cluster III (9.39 m) and minimum in cluster II (7.70 m), length of straight stem was recorded maximum for cluster VIII (12.13m), followed by cluster VII (12.01m) and least in cluster II (9.66m). CAI in DBH was recorded maximum for cluster IV (1.53 cm), followed by cluster V and VII both (1.50cm) and minimum in cluster II (1.21cm). In cluster analysis of Shisham, Gera (2000) mentioned that cluster I consisting of seven provenances followed by cluster II with five provenances and cluster III with two provenances.

Maximum value of MAI in DBH was recorded for cluster VIII (0.97 cm), followed by cluster VII (0.90 cm) and minimum in cluster II (0.68 cm). CAI in height was recorded maximum for cluster VIII (0.70 m), followed by three clusters namely cluster VII, V and IV (0.67 m) and minimum for cluster II (0.37 m). Maximum value of MAI in height was recorded for cluster VIII (0.67 m) followed by two clusters namely cluster VII and IV (0.60 m) and least for cluster II (0.47 m). Volume of stem was recorded maximum for cluster VIII (119.13 m^3) followed by cluster VII (100.53 m^3) and minimum for cluster II (53.09 m^3). Maximum value of CAI of stem volume was recorded for cluster VIII (18.43 m^3) followed by cluster VII (15.20 m^3) and minimum for cluster II (8.34 m^3). In case of MAI of stem volume, its maximum value was recorded for cluster VIII (3.83 m^3) followed by cluster VII (3.63 m^3) and minimum for cluster II (1.67 m^3). Maximum value of leaf area was recorded for cluster VIII (517.71cm^2) followed by cluster, cluster IV (491.00 cm^2) and minimum for cluster II (259.94 cm^2).

Table 8

Mean performance of clusters for growth parameters in *Tectona grandis* of Clonal Seed Orchard

Clusters	Cluster Means											
	DBH (cm)	Tree height (m)	Length of clear bole (m)	Length of straight stem (m)	CAI DBH (cm)	MAI DBH (cm)	CAI Height (m)	MAI Height (m)	Vol. of stem (m^3)	CAI of stem volume (m^3)	MAI of stem volume (m^3)	Leaf area (cm^2)
I	28.74	20.17	8.10	10.36	1.33	0.79	0.49	0.53	79.63	11.76	2.57	434.37
II	25.49	18.43	7.70	9.66	1.21	0.68	0.37	0.47	53.09	8.34	1.67	259.94
III	28.78	20.04	9.39	10.93	1.38	0.81	0.47	0.54	79.03	11.78	2.47	425.56
IV	29.53	21.05	8.56	10.88	1.53	0.80	0.67	0.60	85.77	14.27	2.77	491.00
V	29.61	21.47	8.74	11.01	1.50	0.83	0.67	0.57	91.77	13.43	2.83	478.67
VI	26.37	19.28	9.29	10.64	1.33	0.70	0.43	0.50	61.65	8.68	2.02	319.33
VII	31.01	21.92	8.88	12.01	1.50	0.90	0.67	0.60	106.53	15.20	3.63	472.33
VIII	32.09	22.50	9.64	12.13	1.43	0.97	0.70	0.67	119.13	18.43	3.83	517.71

It can be manifested that cluster VIII consists of most superior close of Teak (ORANP-17), because it gave maximum value for almost all the growth parameters. Next to cluster VIII, best performing cluster is VII (ORANP-16). So, for selection of superior clones of Teak, ORANP-17 and ORANP-16 should be preferred for crop improvement practices.

Conclusion

In the present investigation, large diversity was found in Teak, which provides ample scope for selecting its superior clones for further improvement. While selecting the clones for vegetative propagation, it is quite imperative to ensure that the genotypes chosen are superior for the desired traits and also selected from a genetically diverse population. Considering the importance of identification and deployment of suitable clones for increased wood production, this particular study recommends the vegetative multiplication of tested clone ORANP-17 which manifested highest stem volume of 118.10m^3/ha and MAI of 2.63m^3/ha at the age of 31 years for *ex-situ* mass planting in many current reforestation programs. Further, the genetic analysis also leads to clear understanding of different quantitative traits and their extent of contributions to wood yield. Among all, highest heritability was shown by tree height (99.27%) and DBH (98.81%), however maximum genetic advance was observed for MAI of stem volume, indicating that these plant traits shall be considered for further selection and improvement program on Teak and other tropical hardwood species. The genetic analysis would also help us in understanding, conserving and harnessing the genetic biodiversity of Teak across the world.

Declarations

Author Contribution

Hiranmayee Nayak - Conducted the research Animesh Sinha - Data analysis and verificationNirankar Bhol - Data analysisJai Kumar - Data analysis and wrote the main manuscript

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Figures

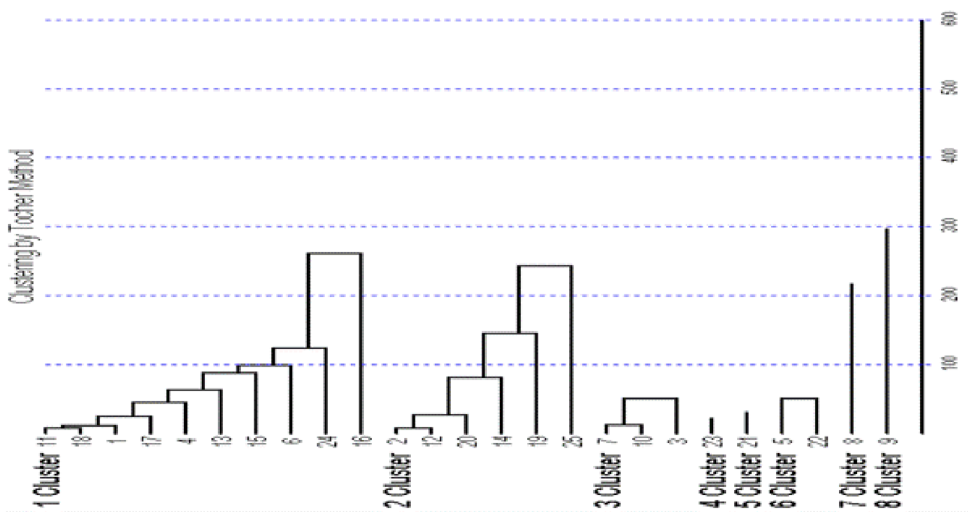

Figure 1

Clustering pattern of Tectona grandis of Clonal Seed Orchard based on genetic divergence among growth parameters