

ESTIMATES OF GENETIC PARAMETERS FROM AN OPEN POLLINATED GENETIC TEST OF TEAK (*TECTONA GRANDIS*)

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SHARMA, R., SWAIN, D. & MANDAL, A. K. 2000. Estimates of genetic parameters from an open pollinated genetic test of teak (*Tectona grandis*). Genetic parameters were estimated from a 7-y-old open pollinated progeny test of teak. The results indicated presence of significant amount of genetic variation in the materials studied. Height, diameter and basal area were found to be under the control of additive gene action as evidenced by their moderately high values of individual tree heritability. The genetic gain values followed a similar trend. Basal area and diameter exhibited positive significant genetic correlation. Clones ORANP-1 and ORANP-5 were found to be the best general combiners for height, diameter and basal area.

Key word: Open pollination - heritability - genetic advance - additive variance

SHARMA, R., SWAIN, D. & MANDAL, A. K. 2000. Anggaran parameter genetik daripada ujian pendebungaan bebas ke atas pokok jati (*Tectona grandis*). Parameter genetik dianggarkan daripada ujian progeni pendebungaan bebas bagi pokok jati yang berumur tujuh tahun. Keputusan menunjukkan wujudnya amaun perubahan genetik yang bererti dalam bahan-bahan yang dikaji. Ketinggian, garis pusat dan luas pangkal didapati di bawah kawalan tindakan gen penambah seperti yang dibuktikan daripada nilai tinggi yang berpatutan bagi keterwarisan pokok individu. Nilai genetik yang dicapai juga mengikut trend yang serupa. Luas pangkal dan garis pusat mempamerkan korelasi genetik yang positif dan bererti. Klon ORANP-1 dan ORANP-5 didapati merupakan penggabung umum yang terbaik bagi ketinggian, garis pusat dan luas pangkal.

Introduction

The increasing pressure of human populations over the years has resulted in decreased wood productivity of forests. This trend will continue if measures to

check population explosion are not enforced strictly. Since it is difficult to increase the area of forest land, efforts need to be concentrated on the existing forest stands to bridge the widening gap between demand and supply of forest products, especially timber. It is increasingly felt that increase in per hectare yield of wood will not be possible unless genetically superior seeds are available for regular plantation programmes.

Attempts are constantly being made to select phenotypically superior trees ("plus trees"), test their genetic merit, make grafts from these and establish seed orchards. Of these, progeny tests help identify the best performers (superior genotypes). Assembling such genotypes in seed orchards and their subsequent cross fertilisation to produce superior seeds in large quantities further helps in raising forest plantations with increased yield.

Teak (*Tectona grandis*), an important timber tree of India, has been used for decades in plantation establishment either as an indigenous or exotic species. It is used for many purposes, but the most important end use is timber and other high value products. Phenotypic variation observed in teak in India is related to variation in geographical conditions which affect the expression of a trait. However, it is the genetic component of this variation that is made use of by the breeder in a breeding programme. As a result of environmental selection, the genetic systems exhibit variability at many levels: within individuals, among individuals within populations, among populations within localities and among populations from different geographic regions. Considering the magnitude of natural genetic diversity and commercial value of the species, genetic improvement via progeny trials to select parents for inclusion in breeding programmes is in progress at a number of locations in the country. One such progeny trial was laid out at Dhandatopa Research Station, Orissa, to study the magnitude of variation among open pollinated families and to identify parents with high general combining ability for use in breeding programmes. General combining ability (gca) of a parent signifies high average performance of its progenies in various crosses, as compared to progenies of other parents in the same test.

Materials and methods

Open pollinated seeds for the present study came from a clonal seed orchard established with 6 clones and 30 ramets of each clone. These clones were produced from plus trees selected from 6 different provenances of Orissa origin. Open pollinated seeds were collected in 1986 when all the clones and all the ramets of each clone flowered and fruited. Teak is primarily an outcrossing species and, therefore, the open pollinated families are the product of outcrossing. Identity of collected seed from the clonal orchard was maintained and seedlings were raised. These were then field planted at spacing of 2.5 × 2.5 m in a replicated experiment at Dhandatopa Research Station, Orissa, in 1987. The experimental progenies were field planted following a randomised complete block design with three replications and 36 trees per plot. Measurements on height (m) and diameter at breast height (cm) were taken on inner 16 trees each year starting one year after

field plantation. Measurements recorded in 1994 were subjected to statistical analysis following Zobel and Talbert (1984) and are presented in this paper. Genetic gain values were calculated at 10% selection intensity.

Results and discussion

Good estimates of genetic parameters form an important basis for formulating an efficient breeding plan. The present study centres around progeny test based on limited number of families grown from open pollinated seeds collected from a clonal seed orchard of teak. Analysis of variance indicated that families were a significant source of variation for height, diameter at breast height (dbh) and basal area (Table 1). As family alone accounted for more than 50% of the total variation for different characters, there exists scope for family-level selection. In family selection inferior families and/or inferior individuals within families are removed. Such selective removal of inferior families help in converting progeny test materials into a productive seedling seed orchard for immediate genetic gains. Non-significant family x replication variation suggests that the development of different characters included in the present study is not susceptible to local environmental variation at the field station. Though the present experiment was conducted in a single locality and, therefore, does not encompass levels of variation that will be encountered by widespread plantings, the results of studies reported by Swain *et al.* (1996), Nagrajan *et al.* (1996) and Gogate *et al.* (1997) using teak clones of central and south Indian origin support the present observation.

Table 1. Analysis of variance for growth characters

Source of variation	d.f.	Height		Diameter (dbh)		Basal area	
		MS	% variation	MS	% variation	MS	% variation
Replication	2	1.805	22.16	0.408	8.82	29.174	6.78
Family	5	4.340**	53.29	2.473**	53.46	252.046**	56.69
Fam. x Rep.	10	1.045	12.83	0.685	14.81	56.407	13.11
Tree within plot (error)	342	0.954	11.71	1.060	22.91	92.529	21.51

** Significant at 1% level.

Individual and family heritability values of seven years ranged 11–22 and 64–77% respectively (Table 2). Estimates of genetic advance (in percentage of the population mean) followed a similar trend. Similar results have earlier been reported by Swain *et al.* (1996) and Nagrajan *et al.* (1996). In addition to individual tree heritability, information on the magnitude of family heritability becomes important when selection is practised on families as well as on individuals (Zobel & Talbert 1984). While heritability values express the proportion of variation in the population that is attributable to genetic differences among individuals, genetic advance indicates average improvement in a progeny over the mean of the parents. Advance is realised by selection in the parental generation and the magnitude of genetic

advance depends on selection intensity, parental variation and heritability. In population improvement programme like this where many selected parents are mated together, only additive genetic variance can be utilised. Additive genetic variance arises due to additive effects of genes. Additivity is the basis for most quantitative inheritance theories and for most breeding efforts. Values of narrow sense heritability in the present study indicate the presence of moderate amount of additive genetic variance for height.

Table 2. Estimates of narrow sense heritability and expected genetic advance

Character	h^2 (%)	Genetic advance	Genetic advance in % of mean
Height	22 (77)	0.39 (0.36)	6.38 (6.30)
Diameter	11 (64)	0.20 (0.24)	3.42 (4.11)
Basal area	14 (69)	2.39 (2.64)	8.66 (9.57)

Figures in parentheses indicate values of heritability and genetic gain at family level.

The genetic correlation coefficients of height with diameter at breast height (dbh) and basal area were positive but non-significant, whereas, for dbh and basal area, the coefficient was positive and significant (Table 3). Such relationship of diameter with basal area suggests that selection for one trait should lead to strong positive indirect responses in the other, whereas non-significant correlation of height with diameter and basal area suggests low genetic gain upon selection.

Table 3. Genetic correlation coefficients among different characters

	Diameter	Basal area
Height	0.1629	0.1521
Basal area	0.9910**	

** Significant at 1% level.

Of the 6 clones, clone ORANP-1 and ORANP-5 were the best as evidenced by their positive gca values (Table 4). The local clone was the poorest among all having negative gca values for all the traits studied. As positive values of general combining ability of parents indicate constellation of additive genes, such parents are expected to throw out good segregants (Swain *et al.* 1999). It is suggested that these elite trees should be used along with other elite clones for establishing advanced generation seed orchards and breeding arboreta. Genetic thinning should also be carried out in the present clonal orchard based on the result obtained in this study. The slow growth rate of the species is a drawback in a tree improvement programme as the superior plus trees are selected at a mature

stage while their breeding values are assessed from progeny tests at a younger age. One must, therefore, rely on a good concordance between juvenile performance and the performance at harvesting age.

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

Clone	Height	Diameter	Basal area
ORANP-1	0.21	0.33	3.49
ORANP-2	0.08	- 0.18	- 1.76
ORANP-3	0.08	- 0.13	- 1.19
ORANP-4	0.03	- 0.01	- 0.26
ORANP-5	0.13	0.15	1.03
Local	- 0.53	- 0.17	- 1.06

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