J. Indian Soc. Coastal Agric. Res. 35(1): 56-63 (2017)

Genetic Variability of Growth Parameters among Different Progenies of *Santalum album* L.

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Received: 18.02.2017 Accepted: 05.05.2017

Sandal (*Santalum album* L.), occupies an important place in the ecological, cultural and spiritual heritage of India. *Santalum album* is an evergreen tree belonging to the family *Santalaceae.* Among 30 progenies evaluated the progeny FCRISA18 was found to be superior in respect of growth attributes and hence the progeny FCRISA18 could be exploited for further tree improvement programme. The variability study indicated that the volume of the progenies registered highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) followed by clear bole height, crown height, diameter at breast height (DBH), basal diameter and tree height. Hence, these parameters could be effectively used as selection criteria to increase tree volume in *Santalum album.* Maximum heritability was recorded in diameter at breast height (DBH) and low heritability was observed in number of branches however volume showed higher heritability. The trend of genetic advance as per cent of mean was maximum in volume followed by clear bole height, crown height and diameter at breast height (DBH) indicating a wide scope of genetic improvement in the species.

(***Keywords:*** *Santalum album, Sandal, GCV, PCV, Heritability, Genetic advance*)

Sandal is a commercially and culturally important plant species belonging to the family *Santalaceae*. Sandal is considered as one of the most valuable trees in the world. The sandal is known for its oil which is pronounced as the most famous East Indian sandal wood oil which is produced from the heartwood of sandal upon distillation. The sandal wood oil has been known in the perfume industries for several centuries. Besides perfume industry the sandal oil and powder obtained from sandal wood found multifarious utility in cultural and religious festivals coupled with the utility in wide range of medicinal use. Particularly in Asian countries such multifarious utility and the associated escalating demand in the global market are noticed in both in perfumery and other utility industries.

The demand for sandal is increasing but at the same time the supply from forests has almost been stopped resulting in wider gap between demand and supply. Due to this wider gap between the actual availability and the growing demand, the prices of sandal wood and the associated value added product have gone up steeply. This necessitated development of sandalwood plantation throughout agro and farm forestry but for want of suitable varieties and the associated management technology the achievement in sandal wood promotion is dismally modest.

Despite being a species endowed with an amplitude of utilities and commanding extensive areas, it has received little research attention in genetic improvement. A knowledge on magnitude, nature and type of variation is a pre-requisite for any tree improvement programme (Zobel and Talbert, 1984). The best gains can be made for characteristics that have a wide range of variation and are strongly under genetic control (Zobel, 1971, Lacase, 1978, Zobel and van Buijitenen, 1989). Since sandal extensively being planted for aromatic and essential oil is very costly to establish, it is essential that the most productive plant material be used. A detailed knowledge of genetic variation within a species is thus a pre-requisite to select seed sources for developing efficient tree breeding strategies. These selected clones need to be tested under field conditions for growth performance, productivity and adaptability to specific sites and agro-climatic conditions. In the selection programme, understanding of such important association between characters is necessary to make an effective profitable selection.

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MATERIALS AND METHODS

The present study was undertaken in order to investigate the progeny evaluation in *Santalum album* genetic resources.

Species under study

The experimental materials for this study consisted of 30 progenies of *Santalum album* selected from various locations of Tamil Nadu. The progeny evaluation experiments were carried out in the field of Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam in a place having longitude and latitude of 11°19′N and 76°56′E and an altitude of 320.0 above MSL with the average rainfall of 922.0 mm in a soil having neutral in reaction (pH 7.1) during 2012-2013.

The investigations were carried out in 32 month old progeny evaluation trial at Forest College and Research Institute, Mettupalayam during 2012 to 2013.

Mean performance of clones at field

A progeny evaluation trial has been laid and thirty different clones were planted in a randomized block design (RBD) replicated three times. The progeny were planted at the spacing of 3 x 3 m. The observations were recorded at 32 months after planting (MAP) as described below.

Table 1. *Details of Santalum album seed source genetic resources and locations*

Location	State	Clones	Latitude	Longitude	Altitude (ft)
Mettupalayam	TamilNadu	FCRISA1	11324743	76934691	1026
Thiruvanamalai		FCRISA2	12140153	79025092	845
Haasanur		FCRISA3	11403500	77073828	2899
Thirupattur		FCRISA4	12322604	78371668	1490
Mettur		FCRISA5	11554994	77404568	857
Coimbatore		FCRISA6	11010036	76565899	1436
Maruthamalai		FCRISA7	11021877	76520401	1719
Sathyamangalam		FCRISA8	11344831	76595707	1360
Amaravathi		FCRISA9	10264343	77143043	1392
Dindugal		FCRISA10	10081426	78015519	1486
Kurangani		FCRISA11	10044966	77150280	2426
Salem		FCRISA12	11403334	78093829	982
Kalakad		FCRISA13	08410840	77183558	807
Trichy		FCRISA14	10453373	78422041	299
Marayoor	Kerala	FCRISA15	10153571	77090617	3233
Nachivayal		FCRISA16	10142105	77083901	3115
Kanthaloor		FCRISA17	10160834	77110329	2538
Chinnar		FCRISA18	10195616	77130605	1551
Thrissur (KAU)		FCRISA19	10325135	76164277	119
Thrissur (KFRI)		FCRISA20	10314479	76210028	217
Shimoga	Karnataka	FCRISA21	13435981	75270631	2082
Bangalore		FCRISA22	13003880	77341431	3090
Mysore		FCRISA23	12163722	76400131	2975
Chikkamagaluru		FCRISA24	13182177	75434277	3789
Kudagu		FCRISA25	12202051	75482700	2986
Hassan		FCRISA26	12543986	75561948	3145
Sirsi		FCRISA27	14362701	74521261	1996
Chitoor	Andhra Pradesh	FCRISA28	13143161	79073003	947
Tirupathi		FCRISA29	13400446	79213950	2252
Hyderabad		FCRISA30	17350102	78414074	1745

Plant height

The plant height was measured from ground level to the tip of the stem and expressed in metres.

Diameter at breast height (DBH)

It is the diameter of the tree which is measured at the stem on 1.37 m (breast height) and expressed in centimetre.

Basal diameter

The basal diameter was measured at the base of the stem (near the ground level) and expressed in centimetre.

Number of branches

The number of branches was counted manually in number wise.

Clear bole height

The bole height was measured by the distance between the ground level and the crown point. It gives the height or length of the clear main stem of a tree and expressed in metres.

Crown height

The crown height was measured vertically from the tip to the point half way between the lowest green branches forming green crown all round and the lowest green branch on the bole and expressed in metres.

Volume

The volume was estimated using the formula prescribed by Chaturvedi and Khanna (1982) for standing trees.

$$\text{Volume} = (\pi r^2 h) \text{ X Form factor}$$

Estimation of genetic parameters

Variability studies

These parameters were estimated as per the method described by Johnson *et al.* (1955) and phenotypic (PCV) and genotypic (GCV) coefficients of variances were computed following Burton (1952).

Genotypic Variance: (GV) $(\sigma^2 g) = (\sigma^2 g - \sigma^2 e)/r$

Phenotypic Variance: (PV) $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Phenotypic Co-efficient of Variability (PCV)

$$\text{PCV (\%)} = \frac{(\text{Phenotypic Variance})^{1/2}}{\text{General mean}} \text{ x 100}$$

Genotypic Co-efficient of Variability (GCV)

$$\text{GCV (\%)} = \frac{(\text{Genotypic Variance})^{1/2}}{\text{General mean}} \text{ x 100}$$

Heritability (h^2)

Broad sense heritability (h^2) was calculated by the following formula

$$h^2 = \sigma^2 g / \sigma^2 p$$

$$\text{Heritability percentage} = h^2 \text{ x 100}$$

Genetic advance

Genetic advance was worked out after Johnson *et al.* (1955).

Genetic advance (GA) = [(Genotypic variance / Phenotypic variance) $^{1/2}$] x K

Where, K = 2.06, a selection differential at 5 per cent selection intensity.

Genetic advance as percentage of mean

GA as percentage of mean = GA/Grand mean x 100

The biometrical traits for describing the genetic parameters, the values recorded in the study were classified and presented. The genetic estimates for biometric attributes were classified as detailed below.

Table 2. *Classification of genetic estimates for biometric attributes*

Genetic parameter	Low	Moderate	High
GCV and PCV	<20	20-30	>30
Heritability	<30	30-60	>60
GA as % of mean	<30	30-60	>60

RESULTS AND DISCUSSIONS

In genetic improvement programme of trees, the selection of superior genotype is very important as it forms the very basis for any tree improvement. The success of any tree improvement programme depends on the amount of genetic variability in a tree species and it has got significant importance for developing effective tree improvement strategies (Vakshasya *et al.,* 1992). The largest, cheapest and fastest gains in most forestry tree improvement programme will accrue if use of suitable species and seed sources or clonal evolution within species is assured (Zobel and Talbert, 1984). Against this back drop the current study has been designed to examine and evaluate the progenies of *Santalum album* in order to identify the superior progeny for higher productivity for its suitability in various sandal wood based industries and pharmaceutical industries.

Mean performance of clones at field

The progeny evaluation trial conducted in the field showed significant differences among 30 progenies of *Santalum album* for the growth characteristics *viz.,* tree height, diameter at breast height (DBH), basal diameter, number of branches, clear bole height, crown height and volume at 32 month after planting (MAP). Considering all the 30 progenies, FCRISA18 showed consistently superior performance in all growth attributes *viz.,*tree height (9.16 m), diameter at breast height (DBH) (8.90 cm), number of branches (12.33), basal diameter (10.17 cm), clear bole height (3.00 m), crown height (6.00 m) and Volume (0.0342 m^3) (Table 3) at 32 MAP investigated, based on volume of the progenies. Current result was supported by numerous workers who also reported the existence of significant differences and superiority of few seed sources, progenies and provenances in various trees like *Azadirachta indica* (Syed *et al.,* 2013) *Populus deltoides* (Jha, 2012), *Pongamia pinnata* (Divakara and Rameshwar Das, 2011), *Gmelina arborea* (Kumar, 2005) *Jatropha curcas* (Ginwal *et al.,* 2004)*, Populus deltoides (Singh et al.,* 2001) and *Dalbergia sissoo* (Tewari, 1994). Genetic selection of rapid juvenile growth rate was also advocated as a means of improving competitive ability of forest trees (Gall and Taft, 1973; Steiner, 1986) which extend the scope of selection of a progeny under evaluation.

Table 3. *Progeny variations of biometric traits for Santalum albumat 32 MAP*

Clone details / Treatments	Tree height (m)	DBH (cm)	No. of Branches	Volume (m^3)	Basal diameter (cm)	Clear bole height (m)	Crown height (m)
FCRISA1	7.33	5.75	14.67	0.0115	7.13	1.20	7.20
FCRISA2	7.02	6.62	11.47	0.0148	7.71	1.88	6.00
FCRISA3	8.17	7.20	12.00	0.0201	7.77	2.05	5.61
FCRISA4	7.59	6.53	13.00	0.0146	8.12	1.71	5.82
FCRISA5	7.76	6.44	12.07	0.0153	7.24	1.89	4.50
FCRISA6	7.68	6.37	12.00	0.0148	7.53	1.82	5.75
FCRISA7	8.53	7.70	12.50	0.0240	8.50	2.30	6.40
FCRISA8	6.68	6.76	11.33	0.0144	7.82	1.97	5.18
FCRISA9	7.25	6.29	11.67	0.0137	7.64	2.07*	5.60
FCRISA10	7.15	6.89	12.87	0.0160	8.04	1.61	4.80
FCRISA11	7.48	7.40	14.87	0.0188	6.91	1.37	7.10
FCRISA12	7.53	7.44	12.73	0.0199	8.00*	1.81	4.50
FCRISA13	8.32	7.53	12.53	0.0223*	8.10	2.11*	6.00
FCRISA14	7.29	6.27	12.87	0.0137	7.40	1.90	5.80
FCRISA15	7.37	6.55	12.50	0.0150	6.60	1.17	6.01*
FCRISA16	8.02	7.00	11.20	0.0185	7.33	1.99	6.03*
FCRISA17	7.85	6.91	12.00	0.0164	6.58	1.85	5.99
FCRISA18	9.16	8.90	12.33	0.0342*	10.17	3.00	6.00
FCRISA19	7.75	7.76	12.38	0.0205	7.74	1.70	5.70
FCRISA20	6.11	6.77	13.00	0.0120	8.13	2.08*	4.40
FCRISA21	7.60	6.85	11.33	0.0156	7.66	1.89	5.99
FCRISA22	7.85	7.63	11.33	0.0147	7.91	1.92	5.84
FCRISA23	7.45	6.45	12.00	0.0165	7.56	1.78	5.12
FCRISA24	6.35	5.89	11.33	0.0186	6.41	1.96	5.63
FCRISA25	6.21	7.63	10.33	0.0189	6.32	1.84	5.47
FCRISA26	7.95	6.89	10.00	0.0147	8.01	1.68	5.94
FCRISA27	7.96	7.22	11.33	0.0163	7.99	1.89	5.99
FCRISA28	8.05	6.55	10.67	0.0185	8.09	1.98	5.99
FCRISA29	8.44	6.84	11.00	0.0200	8.51	1.46	5.48
FCRISA30	8.74	7.52	10.67	0.0206	8.81	2.07	5.76
MEAN	7.62	6.95	12.00	0.0175	7.72	1.87	5.72
SEd$\pm$	0.1313	0.0570	0.8857	0.0026	0.1188	0.1041	0.1443
CD (p= 0.05)	0.2658	0.1155	1.7931	0.0053	0.2406	0.2018	0.2902

*Significant at 5 per cent level

Variability parameters

Success of any tree improvement program depends on the variability present in the material. *Santalum album* can be considered a more exploitable tree crop and therefore, to start the improvement work in this tree crop, the assessment of genetic variability of the progenies material under study becomes imperative. Significant differences that existed among different progenies could be evidenced due to the considerable range of variability with respect to almost all the characters under study. The maximum range of variation was obtained for volume (PCV - 27.67% and GCV - 33.18%) followed by clear bole height (21.84%) and crown height (13.50%). However, low variation was observed in number of branches (PCV - 5.64%) (Table 4).

The coefficient of variations being independent of the scale of the unit of measurement, for different mean values, etc., can be conveniently used for comparison between different populations. In the present study, volume recorded highest phenotypic coefficient of variation (27.67%) and genotypic coefficient (33.18%) of variation. Biometric characters *viz*., tree height, diameter at breast height (DBH), basal diameter, number of branches, clear bole height and crown height exhibited low to intermediate genotypic and phenotypic coefficient of variation (Table 4). Current findings are similar to studies in teak which showed higher genotypic coefficient of variation (GCV) for volume index (Prasad, 1996), number of branches in *Eucalyptus tereticornis* and low genotypic coefficient of variation (GCV) for height (Surendran and Chandrasekeran, 1984; Paramathma, 1992). Similarly low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for height and collar diameter in *Bambusa pallida* (Singh and Beniwal, 1993), low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for plant height and basal diameter in *Melia dubia* (Kumar *et al.,* 2013), *Populus deltoides* (Singh *et al.,* 2001), *Tectona grandis* (Gera *et al.,* 2001) and in *Salix eriocephala* (Lin and Zsuffa, 1993) were observed.

Genotypic coefficient of variation gives an idea of the quantum of genetic variability in a character and provides a mean to compare the genetic variability in the different quantitative characters and it is not possible to estimate heritable variation alone. The genotypic coefficient of variation for tree height, diameter at breast height (DBH), basal diameter, number of branches, bole height, crown height and volume recorded in the current study provided evidences for existence of adequate genotypic variations and thus lend support for exploitation of genetic variability for further improvement in this species (Table. 4). In general, for all the traits, genotypic coefficients of variations were at a higher side than their respective phenotypic coefficient of variations for almost all the traits thus indicating the less environmental effect and true representation of the genotype by the phenotype as evidenced in Poplars (Lone and Tewari, 2008), *Melia dubia* (Kumar *et al.,* 2013), *Madhuca latifolia* (Kanna, 2001), *Ceiba pentandra* (Rajendran, 2001), seed sources of *Jatropha curcas* (Rao *et al.,* 2008; Das *et al*., 2010) and *Pongamia pinnata* (Harini, 2007).

Heritability and genetic advance

Heritability has an important place in tree improvement programme as it provides an index of relative strength of heredity versus environment. Heritability is very important in tree improvement programme (Dorman, 1976). It is also useful for ranking importance of each trait in cross breeding programme. Heritability expresses the degree to which a character is influenced by heredity as compared to the environment. (Kumar *et al.,* 2010).

Table 4. *Genetic estimates of growth attributes of Santalum album clones*

Traits	PCV	GCV	Heritability	Genetic Advance (%)
Tree height (m)	9.88	10.11	0.95	19.89
DBH (cm)	10.05	10.10	0.99	20.60
No. of branches	5.64	10.35	0.29	6.34
Clear bole height (m)	20.76	21.84	0.90	40.64
Basal diameter (cm)	9.95	10.13	0.96	20.15
Crown height (m)	13.15	13.50	0.94	26.38
Volume (m^3)	27.67	33.18	0.69	47.53

Estimation of broad sense heritability showed high values for diameter at breast height DBH (0.99%), basal diameter (0.96%), tree height (0.95%), crown height (0.94%) clean bole height (0.90%) and volume (0.69%) while low heritability was observed for number of branches (0.29) (Table 4). The results are in agreement with the findings of Gera and Sharma (2001) in *Tectona grandis* with high heritability for plant height and collar diameter. Studies on the trait female: male flower ratio, seed yield and plant height had higher broad sense heritability in 32 candidate plus trees (CPTs) of *Jatropha curcas* (Rao *et al.,* 2008) and the heritability varies with changing environment and age.

The diameter at breast height (DBH) registered high heritability (0.99%) which might be due to the complexity of quantitative trait, prone to high environmental influences (Table 4). The current study indicated the predominance of additive gene action for this character as reported in teak (Kumar *et al.,*1997). Gera *et al.* (2000) reported low heritability for collar diameter and inter nodal length but higher heritability for height, number of branches, and survival percentage was observed in *Santalum album*. Moderate to high heritability for height, diameter, and volume were found in *Eucalyptus grandis* and *Pinus elliotti* (Hodge and White, 1992; Lambeth *et al.,* 1994). As the height, diameter at breast height (DBH), clear bole height, crown height, basal diameter and volume showed high heritability percentage, the selection for these traits would be effective and improvement could be made through mass selection.

Higher heritability indicates the effectiveness of selection based on good phenotypic performance but does not necessarily mean a high genetic gain for particular traits. Heritability estimates in broad sense is reliable if accompanied by high genetic advance (Burton, 1952). Similar findings were reported by Wilcox and Farmer (1967) in *Salix eriocephala* and Burdon *et al.* (1992) in *Pinus radiate* clones, Singh (1993) in *Bambusa pallida* and Singh and Beniwal (1993) in *Bambusa balcooa*. In the present study, the trend of genetic advance as per cent of mean was maximum in volume (47.53%) (Table 4) followed by clear bole height, crown height and basal diameter indicating a wide scope of genetic improvement possibility in the species. The findings of current study are in line with those of Ramachandra (1996) in *Acacia catechu*. Other research workers have also reported similar results in *Terminalia arjuna* (Srivastava *et al.,* 1993), *Grewia optiva* (Sharma and Sharma, 1995) and also in *Eucalyptus grandis* (Subramanian *et al.*, 1995) which lend support to the results of current investigation. Number of branches recorded the lower heritability value and genetic advance as percentage of mean. Lower heritability estimates for various growth parameters was also observed in *Casuarina equisetifolia* (Kumaravelu, 1997; Mahadevan *et al**.,*** 1999), *Tectona grandis* (Rao *et al**.,*** 2001) and in *Azadirachta indica* (Chauhan *et al*., 2005).

CONCLUSION

Among the thirty progenies evaluated under field condition, the progeny FCRISA18 proved to be consistently superior for all the biometric traits investigated and current study provided evidences for existence of adequate genotypic variation and thus lend support for exploitation of genetic variability for future tree improvement programme.

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