Article AR2320 DOI: HTTPS://DOI.ORG/10.23910/1.2021.2320

International Journal of Bio-resource and Stress Management

December 2021

Crossref

Print ISSN 0976-3988

Online ISSN 0976-4038

IJBSM 2021, 12(6):759-765

Research Article *Natural Resource Management*

Genetic Variability in Growth Characteristics among Different Clones of *Eucalyptus tereticornis* Sm.

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Citation: Sahoo et al., 2021. Genetic Variability in Growth Characteristics among Different Clones of *Eucalyptus tereticornis* Sm.. International Journal of Bio-resource and Stress Management 2021, 12(6), 759-765. HTTPS://DOI.ORG/10.23910/1.2021.2320.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

Acknowledgement: The authors are highly thankful to the Dean, College of Forestry, OUAT, Bhubaneswar for providing a land facility for the trial and also equally thankful to the Director, Institute of Forest Productivity, Ranchi for providing a laboratory facility for both carrying out research and analysis.

Abstract

The present investigation was carried out at the College of Forestry, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India during August, 2018 to June, 2019 to study the genetic variability in growth characteristics among different clones of *Eucalyptus tereticornis.* Different clones of *Eucalyptus tereticornis* Sm. were planted in RCBD, with 4 replications revealed significant variations among all eight treatments (clones) with respect to 9 different characters. Based on the mean performance, treatment-1 (clone-526) showed maximum value for characters like biomass (1124.17), plant height (247.9 cm), collar diameter (23.25 mm), and a number of leaves plant^{-1} (463.25 number). Similarly, the maximum value was observed in treatment-8 (clone-136) for traits like leaf area (42.70 cm^2), leaf length (15 cm), and leaf width (5.75 cm). The highest leaf length to leaf width ratio (3.57) and lowest number of branches plant^{-1} (18.75 number) were found in treatment-2 (clone-288). All characters had exhibited higher genotypic variance than an environmental variance. Similarly, the genetic coefficient of variation in the case of all variables was also found greater than an environmental coefficient of variation. Heritability was found maximum in plant height (87.35%) and all other characters also showed high heritability. Genetic advance as % of mean was found maximum in biomass (71.15%). Based on the overall mean performance of growth characters, Treatment-1 (Clone-526) was found as a superior clone with respect to the most important character biomass for the test locality. High GCV, heritability, and GAM value for biomass indicated that the character would respond to selection for the improvement program.

Keywords: Biomass, clone, *Eucalyptus tereticornis*, growth, genetic advance, heritability

1. Introduction

Eucalyptus is a genus of the Myrtaceae family endemic to Australia, Tasmania, and nearby islands. Being endemic to Australia, South East Asia and the pacific, Eucalyptus is grown mainly as exotic species (Stape, 2010). It is widely planted throughout the world including in India to provide various products. It is the longitudinally widely cultivated forest tree in the world (Nichols et al., 2010). The members of genus Eucalyptus are mostly planted in tropical and subtropical regions with the total plantation area in the world are reported to be more than 21 million ha. (Midgley, 2013). Eucalyptus plantations occupy more than 20 million hectares globally (Ribeiro et al., 2015). It is one of the most intensively managed commercial forest species in the world leading to a doubling of growth rates in many

Article History

RECEIVED on 27th April 2021 RECEIVED in revised form on 20th October 2021 ACCEPTED in final form on 15th December 2021

areas (Binkleyet al., 2017). Probably more than one million hectares area in India is under Eucalyptus plantations which will increase in the coming decades as demand for the wood is increasing highly (Tumbull, 1999). It occurs over a good range of climate and topography like river flats or hill slopes with alluvial or sandy to gravelly soils. It has been the most successful in summer rainfall conditions with a moderate to fairly severe dry season. It is considered drought-resistant but is susceptible to frost. It is a fast-growing, short-rotation tree and has a high wood density. Eucalyptus species are used in bio energy. Eucalyptus has become one of the world's major sources of woody biomass for energy production (Shepherd et al., 2011) and is leading hardwood sawn wood, pulpwood, fuelwood and timber feedstock (Luo et al., 2014). In India, Eucalyptus is one of the most prime species in an agroforestry model and farmers prefer clonal material for high return in short rotation. In India, agroforestry could be a major land use activity after agriculture and forestry (Dhyani et al., 2013).

In the clonal improvement and mass propagation of Eucalyptus, individual trees are identified, and then selected (candidate plus trees or CPTs) from the existing plantations based on different morphological performance, mobilize and rejuvenate of their first vegetative propagules; production of rooted plants from juvenile shoots; planting and screening in the field testing or in clonal orchards; again rejuvenate the chosen individuals, and begin their mass multiplication by rooting the cuttings. The advantages of clonal plantations could be attributable to fixation of a non-additive component of genetic variance, maintenance of hybrid vigour (Ginwal, 2010) and exploitation of genotypic environmental interactions for the development of site-specific genotypes (White et al., 2007). Commercial Eucalyptus clonal planting materials perform better in volume and productivity than rooted seedlings (Sharda and Verma, 2008). Clonal variation studies will be helpful for a selection of suitable clones for different sites. Genetic variations have been reported for growth and wood traits in a number of Eucalyptus populations such as diameter, wood density, lignin content and S/G ratio in *Eucalyptus globulus* (Stackpole et al., 2011) and *Eucalyptus europhylla* (Hein et al., 2012). Kumar et al. (2010) reported that significant variations were recorded for height and diameter at breast height (DBH) and clear bole length (CBH) for eighteen clones of *Eucalyptus tereticornis* for various growth parameters. Hybridisation and selection programmes have been implemented for various Eucalyptuses in a number of countries resulting in improvement of growth and adaptability traits (Hardener et al., 2011). The future thrust for genetic improvement will be for higher growth, productivity, bio energy, abiotic stress, diseases and insect resistance, etc. Taking the above facts into consideration the present research was undertaken with objectives to study the performance of different clones of Eucalyptus tereticornis Sm., to study parameters of variation in different characters of Eucalyptus tereticornis Sm., and to identify superior clones based on their performance suitable for the test region.

2. Materials and Methods

The present investigation was carried out at the instructional farm, College of Forestry, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India from August, 2018 to June, 2019. The location's latitude is 20°26'9.58" N and the longitude is 85°78'4.45" E. It comes under the agro-climatic zone of the east and south-eastern coastal plain. Its climate is hot and humid. The mean annual rainfall is 1577 mm. The mean maximum summer temperature is 39°C and the mean minimum winter temperature is 11.5°C. Eight clones (treatments) namely T_1 (ITC 526), T_2 (ITC 288), T_3 (ITC 7), T_4 (ITC 316), T_5 (ITC 413), T_6 (ITC 286), T_7 (ITC 71), and T_8 (ITC 136) of *Eucalyptus tereticornis* Sm. each with 20 rametes were collected from the nursery of "Avantha Agritech Ltd", Jaypur, Koraput, Odisha. The planting materials were of 25 days old at the time of collection. The experiment was conducted in a randomized complete block design (RCBD) with 4 replications (blocks) and 8 treatments (clones). The size of each block is 24 meters in length and 7.5 meters in breadth that it having an area of 180 square meters. Each replication (block) contains 8 treatments each with five rametes planted using the random table given by Gomez and Gomez (1984). All recommended cultural practices were carried out while raising the clonal seedlings. For different morphological characters, observations were recorded based on randomly selected plants in each clone in each replication after 300 days of planting. The nine important characters considered were plant height, leaf area and collar diameter, number of branches plant^{-1}, number of leaves plant^{-1}, leaf length, leaf width, L/W ratio, and dry biomass.

2.1. Statistical analysis

The data recorded on different characters were subjected to different statistical analyses for estimation of different parameters following the standard procedures given by Singh and Chaudhary (1985).

2.1.1. Mean

The arithmetic mean is defined as the value arrived at by dividing the sum of the observations by the total number of observations. It was calculated from the following formula:

$\bar{X} = (\Sigma Xi) / n$

Where ` $\bar{X}$' represents Arithmetic mean; `n' total number of observations;

'Σ Xi' is the sum of `n' observations.

2.1.2. Analysis of variance (ANOVA)

ANOVA for each character was carried out for partitioning total variance into components attributed to replication, treatment, and error.

Test for significance was done by `F' test. `F' value for treatment was calculated by dividing the treatment mean sum of squares with the error means the sum of squares. `F' value for replication was calculated by dividing replication

mean sum of squares with error means sum of squares. This calculated `F' value was compared against the tabulated `F' value at error degrees of freedom to test the hypothesis. When the calculated `F' value was greater than the tabulated `F' value, the null hypothesis was rejected and variation was considered significant.

The test of significance, for the difference between means of two treatments, was done by the `t' test for which critical difference (CD) was calculated as follows

CD (at *p*=0.05) = (2MSe/r) ½ x t0.05

Where CD implies to Critical Difference, MSe to error mean sum of squares, `r' to a number of replications, and `t' value at the chosen level of significance (5%) at error degrees of freedom.

2.1.3. Estimation variance components

The phenotypic, genotypic, and environmental variance components for different characters were estimated from the mean sum of squares in ANOVA according to the standard procedure given by Al-Jibouriet al. (1958).

Environmental variance (σ^2e)=MSe

Genotypic variance (σ^2g) = (MSt-MSe)/r

Phenotypic variance (σ^2p) = (σ^2g)+(σ^2e)

Where σ^2g represents genotypic variance, σ^2p is phenotypic variance and σ2e is variance due to the environment.

2.1.4. Coefficient of variation

The coefficient of variation is the ratio of the standard deviation to the mean of the observations. It was calculated as a percentage from the following formula.

CV=(SD/$\bar{X}$)×100

Where CV represents the coefficient of variation and SD represents standard deviation.

Estimation of components of the coefficient of variation

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and environmental coefficient of variation was calculated from the following formula,

PCV=(σ^2p) 1/2 /$\bar{X}$)×100

GCV=(σ^2g) 1/2 /$\bar{X}$)×100

ECV=(σ^2e) 1/2 /$\bar{X}$)×100

Where, σ2p, σ2g, and σ2e are the square root of the phenotypic, genotypic, and environmental variance respectively.

2.1.5. Estimation of heritability

Heritability (h2) in the broad sense of characters was estimated by the formula suggested by Hanson et al. (1956), using the components of variance, as follows.

h2=σ^2g/σ^2 p

Where, σ^2g and σ^2p represent genotypic and phenotypic variance respectively.

2.1.6. Estimation of genetic advance

The expected genetic advance (GA) from selection among treatments for different characters was calculated according to Johnson et al. (1955) as follows.

GA=K×h^2×σp

Where k represents standardized selection differential at 5% selection intensity.

2.1.7. Genetic advance as % of mean

The genetic advance as percentage of mean (GAM) was expressed as a % of the mean for comparison among characters.

GA (as % of mean) or GAM=(GA/Mean)×100

3. Results and Discussion

The variations that exist among the tested clones for different morphological characters were assessed through various statistical tools like analysis of variance, estimation of components of variation, and heritability. The analysis of variance revealed significant differences among the treatments for different characters like biomass, plant height, collar diameter, and number of branches plant^{-1}, number of leaves plant^{-1}, leaf width, leaf area, leaf length, and leaf length to leaf width ratio.

3.1. Performances of the different quantitative characters

The collected data in respect of all 9 quantitative characters were subjected to analysis of variance (ANOVA) following the standard procedure. The mean values, the coefficient of variation (C.V.), along critical difference (CD) at a 5% level of significance are presented in table-1, which revealed a wide range of variation for all traits studied.

3.2. Plant height

The performances of the tested clones had shown significant variation with respect to plant height. The mean performance of plant height ranged from 168.64 cm to 230.71 cm with an overall mean of 200.94 cm (Table 1). The maximum height (247.9 cm) was observed in T_1 followed by T_5 (221.02 cm) and T_8 (218.79 cm). The minimum height (151.45 cm) was observed in T-2 which was statistically at par with T_7 (167.79 cm).

3.3. Collar diameter

Significant variation was observed among all clones for the collar diameter. The overall mean was 21.17 mm (Table 1). The maximum collar diameter (23.25 mm) was observed in T_1 which was statistically at par with T_8 (22.92 mm), T_4 (22.16 mm), and T_6 (21.86 mm). The minimum collar diameter (18.35 mm) was observed in T_7 which was statistically at par with T_2 (18.79 mm).

3.4. Number of branches

All the treatments differed significantly for number of branches. The overall mean was observed at 23.65. T_1 recorded the highest number of branches (27.5 number), which was statistically at par with T_5 (26.25 number).

Table 1: Mean value of growth parameters in different clones of *Eucalyptus tereticornis* Sm.

Treatments	Plant height (cm)	Collar diameter (mm)	Number of branches	Leaf area (cm^2)	Leaf length (cm)	Leaf width (cm)	(L/W)	Number of leaves	Biomass (g)
T_1	247.9	23.25	27.5	37.72	14.3	4.85	2.95	463.25	1124.17
T_2	151.45	18.79	18.75	32.6	13.87	3.95	3.51	269.5	356.18
T_3	185.15	20.76	22.25	32.9	14.1	4.4	3.21	327.25	517.1
T_4	203.88	22.16	24	36.15	14.12	4.62	3.06	373.25	581.89
T_5	221.02	21.25	26.25	39.77	14.75	5.0	2.95	429.75	757.06
T_6	211.59	21.86	24.25	36.88	14.25	4.77	2.98	380.75	684.66
T_7	167.79	18.35	21.75	30.12	12.65	3.95	3.20	288	403.76
T_8	218.79	22.92	24.5	42.70	15	5.75	2.61	384.5	735.74
Grand Mean	200.94	21.17	23.65	36.10	14.13	4.66	3.06	364.53	645.07
SEm±	5.50	0.36	0.48	0.74	0.13	0.14	0.04	11.79	42.85
CD (*p*=0.05%)	17.19	1.84	1.67	2.83	0.70	0.35	0.15	37.28	135.28

3.5. Leaf area

The performance of the leaf area ranged from 30.12 cm^2 to 42.70 cm^2 with an overall mean of 36.10 cm^2 (Table 1). T_8 recorded the highest leaf area (42.70 cm^2) followed by T_5 (39.77 cm^2) and T_1 (37.72 cm^2). The lowest leaf area was observed in T_7 (30.12 cm^2) which was statistically at par with T_2 (32.6 cm^2) and T_3 (32.9 cm^2).

3.6. Leaf length (L)

The leaf length varied from 12.65 cm to 15.0 cm with an overall mean of 14.13 cm (Table 1). T_8 recorded the highest length (15 cm) which was statistically at par with T_5 (14.75 cm) and T_1 (14.3 cm). The lowest leaf length was recorded in T_7 (12.65 cm) followed by T_2 (13.87 cm).

3.7. Leaf width (W)

The performance of the tested clones had shown significant variation with respect to leaf width. The leaf width was found to range from 3.95 cm to 5.75 cm with an overall mean of 4.66 cm. The maximum leaf width ((5.75 cm) was recorded in T-8 followed by T_1 (4.85 cm) and T-6 (4.77 cm). The minimum leaf width (3.95 cm) was recorded both in T_2 and T_7 (Table 1).

3.8. L/W ratio

Significant variation was observed among all clones for the trait L/W ratio. The overall mean was found to be 3.06 (Table 1). The maximum L/W ratio (3.51) was observed in T_2 which was followed by T-3 (3.21). The minimum L/W ratio (2.61) was observed in T_8 which was followed by both T_5 and T_1 (2.95).

3.9. Number of leaves

A perusal of the data in Table 1 showed the number of leaves ranged from 269.5 to 463.25 number with an overall mean of 364.53 number T_1 recorded the highest number of leaves (463.25 number) which was statistically at par with T_5 (429.75 number). The lowest number of leaves was recorded in T_2 (269.5 number) which was statistically at par with T_7 (288 number).

3.10. Total biomass (dry)

Based on the data appended in Table 1, it was found that the tested clones had shown significant variation with respect to total biomass. The biomass ranged from 1124.17 g to 356.18 g with an overall mean of 645.07 g. The maximum biomass (1124.17 g) was recorded in T_1 followed by T_5 (757.06 g) and T_8 (735.74 g). The minimum total biomass (356.18 g) was observed in T_2 which was statistically at par with T_7 (403.76 g). Dhilon and Singh (2010) reported significant differences among seed sources of *Eucalyptus tereticornis* Sm. with respect to growth traits i.e. height and diameter. Different quantitative traits like biomass, plant height, collar diameter, no of branches $plant^{-1}$, leaf length, leaf width, etc. can be considered as desirable attributes as they contribute to timber yield (Kumar and Dhillon, 2016; Marron et al., 2005). Kulkarni (2002) studied the performance of 86 clones and identified 19 clones having clear bole, 16 high productive clones, 19 adaptable to refractory sites, and 6 having disease resistance. In tree improvement programs clones possessing desirable attributes can be used as parents for specific traits. Saravanan (2020) reported clonal variation in growth, biomass production and components in a study of Eucalyptus clones. Srivatav et al. (2020) reported variation in height, girth at breast height(GBH), basal area and volume of trees ha^{-1}. in clones of Eucalyptus. In the present study, we have found certain clones performed better with respect to growth characters and could be selected for the tree improvement program.

3.11. Assessment of genetic parameters

The tested clones of *Eucalyptus tereticornis* Sm. had shown wide genetic variation among themselves for traits studied. Genetic parameters like variance, coefficient of variation, heritability, genetic advance and genetic advance as a percentage of mean were calculated from the mean sum of

squares and are presented in Table 2.

3.12. Variance

The total phenotypic variance was partitioned into genotypic and environmental components of variance according to their contribution to the total variance. In all nine quantitative characters for which significant variation among clones was found, all have higher genotypic variance than the environmental variance. The maximum phenotypic variance (65477.63) was observed in biomass and the least (0.07) in the L/W ratio. In the case of genotypic variance, biomass had the highest (57016.59) value followed by number of leaves (4269.97) and plant height (3775.97). The lowest genotypic variance (0.06) was observed in the L/W ratio. The environmental variance was also showed a similar trend that is maximum (8461.04) in biomass, and minimum (0.01) in L/W ratio. The higher contribution of genotypic variance to total phenotypic variance signifies high heritability of characters, and this can be evidenced from the heritability estimates of characters. This is considered desirable from a breeding point of view. Similar significant differences among clones of different Eucalyptus species have been reported by various workers Gomes and Correia (1995), Lal (2005), Kumar and Bangawa (2006), and Pima et al. (2016).

Table 2: Genetic Parameters of different growth characters in clones of *Eucalyptus tereticornis* Sm.

Growth characters	σ^2p	σ^2g	σ^2e	PCV%	GCV%	ECV%	h^2 %	GA	GA% of mean
Plant height	3912.6	3775.97	136.62	16.35	15.29	5.81	87.35	59.15	29.43
Leaf area	19.73	16	3.72	12.30	11.08	5.34	81.12	7.42	20.55
Collar diameter	4.40	2.83	1.57	9.91	7.94	5.90	64.27	2.77	13.12
Number of Branches	8.45	7.15	1.29	12.28	11.30	4.77	84.69	5.07	21.44
Leaf length	0.66	0.43	0.22	5.75	4.66	3.32	65.71	1.10	7.79
Leaf width	0.39	0.33	0.05	13.42	12.36	5.15	84.88	1.09	23.46
Leaf Length to Leaf Width	0.07	0.06	0.01	9.05	8.41	3.26	86.49	0.49	16.12
Number of Leaves	4912.66	4269.97	642.68	19.22	17.92	6.95	86.91	125.49	34.42
Biomass	65477.63	57016.59	8461.04	39.66	37.01	14.25	87.07	459.01	71.15

σ^2p: Phenotypic variance; σ^2g: Genetic variance; σ^2e: Environment variance; PCV: Phenotypic coefficient of variation; GCV: genotypic coefficient of variation; ECV: Environment coefficient of variation; h^2: heritability; GA: Genetic advance

3.13. Coefficient of variation

The extent of the coefficient of variation among the studied clones for different characters was estimated in terms of coefficient of phenotypic variation (PCV), coefficient of genotypic variation (GCV), and coefficient of environmental variation (ECV). Among the 9 quantitative traits, the PCV ranged from 5.75% in leaf length to 39.66% in biomass. Similarly, the GCV of the characters varied between 4.66% in leaf length to 37.01% in biomass, which represents the presence of significant variability among the clones. Other characters showed low PCV and GCV value. Environmental coefficient of variation (ECV) was highest for biomass (14.25%), while lowest (3.32%) for L/W ratio. High PCV and GCV value and small difference between them in biomass indicate the character is under the control of strong genetic factors and the environment has little contribution towards the variability expression of the character. Biomass could be improved by the selection of superior phenotypes independent of genotypes. It also suggests genotypes with high biomass could be selected for hybridisation and selection programme. It is assumed that high GCV gives rise to variable offspring in segregating generation.

The low environmental coefficient of variation suggests all the characters under study are under genetic control. Huse et al. (2018) reported high PCV and GCV value for biomass and low PCV and GCV value for plant height and diameter in a study of Eucalypt clones which was similar to the findings of the present study.

3.14. Heritability

The broad-sense heritability was observed high (>60%) for all the quantitative characters under study. It ranged from 64.27% in collar diameter to 87.35% in plant height. High heritability was also found in biomass (87.07%), number of leaves (86.91%), L/W ratio (86.49%), leaf width (84.88%) and number of branches (84.69%). High heritability in all the characters under study suggests the genetic control over the variability in character expression and reliability of the above phenotypic characters for selection. It also indicates a very low influence of the environment in the expression of these characters, so these characters should be chosen for improvement of Eucalyptus. Dlamini et al. (2017) found heritability in both height and diameter at breast height was high at family level in a study of 2nd generation progeny test of *Eucalyptus urophylla* suggesting that selection of the best families would be possible at an early stage.

3.15. Genetic advance

In this study, the value of genetic advance (GA) ranges from 0.49 to 459.01. The maximum GA value was recorded in biomass (459.01) followed by number of leaves plant^{-1}

(125.49), plant height (59.15), leaf area (7.42). The character L/W ratio recorded the lowest (0.49) GA value. The genetic advance should be given priority along with the heritability estimate in the process of selection (Johnson et al., 1955).

3.16. Genetic advance as % of the mean (GAM)

Expected genetic advance (GA) under selection (5% selection intensity) among the clones was estimated for each character and was expressed as % of the mean. The estimated GA % under selection for characters varied from 7.79% to 71.15%. The biomass recorded the highest (71.15) GA as % of the mean. Besides high genetic advance as % of the mean (>20%) was observed in number of leaves plant^{-1} (34.42%), plant height (29.43%), leaf width (23.46%), number of branches plant^{-1} (21.44%), leaf area (20.55%) and the lowest (7.79%) was observed in leaf length. Characters with higher genetic advance as % of the mean signify expected higher genetic gain in response to selection at a given selection intensity and vice versa. Silva et al. (2004) also found in *Eucalyptus globules* that for genetic gains selection for additive genetic merit and clonal testing are equally important.

In this experiment biomass recorded high GCV and genetic advance % of the mean, so this trait is controlled by additive gene action and could be selected through direct selection.

4. Conclusion

Treatment-1 (Clone-526) had recorded maximum mean value with respect to five important growth traits such as biomass, plant height, collar diameter, number of branches plant^{-1}, and number of leaves plant^{-1}. Biomass had high GCV (%) and genetic advance (% of the mean) which under additive gene action and could be selected for the improvement programme.

5. Acknowledgement

The authors are highly thankful to the Dean, College of Forestry, OUAT, Bhubaneswar for providing a land facility for the trial and also equally thankful to the Director, Institute of Forest Productivity, Ranchi for providing a laboratory facility for both carrying out research and analysis.

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