(RESEARCH ARTICLE)

Study of genetic divergence among *Eucalyptus tereticornis* clones through principal component analysis (PCA)

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Abstract

Eucalyptus tereticornis is one of the fastest growing multipurpose tree species. It is planted extensively under agroforestry and farm forestry. It was needed to estimate the genetic variability and contribution of yield contributing traits towards the total divergence. The PCA summarizes variability present in studied traits into utilizable form and to practical importance. Therefore, in the present study, eight clones of *E. tereticornis* were studied under field trial for their growth performance and contribution of individual traits towards total divergence were estimated. The eigene value of all three vectors (PCs) were found greater than one, which revealed that all the principal components explained a significant amount of variability present in traits. The proportion of variability explained by PC1 was 48.15 percent, by PC2 was 38.09 percent and by PC3 was 5.75 percent, all together these three vectors explained 92 percent of total variability. In PC1 and PC2, Plant height, biomass, leaf area, number of leaves, number of branches, leaf width and collar diameter were contributed positively towards the divergence hence the selection based on these traits will be rewarding. The times ranked contribution study also confirmed the contribution of L/W ratio (35.71%) and biomass (14.29%) towards the divergence. These traits are very important for the selection of parents in hybridization programs and effective selection of productive clones.

Keywords: *Eucalyptus tereticornis*; Principal Components (PCs); Eigene value; Hybridization; Variability

1. Introduction

Eucalyptus tereticornis belongs to the family Myrtaceae is one of the fastest growing tree species. It is widely planted under agroforestry and farm forestry due to short rotation and diverse utilization. It is used for various purposes viz. for making paper and pulp, sawn timber, pole, extraction of essential oil and by the plywood industry [1]. It is a species of choice for planting under Agroforestry and farm forestry because of its fast-growing nature, weed suppressing ability, high coppicing ability, browse resistance and ability to withstand wide edaphoclimatic conditions [2]. It has the widest latitudinal distribution among all the species of Eucalyptus. It can grow up to a height of 20 to 50 meters with a girth of up to 2 meters.

The populations of the species are genetically diverse due to natural cross pollination, but the productivity under plantations have stagnated due to its over exploitation through intensive selection programs. To obtain maximum return and uniform stand the clonal development programs have also been carried out by the government agencies and private firms. The plantations raised through clones are always beneficial due to fixation of non-additive components of genetic variance, locking of hybrid vigour and exploitation of G X E interaction for developing site specific cultivar/clone [3 and 4]. Estimation of genetic parameters at early stages of growth gives an insight to breeder to devise appropriate strategy and perform early selection based on desirable traits. The genetic divergence in breeding material

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is prerequisite for achieving genetic gain through selection and breeding programs [5]. It is also important to have information on the traits which contribute maximum towards the variability.

Principal component analysis (PCA) is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables (entities each of which takes on various numerical values) into a set of values of linearly uncorrelated variables called principal components which accounts for most of the variation produced by these characters. The PCA summarizes variability present in studied traits into utilizable form and to practical importance [6]. In the present study the contribution of individual traits towards the total variability have been studied. The canonical variate analysis, reduced the number of variables into linear functions which account for most of the variations produced by these characters, called canonical vectors.

2. Material and methods

The experimental material consisted of eight clones of *E. tereticornis* viz. ITC 526, ITC 288, ITC 7, ITC 316, ITC 413, ITC 286, ITC 71, and ITC 136. The field trial was established at the Bhubaneswar (Odisha), located at 20°26'9.58" N and 85°78'4.45" E. The field trial was established in Randomized Block Design (RBD) with four (4) replications and five (5) plants per clone per replication. To study the genetic divergence among planted clones of *E. tereticornis*, growth data viz. plant height (PH), collar diameter (CD), leaf area (LA), number of branches plant^{-1} (NB), number of leaves plant^{-1} (NL), leaf length (LL), leaf width (LW), leaf L/W ratio (L/W ratio) and dry biomass (B) were recorded. The observed data were analysed by using Windostat version 9.2 software (Licensed to IFP, Ranchi). The canonical variate analysis has been done to analyse the clustering pattern and canonical root vectors were calculated and presented in graphical form [7].

3. Results and discussion

Table 1 The eigene value (root), percent variance and percent cumulative variance for three principal components (PCs) and factor loading between PCs and traits studied in *Eucalyptus tereticornis*

		PC I	PC II	PC III
Eigene Value (Root)		171.49	135.67	20.49
% Var. Exp.		48.15	38.09	5.75
Cum. Var. Exp.		48.15	86.24	92.00
Characters		**Factor Loading**		
1.	Plant Height (cm)	0.43	0.35	0.18
2.	Leaf Area (cm2)	0.24	0.49	0.21
3.	Collar Diameter (mm)	0.11	0.08	0.06
4.	No. of Branches	0.16	0.06	-0.31
5.	Leaf Length (cm)	-0.16	-0.32	0.16
6.	Leaf Width (cm)	0.12	0.49	-0.39
7.	L/W Ratio	-0.73	0.49	0.39
8.	No of Leaves	0.22	0.05	0.27
9.	Dry Biomass (g)	0.32	-0.17	0.65

The principal component analysis of eight eucalyptus clones based on correlation matrix of studied economical traits yielded three eigene roots. The estimated eigene value, percent variance, percent cumulative variance and factor loading of studied traits are presented in Table 1. In the present study, yielded three principal components (vectors) described 92 percent of total variability produced by the studied traits. The first principal component captured maximum variability present in the traits and succeeding components account for the remaining variability. Eigene value of all three vectors was found greater than one, which revealed that all the principal components explained a significant amount of variability present in traits. Under the present study, the eigene value observed for PC_1 was 171.49, 135.67

for PC$_2$, and 20.49 for PC$_3$. The proportion of variability explained by PC$_1$ was 48.15 percent by PC$_2$ was 38.09 percent by PC$_3$ was 5.75 percent. The results revealed that the differentiation of genotypes into different clusters was due to high contribution of certain characters towards divergence rather than small contribution of each trait [8, 6 and 9]. in Bitter gourd. The value of factor loading in PC$_1$ was highest for PH (0.43) followed by dry biomass (0.32), leaf area (0.24), NL (0.22), NB (0.16) therefore these characters contributed positively towards divergence. The lowest value of factor loading for PC$_1$ was observed for L/W ratio (-0.73). PC$_2$ accounted for 38.09 percent of total divergence and all the characters except leaf length and dry biomass contributed positively towards divergence. The maximum contribution towards divergence was reported from leaf area (0.49), leaf width (0.49), and L/W ratio (0.49) and the lowest contribution was observed form leaf length (-0.32). in PC$_2$, leaf length and dry biomass contributed negatively towards the genetic divergence. In vector three (PC$_3$) contribution towards total divergence was recorded 5.75 percent with highest contribution from dry biomass (0.65) followed by the L/W ratio (0.39). The lowest value of factor loading for PC$_3$ was observed in leaf width (-0.39) and it is affecting negatively.

3.1. Canonical graph

Table 2 The Principal Component Analysis (PCA) scores for eight clones of *Eucalyptus tereticornis*

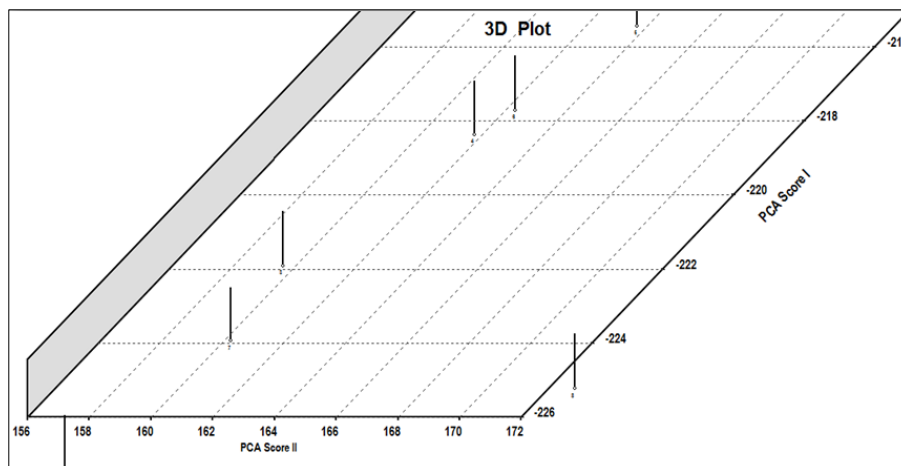|		PC I	PC II	PC III
Sl. No.	Eucalyptus clone	X Vector	Y Vector	Z Vector
1	ITC 526	-212.045	161.969	57.539
2	ITC 288	-225.967	157.177	57.633
3	ITC 7	-220.426	157.893	54.808
4	ITC 316	-216.91	160.088	53.422
5	ITC 413	-213.928	161.952	54.775
6	ITC 286	-216.23	160.636	54.318
7	ITC 71	-222.504	158.583	52.975
8	ITC 136	-223.745	171.149	55.073

Figure 1 Three dimensional principal components scatter plot

The principal component score for the first three vectors PCA I (X vector), PCA II (Y vector) and PCA III (Z vector) are given in Table 2. The highest value of PCA I was observed for ITC 526 (-212.045) and the lowest value for ITC 288 (-225.967). The highest value of PCA II was observed for ITC 136 (171.149) and the lowest value for ITC 288 (157.177). The highest value of PCA III was observed for ITC 288 (57.633) and the lowest value for ITC 71 (52.975). The graphical depiction of the genetic distance between eight clones of *E. tereticornis* was obtained from mean scores of the first two canonical vectors i.e., X vector and Y vector. Using these sores, all the studied clones were plotted for PC$_1$ and PC$_2$. The PC$_1$ and PC$_2$ collectively explained 86.24 percent of total variability. The three-dimensional scatter plot of PC scores of

first two PC axes is presented in Figure 1. The scatter plot revealed that the variance in studied clones was due to all the studied traits except leaf length and dry biomass. The variability explained by these two vectors was accounted for the biomass and growth contributing traits.

The genetic diversity is the outcome of various factors depends on genetic makeup of the genotype along with the geographical diversity. The breeding material must be selected based on genetic diversity and not on geographical diversity alone [5]. The PC_1 explains maximum variance (48.15 %) hence the characters contributing maximum towards divergence can be easily identified and selection can be made based on those characters. Similarly, PC_2 explains 38.09 % variance and the traits responsible for this variance can be identified and utilized for making selection. In PC_1, Plant height, biomass, leaf area, number of leaves, number of branches, leaf width and collar diameter contributed positively towards the divergence while in PC_2 also these traits contributed positively towards the divergence hence the selection based on these traits will be rewarding in selection of productive clone. The times ranked contribution study revealed (Table 3) that L/W ratio (35.71%) contributed maximum followed by dry biomass (14.29%), plant height (10.71), leaf area (10.71), leaf length (10.71) and number of leaves (10.71) towards the total divergence [10], [11], [12], [13], [14], [15], [6].

Table 3 Times ranked contribution of studied traits

Sl. No.	Characters	Times Ranked 1st	(%) Contribution
1	Plant Height (cm)	3	10.71
2	Leaf Area (cm2)	3	10.71
3	Collar Diameter (mm)	0	0.00
4	No. of Branches	0	0.00
5	Leaf Length (cm)	3	10.71
6	Leaf Width (cm)	2	7.14
7	L/W Ratio	10	35.71
8	No of Leaves	3	10.71
9	Dry Biomass (g)	4	14.29

4. Conclusion

Through the principal component analysis (PCA), it can be concluded that the variability present among the eucalyptus clones was primarily due to plant height, dry biomass, number of leaves, leaf width, leaf length-width ratio and leaf area. These traits are very important for the selection of parents in hybridization programs. The effective selection of productive eucalyptus clones can also be carried out based on these traits.

Compliance with ethical standards

Disclosure of conflict of interest

The authors declare no conflict of interest and there is no financial interest to report. It is an original research work and not submitted to any other journal for consideration.

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