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Genetic divergence study for growth characters among clones of *Eucalyptus*

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Abstract
In the study, the genetic divergence in *Eucalyptus* was estimated based on the growth traits of 20 clones grown in the South Gujarat, India. Accordingly, a field experiment was performed using a randomized block design and three replications to compare divergences in diameter at breast height (DBH), mid-diameter, height, form quotient and volume at 6 years of age. Tocher's clustering method was performed using the Mahalanobis distance. The twenty clones were grouped into 6 clusters on the basis of growth attributes. Cluster I was formed with 15 clones and remaining five clones were grouped into 5 separate clusters indicating these five clones are genetically distant from each other. The divergence analysis indicated that promising crosses could be made between cluster IV and VI containing clone C20 and C4 respectively as recorded the largest statistical distance signifying maximum divergence. This may result in substantial segregation for quantitative traits studies and help in further selection for overall improvement of *Eucalyptus* species in South Gujarat condition.

Keywords: *Eucalyptus*, Growth characters, Genetic divergence, Volume

Introduction
Eucalyptus (Myrtaceae family) with astonishing growth characteristics and fast growing in nature tree species are normally found with a natural latitudinal range extending from 7˚N to 43˚39'S and flourishes from coastal areas to areas situated at an altitude of 2000 m, tropical to warm temperate climate and rainfall ranges of 400-4000 mm (Tewari, 1992) [24].

India is one of the largest *Eucalyptus* growing countries with a total area of 1.36 million ha plantations up to 1999 (FSI, 1999) [8] which increased to around 8.00 mha up to 2010 (Aregowda *et al.,* 2010). *Eucalyptus* one of the species among top 10 tree species found in the growing stock of Tree Outside Forest (TOF) area which contributing stem and volume of 3.98 and 2.11 per cent of total stems and total volume respectively (FSI, 2015) [9]. Eucalypts are multipurpose tree species and their wood is in much demand for paper and pulp, plywood, furniture, packing cases and light constructional timber all over the world (Behera, 2016) [2]. Among the *Eucalyptus*, different clones are being developed to get the quality pulpwood plantations which can give higher pulp yield and better growth rate. Wood properties of trees are changing throughout the world (Zobel *et al.*, 1983) [27] and causes of the changes must be known. In order to use wood efficiently, the variation patterns within trees, among tree within species and among species must be understood (Zobel and van Buijtenen, 1989) [26].

The establishment of breeding programs with forest species is important for attaining greater productivity and wood quality without jeopardizing the genetic heritage of the elected populations (Zobel and Talbert, 1984; Martins *et al.*, 2006) [25, 15]. Knowledge of genetic diversity is important for any breeding strategy and provides a scientific basis for the better management of the genetic heritage of forest species (Poltri *et al.*, 2003) [20]. On the other hand, clustering progeny according to similarity has become essential for selecting the crossing cultivars based on quantitative traits of economic interest (Manfio *et al.*, 2012; Silva *et al.*, 2012) [14, 23]. For years, the use of multivariate analysis has been an important tool for genetic diversity studies, helping to organize germplasm banks and determine breeding strategies for different wood species: *Pinus caribaea* (Missio *et al.*, 2007) [16], *Eucalyptus tereticornis* (Chezhian and Ghosh, 2010) [6], *Dalbergia sissoo* (Kumar *et al.*, 2012) [12] and *Eucalyptus camaldulensis* (Brito da Costa *et al.*, 2016) [4] and others. In this study a successful attempt was made to find out the genetic divergence among twenty clones of *Eucalyptus* for growth traits in South Gujarat conditions.

Materials and Methods

The present experiment was carried at College of Forestry, Navsari Agricultural University, Navsari. The established *Eucalyptus* plantation consists of 20 clones planted at 2 x 2m spacing in three replications following Randomized Block Design (RBD). Total 3 ramets per clone were selected randomly and growth parameters such as Diameter at Breast Height (DBH), mid- diameter, tree height, form quotient and volume were recorded at the age of 6 years as per standard procedure. Genetic divergence of clones for growth characters were studied using Mahalanobis D^2- statistics (1936) [13]. Grouping of genotypes into various clusters was made by Tocher's method as described by Rao (1952) [22].

Results and Discussion

Result of genetic divergence for growth parameters among clones shows that volume was contributed to highest genetic divergence with 35.79 per cent (Table 1), followed by mid-diameter (21.05%) and DBH (18.95 %). However, the least contribution was made by form quotient (8.95%). Such a study helps in choosing parents for specific breeding objectives to get the desirable segregates by hybridization besides its taxonomic application. Deve and Parthiban (2014) [7] found volume (41.06%) and height (55.26%) contributed maximum to the total genetic divergence in *Dalbergia sissoo* clones whereas Pande *et al.* (2013) [19] reported GBH (34.39 %) contributed highest in the *Leucaena leucocephala*.

As per D^2 analysis, the entire 20 clones of *Eucalyptus* were grouped into 6 clusters on the basis of growth attributes (Table 2). Cluster I was formed with 15 clones and remaining five clones were grouped into 5 separate clusters indicating these five clones are genetically distant from each other. The clustering pattern of the present study complies with report of Hegde and Varghese (2008) in *E. camaldulensis* where 21 seed sources were grouped into 4 clusters on the basis of growth traits.

In the study, maximum inter cluster distance was found between cluster-IV and cluster-VI (4.99), followed by cluster-IV and cluster-V (4.21) and cluster-III and cluster-VI (3.93). Such diverse in clones characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, chances to obtain favourable transgressive segregates are more on the basis of results obtained. It indicates the maximum divergence between the clones and their heterogeneous origin. Murty and Arunachalam (1966) [18] observed that genetic drift and selection in different environments could cause greater diversity among the inbreeds than their geographical distance.

In the present trial, it was recorded that cluster VI was formed by DBH with highest clonal mean 16.85, followed by tree height with value of 21.99, whereas in cluster V, tree height (clonal mean value of 23.86) contributed more. Therefore, such traits may be used while crossing among the clones belonging to clusters- V and VI. Hegde and Varghese (2008) selected cluster with high mean value of growth parameters like height, DBH, Clear Bole Height (CBL) and Diameter for further hybridization programme in *E. camaldulensis* Dehnh. to exploit heterosis and create variability. Many researchers studied genetic divergence study among different species. For instance, Mohapatra (1996) [17] studied genetic divergence in *Acacia catechu*, Chauhan *et al.* (1997) [5] in *Bauhinia variegata*, Bhat (1999) [3] in *Albizia lebbek*, Jha (2001) [11] in *Dalbergia sissoo* and Poonam (2010) [21] in *Bauhinia variegata.*

Table 1: Contribution of different growth attributes to the total divergence among clones of *Eucalyptus*

Trait	Per cent contribution
DBH	18.95
Mid-diameter	21.05
Tree height	15.26
Form quotient	8.95
Volume	35.79

Table 2: Composition of Euclidean clusters for growth attributes in *Eucalyptus* clones

Cluster	Number of clones	Clones
I	15	C13, C19, C2, C14, C1, C6, C18, C5, C9, C16, C7, C11, C15, C3, C10
II	1	C8
III	1	C12
IV	1	C20
V	1	C17
VI	1	C4

Table 3: Average intra and inter distances (D^2) among different clusters for growth attributes

	I	II	III	IV	V	VI
I	1.22					
II	1.92	0.00				
III	2.41	1.97	0.00			
IV	2.18	2.95	2.44	0.00		
V	3.37	1.63	2.63	4.21	0.00	
VI	3.79	2.30	3.93	4.99	1.83	0.00

Table 4: Cluster mean values for growth attributes among different clones

Trait	I	II	III	IV	V	VI
DBH	13.43	15.39	15.75	13.71	16.01	16.85
Mid-diameter	8.62	10.01	11.41	9.81	10.80	10.49
Tree height	21.05	22.94	22.68	20.67	23.86	21.99
Form quotient	0.64	0.65	0.72	0.72	0.68	0.62
Volume	0.20	0.28	0.32	0.22	0.32	0.31

Conclusion

In the present trial, cluster IV and VI recorded the largest statistical distance indicating maximum divergence. Since wide diversity exists between the clones belongs to cluster IV and VI, the crosses between clones such as C20 and C4 may result in substantial segregation for quantitative traits studies and help in further selection for overall improvement of species in South Gujarat condition.

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