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GENETIC DIVERGENCE IN *POPULUS DELTOIDES* BART

DEEPAK PANDEY, SALIL K. TEWARI* AND SANJAY TRIPATHI

Department of Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar 263145

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ABSTRACT

Genetic divergence using Mahalanobis D^2 analysis among 12 clones of poplar with sixteen component characters at 8 yers of age led to their grouping into five clusters. Four clones fall in cluster I, three in cluster II, two each in cluster III and IV, and only one in cluster V. Maximum and minimum distances were observed between clusters II and III and clusters I and V, respectively.

Key words: Genetic divergence, D^2 static, poplar.

Poplar or cottonwood (*Populus deltoides* Bart) is a unique tree, suitable for agroforestry because of its fast growth habit, and multiple uses. It has been planted widely in Northern India under agroforestry and pure culture system. A quantitative estimation of genetic diversity present among different genotypes helps the breeder to attempt crosses between desirable but diverse genotypes for generating sufficient genetic variability for the rapid progress in any selection programme. Multivariate analysis has been found to be a potent biometrical tool in quantifying the degree of divergence in the germplasm [1, 2]. To achieve breakthrough in yield of *Populus deltoides*, the genetic divergence analysis has been attempted so that the highly diverse genotypes can be selected for attempting crosses between them.

MATERIALS AND METHODS

Twelve clones of *Populus deltoides*, obtained from the Lalkuan Forest Nursery and Wimco Seedlings Ltd., were grown in randomized complete block design with two replications. Twenty trees were maintained in each treatment of four rows at a distance of 5 m betweene rows and 4 m between trees. Observation on sixteen characters were recorded on ten representative trees in each treatment. Mahalanobis' D^2 static (generalized distance) was used to analyze the genetic divergence as suggested by [2].

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*Author for correspondence.

RESULTS AND DISCUSSION

The analysis of variance exhibited significant differences among the clones for all the characters studied. Based on D^2 values, twelve clones were grouped into five clusters according to the method described by Tocher [2]. The criterion used for clustering is that any two genotypes belonging to the same cluster should, at least on an average, show a smaller D^2 value than those belonging to different clusters. The clustering pattern of these twelve genotypes is depicted in Table 1. Twelve clones were grouped in five clusters on the basis of D^2 values. Cluster I contains four genotypes, cluster II three, clusters III and IV two each, and cluster V had only one genotype. The intracluster values ranged from 0 to 0.3 (Table 2), with the maximum value of 0.43 in cluster II, followed by 0.37 in cluster IV, 0.02 in III, and 0.00 in cluster I as it had only one genotype.

Table 1. Clustering pattern of 12 genotypes on the basis of genetic divergence in poplar

Cluster	Clones
I	Lux 69/55, IC, Triplo, 4/68
II	D-121, 19/66, D-61
III	I-214, B.L. Costa 420
IV	6-64, Black hybrid
V	V.L. Onda

The pattern of distribution of these entries in the five clusters showed that there was considerable amount of genetic divergence in these clones. Calculation of intercluster distances revealed the maximum value of 19.3 between clusters II and III, indicating that the clones in cluster II (D-121, 19/66 and D-61) and cluster III (I-214 and B.L. Costa 420) were most divergent. The importance of different plant characters in intercluster divergence was studied further by comparing cluster means for different characters. Significant differences between cluster means in these two clusters were observed for trunk diameter at breast height, tree height, total crown length, crown width, No. of primary branches, branch length, leaf width, branch angle, total duration of leaf fall, and under bark volume (Table 3). It was found that these characters contributed maximum to the genetic distance between clusters II and III. The distance between clusters I (Lux 69/55, IC, Triplo and 4/68) and II (D-121, 19/66 and D-61) was also high. Significant differences between character means were observed in these two clusters for trunk diameter, crown length, crown width, primary branch length, branch number, branch angle, duration of leaf fall, and under bark volume.

Table 2. Average intracluster (in bold) and intercluster distances in poplar

Clusters	I	II	III	IV	V
I	**0.15**	13.80	2.93	4.52	1.13
II		**0.43**	19.26	5.14	8.88
III			**0.02**	12.03	4.16
IV				**0.37**	2.10
V					**0.00**

Intracluster distances given in parenthesis.

While selecting the clones as parents, other practical considerations, such as, disease and insect reaction and quality index should also be taken into account in addition to genetic divergence. The minimum distance between cluster I (Lux 69/55, IC, Triplo and 4/68) and

Table 3. Character means for five clusters of 12 poplar genotypes

Character	I	II	III	IV	V	SE	CD (5%)
Trunk diameter (cm)	22.2	28.1	19.30	19.45	23.00	0.71	1.55
Height (m)	15.7	18.0	14.36	16.74	15.68	0.45	0.98
Clear bole length (m)	4.9	5.6	4.88	5.09	4.60	0.26	0.58
Crown length (m)	10.7	12.4	9.48	11.65	11.08	0.33	0.72
Crown width (cm)	612.9	733.8	473.00	594.70	598.00	12.83	28.24
Branch length (cm)	342.0	396.2	264.70	321.50	379.50	10.05	22.10
No. of branches	35.9	48.4	32.10	44.50	39.65	4.23	9.29
Length of leaf blade (cm)	13.9	13.3	10.27	13.15	11.60	0.68	1.49
Petiole length (cm)	8.9	8.5	6.10	8.25	8.60	0.65	1.42
Leaf length (cm)	22.8	21.8	16.50	21.45	20.20	1.06	2.33
Leaf width (cm)	14.0	14.4	9.75	12.76	11.50	1.24	2.74
Bark thickness (cm)	1.0	1.2	0.92	1.22	1.05	0.03	0.07
Branch angle	80.3	82.7	76.29	80.61	81.61	1.06	2.33
Fall duration (days)	204.2	183.2	214.00	196.00	196.00	2.94	6.47
Under bark tree volume (m^3)	0.3	0.5	0.21	0.37	0.28	0.3	0.06
Over bark tree volume (m^3)	0.3	0.5	0.23	0.44	0.32	0.09	0.19

V (V. L. Onda) indicated that the varieties in these two clusters were relatively closes to each other. The estimation of genetic divergence has wide scope in tree breeding as it helps in identifying the diverse genotypes for a crossing programme [3–5].

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