GENETIC DIVERGENCE IN *PINUS ROXBURGHII*

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Pinus roxburghii, commonly known as Chir pine or Himalayan long-leaved pine, belongs to the family Pinaceae and is one of the most important pines in India. It has a wider adaptability, being less demanding on soil and nutrients than other conifers. This is the most important species for plantation on degraded areas in its zone of distribution. As per altitudinal limits, it grows between 450 and 2300 m which covers the ridges of Shiwalik hills in the outer ranges of the Himalaya. Its distribution in India is confined to Jammu and Kashmir, Himachal Pradesh, Uttranchal, Sikkim, Arunachal Pradesh, Manipur and Morni hills of Haryana.

To make an improvement in any species, the breeder is constantly engaged in an effective choice of desirable parents of high genetic variability so that individuals with desirable character combinations can be selected. Genetically diverse parents are likely to produce high heterotic effect and desirable segregants. Thus the genetic diversity has an obvious significance. Multivariate analysis by means or Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of divergence among the biological populations.

Divergence analysis in forest tree species was employed by Burley and Burrons (1972) in *P. kesiya*, Khosla *et al.* (1979) in *Populus ciliata*, Surendran and Chandrashekharan (1988) in *Eucalyptus tereticornis*, Singh and Chaudhary (1991) in Chilgoza pine, Singh and Chaudhary (1992) in *Prunus armenica*, Chauhan *et al.* (1997) in *Bauhinia variegata*, and Chauhan and Hosalli (1998) in *Leucaena varieties*. The present investigation was aimed at ascertaining the nature and magnitude of genetic divergence present among 48 plus trees of *P. roxburghii* and further utilisation in hybridisation programme.

The material for the present study was procured on the basis of compartment history files, vis-a-vis information obtained from the territorial staff of the forest department of Himachal Pradesh, India. The best quality, similar-aged stands with an average age of 60 ± 15 years were selected in different forest divisions in the state of Himachal Pradesh. From these stands, 48 phenotypically superior trees were selected for best growth form and high resin yield with the help of scoring method (Ledig 1974) by comparing with five dominant and co-dominant trees (check tree). Thirty cones per tree were randomly selected, out of which 10 cones per replicate were taken, thus having in all three replicates. Data were recorded on cone length, cone width, cone weight, seeds per cone, seed length, seed width and 100 seed weight. The data were statistically analysed for each character in a randomised block design. Genetic divergence was determined using Mahalanobis D^2 statistics (Mahalanobis 1936). Group constellation was formulated after computation of D^2 values by the method suggested by Tocher and reported by Rao (1952).

The analysis of variance revealed highly significant differences for all the traits, indicating the existence of huge genetic variability among the plus trees. Based on the relative magnitude of D^2 values, 48 plus trees were grouped into 9 clusters (Table 1). Maximum numbers of plus trees were grouped in cluster VII (10 plus trees), followed by cluster II and cluster IX (9 and 8 plus trees respectively).

Table 1 Distribution of 48 plus trees in different clusters

Cluster No.	No. of plus trees in each cluster	Collection number of the plus trees
I	6	22, 30, 31, 32, 36, 48
II	9	4, 7, 10, 14, 18, 35, 39, 41, 45
III	1	42
IV	5	3, 23, 28, 40, 47
V	3	1, 16, 29
VI	1	13
VII	10	2, 9, 11, 19, 21, 24, 26, 33, 34, 43
VIII	5	8, 12, 20, 38, 46
IX	8	5, 6, 15, 17, 25, 27, 37, 44

Table 1 shows that some plus trees from different locations are accommodated in the same cluster (tree numbers 22, 30, 36 and 48 in cluster I; 3, 23 and 40 in cluster IV; 1 and 29 in cluster V; 2, 11, 19, 21, 24 and 43 in cluster VII; 38 and 46 in cluster VIII; and 5, 6, 15, 17, 27 and 44 in cluster IX). This indicates their close affinity. On the other hand, plus trees from the same location/ area were distributed to different clusters (tree numbers 13 and 14, 32 and 33, 4 and 5, 43 and 44, 47 and 48, 34 and 35, and 18 and 19), indicating that geographical diversity may not necessarily be related to genetic diversity. These findings are in general agreement with Pandey *et al.* (1995), Chauhan *et al.*(1997), and Chauhan and Hosalli (1998) in different forest tree species.

Intra-cluster distance ranged from 0.001 (Cluster III) to 1.808 (Cluster IV). Maximum inter-cluster distance (9.055) was found between cluster V and cluster VI, followed by cluster III and VI (9.001), suggesting wide diversity between the groups. The crosses made between the genotypes from the above clusters may give transgressive segregants. On the other hand, minimum distance (1.863) was recorded between cluster VII and IX, indicating minimal diversity between these clusters. On the basis of inter- and intra-cluster distances, clusters III, IV, V, VI and VIII may be considered as most diverse and can be utilised for hybridisation when selecting trees for breeding purposes.

Besides high genetic divergence, the performance of plus trees for characters with maximum contribution towards genetic divergence should also be given due consideration (Table 2). The relative contribution (Table 3) of different characters towards genetic divergence showed that cone length gave maximum contribution (55.9%), followed by cone width (18.4%) and cone weight (10.9%).

Comparison of cluster means for eight characters (Table 3) indicated that different characters showed considerable differences between the clusters. Maximum cone length and cone weight were recorded for cluster IV, followed by cluster VIII. Cluster VIII also recorded maximum cone width and seeds/cone, followed by cluster III. Cluster VI recorded maximum values for seed length, seed width, seed thickness and 100 seed weight. Considering the cluster distances and cluster means, clusters IV, VI and VIII may be employed for improvement programme in *P. roxburghii.*

Table 2 Inter- and intra-cluster distances of the genotype clusters

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	<u>1.319</u>								
II	2.266	<u>1.277</u>							
III	5.540	5.984	<u>0.001</u>						
IV	4.040	2.324	5.825	<u>1.808</u>					
V	4.753	6.588	4.261	7.501	<u>1.632</u>				
VI	4.432	3.315	9.001	4.902	9.055	<u>0.002</u>			
VII	2.364	2.205	3.940	3.178	5.049	5.087	<u>1.196</u>		
VIII	3.913	2.403	5.532	2.589	7.323	4.349	2.447	<u>1.729</u>	
IX	2.139	3.454	3.595	4.480	3.366	6.070	1.863	4.060	<u>1.308</u>

Underscored values are intra-cluster distances

Table 3 Mean performance of clusters with respect to different traits

Cluster No.	Cone length (cm)	Cone width (cm)	Cone weight (g)	Seeds/ cone	Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100 seed weight (mm)
I	13.22	5.66	130.68	45.15	11.53	6.27	3.94	11.04
II	14.88	6.06	180.63	56.61	12.28	6.65	3.87	11.86
III	13.32	6.24	150.50	71.33	9.67	5.18	3.12	6.90
IV	17.80	5.84	236.51	55.54	11.99	6.62	3.64	10.83
V	10.52	5.21	60.60	41.44	9.78	5.29	3.49	6.49
VI	14.21	5.88	185.94	61.83	12.60	7.33	4.41	15.54
VII	13.62	6.19	155.98	66.49	11.41	6.14	3.70	9.89
VIII	16.72	6.34	193.21	79.35	11.86	6.27	3.95	11.07
IX	12.51	5.70	129.68	54.84	10.46	5.89	3.73	9.14
Per cent variation explained by each root	55.86	18.39	10.90	5.19	3.20	3.11	1.92	1.42

The study revealed maximum genetic variability among the plus trees and the characters studied, i.e. cone length, cone width and cone weight showed highest genetic diversity. On the basis of inter- and intra-cluster distances, clusters IV, VI and VIII were most divergent and may be utilised in hybridisation programme in *P. roxburghii.*

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