

Divergence studies of white willow (*Salix alba* L.) germplasm

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The present study was carried out with the aim to determine genetic diversity in *Salix alba* germplasm/plus trees by employing the various catkin, seed and seedling characteristics. Divergence studies revealed grouping of 20 plus trees of *S. alba* into five clusters, with maximum plus trees in clusters I and II. There was maximum (748.77) cluster distance between clusters V and IV among all the clusters. This was followed by clusters I and IV (598.23). It indicates that there exists wide diversity between these groups. Cluster V had maximum for majority of the catkin, seed and seedling characteristics under study. The plus trees/genotypes in the clusters which are more divergent can be used for future breeding/tree improvement programmes of the species.

Keywords: Clustering, divergence, germplasm, plus trees, *Salix alba*.

WITH a total of 450–520 species, *Salix* is to a large extent distributed in the Northern Hemisphere of the earth^{1,2}. The species are found in all the continents with the exception of Antarctica and Australia^{3,4}. In India, there are about 33 *Salix* species which have majorly been categorized as shrubs, except *S. alba*, *S. babylonica*, *S. daphnoides*, *S. fragilis*, *S. elegans* and *S. tetrasperma*. In the Kashmir valley, the genus *Salix* is represented by 23 species, of which 15 reach alpine/subalpine limits⁵. White willow (*Salix alba* L.) is a moderate to a large deciduous tree with ascending branches and spreading but light crown, attaining a height of 20–25 m and a diameter of 60 cm. Under native habitat, trees are known to attain a height of 30 m and 1 m in diameter. White willow is primarily utilized for cricket bats and polo balls, fruit boxes, artificial limbs, match-wood, honey-comb frames, tool handles, fibre-boards, agricultural implements and boats; it is as durable as oak⁶. Tender shoots are woven into baskets and ropes. Dried inner bark is powdered and made into bread. Decoction of tender twigs is given as a beverage; also used as an adulterant to tea. Bark yields, tannin (5–7%) and salicin, are utilized as haemoptysis in rheumatism, diarrhoea and dysentery⁷. The tree is extensively planted in cold deserts along with other *Salix* species for conservation and reclamation of soil in catchment areas, to prevent erosion along stream banks, as live fence for check dams, on roadside avenues for recreation

and agro-forestry. The white willow has a wide natural distribution over the whole of Europe, except the extreme north, and also occurs in Western Asia and in small parts of North Africa. *S. alba* belongs to the boreal-Mediterranean type of habitat. Its natural distribution ranges from the British Isles (excluding Scotland) in the west, to western Siberia in the east and from southern Scandinavia in the north to the Near East, Palestine, Morocco and Algiers in the south. In the South it reaches altitudes of 2400 m amsl and in the north about 600 m amsl⁸. In India, it is extensively cultivated in the Western Himalaya, up to 2400 m amsl, mostly in Kashmir and Kulu valleys along river streams, canal banks and around lakes. It is also reported to have been raised in dry temperate zone of Lahaul and Ladakh at a much higher altitude, mainly for fuel-wood and fodder⁶. Diversity analysis has relevance in genetic resource conservation, breeding and evolution. It is essential to possess information on genetic divergence of desired traits in order to start a breeding programme⁹ for improvement and conservation of a species^{10,11}. Diverse parents when hybridized will result in variable progeny. There are chances of obtaining variants with desired characters. It is in this context that diversity analysis using Mahalanobis D^2 statistics has been used in various tree species such as *Jatropha curcas*¹², *Pongamia pinnata*^{13,14}, wild apricot¹⁵ and *Madhuca latifolia*¹⁶. However, no such information is available with respect to *S. alba* in the Kashmir valley and as such an effort has been made in this direction. In this context, twenty plus trees of *S. alba* were used for the present study.

The study was conducted in the Faculty of Forestry, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST-K). Twenty plus trees of *S. alba* were selected on the basis of outstanding phenotypic characteristics from different places following comparison tree method (Table 1). These plus trees were marked and recorded for various catkin and seed characteristics, viz. catkin length (cm), catkin width (mm), number of capsules/catkin, capsule diameter (mm), 100-catkin weight (g), 1000-seed weight (mg) and germination percentage. Simultaneously, progeny trial of these plus trees was laid out in the Faculty nursery in a mist chamber, which was maintained according to the standards. The experimental design used for the present study was randomized complete block design with three replications. The progeny trial was evaluated at the end of the growing season for various seedling morphometric characteristics (growth, biomass and leaf traits). The data were analysed using Mahalanobis D^2 statistics for estimating genetic divergence among the *S. alba* germplasm/plus trees⁹. The clusters were formed according to Tocher's algorithm¹⁷. In this process, closely associated genotypes are grouped together in one cluster on the basis of similarity or dissimilarity. The process continues until all the genotypes are resolved into different clusters. It is

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Table 1. Characteristics of *Salix alba* plus trees used in the present study

Plus trees	Source	Height (m)	DBH (cm)	Volume (m ³)	Bole height (m)	Crown diameter (m)
CPT-26	Sehpora (Ganderbal)	13.2	34.9	0.81	6.0	4.2
CPT-86	Sonawari (Bandipora)	13.6	22.8	0.36	6.2	3.4
CPT-75	Ajas (Bandipora)	12.4	23.4	0.34	5.4	2.7
CPT-45	Tulmulla (Ganderbal)	10.7	27.2	0.40	4.7	2.5
CPT-98	Sumba (Bandipora)	14.0	34.5	0.84	6.5	3.8
CPT-56	Ashtangoo (Bandipora)	12.6	23.4	0.35	5.8	2.7
CPT-37	Wakura (Ganderbal)	14.4	23.5	0.40	6.2	3.2
CPT-12	Haran (Ganderbal)	14.5	35.0	0.89	6.1	4.2
CPT-42	Tulmulla (Ganderbal)	11.6	31.2	0.57	5.1	3.5
CPT-23	Gundrehman (Ganderbal)	11.6	28.2	0.46	5.2	3.4
CPT-79	Kaimbachoo (Bandipora)	14.0	31.1	0.68	5.8	3.5
CPT-92	Saderkote (Bandipora)	10.8	25.5	0.35	4.6	2.8
CPT-6	Dab (Ganderbal)	11.9	28.8	0.50	5.4	4.0
CPT-50	Butwana (Ganderbal)	11.8	25.2	0.37	5.2	3.9
CPT-4	Shalbugh (Ganderbal)	12.2	27.2	0.45	5.3	3.7
CPT-53	Aloosa (Bandipora)	11.7	31.2	0.57	5.1	3.2
CPT-81	Hajin (Bandipora)	11.1	31.2	0.54	5.1	2.8
CPT-62	QuilMuqaam (Bandipora)	11.9	25.8	0.40	5.4	2.8
CPT-17	Chandun (Ganderbal)	11.9	27.2	0.44	5.2	3.0
CPT-69	Zaalwan (Bandipora)	13.6	33.6	0.77	5.4	4.1

DBH, Diameter at breast height.

Table 2. Composition of Euclidean clusters for catkin, seed and seedling characteristics of *S. alba* genotypes

Cluster	Number of plus trees	Plus trees
I	9	CPT-98, CPT-4, CPT-75, CPT-92, CPT-50, CPT-69, CPT-12, CPT-37, CPT-81
II	8	CPT-45, CPT-56, CPT-86, CPT-23, CPT-42, CPT-79, CPT-26, CPT-17
III	1	CPT-62
IV	1	CPT-53
V	1	CPT-6

Table 3. Cluster distance (intra and inter) for catkin, seed and seedling characteristics of *S. alba* genotypes

Cluster	I	II	III	IV	V
I	102.98	266.77	180.42	598.23	204.68
II		104.40	193.62	221.86	380.74
III			0.00	568.17	367.42
IV				0.00	748.77
V					0.00

this clustering pattern which gives an insight into the diversity pattern of a particular germplasm.

Mahalanobis D^2 statistics resolved 20 plus trees of *S. alba* into five clusters (Table 2). There were nine and eight plus trees in clusters I and II respectively. However, the rest of the clusters had only one plus tree each (Figure 1). The present findings also confirm that geographic and genetic diversity are not related to each other. It may be attributed either to the scattered distribution of plus trees from one geographic region to different clusters or plus

trees from different geographic regions may group together in one cluster. Table 3 presents the intra- and inter-cluster distances. This table clearly indicates that cluster II has the highest intra-cluster distance (104.40), whereas it was lowest for clusters III, IV and V having only one plus tree each. Clusters V and IV have maximum inter-cluster distance (748.77), followed by clusters IV and I (598.23). This suggests that there is wide genetic diversity between the groups. However, clusters III and I have minimum inter-cluster distance (180.42). Table 4 presents the cluster means. Significant variation is observed among these clusters for all the selected traits. Cluster V has maximum mean values for catkin length, catkin width, capsule diameter, 100-catkin weight, 1000-seed weight, shoot height, length/width ratio, number of leaves per plant and leaf angle. Cluster I has maximum mean values for survival percentage, root length, collar diameter, aboveground biomass, belowground biomass and total biomass. Cluster III has maximum mean values for leaf length, leaf width, petiole length and position of maximum width. Cluster IV has

Table 4. Cluster mean value for catkin, seed and seedling characteristics of *S. alba* genotypes

Parameter	Cluster mean				
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Catkin length (cm)	7.97	6.43	5.23	8.83	9.13
Catkin width (mm)	7.83	7.28	9.33	4.77	9.43
Capsules/catkin	81.52	68.46	72.62	84.67	67.3
Capsule diameter (mm)	3.18	2.60	1.30	3.50	3.81
100-Catkin weight (g)	82.64	70.89	61.37	98.73	107.33
1000-Seed weight (mg)	89.95	77.18	67.73	108.10	118.53
Germination percentage	91.93	85.29	84.00	96.6	93.33
Survival percentage	90.30	81.00	87.00	76.33	90.00
Shoot height (cm)	27.79	19.10	24.60	17.80	28.90
Root length (cm)	13.39	9.40	11.57	8.37	12.20
Collar diameter (mm)	3.12	1.90	2.47	1.90	1.50
Aboveground biomass (g)	2.64	1.59	2.37	1.80	2.07
Belowground biomass (g)	1.43	0.94	1.30	1.17	1.17
Total biomass (g)	4.07	2.53	3.67	2.97	3.23
Root/shoot ratio	0.55	0.60	0.55	0.65	0.57
Leaf length (cm)	8.69	8.40	9.93	8.13	7.53
Leaf width (cm)	1.51	1.48	1.77	1.43	1.26
Length/width ratio	5.76	5.73	5.60	5.61	5.80
Petiole length (mm)	1.27	1.23	3.78	2.30	1.80
Position of maximum width (cm)	3.46	3.13	4.07	3.37	2.70
Number of leaves/seedling	7.43	4.79	6.77	3.47	7.50
Leaf angle (°)	56.56	59.36	57.30	54.47	62.83

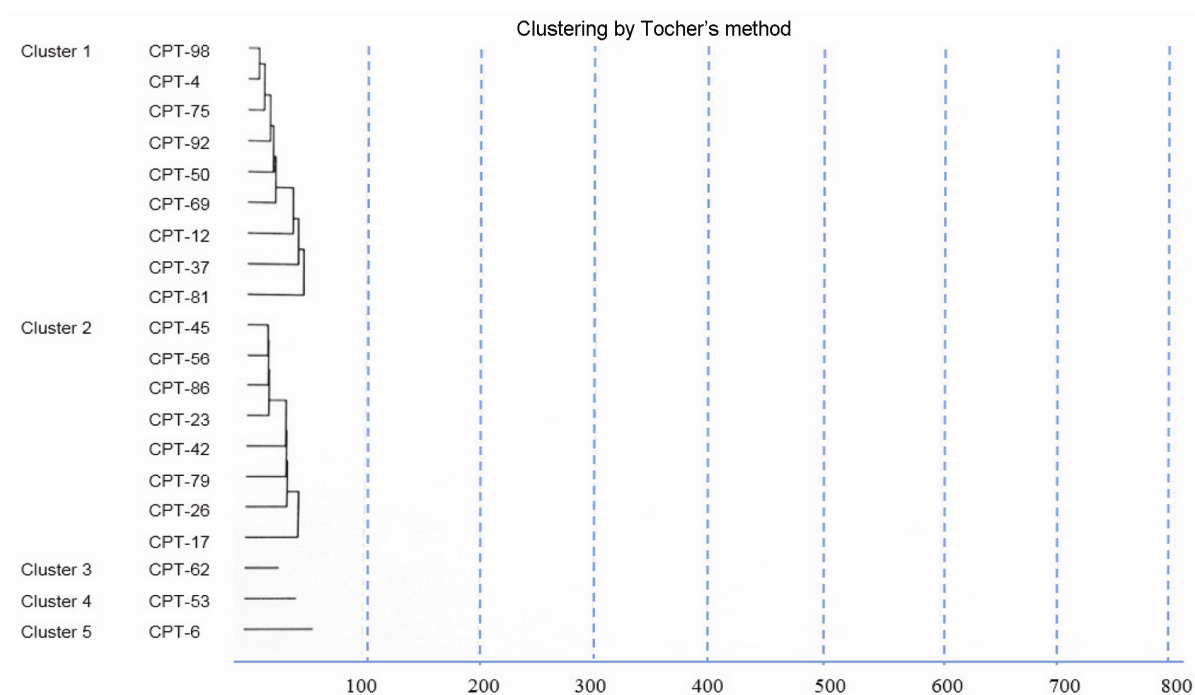


Figure 1. Dendrogram depicting different clusters of genotypes in *Salix alba* germplasm.

highest mean values for number of capsules per catkin, germination percentage and root/shoot ratio.

Divergence in plants is a pre-requisite for selection and further improvement of tree species. The knowledge on diversity of plants is important for planning future collections as well as for efficient utilization of genetic re-

sources. Besides, it is also considered as an important tool in realizing the potential of a plant species for maximum growth, yield and other associated traits. In this context, a number of statistical tools such as Mahalanobis D^2 analysis, cononical and principal component analysis have been at the forefront. However, D^2 statistics is one

of the popular tools to analyse genetic diversity. It helps determine the relative contribution of different component traits in the total variability. Besides, it is also equally important in determining the degree of variability between populations. This is essential while selecting parents with wide diversity in order to have fruitful recombinations. In the present study, 20 plus trees/genotypes of *S. alba* were resolved into five clusters following non-Euclidean hierarchical cluster analysis (Table 2 and Figure 1). This type of clustering pattern revealed no relation between geographical and genetic diversity. The genetic diversity may be attributed to different factors such as differential adoption methods, selection criteria, selection pressure and environment factors¹⁸, which indicates that genetic drift resulted into greater diversity than that of geographic diversity¹⁹. Earlier studies in *Jatropha curcas*¹², *Pongamia pinnata*¹³ and *Madhuca latifolia*¹⁶ are in line with the present findings, where no relation was observed between genetic diversity and geographical distribution. This can be attributed to the changes that these trees may have undergone during the process of selection. Plus trees in clusters II and I could be used for hybridization within groups as they were diverse and had maximum intra-cluster distance. Similarly, wider genetic diversity was observed between clusters V and IV, as they had maximum inter-cluster distance, followed by clusters IV and I. Thus, these groups can be utilized for hybridization, which will definitely yield fruitful results in the form of variable segregants having desired traits. This will be helpful in the improvement of the tree species in question.

11. Gradual, L., Kjaer, E. D., Suangtho, P. and Kaossard, A., Conservation of genetic resources of teak (*Tectona grandis*) in Thailand. Technical Note No. 52, Danida Forest Seed Center, Denmark, 1999.
12. Rao, G. R., Korwar, G. R., Shanker, A. K. and Ramakrishna, Y. S., Genetic associations, variability and diversity in seed characters, growth, reproductive phenology and yield in *Jatropha curcas* (L.) accessions. *Trees*, 2008, **22**, 697–709.
13. Rao, G. R., Shanker, A. K., Srinivas, I., Korwar, G. R. and Venkateswarlu, B., Diversity and variability in seed characters and growth of *Pongamia pinnata* (L.) Pierre accessions. *Trees*, 2011, **25**, 725–734.
14. Divakara, B. N. and Das, R., Variability and divergence in *Pongamia pinnata* for further use in tree improvement. *J. For. Res.*, 2011, **22**(2), 193–200.
15. Singh, N. B. and Chaudhary, V. K., Multivariate analysis of genetic divergence in wild apricot (*Prunus armeniaca* Linn.). *Indian J. For.*, 1992, **15**, 211–216.
16. Divakara, B. N., Relationship of seed traits on initial progeny growth performance and divergence studies in *Madhuca latifolia* Macb. for further use in tree improvement. *J. Trop. For. Environ.*, 2014, **4**(2), 11–23.
17. Rao, C. R., *Advanced Methods in Biometrical Research*, John Wiley, New York, 1952.
18. Vivekananda, P. and Subramanian, S., Genetic divergence in rainfed rice. *Oryza*, 1993, **39**, 60–62.
19. Singh, A. K., Singh, S. B. and Singh, S. M., Genetic divergence in scented and fine genotypes of rice (*Oryza sativa* L.). *Ann. Agric. Res.*, 1996, **17**, 163–166.

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1. Argus, G. W., Infrageneric classification of *Salix* L. (Salicaceae) in the New World. *Syst. Bot. Monogr.*, 1997, **52**.
2. Skvortsov, A. K., *Willows of Russia and Adjacent Countries: Taxonomical and Geographical Revision* (transl. from: Skvortsov, A.K., *Willows of the USSR: Taxonomic and Geographic Revision*, Nauka, Moscow), 1968, Joensuu University, Joensuu, Finland, 1999.
3. Kuzovkina, Y. A. and Quigley, M. F., Willows beyond wetlands: uses of *Salix* L. species for environmental projects. *Water Air Soil Pollut.*, 2005, **162**, 183–204.
4. Trybush, S., Jahodova, S., Macalpine, W. and Karp, A., A genetic study of *Salix* germplasm resource reveals new insights into relationships among subgenera, sections and species. *Bioenergy Res.*, 2008, **1**(1), 67–79.
5. Dar, U. and Kachroo, P., *Alpine Flora of Kashmir Himalaya*, Scientific Publishers, Jodhpur, 1983, p. 169.
6. Luna, R. K., *Plantation Trees*, Publishing Corporation, International Book Distributors, Dehradun, 1995, pp. 640–645.
7. CSIR, *Plants for Reclamation of Wastelands*, CSIR, New Delhi, 1990.
8. Weber, E., Genetic Der *Salix alba* L. *An. Za Sumarstvo*, 1974, **6**, 5–25.
9. Chaturvedi, O. P. and Pandey, N., Genetic divergence in *Bombax ceiba* L. germplasm. *Silvae Genet.*, 2001, **50**, 99–102.
10. Ayad, W. G., Hodgkin, A. J. and Rao, U. R., Molecular Genetic Techniques for Plant Genetic Resources. International Plant Genetic Resources Institute Report, Maccarese, Rome, 1995.

Estimating net primary productivity of croplands in Indo-Gangetic Plains using GOME-2 sun-induced fluorescence and MODIS NDVI

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Recently evolved satellite-based sun-induced fluorescence (SIF) spectroscopy is considered as a direct measure of photosynthetic activity of vegetation. We have used monthly averages of satellite-based SIF retrievals for three agricultural year cycles, i.e. May to April for each of the three years, viz. 2007–08,

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