

Willow Improvement in India with a Special Reference to Work Done at Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni

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Introduction

Willow (*Salix*) being a multipurpose species across the globe is well recognized in short rotation forestry. In India, its importance is well noticed in sports industry, as household timber because of its myriad uses. Willow is the life line in Lahual Spiti dry temperate region of H.P.

The willows, belonging to the genus *Salix* (Salicaceae), are one of the most important taxonomic entities of the world because of the great number of species and varieties. Willows are commonly found in three groups namely: Arborescent willows, osiers or basket willows and sallows or pussy willows; i.e., low shrubs to small trees with multiple stems. There are about 330-500 species worldwide (Argus, 1997) occurring mostly in the Arctic and north-temperate zone, only few species occur in the southern hemisphere covering tropical and subtropical zones. There are 103 species in North America, few in Africa and 65 species in Europe. In Asia, *Salix* centre of abundance is in China with 275 species including endemics (Zhenfu *et al.*, 1999) and there are about 120 species in the former Soviet Union (Argus, 1999). Around 33 species of willows are reported from India out of which, seven species of tree willows, namely *S. tetrasperma*, *S. acmophylla*, *S. alba*, *S. fragilis*, *S. babylonica*, *S. daphnoids* and *S. excelsa* are found from northern temperate parts of Jammu and Kashmir to Arunachal Pradesh. However, *S. tetrasperma* is occurring throughout the country and *S. acmophylla* is distributed in north-west India, and rest of the species are confined to sub Himalayan track to higher reaches (WoI, 1972). The area under indigenous *Salix* species in the country is 108,000 hectare and only 28,300 hectare is under agroforestry (NPC, 2012). Sinha and Sharma (2002) have emphasized the suitability and growth pattern of *Salix* species in Himalayan foothills. Phenological study of *Salix* species has been completed in Indian conditions (Choudhary *et al.*, 2011). In addition to the naturally occurring hybrids in various parts of the world, a considerable number of hybrids have been artificially produced by controlled mating (Newsholme, 2003). Many examples of successful inter- and intra-specific hybridization on willows have been reported (Argus, 1974; Hathaway, 1977; Scott, 1984; Zsuffa *et al.*, 1984; Kajba *et al.*, 1998, 1999; Larsson, 2000; Kopp *et al.*, 2001). Scott (1984) identified 54 species worldwide for biomass production breeding that produced hybrids having high productive potential and better adaptability to climatic and edaphic factors. Several different forms in terms of habit, utilization properties and value addition for *Salix* in the Himalayan region are the result of natural hybridization

(Biswas and Hussain, 2008). Many hybrids of *Salix* species (willow) have been developed through control-pollination in India (UHF, 2012). The productivity of hybrid clones of willow is reported to be 44 m³/ha/yr in Argentina, 50 m³/ha/yr in China, 67.2 m³/ha/yr in Turkey and, 70 m³/ha/yr in Croatia (Singh *et al.*, 2011). In India clone J-799 recorded maximum diameter at breast height (16.50 cm) and volume index (0.554 m³) followed by NZ-1140 and 131/25 clones in five year growth. Bole straightness was registered highest in clone J-795 which was at par with clones 194, PN-721 and 131/25 (Sharma *et al.*, 2011).

Willow Research in India

Collection, Nursery Evaluation, Field Testing and Multilocation Trials of Willow Germplasms

Willow (*Salix*) being a multipurpose species across the globe is well recognized in short rotation forestry. In India, its importance is well noticed in sports industry, as household timber because of their myriad uses. Willow is the life line in Lahual Spiti dry temperate region of Himachal Pradesh (H.P.). The very ecology and economics is based on the cultivation of this plant group; i.e., *Salix* species. There was large scale drying of willow plants in the region and as a result Himalayan Forest Research Institute (HFRI) at Shimla and university sent the team of scientists to ascertain the probable causes of mortality. Apart from other recommendations given by both teams separately, the replacement of old germplasm by new clones was one of the major course of actions suggested. Accordingly, the Department of Tree Improvement and Genetic Resources took the lead in researchable issues on willow.

Germplasm collection

Over the years two hundred clones/strains/species were procured from 20 different countries covering five continents namely Europe, North America, South America, Asia and Africa. These clones were subjected to repeated nursery screening in the year 2003-2005 followed by field testing (Sharma *et al.*, 2011).

Nursery evaluation of arborescent willow germplasms

Nursery evaluation of 75 clones of willow: The introduced clones were screened in the nursery twice. In the third testing juvenile growth traits were studied in the 75 introduced clones of *Salix* species. The clones were screened in the nursery by applying augmented completely randomized design with three check clones (SI-64-017, SI-63-007, Kashmiri willow) for phenotypic, genotypic, their correlations and principal component analysis. Significant

differences were recorded for morphological traits among clones, except in leaf length among test clones and volume index, leaf length and petiole length among check versus test clones. The clones SI-63-016, J-799, PN-722, NZ-1002, PN-733, PN-731, SN-2, Sx61, 194 and 084/03 were found superior to check clones for the growth traits, viz., plant height, basal diameter and volume index. Heritability in broad sense (91.08 per cent) and genetic gain (75.24 per cent) were found highest for leaf breadth and volume index, respectively. Maximum positive and significant correlation coefficient (0.959) was recorded for basal diameter with volume index. Principal component analysis through correlation matrix revealed that three out of eight components contributed 85.03 per cent of the overall variation out of which the first principal component ($\bar{\epsilon}=3.086$) explained 38.57 per cent of the variance weighted maximum (0.937) by volume index (Singh *et al.*, 2012a).

Nursery evaluation of 25 clones: Twenty-five clones were evaluated for various growth characteristics. Maximum values for plant height (290.35cm) and collar diameter (17.38 mm) were recorded for clone 799 (U.K.), respectively. The highest value for shoot fresh weight (243.25 g), shoot dry weight (138.94 g), root fresh weight (184.05 g) and root dry weight (102.87 g) were recorded for Kashmir willow (U.K.). Heritability percentage (broad sense) was recorded to be maximum (99.78 per cent) for leaf area. Maximum genetic gain (61.58 per cent) was recorded for leaf area that was closely followed by number of branches (60.39 per cent). Growth characteristics were found to have positive and significant correlation with most of the characters (Joshi, 2009).

Principal component analysis (PCA), employed in the present study taking 12 important parameters, proved useful in extracting the most important factors. Three principal components contributed 83.49 per cent variance. First principal component contributed 59.55 per cent for 10 characters followed by second principal component 12.6 per cent for plant height and third one 11.33 per cent for leaf area. In the first PCA high loadings for traits such as total dry weight (0.966), total fresh weight (0.953), shoot fresh weight (0.928), shoot dry weight (0.921) and root fresh weight (0.901) represented those which are most likely to be important for selection and further improvement of willow. The study reveals that maximum weightage should be given to total dry weight due to its maximum variable loading for the initial selection of clones followed by plant height for the biomass improvement of willow (Singh *et al.*, 2012b).

Nursery evaluation of 23 clones of willow: Quantitative genetic parameters on growth characteristics, viz., height,

collar diameter, volume index, number of branches, number of nodes, internodal length, leaf display, leaf area, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight and total dry biomass were studied on 23 tree willow clones in order to analyse the variation in performance of these clones in the foothills of Himalaya mountains in India. Among all these parameters dry shoot weight showed widest range of values (4.68- 378.05 g, mean 117.86 g), followed by volume index (9.29-721.50, mean 356.42) whereas narrowest range was recorded for leaf display (195.0-291.0, mean 238.17). Regarding coefficient of variation, genotypic coefficient of variation (GCV), was maximum (81.78 per cent) for number of branches, while minimum (10.22 per cent) was exhibited by leaf display. All the biomass parameters, viz., fresh shoot weight, dry shoot weight, root fresh weight, root dry weight and total dry biomass showed higher genotypic coefficient of variation; i.e., 73.66 per cent, 72.06 per cent, 75.82 per cent, 71.21 per cent and 70.72 per cent, respectively in comparison with other parameters. Phenotypic coefficient of variation (PCV) followed same pattern with slightly higher values for all the parameters than GCV. Heritability percentage was recorded to be maximum (h^2 b.s. = 96.10) in leaf display (days). It was followed by number of branches (h^2 b.s. = 96.00) and root fresh weight (h^2 b.s. = 96.00), height (h^2 b.s. = 95.80), root dry weight (h^2 b.s. = 95.80) and total dry biomass (h^2 b.s. = 94.90) and the minimum heritability (h^2 b.s. = 78.10) was registered for inter nodal length. Genetic gain as per cent of mean varied from 20.64 to 164.74 for leaf display and number of branches, respectively. All five biomass parameters, viz., fresh shoot weight, dry shoot weight, root fresh weight, root dry weight and total dry biomass showed higher genetic gain as per cent of mean 145.42, 142.15, 153.06, 143.59 and 141.96, respectively. Genetic gain for height was recorded to be 67.51 per cent (Singh and Huse, 2004c; Huse *et al.*, 2005; 2012).

Height, collar diameter and volume index, all at genetic level, showed a positive significant correlation with all the growth and biomass parameters except internodal length, which showed positive non-significant correlation coefficient with height. Number of branches exhibited positive significant correlation with all combination traits except the positive non-significant genotypic correlation with number of nodes and negative non-significant correlation with leaf area. Leaf display (days) reported positive significant correlation at both genotypic and phenotypic level with all growth and biomass traits except a positive but non-significant correlation with leaf area. Leaf area showed positive significant correlation with many growth and biomass

parameters but a positive and non-significant correlation with leaf display, root fresh weight and root dry weight was also found. Leaf area also showed a negative non-significant correlation with number of branches and internodal length. All the biomass parameters, viz., fresh shoot weight, dry shoot weight, root fresh weight, root dry weight and total dry biomass showed significant and positive genotypic correlation coefficient among themselves and with all growth and biomass parameters except positive non-significant correlation of leaf area with fresh root weight and dry root weight at both genotypic and phenotypic level. All the parameters showed higher genotypic correlation coefficient (GCC) than phenotypic correlation coefficient (PCC), with exception of correlation between fresh shoot weight and dry shoot weight which had both type of correlation coefficients (genotypic and phenotypic) same (0.997) and higher phenotypic correlation coefficient between number of nodes and number of branches (GCC = 0.138 and PCC = 0.141) and between root fresh weight and leaf area (GCC = 0.125 and PCC = 0.128). Indirect selection can be effectively undertaken for the characters, having positive and significant correlations among themselves (Singh *et al.*, 2003; Singh and Huse, 2004d).

A viable alternative to index selection is the use of principal component analysis. This was found useful in poplar selection as a way to reduce the complexity of multidimensional data sets. By using the principal component analysis, four principal components were extracted: The first one had given value accounting for 50 per cent with 13 variables of growth traits – plant height, collar diameter, volume index, number of branches, number of nodes, leaf display, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight, total dry biomass, wood per cent and fibre length; the second one (15 per cent; four variables – inter nodal length, leaf area, photosynthesis rate and transpiration), the third one (08 per cent; one variable – relative density), and the fourth one (06 per cent; three variables – moisture per cent, bark per cent and water use efficiency). Eigen values indicated that first three components explain 75 per cent of the overall variation in the data. For timber production, the above ground biomass, plant height, and diameter of first principal component should be given higher weighting for the selection of clones (Singh *et al.*, 2004).

Field testing of willow clones

The five years growth performance was evaluated on the willow clones raised in the experimental field at University Campus, Nauni. J-799 has given maximum average plant height (19.33m) which is at par with the clone NZ-1140 (16.33 m)

followed by SI-63-007(14.30 m). As regards, diameter at breast height and volume index clone J-799 registered first rank followed by NZ-1140 and 131/25 recording 16.50 cm and 0.554 m³, 15.30 cm and 0.386 m³; 15.30 cm and 0.368 m³, respectively. Bole straightness was recorded maximum in clone J-795 which was at par with clones 194, PN-721 and 131/25. Heritability in broad sense (46.36 per cent) for bole straightness and genetic gain (67.95 per cent) of the volume index was found highest. Genotypic, phenotypic and environment coefficients of variations were recorded highest for volume index. Genetic correlation coefficient was highest between diameter at breast height and volume index (0.921). On the basis of five year growth performance, most promising five clones namely J-799, NZ-1140, 131/25, SI-63-007 and PN-731 were found suitable for lower and mid-hills of Himachal Pradesh (Sharma *et al.*, 2011; NPC, 2012). Clone J-799 exhibited maximum tree height of 21.23 meters, diameter at breast height 22.75 cm and volume index of 1.119 m³ in 6 years in the same experiment (Table 1) (UHF, 2012).

In another field experiment, 15 selected clones were planted in farmer field at Gandhigram, District Solan, H.P. in February 2007 to assess the performance under agroforestry (with peas, tomatoes and oil seeds). The growth data was recorded in February 2012. Perusal of the data revealed that maximum plant height (18.31 m), diameter at breast height (24.62 cm) and volume index (0.861 m³) were obtained by clone J799. Lowest plant height (5.45 m) collar diameter (7.56 mm) and volume (0.036 m³) were found in clone SE-63-016. Kashmiri willow (*S. alba cv coerulea*) (control) did not perform well and gave plant height, diameter at breast height and volume index of 7.39 m, 10.21 cm and 0.071 m³, respectively. Overall clone J-799 was found to be the best followed by clone SI-64-017 and 084/03 (NZ-1002) (UHF, 2012).

Assessment of site specific clones

On the basis of five year growth stability parameters were worked out with respect to plant height. Clones J799,

131/25 and 194 were found suitable for rich environments. Clone SE-63-016 was found suitable for average environment for both the characters; i.e., plant height and diameter at breast height. Clone SI-63-007 was adaptive to overall environments but only for plant height character. For poor environments, clones NZ-1179 for plant height and PN-722, PN-721 for diameter at breast height are found suitable. Clones NZ-1040, NZ-1140, NZ-1130 were found most adaptive to rich environments for diameter at breast height.

Multilocation trials

Multi-location trials of 18 superior selected *Salix* clones have been carried out at 10 sites in H.P. and 26 locations in 13 states to study the genotype x environment interaction at different sites for analysis of suitability of clones for a particular site.

Multilocation trial of 18 superior clones planted at Rajgarh (Mandi), Tiuri (Una) and Devamanal (Sirmour) in Febuary 2011 were evaluated in the first week of February 2012. The data revealed that the maximum height at Tiuri (Una) was attained by clone NZ1002 (510 cm) which is at par with clones V-311, PN-722, NZ-1140, J-795, SI-64-017, SI-63-007 and PN 721. At Rajgarh (Mandi) maximum height (281.67 cm) was recorded in the clone J-799 which is at par with the clones PN-722, NZ-1040, Kashmiri willow, SI-63-007, SI-64-017, 194, NZ-1179, NZ-1140 and MB-368. The clone NZ-1179 recorded maximum height (199cm) at Devamanal (Sirmour) which is at par with clones PN722, SE-63-016, Kashmiri willow and J799. The clone NZ-1002 recorded maximum basal diameter (62.19 mm) at Tiuri (Una) which is at par with clones SI-64-017, PN-722, V-311, NZ-1040, 131/25, PN-721, NZ-1140, NZ-1130 and SI-63-007. At Rajgarh (Mandi) clone J799 attained maximum basal diameter (13.06 mm) which is at par with clones SI-64-017, PN-722, 194, Kashmiri willow, NZ-1040, NZ-1140 and SE-63-016. The clone NZ-1179 recorded maximum basal diameter (16.10mm) at

Table 1. Growth performance of best clones at different multilocation sites

Site	Height (cm)		Basal diameter (mm)		Volume index (cm ³)	
	Clone	Value	Clone	Value	Clone	Value
Devamanal (Sirmour) (1-yr-old)	NZ-1179	199	NZ-1179	16.2	Kashmiri willow (<i>Salix alba</i>)	618
Rajgarh (Mandi) (1-yr-old)	J799	281.67	J799	13.06	J799	485.91
Tiuri (Una) (1-yr-old)	NZ-1002	510	NZ-1002	62.19	NZ-1002	24389.3
Devamanal (Sirmour) (2-yr-old)	J799	557	J799	48.6	J799	15844.5
Gandhigram (Solan) (5-yr-old)	J799	1831	J194	246.2**	J194	0.861*
Nauni (6-yr-old)	J799	2122	J799	227.5**	J799	1.119*

*Volume index in cubic meter; ** Diameter at breast height.

Devamanal (Sirmour) which is at par with clones Kashmiri willow and SI-64-017 (UHF, 2012).

Reproductive Biology, Crossing Pattern and Hybridization in *Salix* Species

Phenological behavior of different *Salix* species

Six staminate and seven pistillate species were selected for reproductive biology studies. Observations were recorded on different vegetative and reproductive characters in 2008-2009 and 2009-2010. Analysis of variance revealed significant variation among different species with respect to the duration taken for completion of different phenological events. *Salix tetrasperma*, *S. acmophylla*, *S. babylonica* and *S. alba* were reported to initiate most of phenological events earlier than other species. *S. nigra* was found to be last in initiation of different phenological events. There was delay in initiation of first phenological event by different species by at least seven days in 2010 as compared to 2009. Maximum period of vegetative growth was recorded for both staminate and pistillate *S. matsudana* followed by pistillate *S. jessonensis* whereas minimum period was judged for both staminate and pistillate *S. alba*.

The male flower buds burst earlier than the vegetative bud whereas in female the flower buds burst after the leaves started emerging in all the species. *S. tetrasperma*, *S. jessonensis*, *S. acmophylla*, *S. alba* and *S. babylonica* remained leafless from 3rd week of November to 1st week of February, whereas *S. matsudana* and *S. nigra* remained leafless from 2nd week of December till 2nd week of March. Both pistillate and staminate *S. alba* recorded maximum leafless period (100.80, 103.70 and 101.00, 114.67 mean days), respectively in two successive years.

Flower buds of all the species under study from emergence to maturity were examined and divided into five different stages according to their development and maturity. Among staminate species catkin length ranged between 2.00 cm (*S. babylonica*) to 4.94 cm (*S. tetrasperma*). Maximum female catkin length (6.06 cm) was recorded for *S. nigra* where minimum (1.06 cm) was recorded for *S. jessonensis*. Maximum capsule (fruit) length (6.80 cm) was recorded for *S. tetrasperma* whereas minimum capsule (fruit) length of 3.78 mm was recorded for *S. babylonica*. *S. acmophylla*, *S. tetrasperma*, *S. jessonensis* and *S. gracilistyla* were among early flowering species whereas *S. udensis* flowered in staggered manner from last week of January to last week of March. Species like *S. babylonica* and *S. alba* initiated flowering between last week of February and 1st week of March whereas *S. matsudana* and *S. nigra* flowered between 2nd and 4th week of March. *S. tetrasperma*

and *S. babylonica* fruit took maximum and minimum time, respectively for its development. Seed dispersal was noticed earlier in *S. tetrasperma*, *S. jessonensis*, *S. acmophylla* and *S. babylonica* dispersing their seeds during last week of March followed by *S. alba* and *S. matsudana* in 2nd week of April. *S. nigra* dispersed its seeds in last week of April. The length of receptive period of each species varied between three to six days with *S. babylonica* recording minimum (three days) and *S. nigra* maintaining a receptive appearance for six days after pollination. Pollen germination was observed in stigmas that were of age group between 48 to 72 hours for *S. tetrasperma*, *S. alba*, *S. matsudana* and *S. babylonica* (Choudhary *et al.*, 2011).

Pollen study of *Salix* species

Pollen grains of different species/clones were collected in bulk from January to March during 2009 and 2010 both by solvent method and by direct extraction from catkins. The collected pollen grains were stored in sealed desiccators for further use in breeding programmes and for studying the effect of temperature and duration of storage on pollen viability percentage. The size of pollen ranged between 40.49 μ in clone 131/25 to 20.20 μ in *S. babylonica*. *In-vitro* pollen germination percentages of directly collected controls, viz., *S. tetrasperma* (control 1) and *S. alba* (control 2) were maximum 54.28 per cent, 59.60 per cent and 63.58 per cent, 62.88 per cent in 2009 and 2010, respectively as compared to pollen extracted with toluene. Average pollen germination percentage was more in the year 2010 as compared to average pollen germination in 2009. Similarly pollen viability percentages of pollen extracted with toluene were lower than both of the directly collected controls in 2009 and 2010. Maximum viability percentage (79.63 per cent) of toluene extracted fresh pollen was recorded for *S. tetrasperma* (TWE) in 2009. In the year 2010 maximum viability percentage (80.50 per cent) of toluene extracted pollen was recorded for *S. tetrasperma* clone TFB.

The long term storage showed a linear declining trend in the viability percentage among different species/clones stored at -20°C and 4°C temperature in 2009 and 2010. Decline in pollen viability was at higher rate within first three months at -20°C as compared to 4°C -20°C temperature with controlled humidity was found effective in long term storage of pollens for breeding programmes.

Different pollen vectors that consistently visited the flowers of different *Salix* species included flies, wasps, honey bees and bumble bees. These insect visited flowers all the day but maximum activity was observed between 8.30 am to 11.30 am which coincided with the pollen shedding and anthesis (Choudhary *et al.*, 2011).

Crossing pattern and controlled hybridization

The crossability pattern and genetic variation among controlled pollinated progenies of tree willows (*Salix* spp.) was studied during 2008-2010. The investigations included the study on reproductive biology of different *Salix* species, pollen collection, storage, germination and pollen viability of different species/clones, assessment of crossability relationship among selected species, controlled hybridization among selected willow clones using incomplete diallel mating design for production of hybrids, revealing molecular genetic variation among selected species/clones that also included the parents involved in hybridization and paternity analysis of hybrids (Table 2).

Species, viz., *S. tetrasperma* and *S. matsudana* showing higher compatibility rate and values of crossability parameters in intra-specific cross combinations. *S. matsudana* and *S. alba* were found highly compatible and showed higher values of crossability parameter among inter-specific combinations should be involved in inter-specific breeding programme. Intra-specific crossing in the species, viz., *S. tetrasperma* and *S. matsudana* [*S. tetrasperma* (LP) x *S. tetrasperma* (TWE), *S. tetrasperma* (LNF) x *S. tetrasperma* (LNM), *S. tetrasperma* (LP) x *S. tetrasperma* (TFB) and *S. matsudana* (PN-227) x *S. matsudana* (PN7-22)] was found easier and genotype may be used for objective specific breeding. Pollen parents, viz., *S. tetrasperma* (TFB), *S. tetrasperma* (TWE) and *S. tetrasperma* (LNM) with significant and positive GCA effects for all crossability parameters may be accommodated in breeding programmes. Similarly female parents, viz., *S. tetrasperma* (LP) and *S. tetrasperma* (LNF) with significant and positive GCA effect for the number of seed per catkin and germination per cent respectively may be used for improvement through intra-specific hybridization. Since dominance variance excelled additive variance, non additive genetic components had played role for all the

characters which suggested the need for exploitation of hybrid vigour by heterosis breeding and population improvement by recurrent selection.

Based on hybrid vigour over check cross, significant desirable SCA effects and mean performance of with respect to crossability parameters, combinations, viz., *S. tetrasperma* (LNF) x *S. tetrasperma* (LNM), *S. tetrasperma* (LNF) x *S. tetrasperma* (TFB), *S. tetrasperma* (LG) x *S. tetrasperma* (TFB), *S. tetrasperma* (LN) x *S. tetrasperma* (TFB) and *S. matsudana* (PN227) x *S. alba* (Kashmiri) were found promising. These combinations showed desirable heterotic effects for most of the nursery growth characters which indicated hybrid vigour over check cross. High broad sense heritability coupled with high genetic gain for the nursery growth traits indicated additive gene effects had played dominant role and selection among full sib families would be effective for further improvement of the characters (Choudhary *et al.*, 2011).

Seed germination and nursery growth performance of hybrids

Analysis of variance for different nursery growth traits of the important crosses revealed significant variations among full-sib families. However, non-significant variation was observed for 100 seed weight among full-sib families. Germination percentage showed the widest range of values (33.40-85.00 per cent) with a mean value of 60.84 per cent followed by plant height (16.98-66.79 cm, mean 27.50 cm) and the narrowest by internodal length (0.78-2.84, mean 1.72). The genotypic and phenotypic variances were maximum for germination percentage (403.63 and 414.19), while minimum was exhibited by internodal length (0.27cm and 0.28 cm) respectively. Plant height exhibited the maximum (291.21 per cent) genotypic coefficient of variation while the minimum was noticed for internodal length (39.95 per cent). Maximum phenotypic coefficient of variation (291.52 per cent) was exhibited by number of leaves while the minimum (40.58 per cent) was

Table 2. Controlled crossing (hybridization) scheme involving five female and five male (incomplete diallel)

S. no.	Female	Pollen parent				
		<i>S. tetrasperma</i> (TFB)	<i>S. tetrasperma</i> (TWE)	<i>S. tetrasperma</i> (LNM)	<i>S. alba</i> (SI-63-007)	<i>S. alba</i> (Kashmiri)
1.	<i>S. tetrasperma</i> (LP)	×	×	×	×	-
2.	<i>S. tetrasperma</i> (LNF)	×	×	×	×	×
3.	<i>S. tetrasperma</i> (LG)	×	×	-	×	×
4.	<i>S. tetrasperma</i> (LN)	×	×	×	×	×
5.	<i>S. matsudana</i> (PN-227)	×	-	×	-	×

(×) Crosses obtained; (-) Not produced viable seeds.

LN: Local nala (*S. tetrasperma*), LNF: Local nala female (*S. tetrasperma*), LNM: Local nala male (*S. tetrasperma*), TFB: *S. tetrasperma* floriculture block, TWE: *S. tetrasperma* entomology field, LP: *S. tetrasperma* polyhouse, LG: *S. tetrasperma* germplasm block.

estimated for internodal length. Heritability percentage (broad-sense) was maximum in plant height (99.79 per cent) whereas, minimum was recorded by number of leaves (87.73 per cent). Germination percentage had the maximum genetic advance (40.86) while the minimum genetic advance was exhibited for internodal length (1.06 cm). Maximum genetic gain was observed in plant height (114.3 per cent) while the minimum was recorded in leaf area (57.56 per cent).

Germination percentage and survival percentage expressed maximum significant positive genotypic (0.917) and phenotypic (0.905) correlation among themselves. Plant height expressed significantly positive correlation with number of leaves (0.669) at genotypic level whereas it exhibited significantly positive correlation with internodal length at both genotypic (0.826) and phenotypic level (0.820). Collar diameter was found significantly positive correlated with germination percentage and survival percentage at both genotypic (0.847 and 0.868) and phenotypic (0.838 and 0.861) levels respectively. Similarly leaf area was found positive and significant correlated with internodal length and germination percentage at both genotypic (0.807 and 0.794) and phenotypic (0.802 and 0.772) level. Number of leaves exhibited positive and significant correlation with internodal length (0.822 and 0.811), germination percentage (0.798 and 0.762) and survival percentage (0.748 and 0.728) at both genotypic and phenotypic levels respectively (Choudhary *et al.*, 2011).

The control breeding/hybridization work in *Salix* clones was continued during the year 2011 and 2012 involving eight females and 16 males. Highest percentage of successful crosses (92.38 per cent) were obtained between clone PN 227 (*S. matsudana*) x SI-63-007 (*S. alba*), whereas, percent of catkins in which seeds were obtained was highest (82.78 per cent) in cross between J799 (*S. matsudana* x *S. alba*) x NZ1140 (*S. matsudana* x *S. alba*). One year old seedling performance in nursery revealed maximum mean height (322.64 cm) by hybrids of PN 227 x SI-63-007 followed by PN227 (*S. matsudana*) x 131/25 (*S. babylonica* x *S. alba*). Collar diameter (18.94mm) and number of branches (52.2) were also recorded highest in hybrids of cross PN 227 x SI-63-007 (UHF, 2012).

Clonal evaluation of hybrids in the nursery field after clonal trial

Salix hybrids developed in the department in the year 2010 were planted in nursery at 50 cm x 40 cm distance in three replications in March 2011 and analysed in November 2011 for the main characters plant height and basal diameter. Maximum height (260 cm) and basal diameter (20.72 mm) was

recorded in the clone UHFS 24/10 and UHFS 17/10, respectively (UHF, 2012).

Evaluation of *Salix* Clones with Respect to Wood and Photosynthetic Traits

Evaluation of genetic parameters for wood characteristics in clones of willow

In order to assess adaptation or to have desirable attributes, an intensive nursery evaluation of twenty three initially screened clones including two locals was undertaken so as to rapidly incorporate in to breeding programmes. The maximum moisture content (47.55 per cent) and fibre length (0.78 mm) were recorded in clone SE-69-002 (*Salix matsudana*), maximum density (0.52 g cm⁻³) was recorded for clone SI-64-010 (*S. alba*). While, maximum wood (78.33 per cent), and minimum bark (21.67 per cent) was recorded for Kashmiri willow. High heritability in broad sense (83.10 per cent) was recorded for bark percentage among wood characters. Genetic gain was maximum for bark percentage (21.33 per cent) closely followed by fibre length (16.67 per cent) (Singh and Huse, 2004a; Huse *et al.*, 2012).

In an another experiment the variation in wood basic density and fibre length was assessed in twenty-five promising willow clones. Analysis of variance at the end of first year growth showed significant difference among clones with respect to both the characters. Value of basic density ranged from 0.40 to 0.58g/cc with clone SE-75-001 registering maximum value (0.58g/cc). Fibre length varied from 0.59 mm to 0.81mm. The clone Kashmir willow (U.K.) and SE-75-001(Italy) stands out because of their long fibre and high wood density, respectively. Moderately high heritability values 56.10 and 55.2 per cent for wood density and fibre length respectively indicated strong genetic control to warrant selection and breeding programme (Joshi, 2009).

Physicochemical characteristics of wood of promising willow clones

Studies on wood of 21 promising willow clones revealed significant variation between physicochemical characteristics of wood of promising willow clones. Among different physical characteristics clone 212/03 registered maximum height, diameter and wood percentage of 12.43m, 9.87 cm and 87.07 per cent, respectively. The maximum bark percentage of 36.13 per cent was exhibited in clone SI-63-016. Also moisture content, specific gravity and fibre length showed significant variation. The maximum moisture content of 110.49 was found in clone 131/25, specific gravity of 0.81 in clone MB-368 and fibre length of 1.93 mm in clone 172. The maximum cold water

extractives, hot water extractives, alcohol-benzene extractives, lignin and holocellulose contents was noticed in clones SI-64-17 (7.67 per cent), NZ-1002 (11.33 per cent), PN-721 (7.10 per cent), V-99 (26.33 per cent) and 131/25 (79.33 per cent), respectively. The wood percentage had highly significant positive correlation with other studied physical parameters, viz., diameter and height. Also significant positive correlation was seen between diameter and height, moisture content and holocellulose content, and moisture content and height. Highly significant negative correlation was observed in bark percentage and wood percentages followed by bark percentage vs. diameter, fibre length vs. hot water extractives, bark percentage vs. height and diameter vs. specific gravity. Highly significant positive genotypic and phenotypic correlation coefficients were obtained between diameter and wood percentage while highly negative genotypic and phenotypic correlation coefficients were noticed between wood percentage and bark percentage. The values for phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain ranged between 2.51-35.63 per cent, 2.09-30.49 per cent, 24.00-92.00 per cent, 0.03-31.20 and 3.95-53.73 per cent, respectively (Kilemwa, 2010).

Genetic variability of photosynthetic traits studied on tree willows

Twenty-three tree willow clones comprising of seven species were studied for variability of photosynthetic traits and their relationship at establishment year. Photosynthesis, transpiration and instantaneous water use efficiency (WUEi) were determined and the data were further subjected for the estimation of genotypic and phenotypic coefficient of variability (GCV and PCV), heritability and genetic gain (as per cent of mean). Clone SE-69-002 (*Salix matsudana*) showed highest photosynthesis ($16.51 \mu \text{ mol m}^{-2} \text{ s}^{-1}$) and transpiration ($9.09 \text{ m mol m}^{-2} \text{ s}^{-1}$) rate. Clone Sx61 (*S. udensis*) excelled for water use efficiency ($3.09 \mu \text{ mol Co}_2/\text{m mol H}_2\text{O}$). The maximum GCV (39.99) was recorded for transpiration, followed by photosynthesis (38.36) and least in case of WUEi (19.71). Heritability (h^2 b.s.) was recorded maximum (85.30 per cent) for transpiration, 80.00 per cent for photosynthesis and 26.55 per cent for WUEi. A positive significant correlation ($r = 0.754$) was observed between photosynthesis and transpiration. WUEi showed significant negative correlation ($r = -0.364$) with transpiration whereas positive non significant ($r = 0.209$) correlation with photosynthesis. Certain clones showed high rate of photosynthesis along with increasing dry weight biomass (Singh and Huse, 2004b; Huse *et al.*, 2008, 2011a, 2011b).

Molecular Profiling of *Salix* Clones

Molecular characterization and assessment of intra-specific relationship among *S. alba* clones using RAPD markers

Genetic diversity and relationship among thirty six genotypes of *Salix alba* were studied using RAPD markers. Five random decamer primers were used to generate 55 RAPD markers by PCR ranging in size 280bp to 1650 bp and all of them were found to be polymorphic with an average of 11.0 RAPD marker per primer. The genetic similarity ranged from 0.418 to 0.873. The lowest similarity value (0.418) was recorded between 668 (T_3) (Lockinge) and SI-2/61(T_{18}) from Netherlands and Hungary, respectively. The maximum similarity value (0.873) was observed between SI-64-063 (T_{10}) (Italy) and Veliki bajar (T_7) (Hungary), respectively (Table 3). The UPGMA clustering (Fig. 1) result indicated that clone 668 (Lockinge) from the Netherlands has most divergent genotype. The dendrogram also reveals that the distribution of various genotype into clusters and within cluster was somewhat random although some of the genotype belonging to same country were placed in same cluster. The results of RAPD analysis indicated that genetic diversity from the Netherlands showed maximum variation and genotype from U.K. were found to be most similar having minimum mean genetic distance. Yugoslavia and the Netherlands had maximum mean genetic distance whereas Turkey and the Netherlands were found to be the closest.

Molecular characterization *Salix* clones using RAPD and SSR markers

Twenty-five promising willow clones were selected after nursery screening twice. These genotypes belong to six countries. Molecular diversity among the clones was estimated using sixteen RAPD and fourteen SSR primers. A total of 363 markers were generated and out of which 351 were polymorphic, showing high (96.7 per cent) rate of

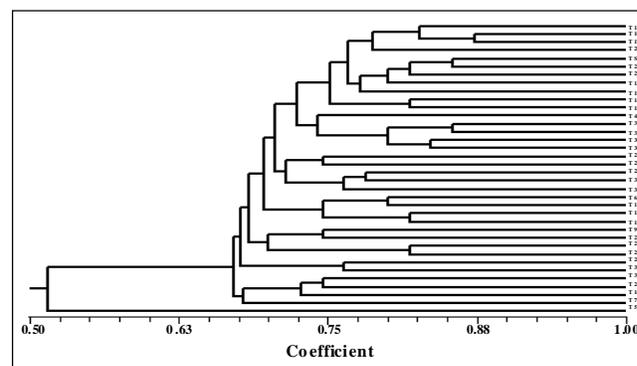


Fig. 1. Dendrogram based on UPGMA analysis of 36 clones of willow using RAPD markers.

Table 3. RAPD based genetic distances within and among different populations (source countries)

Country		UK	Hungary	Italy	The Netherlands	Yugoslavia*	Turkey
UK	Mean	0.234	-	-	-	-	-
	Maximum	0.346	-	-	-	-	-
	Minimum	0.164	-	-	-	-	-
Hungary	Mean	0.296	0.282	-	-	-	-
	Maximum	0.509	0.418	-	-	-	-
	Minimum	0.200	0.182	-	-	-	-
Italy	Mean	0.305	0.293	0.345	-	-	-
	Maximum	0.473	0.473	0.491	-	-	-
	Minimum	0.182	0.127	0.182	-	-	-
The Netherlands	Mean	0.258	0.334	0.332	0.385	-	-
	Maximum	0.527	0.582	0.564	0.564	-	-
	Minimum	0.218	0.164	0.145	0.291	-	-
Yugoslavia	Mean	0.320	0.279	0.304	0.437	0.352	-
	Maximum	0.418	0.400	0.418	0.545	0.382	-
	Minimum	0.218	0.236	0.200	0.236	0.309	-
Turkey	Mean	0.302	0.318	0.331	0.352	0.289	0.276
	Maximum	0.418	0.400	0.455	0.509	0.400	0.345
	Minimum	0.145	0.218	0.218	0.236	0.218	0.218

* Indicates Yugoslavia and Croatia combined.

polymorphism. Out of thirty, eighteen primers showed 100 per cent polymorphism. RAPD widely scored over SSR markers in polymorphic information content. UPGMA dendrogram based on both RAPD and SSR markers resolved into four major clusters. The similarity coefficient (Fig. 2) among 25 clones of willow ranged from 0.71 to 0.86. Maximum similarity (86 per cent) was observed between 795 (T_{11}) and PN-721(T_{14}) and SI-63-007(T_{12}) and V-99(T_{13}). Thus, these genotypes showed maximum degree of similarity in their genetic makeup. However the minimum values were observed between SE-69-002 (T_{24}) and 84/11(T_6) (0.71) followed by SE-69-002 and 17-93-A (T_2) (0.72). RAPD and SSR analysis proved helpful for estimating the magnitude of genetic diversity at molecular level. The clustering further indicated that the geographic distribution may not be the true index of genetic diversity in willow clones. On the basis of banding pattern, RAPDs and SSRs were effectively used for molecular characterization of willow clones used in this study (Joshi, 2009).

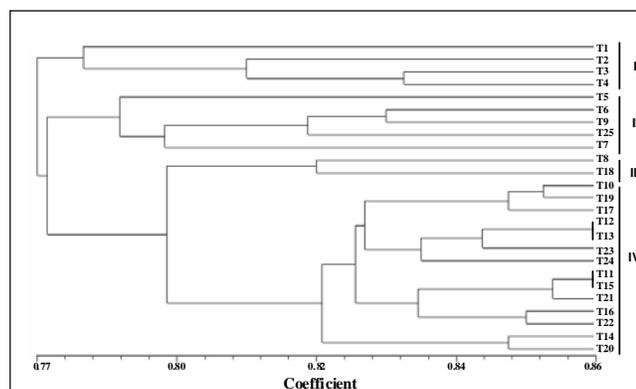


Fig. 2. Dendrogram based on UPGMA analysis of 25 clones of willow using RAPD and SSR markers.

Molecular analysis of parents used for crossing through RAPD and SSR molecular markers

Seventeen RAPD and 10 SSR primers were effective in revealing polymorphisms among different species/clones of willows. A total of 92 scorable bands with an average of 4.11 bands per primer were obtained in RAPD study. Out of the total, 92 scorable bands, 72 showed polymorphism and 20 bands exhibited monomorphism resulting in 78.26 per cent polymorphism among 22 genotypes. Three out of 17 primers exhibited 100 per cent polymorphism. The amplified product obtained in the study ranged between 50-4282 bp. Jaccard's similarity correlation coefficient ranged from 0.43 between *S. acmophylla* and *S. pierotii* and *S. pierotii* and 799 to 0.91 between two male genotypes (SI-63-007 and Kashmiri) of *S. alba*. The dendrogram exhibited seven clear clusters.

Out of 10 SSR primers only seven primers produced SSR profiles with intense banding pattern and generated a unique set of amplification products. Out of the total 24 scorable bands, 16 showed polymorphism and eight bands exhibited monomorphism with an average of 3.43 bands per primer. A unique band of approximately 100 bp was generated by SB-80 for *S. udensis*. Jaccard's similarity correlation coefficient values (Fig. 3) was highest value (0.98) between two male genotypes of *Salix tetrasperma* [*S. tetrasperma* (TFB) and *S. tetrasperma* (LNM)] and lowest (0.64) between *S. udensis* and *S. nigra*, *S. udensis* and *S. tetrasperma* (TWE) and between *S. matsudana* (PN-722) and *S. pierotii* and 799. The dendrogram exhibited six clear clusters with *S. udensis* coming out as an outlier.

Molecular analysis of hybrids through RAPD molecular markers

The important hybrids obtained after the completion of hybridization programme were tested for their paternity

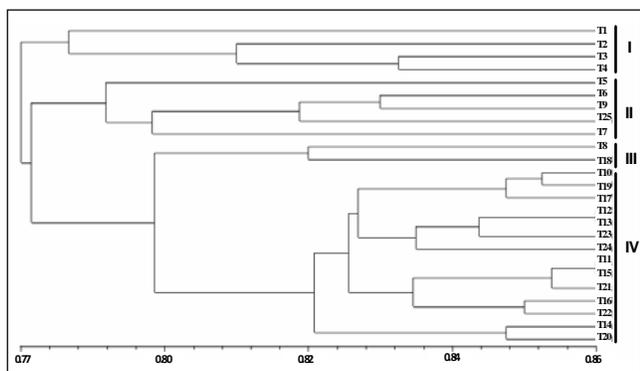


Fig. 3. Dendrogram based on UPGMA analysis of willow clones using RAPD and SSR markers.

using four RAPD markers. RAPD banding pattern obtained after the amplification of genomic DNA of both the parents and their hybrid revealed that all the nine hybrids were true to type. The RAPD fragments obtained after PCR amplification were subjected to analysis for obtaining their similarity coefficient with respect to their parents. Results disclosed that six out of nine hybrids were highly similar to their male parents, whereas, three hybrids showed more similarity towards female parents. Hybrid (*S. tetrasperma* (LG) x *S. tetrasperma* (TWE)) recorded 100 per cent and 70 per cent similarity with male and female parent respectively suggesting dominant control of male parent. Similarly hybrids [(*S. tetrasperma* (LG) x *S. tetrasperma* (TFB)) and *S. tetrasperma* (LN) x *S. tetrasperma* (TWE)] also recorded 100 per cent similarity with male parent. Maximum similarity (96 per cent) with female parent was recorded in *S. matsudana* (PN-227) x *S. matsudana* (PN-722) suggesting dominating control of female parent. Two other hybrids and [*S. alba* (SI-64-017) x *S. matsudana* (PN-722)] and [*S. matsudana* (PN-227) x NZ-1002] also recorded high similarity (87 per cent and 71 per cent) with their female parent, respectively (Choudhary *et al.*, 2011).

Diversity study on natural population through AFLP molecular markers

In Kashmir, *Salix* is cultivated on large scale. There are diverse cultivars of *Salix* found in Kashmir Valley but they are not well demarcated due to similarities in certain morphological characteristics. Andleeb *et al.* (2011) found high diversity in four cultivars of *Salix viminalis* on genetic level assessed with amplified fragment length polymorphism (AFLP). The four primers used generated a total of 240 bands of which 197 (82 per cent) were polymorphic.

Establishment of Germplasm Bank-cum-*Ex situ* Conservation Blocks and Demonstration Plot

UHF Nauni has largest germplasm collection of willow in India consisting of 200 introduced clones, 70 local collections and 5,000 hybrids. Two germplasm banks are maintained along with one VMG at the university.

Economic Studies

Biswas and Hussain (2008) and Rather *et al.* (2010) studied the livelihood of willow dependent communities of the Indian trans-Himalayas region and found that the economic benefits of willow diversity have been well understood by the dependent communities of the region in terms of gains through marketing and continual improvement in quality, aesthetics and design. A traditional method for the development of this resource through conscious and sub-conscious selection of material for small-scale planting and utilization exists in the region despite the introduction of exotic willow (*Salix alba* cv *calve* = *S. caerulea* Smith) during the early decades of the last century in the Kashmir Himalayas. Lesser known uses of willows in the trans-Himalayan region are for making charcoal and Kangri (fire pot) from twigs, chips, etc. to overcome severe winter conditions, as cattle feed from foliage during lean seasons and wickerwork for the manufacture of baskets, flower vases, trays, chairs and other novelty items. Maximum yield/ha of wicker willow has been found in Srinagar (12.69t/ha) and minimum in Anantnag 11.20 t/ha. Subsequently, wicker willow contributes about 35.34 per cent to the farmers average income in Srinagar as against lowest of 1.27 per cent in Pulwama. Numbers of processing units varies from district to district and are maximum in Srinagar and Baramulla as against the minimum in Budgam, Anantnag and Pulwama. The willow- dependent communities carry out weaving jobs about six days a week, 25 days a month and 300 days a year. In the rural/forest villages of the region, viz., Hakimgund and Kachen in Srinagar District of Kashmir, 33 out of a total of 95 family members, are workers. Studies indicate that the income from the weaving per family ranges from Rs. 4,000 to Rs. 17,513,125 and the total income of as many as 14 families reaches Rs. 20,525,360). Thus, the willow bioresource provides a sustainable livelihood. Some of the families have been involved in weaving for over six decades and are recognized for their traits and grass-root innovation.

Kashmir manufactured bats on account of less accessibility to the outside market have not touched popularity and export potential as otherwise it should have

been. With this in view a survey was conducted by Hussain and Biswas (2008) to explore the willow-based industrial and market potentials. The mechanical properties taken into consideration by the local manufacturers and also the production status and market trends were studied in Kashmir Valley. The present annual turnover of the products from *Salix* in Kashmir is 600 million in Indian rupees. The production is targeted to the demand of the Indian market presently.

There are number of cultivars of *Salix* species suitable for manufacturing of bat. Over 80 per cent of all cricket bats today are made in India. The remaining 20 per cent (probably less) of bats are mostly made in Australia, England, South Africa, Pakistan, and New Zealand. Around 30 million bats of international standard are required every year which require massive propagation of willow under small scale forestry to harness the potential of this industry. Cricket bat industries are very well established at Meerut and Jalandhar (Bhat, 2004) with annual turnover of approx. Rs. 250 crore, each at both the cities. Approx. 40 cm diameter can be obtained in 9-14 years depending on clone, site and cultural practices. However, such diameter can be achieved earlier (8-10 years) provided more productive clones and intensive cultural management are involved in agroforestry models (Quardri, 1980). Due to lack of willow wood (*S. alba coerulea*) in sufficient quantity, poplar and other species of willow are being used for manufacturing of around 40 per cent substandard bats. (Bhat, 2004; J and K, 2009; Mohamin 2011). During the Cricket World Cup, 2011, cricket bat production went upto 1,200 per day against 400 per day in one the leading factories (BDM) based at Meerut, U.P. They are made of English willow which start as low as Rs. 600 and goes up 21,000 or more per bat (WP, 2011).

Highlights/Significant Achievements at Dr. Y.S. Parmar University of Horticulture and Forestry Nauni, Solan, H.P.

- Nursery testing of selected 78 clones.
- Study of physiological traits and wood characteristics of 25 clones.
- Evaluation of field trial at an age of five years.
- Stability analysis of 18 clones was studied.
- Reproductive biology was worked on important clones for undertaking hybridization/breeding work.
- About 5,000 hybrids (F_1 s) plants developed through control-pollination by involving outstanding (field tested) clones and selections

of local species (*Salix tetrasperma*). Nursery assessment is in progress.

- Assessment of genetic variation in *Salix alba* using RAPD technique.
- Molecular diversity was estimated using RAPD and SSR primers on promising clones of willow.
- Supply of willow germplasm 26 institutes, NGOs and state forest departments.
- Performance trial at 10 places in H.P.
- Two germplasms and one V.M.G are established.
- Largest germplasm collection of willow in India.
- Promising five clones namely J-799, NZ-1140, 131/25, SI-63-007 and J-194 are recommended for plantation in mid-hills of Himachal Pradesh.
- Clone SI-64-017, NZ-1040, V-311, NZ 1002, 131/25 and PN 722 were found suitable in subtropical area (zone 1) of Himachal Pradesh.
- PN-731 and SI-64-017 were found promising in northern tropical zone based on field trial (Kanpur and Gonda).
- Hybrids have been developed involving out performing clones *S. alba*, hybrid clones and local species (*S. tetrasperma* and *S. babylonica*).
- Outstanding hybrids developed by the university will be made available to planting agencies in 2013.
- Clone J-799 exhibited 22.57 meters plant height and 28.75 cm (approx. one foot) diameter in six years. This growth is much better than any outstanding clones of poplar grown at Nauni, Solan.

References

- Andleeb, L; Munshi, A.H. and Dar, A.R. 2011. Genetic diversity in *Salix viminalis* in the Kashmir Valley, India. *American Journal of Biochemistry and Molecular Biology* 1(2):178-184.
- Argus, G.W. 1974. An experimental study of hybridization and pollination in *Salix* (willow). *Canadian Journal of Botany*, 52(7): 1613-1619.
- Argus, G.W. 1997. Infrageneric classification of *Salix* (Salicaceae) in the new world. Systematic Botany Monographs, Vol. 52. American Society of Plant Taxonomists, USA. 121p.
- Argus, G.W. 1999. Classification of *Salix* in the new world. [Available at: www.ou.edu/cas/botany-micro/ben2227.html].
- Bhat, M.A. 2004. Diagnostic study report of cricket bat-manufacturing cluster-Anantnag. New Delhi. 41p.
- Biswas, Sas and Hussain, S.S. 2008. Livelihood studies of willow-dependent communities of the Indian

- trans-Himalayan region with emphasis on sustainable management of the bioresource and improved well-being. *In: 23rd Session of the International Poplar Commission, Beijing, 27-30th October 2008. Abstracts. The author. p.20.*
- Choudhary, P.; Singh, N.B.; Sharma, J.P., Thakur, I.K., Sharma, A. and Verma, A. 2011. Phenological behaviour and reproductive biology of important fast growing *Salix* species. *Indian Journal of Ecology*, 38(Special Issue): 99-106.
- Hathaway, R.L. 1977. Early growth of *S. matsudana* x *S. alba* hybrids. *New Zealand Journal of Forestry Science*, 7(2): 207-213.
- Huse, S.K., Singh, N.B.; Gupta, A. and Anand, R.K. 2008. Genetic improvement of tree willows in India. *In: Chauhan, S.K.; Sharma, S.C.; Chauhan, R. and Gill, S.S. Eds. Exotics in Indian forestry. Udaipur, Agrotech Publishing Academy, pp. 591-514.*
- Huse, S.K.; Singh, N.B. and Anand, R.K. 2011a. Genetic variability of photosynthetic traits and their relationship with growth and biomass parameters studied on tree willows. *Indian Journal of Agroforestry*, 13(2): 41-46.
- Huse, S.K.; Singh, N.B. and Anand, R.K. 2011b. Genetic variability of photosynthetic traits and their relationship with growth parameters studied on tree willows. *In: IUFRO Symposium on Short Rotation Forestry: Synergies for Wood Production and Environmental Amelioration, Ludhiana, 10-12 February 2011. p. 85.*
- Huse, S.K.; Singh, N.B. and Sankhyan, H.P. 2005. Variation in quantitative genetic parameters studied on growth traits in *Salix* species. *In: National Symposium on Changing Concepts of Forestry in 21st Century, Solan, 21-22 October 2005. Souvenir and abstracts. Nauni, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni. p. 77.*
- Huse, S.K.; Singh, N.B.; Anand, R.K. and Sharma, J.P. 2012. Variation in quantitative genetic parameters studied on growth and biomass traits in *Salix* clones. *Indian Journal of Genetics and Plant Breeding* [Accepted].
- Hussain, S.S. and Biswas, Sas. 2008. Indian willows-based cricket bats of international significance of trade and income. *In: 23rd Session of the International Poplar Commission, Beijing, 27-30th October 2008. Abstracts. The author. p. 87.*
- J and K (Jammu and Kashmir ban on willow movement boosts smuggling). 2009. *Economic Times*, 14th November, 2009.
- Joshi, S. 2009. Molecular characterization of promising willow clones. M.Sc. thesis. Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni. 74p.
- Kajba, D.; Bogdan, S. and Prataric, P. 1999. Growth of white willow clones in mixed plantation with black alder (*Alnus glutinosa*) on the peat clay type of soil. *Sumarski*, 11-12: 523-531.
- Kajba, D.; Krstinic, A. and Komlenovic, N. 1998. Arborescent willow biomass production in short rotations. *Sumarski*, 3-4: 139-145.
- Kilemwa, A.M. 2010. Studies on physico-chemical characteristics of wood of promising willow clones. Nauni, Dr. Y.S. Parmar University of Horticulture and Forestry. 93p.
- Kopp, R.F.; Smart, L.B., Maynard, C.A.; Tuskan, G.A. and Abrahamson, L.P. 2001. The development of improved willow clones for eastern North America. *Forestry Chronicle*, 77(2): 287-292.
- Larsson, S. 2000. Genetic improvement of willows for short-rotation coppice. *Biomass and Bioenergy*, 15: 23-26.
- Mohamin, A. 2011. Female bat better. *Kashmir Life*, 3(4): 3-6.
- Newsholme, C. 2003. Willows: The genus *Salix*. Portland, Timber Press.
- NPC (India. National Poplar Commission). 2012. Country report on poplars and willows period: 2008 to 2011 Dehradun, ICFRE. 64p.
- Quardi, S.T. 1980. On activities related to poplar and willow cultivation, exploitation and utilization in Jammu and Kashmir state for the period 1975-79. *Foliage*, 2(1): 15-25.
- Rather, Tareq Ahmad; Qaisar, K.N. and Khan, M.A. 2010. Status and distribution of wicker willow in Kashmir. *Indian Journal of Traditional Knowledge*, 9(2): 403-406.
- Scott, K.G. 1984. Improving the biomass potential of willow by selection and breeding. *In: Perttu, K., Ed. Ecology and management of forest biomass production systems. Uppsala, Swedish University of Agricultural Sciences. pp. 233-260.*
- Sharma, J.P.; Singh, N.B.; Sankhyan, H.P.; Chaudhary, P. and Huse, S.K. 2011. Estimation of genetic parameters of newly introduced tree willow clones in Himachal Pradesh, India. *Genetika*, 43(3):487-501.
- Singh, N.B. and Huse, S.A. 2004a. Improvement of tree willows in India. I. Variation of wood characteristics. *In: 22nd Session of International Poplar Commission, Santiago, 29th November to 2nd December, 2004. Abstracts. The author. p. 48.*
- Singh, N.B. and Huse, S.A. 2004b. Improvement of tree willows in India. II. Genetic variability of photosynthetic

- traits and their relationship. *In: 22nd Session of International Poplar Commission, Santiago, 29th November to 2nd December 2004. Abstracts. The author. p. 49.*
- Singh, N.B. and Huse, S.A. 2004c. Improvement of tree willows in India. III. Variation on quantitative genetic parameters on growth traits. *In: 22nd Session of International Poplar Commission, Santiago, 29th November to 2nd December 2004. Abstracts. The author. p. 50.*
- Singh, N.B. and Huse, S.A. 2004d. Improvement of tree willows in India. IV. Estimates of genotypic and phenotypic correlation coefficients and response to indirect selection. *In: 22nd Session of International Poplar Commission, Santiago, 29th November to 2nd December 2004. Abstracts. The author. p. 51.*
- Singh, N.B.; Huse, S.A.; Gupta, R.K. 2004. Principal component analysis of tree willow clones for genetic improvement of quantitative traits. *In: 22nd Session of International Poplar Commission, Santiago, 29th November to 2nd December, 2004. Abstracts. The author. p.52.*
- Singh, N.B.; Sankhyan, H.P. and Huse, S.A. 2003. Clonal variation in arborescent willow (*Salix* species). *In: International Conference on World Perspective on Short Rotation Forestry for Industrial and rural Development, Nauni, 7-13 September 2003. Abstracts. Nauni, Dr. Y.S. Parmar University of Horticulture and Forestry. p.50.*
- Singh, N.B.; Sharma, J.P.; Choudhary, Punit; Sankhyan, H.P. and Sankanur, M. 2012b. Principal component analysis of fast growing willow clones for quantitative traits under short rotation forestry. *Annals of Forestry* [Accepted].
- Singh, N.B.; Sharma, J.P.; Huse, S.K.; Thakur, I. K.; Gupta, R. K. and Sankhyan, H.P. 2012a. Heritability, genetic gain, correlation and principal component analysis in introduced willow (*Salix* species) clones. *Indian Forester* [Accepted].
- Singh, N.B.; Sharma, J.P.; Sankhyan, H.P.; Thakur, I.K. and Gupta, R.K. 2011. Four years' performance of selected tree willow clones in Himachal Pradesh (genotype x environment interactions and stability analysis). *In: IUFRO Symposium on Short Rotation Forestry: Synergies for Wood Production and Environmental Amelioration, Ludhiana, 10-12 February 2011. Abstracts. Ludhiana, PAU. p.72.*
- Sinha, A.R. and Sharma R.C. 2002. Suitability and growth pattern of *Salix* in Himalayan foothills. *Indian Forester*, 128: 355-357.
- UHF (Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni). 2012. Annual report 2011-12. The author. 45p.
- WoI (Wealth of India: A dictionary of Indian raw material and industrial products). 1972. Vol. 9. New Delhi, CSIR. 471p.
- WP (Willow power: As India march into the final bat industry hits a ton). 2011. Hindustan Times, 1st April, 2011.
- Zhenfu, F.; Shidong, Z. and Skvortsov, A. 1999. Salicaceae. *In: Zhengnys, W. and Reven, P.H Eds. Flora of China. St. Louis, Missouri Botanical Garden Press. pp.139-274.*
- Zsuffa, L. Mosseler, A and Raj, Y. 1984. Prospects for interspecific hybridization in willows for biomass production. *In: Perttu, K. Ed. Ecology and management of forest biomass production systems. Sweden, Department of Ecology and Environmental Protection, Swedish University of Agricultural Sciences. pp. 261-281. ●*