



Estimates of Genetic Parameters for Growth, Leaf and Biomass Traits of Indian Willow (*Salix tetrasperma* Roxb.)

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ABSTRACT

Indian Willow (*Salix tetrasperma* Roxb.) genotypes were collected from 20 sites in North India covering Uttarakhand, Himachal Pradesh, Punjab and Jammu and Kashmir and one genotype from Rajasthan and evaluated in experimental fields to study genetic variability in growth, leaf and biomass characters. The high heritability coupled with high genetic advance as percentage mean were recorded for root length, inter nodal length, plant height, root to shoot ratio, leaf area, lamina breadth and petiole length and the biomass characters, indicating that selection for these characters could be more effective due to additive gene action.

Key Words:

Diversity, Genetic, Genotypes, Indian Willow, *Salix tetrasperma*,

INTRODUCTION

Willows (*Salix* species) are widespread in diverse ecological niches, being native to the northern hemisphere (Argus 1997). They were the part of an ancient civilization with many necessities such as furniture, snowshoes, arrow shafts, fish traps, nets and ropes, as well as shelter, fences and medicinal remedies. The genus comprises around 520 species worldwide, which show considerable variation in plant size, growth habit and morphological characteristics, ranging from small shrubs to large trees (Newsholme 1992). Asia is considered to be the original center of genus *Salix* with about 275 species exist in China, of which 189 are endemics (Fang 1987). In India, out of 37 species, there are about 33 indigenous and 4 exotic species of willows (Sharma et al. 2011). The indigenous species are found in various forms like shrub, osier and tree out of which 7 species are tree habit, which grow

over a large area ranging from the northern temperate parts of Jammu and Kashmir to Arunachal Pradesh. Most of the arborescent species of *Salix* are confined to the hilly regions of the country except *S. tetrasperma*, which is occurring from tropical to temperate regions of India (Sharma et al. 2015).

Genetic diversity is the amount of genetic variability among individuals of a variety or population of a species (Brown 1983). It results from many genetic differences found among individuals due to differences in DNA sequence, biochemical characteristics and morphological characters. In order to isolate local evolutionary and adaptation, biologists have developed in experimental fields (common garden) by growing individuals from different populations in a common environment for a short period (De Villemereuil et al. 2016). These experiments are used to characterize genetic patterns of natural geographic variation i.e. clinal and ecotypic,

understanding the differential selective forces behind the genetic variation and developing preliminary seed transfer guidelines. These experiments have the advantages of evaluating more number of populations in limited area, generating large amount of data in short time and low experimental error due to homogeneous experimental environment (White et al. 2009). To find the genetic variability in Populations of the Indian willow of collected genotypes from the study area were evaluated in experimental fields (common garden) tests.

MATERIAL AND METHODS

The survey was carried out in the Himalayan regions of J&K, Himachal Pradesh, Punjab and Uttrakhand in North India to identify different populations of indigenous Indian willow (*Salix tetrasperma*). Germplasm was collected on the basis of field observations and interaction with local people. Total numbers of sites/population were 20 and 6 genotypes based upon availability

per site/population were selected (Table 1). Distance among the genotypes within sites varied at least 200 meters to 4 km depending upon availability, as it is a scattered in distribution. Locational data was recorded with instrument GARMIN GPS III Plus (Table 1). Three genotypes from Udaipur, Rajasthan state were procured through Forest Department, Rajasthan in the year 2012 and were included in the experiment making the total sites to 21. The experiment was carried out under protected condition in glasshouse of the Department in polybags of size 4"x9". Polybags of uniform size were filled with mixture of sand, soil and farm yard manure in the ratio of 1:2:1. The minimum and maximum temperature was manually recorded with the help of ordinary thermometer inside the glasshouse. Growth characters were recorded in December while, leaf characters were recorded in the July at full maturation of leaf. Genetic parameters were calculated as per standard methods.

Table 1: Latitudinal, longitudinal and altitudinal ranges of collection sites/ population.

Sr No	Site	Latitude Range (°N)	Longitude Range (°E)	Altitude Range (amsl*)
1	Devamanal	30°47'356"-30°47'572"	77°26'217"- 77°26'423"	1668-1784
2	Jakholi	30°24'243"-30°24'616"	78°52'062"- 78°52'706"	1181 -1630
3	Rampur	31°22'975"-31°23'587"	77°32'127"- 77°35'349"	898 - 987
4	Rupnagar	30°54'390"-30°54'482"	76°27'778"- 76°38'001"	251-262
5	Tandi	30°51'705"-30°51'797"	76°08'320"- 76°08'365"	296-300
6	Suhanpur	31°26'085"-31°31'449"	75°21'327"- 75°26'049"	119-234
7	Dasua	31°40'161"-32°13'265"	75°32'021"- 76°08'837"	228-271
8	Kangra	31°28'070"-32°12'729"	75°24'752"- 76°14'700"	686-715
9	Hamirpur	31°41'141"-31°46'614"	76°25'286"- 76°30'624"	487-811
10	Namhol	31°14'910"-31°15'748"	76°49'367"- 76°51'253"	996-1192
11	Bhunter	31°50'642"-31°50'447"	77°03'096"- 77°09'596"	1089-1127
12	Chinani	33°02'285"-33°02'513"	75°16'843"- 75°16'931"	1096-1137
13	Rajouri	33°18'541"-33°20'301"	74°19'160"- 74°19'738"	829-841
14	Jammu	32°48'256"-32°49'363"	74°45'583"- 74°46'470"	262-313
15	Pauri Garhwal	29°49'022"-30°09'029"	78°37'004"- 78°46'435"	671-1472
16	Jyolikote	29°21'062"-29°21'299"	79°28'615"- 79°28' 920"	1210-1222
17	Deothi	30°55'721"-30°55'853"	77°03'270"- 77°03'388"	1413-1435
18	Balh	31°32'063"-31°32'190"	76°50'810"- 76°50'841"	1140-1167
19	Chowari	32°25'846"-32°25'964"	76°00'030"- 76°00'398"	972-1002
20	Chamba	32°33'337"-32°33'549"	76°05'157"- 76°05'923"	888-904
21	Udaipur	25°06'421"-25°06'495"	73°46'463"- 73°46'476"	360-384

*Above mean sea level

RESULTS AND DISCUSSION

Growth characters

Growth characters has coefficient of variation range from 4.55 percent in root length to 9.46 percent in number of nodes. Genetic parameters for growth characters depicts the highest magnitude of PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation) for characters viz. number of nodes (27.34 %, 25.65 respectively), followed by internodal length (26.43 %, 25.62 %), root to shoot ratio (26.16 %, 24.77 %), basal diameter (24.95 %, 23.13 %) and plant height (23.03 %, 21.64 %). The moderate PCV (Phenotypic Coefficient of Variation) and GCV (Genotypic Coefficient of Variation) was recorded for root length (18.00%, 17.42%). Similar results were obtained in provenance trial of *Populus ciliata* (Uniyal and Todaria 2006).

Heritability was recorded more than 85 percent with highest estimates for growth characters for internodal length (93.95%) and root length (93.60 %). While, high genetic advance as percentage of mean were observed for internodal length (51.15 %), followed by number of nodes (49.58 %) and root to shoot ratio (48.32 %) (Table 2).

Leaf characters

Minimum coefficient of variation (3.27 %) was recorded in leaf petiole length that varies up to 15.47 per cent in maximum breadth of lamina. Among leaf characters, leaf area (31.27 %, 30.45 %), maximum leaf breadth (29.97 %, 28.85 %), petiole length (27.41 %, 27.21 %) and leaf unfolding days (26.05 %, 22.01 %) recorded high PCV and GCV respectively. Number of leaf teeth and lamina length also recorded high PCV. The moderate PCV and GCV was recorded for leaf length (19.77 %, 19.42 %) and foliage duration (15.32 %, 15.11 %), respectively. Lamina length (19.72 %) and number of leaf teeth (19.44 %) also recorded moderate GCV (Table2).

For leaf characters, the highest heritability estimate were observed for petiole length (98.58

%), followed by foliage days (97.27 %), leaf length (96.47 %), lamina length (96.24 %), leaf area (94.77 %) maximum breadth of leaf (92.65%), number of leaf teeth (83.98%) and leaf unfolding days (71.37 %). Similarly for leaf characters high genetic advance as percentage of mean were observed for leaf area (61.09 %), maximum breadth of leaf (57.21 %), petiole length (55.66 %), lamina length (39.85 %), leaf length (39.29 %), leaf unfolding days (38.30 %), number of leaf teeth (36.70 %) and foliage duration (30.70 %).

Biomass characters

Maximum coefficient of variation (16.04 %) was recorded in root dry weight, while minimum (9.68 %) for total fresh plant weight. Genetic parameters for biomass traits were higher than other types of characters. Highest PCV was recorded for shoot fresh weight (50.76 %), followed by total shoot weight (43.83 %), root fresh weight (43.69 %), root dry weight (43.71 %), shoot dry weight (42.90 %) and total dry weight (42.01 %).

For biomass characters, the highest heritability estimate were observed for total shoot weight (95.12 %) followed by shoot fresh weight (94.08 %), root fresh weight (93.06 %), total dry weight (90.50 %), shoot dry weight (89.13 %) and root dry weight (86.52 %). For biomass characters all observed high genetic advance as percentage of mean with highest in shoot fresh weight (98.37 %), followed by total shoot weight (85.89 %), root fresh weight (83.75 %), shoot dry weight (78.77 %) total dry weight (78.31 %) and root dry weight (77.90 %).

The magnitude of PCV was higher than the corresponding GCV for all the traits. This might be due to the interaction of the genotypes with the environment to some degree or environmental factor influencing the expression of these traits as previously reported in *Salix* species (Singh et al. 2012, and Sharma et al. 2017). Close correspondence between phenotypic and genotypic coefficient of variation were observed *i.e.* sufficient variability among the traits is present

Table 2. Estimates of coefficient of variation, heritability, genetic advance and genetic gain for growth, leaf and biomass parameters among *Salix tetrasperma* genotypes.

Characters	Coefficient of Variation	Coefficient of variation (%)		Heritability (%)	Genetic Advance	Genetic Gain (%)
		Phenotypic	Genotypic			
Growth Characters						
Plant height (cm)	7.86	23.03	21.64	88.35	21.89	41.91
Basal diameter (mm)	9.35	24.95	23.13	85.95	1.90	44.18
Internodal length (cm)	6.48	26.43	25.62	93.95	0.89	51.15
Number of nodes	9.46	27.34	25.65	88.03	13.73	49.58
Root length (cm)	4.55	18.00	17.42	93.60	6.29	34.71
Root/shoot	8.52	26.16	24.77	89.68	0.17	48.32
Leaf characters						
Leaf unfolding days	13.93	26.05	22.01	71.37	5.23	38.30
Total foliage duration	3.35	15.32	15.11	97.27	75.94	30.70
Lamina length (cm)	3.90	20.10	19.72	96.24	5.27	39.85
Maximum breadth of lamina (cm)	15.47	29.97	28.85	92.65	1.09	57.21
Leaf length (cm)	3.71	19.77	19.42	96.47	5.49	39.29
Petiole length (cm)	3.27	27.41	27.21	98.58	0.42	55.66
Number of leaf teeth	8.49	21.21	19.44	83.98	1.61	36.70
Leaf area (cm ²)	7.15	31.27	30.45	94.77	10.57	61.06
Biomass characters						
Shoot fresh weight (g)	12.35	50.76	49.23	94.08	9.71	98.37
Root fresh weight (g)	11.51	43.69	42.15	93.06	7.76	83.75
Total fresh plant weight (g)	9.68	43.83	42.75	95.12	16.44	85.89
Shoot dry weight (g)	14.14	42.90	40.50	89.13	4.00	78.77
Root dry weight (g)	16.04	43.71	40.66	86.52	4.04	77.90
Total dry plant weight (g)	12.95	42.01	39.96	90.50	8.04	78.31

among the genotypes. Hence, the enough scope of improvement of these traits. Causes of such variability are generally attributed either to genetic characters of source population/plant (Uniyal and Todaria 2006), or to impact of mother plant environment (Fenner 1991).

Genetic improvement of any character is difficult without having sufficient heritability, genetic advance and genetic variability. Hence, heritability and genetic advance are the important parameters for selecting a genotype that permits greater effectiveness of selection by separating out the environmental influence from total variability. Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson et al. 1955).

Foliage duration showed high heritability coupled with low genetic gain (genetic advance as percentage of mean) High heritability with moderate genetic advance as percentage of mean was shown for lamina length by leaf unfolding days, leaf length and number of teeth. High heritability coupled with low genetic advance shows that character is controlled by non-additive genes (Panse 1957). High heritability but moderate genetic gain was obtained for petiole length in *Willow* clones (Singh et al. 2012).

The high heritability coupled with high genetic advance as percentage mean were recorded for root length, inter nodal length, plant height, root to shoot ratio, basal diameter, leaf area, lamina breadth and petiole length and all the other biomass characters studied, indicating that selection for these characters could be more effective due to additive gene action. Similar

results were obtained while evaluating *Salix* clones in nursery for basal diameter, leaf breadth and petiole length characters by Singh et al. (2012) and for plant height by Sharma et al. (2015). In contrary to our studies Sharma et al. (2017) got low medium heritability with high genetic gain for plant height, green stem biomass. This might be due to fact that homogeneity of experimental environment is more under glass house condition that increased heritability. Ramesh and Khurana (2008) found high heritability for seedling height, basal diameter, root fresh weight, and root dry weight and low heritability for number of branches while evaluating different provenances of *Populus alba* from Himachal Pradesh and Jammu and Kashmir.

The variability estimates computed for each trait exhibited high variability among all the genotypes with maximum coefficient of variation in root dry weight followed by maximum lamina breadth. The high heritability coupled with high genetic advance as percentage mean were recorded for root length, inter nodal length, plant height, root to shoot ratio, leaf area, lamina breadth, petiole length and all the biomass characters, indicating that selection for these characters could be more effective due to additive gene action.

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