

## LINE × TESTER ANALYSIS FOR GROWTH AND BIOMASS CHARACTERISTICS OF *SALIX*

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Line × tester analysis was carried out in willows (*Salix* spp.) to determine the genetic interaction in the expression of various quantitative characters related to productivity. Combining ability revealed that the estimates of GCA variance ( $\sigma^2$  GCA) were more than the SCA variance ( $\sigma^2$  SCA) for all the characters studied. Later the gene action study revealed that additive variance was observed more than the dominance variance for all the parameters studied. The proportional contribution of lines were higher than individual contribution of testers or line × tester interaction except for fresh root weight, dry shoot weight, dry root weight and total dry weight where the contribution of interactions was more. Line PN 227 and tester Austree and J 795 were found to be good general combiners and thus appeared to be worthy of exploiting in *Salix* improvement through breeding and recurrent selection followed by cloning for developing commercial superior clones. On the basis of mean performance and significant desirable SCA effects, the combinations PN 227 × Austree, PN 227 × NZ 1140 and J 799 × Austree were found to be the most promising families for growth and biomass

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characters and are recommended for within family selections followed by heterotic breeding.

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### INTRODUCTION

Willows belong to the genus *Salix* of family Salicaceae, represented by 330-500 species in the world, mainly distributed in North-temperate zone (ARGUS, 1997). Willows are among the most advanced biomass crops in temperate and sub-tropical regions because of their potential for high yields in short cultivation cycles, ease of vegetative propagation and ability to resprout after multiple harvests (KEOLEIAN and VOLK, 2005). Short rotation *Salix* plantations have the potential to accelerate the shift of wood supply from natural forests to plantations. In India about 33 species of *Salix* has been reported, out of these 8 species are of tree form which are mostly confined to temperate regions except *S. tetrasperma*, *S. babylonica* and *S. alba* covering tropical and sub-tropical riparian areas of entire country (SINGH *et al.*, 2013).

*Salix* species are multipurpose agroforestry trees which serves not only purpose of producing fodder, fuel and timber but also as a phytoremediation measure (ZALESNY and BAUER, 2007). Willows wood is used for sport goods, furniture, reconstituted wood products, veneer plywood, paper and pulp, as a substrate for shitake mushroom, *etc.* These attributes make willows ideally suitable for supporting rural livelihoods and contributing to sustainable development particularly in developing countries and countries with economies in transition. It is also the lifeline in Lahaul & Spiti dry temperate region of Himachal Pradesh. Apart from this, willow energy plantations can create new habitat opportunities for wildlife in degraded ecosystems.

Selecting parents on the basis of performance, adaption and genetic variability does not lead necessarily to useful results. This is because of the differential ability of the parents, which depends upon the complex interactions among the genes and cannot be judged by the performance alone (ALLARD, 1960). The parents, which perform well in the cross combinations are of great importance in the breeding program. The information about combining ability and relative magnitude of genetic variance with respect to traits of economic importance is essential for exploitation of the existing gene action in the population. Line  $\times$  Tester analysis is, therefore, of great value to plant breeders as an attempt to select parents to be used in hybrid production and also for those whose primary objective is to transfer specific character as it assists them in identifying desirable parents for producing potential segregating populations for selection.

### MATERIALS AND METHODS

Over the year's two hundred clones/ strains/ species were procured from twenty different countries covering five continents namely Europe, North America, South America, Asia and Africa and raised in the germplasm block of Naganji nursery of Department of Tree Improvement and Genetic Resources (Latitude-30° 51' N and Longitude-76° 11' E), which is located at an altitude of 1200 m above sea level. These clones were screened repeatedly in the nursery followed by field testing. The selected superior clones (Table 1) were involved in control crossing using Line  $\times$  Tester (4  $\times$  4 factorial) with 8 parents in 2013-2014. The seedlings were raised and the clonal cuttings of five outperforming individuals per family and parents were raised in RBD (Randomized Block Design) and were evaluated for growth and biomass characters in 2014-2015.

Observations were recorded for plant height (cm), collar diameter (mm), number of branches per plant, number of leaves per plant, leaf area (cm<sup>2</sup>), root length (cm), fresh shoot weight (g), fresh root weight (g), dry shoot weight (g), dry root weight (g), total fresh weight (g) and total dry weight (g). The mean values of five clones per replication for F<sub>1</sub> generations of 16 crosses along with 8 parents for each trait were subjected to statistical analysis using the model suggested by SINGH and CHAUDHARY (2001). An attempt has been made to understand the genetic system controlling inheritance of yield, its components and the combining ability analysis from a Line × Tester mating design.

Table 1. List of clones involved in control crossing

Sr. no.	Clones	Species	Source country/originally developed	Used as
1	J 795	<i>S. matsudana</i> × <i>S. alba</i>	UK/China	Male
2	J 799	<i>S. matsudana</i> × <i>S. alba</i>	UK/China	Female
3	<i>S. tetrasperma</i>	<i>S. tetrasperma</i>	India (Rajasthan)	Male
4	Austree	<i>S. alba</i> × <i>S. matsudana</i>	UK/Newzealand	Male
5	NZ 1140	<i>S. matsudana</i> × <i>S. alba</i>	UK	Male
6	PN 227	<i>S. matsudana</i>	Newzealand	Female
7	<i>S. tetrasperma</i>	<i>S. tetrasperma</i>	Local selection, H.P., India	Female
8	<i>S. babylonica</i>	<i>S. babylonica</i>	Local selection, H.P., India	Female

## RESULTS AND DISCUSSION

Highly significant variances were observed among parents and crosses for all the observed traits demonstrating the presence of wider genetic difference among the parents and crosses (Table 2 to 5). Variations with respect to hybrid willows performance have earlier been reported (LI and WU, 1997; RONNBERG and GULBERG, 1999; ARADOTTIR *et al.*, 2007; CHAUDHARY, 2011).

Mean values listed in table 2 and 3 revealed that the overall performance of following hybrids: PN 227 × J 795 for plant height (269.51 cm), collar diameter (16.34 mm), number of leaves per plant (311.75), root length (70.75 cm), total fresh weight (277.33 g), total dry weight (132.83 g); J 799 × Austree for plant height (266.42 cm), collar diameter (16.70 mm), number of leaves per plant (316.38), root length (72.33 cm), shoot fresh weight (200.22 g), root fresh weight (96.00 g), total fresh weight (296.22 g), total dry weight (127.01 g); PN 227 × Austree for plant height (289.98 cm), collar diameter (15.27 mm), number of leaves per plant (260.33), root length (73.78 cm), shoot fresh weight (217.83 g), shoot dry weight (123.50 g), root fresh weight (105.67 g), total fresh weight (323.50 g), total dry weight (164.83 g); PN 227 × NZ 1140 for plant height (263.50 cm), collar diameter (16.16 mm), number of leaves per plant (323.71), root length (72.67 cm), shoot dry weight (109.00g), root fresh weight (105.33g), total fresh weight (297.67 g), total dry weight (143.08g) and J 799 × J 795 for plant height (245.42 cm), collar diameter (13.61 mm), number of leaves per plant (253.17), root length (68.20 cm), shoot fresh weight (213.30g), total fresh weight (276.30 g), total dry weight (128.95g) were found outstanding for most of the growth and biomass traits. For number of branches per plant *S. babylonica* × NZ 1140 (6.00) performance was promising with minimum mean values as desired for the clean bole production.

Table 2. Mean table for morphological traits in *Salix*

Sl. No.	Crosses/hybrids	Plant height (cm)	Collar diameter (mm)	No. of branches per plant	No of leaves per plant	Leaf area (cm <sup>2</sup> )	Root length (cm)
1	PN 227 × NZ 1140	263.50	16.16	20.34	323.71	19.25	72.67
2	PN 227 × Austree	289.98	15.27	19.13	260.33	17.02	73.78
3	PN 227 × J 795	269.51	16.34	23.01	311.75	15.37	70.75
4	PN 227 × <i>S. tetrasperma</i>	155.00	14.66	12.43	129.55	20.07	63.83
5	J 799 × NZ 1140	146.55	14.85	11.08	158.83	17.87	60.37
6	J 799 × Austree	266.42	16.70	21.85	316.38	21.36	72.33
7	J 799 × J 795	245.42	13.61	13.07	253.17	18.63	68.20
8	J 799 × <i>S. tetrasperma</i>	252.08	14.81	17.32	274.23	18.50	61.85
9	<i>S. babylonica</i> × NZ 1140	150.83	12.27	6.00	100.83	21.23	60.33
10	<i>S. babylonica</i> × Austree	141.67	12.78	13.00	120.67	21.19	51.00
11	<i>S. babylonica</i> × J 795	149.25	14.22	15.55	91.83	15.62	57.85
12	<i>S. babylonica</i> × <i>S. tetrasperma</i>	130.68	12.63	10.25	132.00	19.55	57.33
13	<i>S. tetrasperma</i> × NZ 1140	162.52	14.13	12.28	103.62	24.40	47.99
14	<i>S. tetrasperma</i> × Austree	143.00	13.19	7.38	143.67	25.72	54.18
15	<i>S. tetrasperma</i> × J 795	132.33	13.66	10.42	128.33	25.03	51.54
16	<i>S. tetrasperma</i> × <i>S. tetrasperma</i>	126.57	14.88	12.23	135.55	23.89	53.92
	Mean	189.10	14.38	14.09	186.53	20.30	61.12
	Parents						
1	PN 227 (Female)	218.50	10.80	10.83	265.33	20.72	65.83
2	J 799 (Female)	247.50	16.09	18.50	280.30	19.81	62.10
3	<i>S. babylonica</i> (Female)	215.00	15.46	18.17	216.15	17.87	52.22
4	<i>S. tetrasperma</i> (Female)	95.00	10.23	7.00	80.59	21.84	52.89
5	NZ 1140 (Male)	203.80	13.08	15.83	247.13	18.48	64.50
6	Austree (Male)	260.83	17.81	32.00	324.62	20.44	65.10
7	J 795 (Male)	257.50	14.47	17.00	276.10	17.47	62.67
8	<i>S. tetrasperma</i> (Male)	116.67	12.88	7.05	112.20	22.55	59.83
	Mean	201.90	13.85	15.80	225.30	19.90	60.64
	CD Parents	29.61	1.36	3.72	47.98	2.52	4.80
	CD crosses	29.61	1.36	3.72	47.98	2.52	4.80
	CD Parents v/s crosses	9.07	0.42	1.14	14.69	0.77	1.47

In quantitative genetics, genotypic value of an individual is determined by various types of gene actions such as additive, dominance and their interactions. Additive and dominance genetic variances are important to breeders, suggesting how far a particular trait is amenable to selection in segregating generations or is useful for hybrid development. The estimates of general combining ability variance ( $\sigma^2$  GCA) were more than the specific combining ability variance ( $\sigma^2$  SCA) for all the character studied (Table 6) indicating the presence of additive gene action governing these traits. Similarly, the additive variance was observed more than the

dominance variance for all the parameters, which suggested the major role of additive gene action and improvement through hybridization can be continued to the second generation of heterozygotic parents in order to achieve transgression effects. Studying the traits affecting the biomass production of *Salix eriocephala* using an incomplete factorial design a large percentage of total variance was additive for all the traits and heritability estimates were low to moderate, suggesting that phenotypic expression of the traits are predictable and can be improved through breeding (CAMERON *et al.*, 2008).

Table 3. Mean table for morphological traits in *Salix*

Sl. No.	Crosses/hybrids	Shoot fresh weight (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)	Total fresh weight (g)	Total dry weight (g)
1	PN 227 × NZ 1140	192.33	109.00	105.33	39.08	297.67	143.08
2	PN 227 × Austree	217.83	123.50	105.67	43.00	323.50	164.83
3	PN 227 × J 795	194.67	96.67	82.67	40.83	277.33	132.83
4	PN 227 × <i>S. tetrasperma</i>	168.33	84.33	58.33	43.33	226.67	131.00
5	J 799 × NZ 1140	196.10	99.10	62.33	56.06	258.43	155.16
6	J 799 × Austree	200.22	84.22	96.00	51.79	296.22	127.01
7	J 799 × J 795	213.30	87.97	63.00	42.65	276.30	128.95
8	J 799 × <i>S. tetrasperma</i>	145.75	75.75	70.67	33.96	216.42	104.04
9	<i>S. babylonica</i> × NZ 1140	145.00	55.00	66.00	38.00	211.00	93.00
10	<i>S. babylonica</i> × Austree	165.00	95.00	72.00	33.33	237.00	128.33
11	<i>S. babylonica</i> × J 795	196.67	99.67	58.67	46.00	255.33	156.67
12	<i>S. babylonica</i> × <i>S. tetrasperma</i>	134.17	54.17	64.00	30.33	198.17	91.17
13	<i>S. tetrasperma</i> × NZ 1140	183.11	98.11	71.00	37.06	254.11	141.83
14	<i>S. tetrasperma</i> × Austree	116.33	56.33	59.00	37.36	175.33	93.69
15	<i>S. tetrasperma</i> × J 795	167.67	97.67	60.67	38.83	228.33	133.17
16	<i>S. tetrasperma</i> × <i>S. tetrasperma</i>	133.00	73.00	65.33	49.44	198.33	122.44
Mean		173.10	86.84	72.54	41.32	245.63	128.00
Parents							
1	PN 227 (Female)	187.00	105.33	75.00	38.67	262.00	143.67
2	J 799 (Female)	192.44	102.44	64.67	46.38	257.11	145.49
3	<i>S. babylonica</i> (Female)	160.89	90.89	65.67	29.67	226.55	122.22
4	<i>S. tetrasperma</i> (Female)	106.11	56.11	51.00	27.50	157.11	86.94
5	NZ 1140 (Male)	196.11	100.77	88.00	38.39	284.11	149.16
6	Austree (Male)	198.87	101.87	86.67	49.67	285.53	141.53
7	J 795 (Male)	185.67	90.67	88.67	40.27	274.33	134.27
8	<i>S. tetrasperma</i> (Male)	90.83	50.83	45.67	22.92	136.50	73.75
Mean		164.74	87.36	70.60	36.69	235.41	124.63
CD Parents		15.96	15.02	16.69	11.48	26.42	32.05
CD crosses		15.96	15.02	16.69	11.48	26.42	32.05
CD Parents v/s crosses		4.89	N.S	5.11	3.52	8.09	N.S

Table 4. Estimation of variance components for morphological characters in *Salix*

Sl. No.	Variance components	Plant height	Collar diameter	No. of branches per plant	No. of leaves per plant	Leaf area	Root length
1	Variances of GCA ( $\delta^2_g$ )	1686.28	0.68	8.77	3219.20	5.28	36.24
2	Variances of SCA ( $\delta^2_s$ )	502.01	0.16	4.44	975.48	0.26	4.321
3	Additive variance (D)	6745.11	2.72	35.10	12876.79	21.14	144.98
4	Dominance variance (H)	2008.05	0.62	17.75	3901.93	1.02	17.29
5	Contribution of testers	8.05	0.55	7.88	4.41	10.12	3.01
6	Contribution of lines	63.01	60.56	48.07	65.03	71.80	78.80
7	Interactions	28.93	38.89	44.05	30.56	18.08	18.19

The proportional contribution of lines ranged from 18.85 % (total dry weight) to 78.80 % (root length) whereas for testers it ranged from 0.55 % (collar diameter) to 33.69 % (shoot fresh weight) (Table 4 and 5). However, the proportional contribution of line  $\times$  tester interaction ranged from 18.08 % (leaf area) to 72.63% (root dry weight) indicating the importance of combination of specific parents. The proportional contribution of lines was higher than individual contribution of testers or line  $\times$  tester interaction except for root fresh weight, shoot dry weight, root dry weight and total dry weight where interactions contribution was more.

Table 5. Estimation of variance components for morphological characters in *Salix*

Sl. No.	Variance components	Shoot fresh weight	Root fresh weight	Shoot dry weight	Root dry weight	Total fresh weight	Total dry weight
1	Variances of GCA ( $\delta^2_g$ )	427.44	99.25	124.00	8.19	775.82	123.75
2	Variances of SCA ( $\delta^2_s$ )	120.96	22.33	80.40	3.06	180.65	50.65
3	Additive variance (D)	1709.78	396.98	495.98	32.77	3103.28	494.99
4	Dominance variance (H)	483.85	89.31	321.61	12.23	722.59	202.59
5	Contribution of testers	33.69	23.40	21.78	3.51	26.51	19.43
6	Contribution of lines	37.68	37.46	28.67	23.86	45.59	18.85
7	Interactions	28.63	39.13	49.55	72.63	27.90	61.72

#### GCA and SCA effects

Line PN 227 exhibited the highest positive GCA effects (Table 6 and 7) for most of the traits and proved to be the best combiner for most of the growth and biomass traits. Among the testers Austree expressed highest GCA effects and excelled the characters associated with plant height, collar diameter, number of leaves per plant, leaf area, root length and root fresh weight.

For dry root weight tester NZ 1140; for shoot fresh weight, shoot dry weight, total fresh weight and total dry weight, tester J 795 exhibited the highest positive GCA effects. For number of branches per plant tester NZ 1140 depicted high desirable (negative) GCA effect. Significant within and between family differences and large general combining ability effects for willow clones has been reported by CHAUDHARY (2011). Different parents expressing high desirable general combining ability effects on various characters have been earlier studied on line  $\times$  tester analysis in *P. deltoides* and mulberry genotypes (SINGH, 2002; VIJAYAN *et al.*, 2008). Thus, for recurrent selection based on GCA effects, parents PN 227, Austree and J 795 appears more appropriate in crossing programme directed towards clonal improvement in *Salix* species.

Table 6. General combining ability effects of different parents for morphological characters in *Salix*

Parents		General combining ability effects				
Females	Plant height	Collar diameter	No. of branches per plant	No. of leaves per plant	Leaf area	Root length
PN 227	55.42*	1.22*	4.64*	69.81*	-2.37*	9.14*
J 799	38.53*	0.61*	1.75*	64.12*	-1.20*	4.57*
<i>S. babylonica</i>	-45.97*	-1.41*	-2.88*	-75.20*	-0.90*	-4.49*
<i>S. tetrasperma</i>	-47.98*	-0.42	-3.51*	-58.74*	4.47*	-9.22*
Males						
NZ 1140	-8.23	-0.03	-1.66*	-14.78	0.40	-0.78
Austree	21.19*	0.10	1.25	23.73*	1.03*	1.70*
J 795	10.05*	0.07	1.43*	9.74	-1.63*	0.96
<i>S. tetrasperma</i>	-23.00*	-0.14	-1.03	-18.69*	0.21	-1.89*
SEgi	5.02	0.24	0.65	8.43	0.44	0.84
C.D	14.28	0.68	1.86	23.99	1.26	2.40

\* Significant at 5 % level of significance

The specific combining ability effect (Table 8 and 9) clearly revealed that it would not be possible to isolate crosses where all attributes are in the most desirable combinations. Significant positive SCA effects were observed for PN 227  $\times$  NZ 1140 (Plant height, no. of leaves and shoot fresh weight); PN 227  $\times$  Austree (plant height, fresh shoot weight, dry shoot weight, total fresh weight); PN 227  $\times$  J 795 (no. of leaves), J 799  $\times$  NZ 1140 (dry root weight); J 799  $\times$  Austree (collar diameter, no. of leaves, root length, fresh root weight, total fresh weight); J 799  $\times$  *S. tetrasperma* (plant height and no. of leaves); *S. babylonica*  $\times$  NZ 1140 (root length); *S. babylonica*  $\times$  J 795 (collar diameter, fresh shoot weight, dry shoot weight, dry root weight, total fresh weight, total dry weight); *S. babylonica*  $\times$  *S. tetrasperma* (no. of leaves); *S. tetrasperma*  $\times$  NZ 1140 (Plant height, fresh shoot weight, dry shoot weight, total fresh weight); *S. tetrasperma*  $\times$  J 795 (leaf area) and *S. tetrasperma*  $\times$  *S. tetrasperma* (collar diameter, root length, dry root weight, total fresh weight). However, for number of branches per plant PN 227  $\times$  *S. tetrasperma*, *S. tetrasperma*  $\times$  Austree, J 799  $\times$  J 795, *S. babylonica*  $\times$  NZ 1140, J 799  $\times$  NZ 1140 were found to be the best cross combinations with desired negative SCA effects.

Table 7. General combining ability effects of different parents for morphological characters in *Salix*

Parents	General combining ability effects					
	Shoot fresh weight	Shoot dry weight	Root fresh weight	Root dry weight	Total fresh weight	Total dry weight
Females						
PN 227	20.20*	16.53*	15.46*	0.25	35.66*	14.19*
J 799	15.75*	-0.08	0.46	4.80*	16.21*	0.84
<i>S. babylonica</i>	-12.88*	-10.88*	-7.38*	-4.40*	-20.26*	-10.66
<i>S. tetrasperma</i>	-23.06*	-5.56*	-8.54*	-0.64	-31.61*	-5.17
NZ 1140	6.04*	3.46	3.63	1.23	9.67*	5.32
Males						
Austree	1.75	2.92	10.63*	0.05	12.38*	0.52
J 795	19.98*	8.65*	-5.29*	0.76	13.69*	9.95
<i>S. tetrasperma</i>	-27.78*	-15.03*	-7.96*	-2.05	-35.74*	-15.79*
SEgi	2.80	2.64	2.93	2.02	4.63	5.63
C.D	7.98	7.51	8.35	5.74	13.21	16.02

\*Significant at 5 per cent level of significance

Table 8. Specific combining ability effects among different crosses for morphological characters in *Salix*

Crosses	Specific combining ability effects					
	Plant height	Collar diameter	No. of branches	No. of leaves	Leaf area	Root length
PN 227 × NZ 1140	27.33*	0.59	3.27*	82.15*	0.93	3.19
PN 227 × Austree	24.30*	-0.44	-0.86	-19.73	-1.93*	1.82
PN 227 × J 795	14.97	0.66	2.86*	45.67*	-0.93	-0.47
PN 227 × <i>S. tetrasperma</i>	-66.50*	-0.81	-5.27*	-108.69*	1.93*	-4.54*
J 799 × NZ 1140	-72.84*	-0.11	-3.09*	-77.04*	-1.62	-4.54*
J 799 × Austree	17.62	1.61*	4.77*	41.99*	1.24	4.94*
J 799 × J 795	7.76	-1.46*	-4.19*	-7.23	1.18	1.55
J 799 × <i>S. tetrasperma</i>	47.46*	-0.04	2.52	42.27*	-0.80	-1.95
<i>S. babylonica</i> × NZ 1140	15.96	-0.67	-3.54*	4.28	1.44	4.49*
<i>S. babylonica</i> × Austree	-22.63*	-0.30	0.54	-14.40	0.76	-7.33*
<i>S. babylonica</i> × J 795	-3.90	1.17*	2.92*	-29.24	-2.15*	0.26
<i>S. babylonica</i> × <i>S. tetrasperma</i>	10.57	-0.20	0.07	39.36*	-0.05	2.59
<i>S. tetrasperma</i> × NZ 1140	29.65*	0.20	3.36*	-9.39	-0.75	-3.14
<i>S. tetrasperma</i> × Austree	-19.29	-0.88	-4.45*	-7.86	-0.07	0.57
<i>S. tetrasperma</i> × J 795	-18.82	-0.38	-1.59	-9.20	1.90*	-1.33
<i>S. tetrasperma</i> × <i>S. tetrasperma</i>	8.46	1.05*	2.68*	26.45	-1.08	3.90*
SE	10.40	0.48	1.31	16.86	0.88	1.69
C.D	29.61	1.36	3.72	47.98	2.52	4.80

\*Significant at 5 per cent level of significance

On the basis of mean performance and overall significant desirable SCA effects PN 227 × Austree, PN 227 × NZ 1140 and J 799 × Austree were found to be the best cross combinations.



Thus, majority of the cross combinations exhibiting desirable SCA effects, had at least one of the parents as good or average combiner. Similar observations have also been expressed by earlier workers on willows and poplar species (LI and WU, 1996; RONNBERG and GULBERG, 1999; SINGH, 2002; CHAUDHARY, 2011) who were of the opinion that desirable SCA effects could be obtained from crosses involving atleast one of the parents with good or average general combining ability. However some of the crosses exhibited desirable SCA effects involving both the parents as poor combiners (*S. babylonica* × NZ 1140, *S. babylonica* × *S. tetrasperma*, *S. tetrasperma* × *S. tetrasperma*). This effect has been widely studied by LI *et al.* (1997); BISOFFI (1999); SINGH (2002) and SARESH (2013) who were of the opinion that the chances for obtaining the highest estimates of specific combining ability effects are from crosses involving diverse parents and it is not necessary that parents having higher estimates of general combining ability effects would always give higher estimates of specific combining ability effects. However, sometimes specific interaction effects, most likely complementary of poor × poor crosses, may perform better than high × high and high × low general combining ability combinations indicating that a high magnitude of non-additive component was responsible for confirming the highest rank to the pertinent cross combination.

*Table 9. Specific combining ability effects among different crosses for morphological characters in Salix*

Crosses	Specific combining ability effects					
	Fresh shoot weight	Dry shoot weight	Fresh root weight	Dry root weight	Total fresh weight	Total dry weight
PN 227 × NZ 1140	-7.00	2.16	13.71*	-3.71	6.71	-5.17
PN 227 × Austree	22.79*	17.20*	7.04	1.38	29.83*	21.38
PN 227 × J 795	-18.61*	-15.36*	0.96	-1.49	-17.65	-20.06
PN 227 × <i>S. tetrasperma</i>	2.82	-4.01	-21.71*	3.82	-18.89*	3.85
J 799 × NZ 1140	1.21	8.88	-14.29*	8.71*	-13.08	21.05
J 799 × Austree	9.62	-5.46	12.38*	5.62	22.00*	-2.30
J 799 × J 795	4.48	-7.44	-3.71	-4.23	0.77	-9.79
J 799 × <i>S. tetrasperma</i>	-15.31*	4.02	5.63	-10.11*	-9.69	-8.96
<i>S. babylonica</i> × NZ 1140	-21.25*	-24.42*	-2.79	-0.15	-24.04*	-29.61*
<i>S. babylonica</i> × Austree	3.04	16.12*	-3.79	-3.64	-0.75	10.53
<i>S. babylonica</i> × J 795	16.48*	15.06*	-0.21	8.32*	16.27*	29.42*
<i>S. babylonica</i> × <i>S. tetrasperma</i>	1.74	-6.76	6.79	-4.53	8.53	-10.34
<i>S. tetrasperma</i> × NZ 1140	27.04*	13.37*	3.88	-4.86	30.41*	13.73
<i>S. tetrasperma</i> × Austree	-35.45*	-27.86*	-15.63*	-3.37	-51.07*	-29.61*
<i>S. tetrasperma</i> × J 795	-2.34	7.74	2.96	-2.60	0.61	0.43
<i>S. tetrasperma</i> × <i>S. tetrasperma</i>	10.75	6.75	9.29	10.82*	20.04*	15.45
SE	5.61	5.28	5.86	4.03	9.28	11.26
C.D	15.96	5.02	6.69	11.48	26.42	32.05

\*Significant at 5 per cent level of significance

## CONCLUSION

On the basis of Line  $\times$  Tester analysis it is hereby concluded, that line PN 227 and tester Austree and J 795 were found to be good general combiners and thus appeared to be worthy of exploiting in *Salix* improvement through breeding and recurrent selection followed by cloning for developing commercial superior clones. Since the additive genetic component had predominant role for all the characters, improvement through hybridization should be continued to the second generation of heterozygotic parents in order to achieve transgression effects. On the basis of mean performance of hybrid clones and significant desirable SCA effects PN 227  $\times$  Austree, PN 227  $\times$  NZ 1140 and J 799  $\times$  Austree were found to be the most promising families for growth and biomass characters and are recommended for within family selections followed by heterotic breeding.

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**LINIJA × TESTER ANALIZA ZA PORAST I KARAKTERISTIKE BIOMASE KOD  
RODA *SALIX***

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Izvod

Linija × tester analiza urađena je kod vrbe (*Salix* spp.) da bi se odredila genetička interakcija u ekspresiji različitih kvantitativnih karakteristika povezanih sa produktivnošću. Kombinaciona sposobnost je pokazala da je procenjena GCA varijansa ( $\sigma^2$  GCA) bila veća od SCA varijanse ( $\sigma^2$  SCA) za sva ispitivana svojstva. Kasnije proučavanje pokazalo je i da je aditivna varijansa bila veća od dominantne varijanse za sve proučavane parametre. Proporcionalni doprinos linija bio je veći od individualnog doprinosa testera ili ukrštanja linija x tester, osim za svežu masu korena, suhu masu izdanka, suhu masu korena i ukupnu suhu masu, kod koje je doprinos interakcije bio značajniji. Za liniju PN 227 i testere Austree i J 795 utvrđeno je da su dobri generalni kombinatori i samim tim korisni za upotrebu u poboljšanju roda *Salix* kroz oplemenjivanje i rekurentnu selekciju, praćenu kloniranjem za razvijanje komercijalno superiornih klonova. Na osnovu performansi i efekata SCA, za kombinacije PN 227 × Austree, PN 227 × NZ 1140 i J 799 × Austree, utvrđeno je da su najpovoljnije za rast i osobine biomase, i da se mogu preporučiti sa unutar-familijsku selekciju, praćenu klasičnim oplemenjivanjem. na bazi heterozisa.

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