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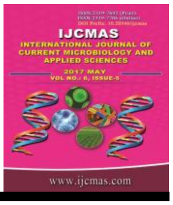

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Estimates of Genetic Parameters and Correlation in Catkin and Seed Traits of *Salix alba*

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ABSTRACT

Keywords

Catkin-seed, *Salix alba*, CPT's, Correlation and heritability.

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Twenty candidate plus trees (CPT's) of *Salix alba* were selected from different locations of Kashmir valley following comparison tree method. Significant variation and association were observed among all the selected CPT's for catkin and seed traits. CPT-12 had maximum for majority of the characters. Heritability in broad sense was high for all the characters under study with maximum (0.936) for capsule diameter followed by high to moderate gain indicating the additive gene action. Germination percentage was found to have positive and significant correlation with catkin and seed weight. CPT-12, CPT-6 and CPT-53 were found to be best on the basis of these characters.

Introduction

The *Salix* species belong to the family *Salicaceae*. There are about 450-520 species of *Salix* known from all around the world which are distributed mostly in the Northern Hemisphere (Argus, 1997; Skvortsov, 1999). In India there are about 33 *Salix*species which have majorly been categorized as shrubs except *Salix alba*, *S. babylonica*, *S. daphnoids*, *S. fragilis*, *S. elegas*and *S. tetrasperma*. In Kashmir valley, the genus *Salix* is represented by 23 species of which 15 reach alpine/subalpine limits (Dhar and Kachroo, 1983). The genus *Salix*is very heterogeneous and shows considerable variation in size, growth form, and crown architecture. The *Salix* species are eco-friendly, multipurpose, fast growing and are widely used for plantation world over. These are being cultivated for a variety of end uses viz. baskets, cricket bats, hurdles, furniture, plywood, paper and pulp, rope making etc (Verwijst, 2001; Kuzovkina *et al.*, 2008). *Salix alba* is a moderate to a large deciduous tree with ascending branches and spreading but light crown, attaining a height of 20-25 m and a diameter of 60 cm. under its native habitat, trees are known to attain a height of 30 m and I m in diameter. Bark is reddish green or brown, smooth in younger trees, fissuring longitudinally with age. Leaves are long lanceolate, acuminate silky, grayish green, silvery white underneath, finely serrated, petiole about 1 cm; shoots are first silky then olive green and very supple.

Flowers male and female in separate catkins. Fruits ovoid-conic capsules. Seeds minute, yellow, ovoid with silky hairs which help in dispersal (Luna, 1995). The growth statistics of *Salix alba* can be compared with a good clone of poplar. In order to diversify the plantation of tree species with integration of agriculture crops, willow is most eco-friendly and farmer's choice. The cricket bat and artificial limbs industry is solely depending on the wood of *Salix alba* and there is ready made market for willow based wood industry (Saini and Sharma, 2001). White willow is primarily utilized for cricket bats and polo balls, fruit boxes, artificial limbs, match-wood, honey-comb frames, tool handles, fibre-boards, agricultural implements, boats etc. used as a fence post, it is as durable as oak (Luna, 1995). The effectiveness of tree improvement programme depends upon the nature and magnitude of existing genetic variability and also on the degree of transmission of traits or heritability (Zobel and Talbert, 1984), because genetic variation is the fundamental requirement for maintenance and long-term stability of forest ecosystem. The rate of tree improvement can be increased or decreased by influencing the selection differential or heritability, or by reducing the total variance (Bagchi, 1995). The knowledge of genetic variability and association between catkin and seed traits is considered to provide considerable help in genetic improvement of the species. Hence, the present investigation was envisaged to evaluate the source variation in different catkin and seed traits of *Salix alba*.

Material and Methods

Twenty CPT's of *Salix alba* were selected following comparison tree method. Mature catkins (yellowish) were collected from these CPT's in the month of May 2015 when the capsules of catkins were ready to burst (mature). Care was taken to collect dry catkins from the marked trees. Sufficient catkins were collected from each CPT. These catkins were analyzed for various characteristics viz. catkin length (cm), catkin width (mm), number of capsules/catkin, capsule diameter (mm), 100-catkin weight (g), 1000-seed weight (mg) and germination percentage.

The germination percentage was worked out as per the following formula:

$$\text{Germinationpercentage} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds used}} \times 100$$

Analysis of variance was carried out following the procedure given by Gomez and Gomez (1984).

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were computed as per the method suggested by Burton (1952):

$$\text{PCV} = \frac{\sqrt{\text{Vp}}}{\text{mean}} \times 100 \quad \text{and} \quad \text{GCV} = \frac{\sqrt{\text{Vg}}}{\text{mean}} \times 100$$

Where, Vp is phenotypic variance and Vg is genotypic variance

Heritability (H^2) in broad sense was estimated as per the procedure presented by Burton and Dewane (1953), Johnson *et al.*, (1955), Hanson *et al.*, (1956) and Allard (1960).

$H^2 = \frac{\text{Vg}}{\text{Vp}}$ Where, Vg is genotypic variance and Vp is phenotypic variance

Genetic advance (GA) was worked out using the formula given by Lush (1949) and Johnson *et al.*, (1955).

$$\text{GA} = \frac{\text{Vg}}{\text{Vp}} \times (\text{Vp})^{0.5} \times \text{K}$$

Where, Vg is genotypic variance of the trait, Vp is phenotypic variance of the trait and K is selection differential, (K=2.06 at 5 percent selection intensity).

Genetic gain (GG) was estimated as per the method suggested by Johnson *et al.*, (1955).

$$GG = \frac{GA}{mean} \times 100$$

Where, GA is genetic advance of the trait

Genotypic (r_g) and phenotypic (r_p) correlation coefficients were worked out for all the possible pairs of characters (Goulden, 1952).

$$r_g = \frac{Cov.xy(g)}{\sqrt{Vx(g) \times Vy(g)}}$$ and

$$r_p = \frac{Cov.xy(p)}{\sqrt{Vx(p) \times Vy(p)}}$$

Where, Cov.xy(g) and Cov.xy(p)are the genotypic and phenotypic covariance for a pair of characters and Vx(g),Vy(g)Vx(p)and Vy(p) are the genotypic and phenotypic variances for the respective characters.

Results and Discussion

In the present investigation, significant variation was observed among the CPT's of *Salix alba* with respect to catkin and seed traits (Table 1). These traits varied from 4.6 cm to 9.9 cm for catkin length, 4.4 mm to 10.2 mm for catkin width, 53.0 to 100.7 for number of capsules per catkin, 1.3 mm to 4.0 mm for capsule diameter, 56.0g to 107.3 g for 100-catkin weight, 61.2 mg to 118.5 mg for 1000-seed weight and 79.6 % to 97.6 % for germination. Analogous with the present findings, significant variation was reported in seed and pod traits of candidate plus trees of *Pongamia pinnata* (Kaushik *et al.*, 2007; Sahoo *et al.*, 2011; Pavithra *et al.*, 2013 and Gawali *et al.*, 2015). Tomar and Rattan (2012) revealed significant variation in fruit and seed characters of *Hippophae salicifolia*. Wani and Ahmad (2013) explored variability in germination parameters of candidate plus trees of *Madhuca indica*. Significant variation in *Albizia procera* for pod, seed and germination characters was observed by Gera *et al.*, (2001). Studies conducted with respect to variation in pod, seed and germination parameters in *Jatropa curcas* (Ginwal *et al.*, 2005; Rao *et al.*, 2008), *Albizia lebbek* (Luna *et al.*, 2006) and *Dalbergia sissoo* (Srivastava *et al.*, 2001, Singh and Sofi, 2011) are in congruity with the present findings.

Genetic parameters of catkin and seed characters of *Salix alba* have been presented under table 2. It is clearly evident that phenotypic variance and phenotypic coefficient of variation were greater than the respective genotypic variance and genotypic coefficient of variation for all the characters under study. Fair differences between PCV and GCV of the characters under study indicate the heritable nature of these traits. All catkin and seed characters exhibited high heritability ranging from 0.936 for capsule diameter to 0.841 for seed weight. High heritability estimates for all pod and seed traits were reported by Divakara and Das (2011) and Gawali *et al.*, (2015) in *Pongamia pinnata* which is in conformity with the present findings. Ginwal *et al.*, (2005) reported high heritability estimates for germination in *Jatropa curcas*. Johnson *et al.*, (1955) reported that heritability estimates along with expected gain is more useful and realistic than heritability alone predicting the resultant effect for selecting the best genotype. In this study genetic advance and genetic gain showed sizeable range indicating the scope for improvement in these characters. Genetic gain was high to moderate for all the characters. High heritability along with high to moderate genetic gain for catkin and seed traits indicate the influence of additive gene action in the expression of these characters

Association is usually determined by studying the correlations existing between various characters under study. The phenotypic correlation coefficient gives the extent of relationship between the two characters which include the genetic and environmental influences whereas genotypic correlation coefficient indicates the real association between two traits and may be useful in selection (Johnson *et al.*, 1955).

Table.1 Variability in catkin and seed traits of selected CPT's of *Salix alba*

CPT's	Catkin length (cm)	Catkin width (mm)	Capsules/ Catkin	Capsule diameter (mm)	100- Capsule Weight (g)	1000- Seed Weight (mg)	Germination percentage
CPT-26	5.9	4.4	59.7	1.6	64.7	69.1	79.6
CPT-86	7.6	6.7	76.0	3.3	82.2	95.3	88.0
CPT-75	8.5	9.0	89.7	3.7	95.5	104.6	91.0
CPT-45	4.6	7.7	53.0	3.9	57.5	61.2	87.3
CPT-98	8.0	7.0	83.3	2.3	85.3	89.6	97.3
CPT-56	5.6	8.6	62.6	2.5	62.6	62.1	85.0
CPT-37	8.9	10.3	90.7	3.8	90.2	93.6	95.0
CPT-12	9.9	4.9	100.6	4.0	101.9	111.4	97.6
CPT-42	4.8	6.4	67.0	1.3	56.2	64.8	86.0
CPT-23	7.6	8.3	82.0	3.5	80.3	86.1	81.0
CPT-79	6.3	7.5	57.3	3.6	76.8	68.1	90.0
CPT-92	6.9	5.4	92.7	2.3	63.4	86.0	89.0
CPT-6	9.1	9.4	67.3	3.8	107.3	118.5	93.3
CPT-50	7.5	8.5	77.3	3.4	78.3	87.1	89.0
CPT-4	9.2	6.5	95.6	2.4	78.5	79.2	85.0
CPT-53	8.8	4.8	84.7	3.5	98.7	108.1	96.6
CPT-81	5.1	8.6	56.3	1.3	56.0	67.7	80.3
CPT-62	5.2	9.3	72.6	1.3	61.4	67.7	84.0
CPT-17	8.7	8.7	90.0	3.6	100.2	110.1	95.3
CPT-69	7.4	10.2	58.0	2.3	81.1	90.2	91.3
Mean	7.3	7.6	75.8	2.9	78.9	86.1	89.1
CD$_{0.05}$	0.8	0.9	8.3	0.4	11.5	12.5	3.5
SE (m)	0.3	0.3	2.9	0.1	4.0	4.4	1.2
CV %	7.0	7.2	6.6	8.4	8.8	8.7	2.3
Min.	4.6	4.4	53.0	1.3	56.0	61.2	79.6
Max.	9.9	10.2	100.7	4.0	107.3	118.5	97.6

Table.2 Estimates of genetic parameters of catkin and seed characteristics of *Salix alba*

S.No.	**Parameters**	**Variance**		**Coefficient of Variation**		**Genetic components**		
		Vp	**Vg**	**PCV**	**GCV**	**H^2**	**GA**	**GG**
1	Catkin length (cm)	2.8	2.6	23.1	22.0	0.902	3.1	43.3
2	Catkin width (cm)	3.4	3.1	24.2	23.1	0.911	3.4	45.5
3	Capsules/catkin	239.6	214.6	20.4	19.3	0.894	28.5	37.6
4	Capsule diameter (mm)	0.9	0.8	33.6	32.5	0.936	1.8	65.0
5	100-Catkin weight (g)	303.9	255.7	22.0	20.2	0.842	30.2	38.3
6	1000-Seed weight (mg)	366.3	309.2	22.2	20.4	0.841	33.2	38.6
7	Germination percentage	45.3	40.7	7.5	7.1	0.903	12.5	14.0

Table.3 Genotypic (G) and phenotypic (P) correlation matrix between catkin and seed characteristics of *Salix alba*

Parameters	Type	Catkin width (mm)	Capsules/ catkin	Capsule diameter (mm)	100-Catkin weight (g)	1000-Seed weight (mg)	Germination percentage
Catkin length (cm)	P G	0.212* 0.235*	0.577** 0.581**	0.263* 0.267*	0.385** 0.392**	0.287* 0.295*	0.101 0.109
Catkin width (mm)	P G		-0.038 -0.035	1.090 1.087	0.202* 0.209*	0.157 0.165	0.086 0.091
Capsules/catkin	P G			-0.153 -0.150	0.108 0.106	0.034 0.046	-0.018 -0.016
Capsule diameter (mm)	P G				0.282* 0.286*	0.302** 0.313**	-0.021 -0.019
100-Catkin weight (g)	P G					0.417** 0.425**	0.476** 0.482**
1000-Seed weight (mg)	P G						0.359** 0.366**

**=significant at 5%, *=significant at 1%

Correlation coefficients of catkin, seed characteristics have been worked out between all the possible pairs and presented under table 3. Catkin length was positively correlated with almost all other catkin and seed characters having maximum correlation (0.577, 0.581) with number of capsules per catkin. Catkin weight displayed positive correlation with seed weight (0.417, 0.425). Germination percentage was positively correlated with catkin weight (0.476, 0.482) and seed weight (0.359, 0.366). Tomar and Rattan (2012) have reported highly significant correlation between fruit length and fruit width in *Hippophae salicifolia*. Positive and significant correlation coefficients were reported between cone and seed traits in *Pinus gerardiana* (Singh and Chaudhary, 1993) which corroborates the present results. There was positive and significant correlation (genotypic and phenotypic) between 100-catkin weight and 1000-seed weight. In consonance with the present findings, Sahoo *et al.*, (2011) while working on CPT's of *Pongamia pinnata* has reported high estimates of genotypic correlations than the corresponding phenotypic correlations between pod length and pod breadth; 100-pod weight, and pod thickness; 100-seed weight and 100-pod weight indicating the presence of strong inherent association. Germination percentage was found to have positive and significant correlation with 100-catkin weight and 1000-seed weight. Positively significant correlation between germination and seed weight has been reported by Singh and Sofi (2011) in *Dalbergia sissoo* and Pavithra *et al.*, (2013) in *Pongamia pinnata.*

In conclusion, from the present investigation, it is clear that there existed wide variation among the selected CPT's of *Salix alba* with respect to catkin and seed characters. CPT-12, CPT-6 and CPT-53 were found to be best on the basis of these characters which revealed promise in their further exploitation for plantation and selection for improvement. High genotypic correlation coefficient between pod and seed characters revealed that the traits are genetically controlled and selection can be very effective in tree improvement programmes of this tree species.

References

Allard, R.W. 1960. Principles of plant breeding. John Wiley & Sons. Inc. New York, p 485.

Argus, G.W. 1997. Infrageneric classification of *Salix* L. (*Salicaceae*) in the New World. *Systematic Botany Monographs*, 52.

Bagchi, S.K. 1995. Selection differential and predicted genetic gain in *Tectonagrandis*. *Indian Forester*, 121(6): 482–490.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*, 1: 227-283.

Burton, G.W., Dewane, C.H. 1953. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agron. J.*, 45: 478-481.

Dar, U., Kachroo, P. 1983. Alpine flora of Kashmir Himalaya. Scientific publishers, Jodhpur, India, pp. 169.

Divakara, B.N., Das, R. 2011. Variability and divergence in *Pongamiapinnata* for further use in tree improvement. *J. Forestry Res.*, 22(2): 193−200.

Gawali, A., Wagh, R., Sonawane, C. 2015. Evaluation of genetic variability and correlation in pod and seed traits of *Pongamiapinnata* (L.) Pierre. germplasm for genetic tree improvement. *Forest Res.*, 4(3): 1-6.

Gera, N., Gera, M., Purohit, M., Agarwal, R. 2001. Intra-population variation in *Albiziaprocera*: Pod, seed and germination characteristics. *Indian Forester*, 127(9): 963-972.

Ginwal, H.S., Phartyal, S.S., Rawat, P.S., Srivastava, R.L. 2005. Seed source variation in morphology, germination and seedling growth of *Jatrophacurcas* Linn. in Central India. *Silvae Genetica*, 54(2): 76-80.

Gomez, K.A., Gomez, A.A. 1984. Statistical procedure for Agricultural Research. 2nd edition.John Wiley ans Sons, Inc, New York.

Goulden, C.H. 1952. Some distance properties of latent root and vector methods used in multivariate analysis. *Biometrica*, 53: 325−338.

Hanson, C.H., Robinson, H.F., Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.*, 48(6): 268-272.

Johnson, H.W., Robinson, H.F., Comstock, R.E. 1955. Estimation of genetic and environmental variability in Soya beans. *Agronomy J.*, 47: 314-318.

Kaushik, N., Kumar, S., Kumar, K., Beniwal, R.S., Kaushik, N., Roy, S. 2007. Genetic variability and association studies in pod and seed traits of *Pongamiapinnata* (L.) Pierre in Haryana, India. *Genet. Resour. Crop Evol.*, 54: 1827–1832.

Kuzovkina, M.A., Wieh, M., Romero, M.A., Charles, J., Hurt, S., Mclvor, I., Karp, A., Trybrush, S., Labrecque, M., Teodorera, T..I, Singh, N.B., Smart, L.B., Volk, T.A. 2008. *Salix*: Botany and global horticulture. *Horticulture Rev.*, 34: 447-489.

Luna, R.K. 1995. Plantation trees. Publishing Corporation. IBD, Dehradun, pp 640-645.

Luna, R.K., Nautiyal, S., and Kumar, R. 2006. Seed source variation in Black Siris (*Albizialebbek* Benth.). *Indian Forester*, 132(2): 149-155.

Lush, J.L. 1949. Heritability of quantitative characters in farm animals. *Proceedings of the 8th international congress on genetics*, Genetics supplement volume. *Heredits*, 356-395.

Pavithra, H.R., Gowda, B., Prasanna, K.T., Shivanna, M. 2013. Pod and seed traits in candidate plus trees of *Pongamiapinnata* (L.) Pierre from southern peninsular India in relation to provenance variation and genetic variability. *J. Crop Sci. Biotech.*, 16(2): 131-142.

Rao, G.R., Korwar, G.R., Shanker, A.K., Ramakrishna, Y.S. 2008. Genetic associations, variability and diversity in seed characters, growth, reproductive phenology and yield in *Jatrophacurcas* (L.) accessions. *Trees*, 22: 697–709.

Sahoo, D.P., Rout, G.R, Das, S., Aparajita, S., Mahapatra, A.K. 2011. Genotypic variability and correlation studies in pod and seed characteristics of *Pongamiapinnata* (L.) Pierre in Orissa, India. *Int. J. Forestry Res.*, 1: 1-6.

Sahoo, D.P., Rout, G.R., Das, S., Aparajita, S., and Mahapatra, A.K. 2011. Genotypic variability and correlation studies in pod and seed characteristics of *Pongamiapinnata* (L.) Pierre in Orissa, India. *Int. J. Forestry Res.*, 1: 1-6.

Saini, B.C., Sharma, P. 2001. *Salix* - a multipurpose tree for future agro-forestry. *ENVIS For. Bull.*, 1(1): 18-20.

Singh, N.B., Chaudhary, V.K. 1993. Variability, heritability and genetic gain in cone and nut characters of Chilgoza pine (*Pinusgerardiana* Wall.). , 42(2,3): 61-63.

Singh, O., Sofi, A.H. 2011. Clone variation of seed traits, germination and seedling growth in *Dalbergiasissoo* Roxb. clonal seed orchard. *Ann. For. Res.*, 54(2): 139-149.

Skvortsov, A.K. 1999. Willows of Russia and adjacent countries: Taxonomical and geographical revision (transl. from: Skvortsov, A.K. 1968. Willows of the USSR: Taxonomic and geographic revision. Nauka, Moscow). Joensuu: Joensuu University.

Srivastava, S.K., Verma, N., Mishra, C.M., Dubey, P., Burfal, B.S. 2001. Evaluation of seed source variation on different parameters of *Dalbergiasissoo* Roxb. *Indian Forester*, 127(3): 358-362.

Tomar, A., Rattan, V. 2012. Source variation in fruit, seed and seedling traits of *Hippophaesalicifolia*. *Int. J. Pharm. & Life Sci.,* 3(12): 2181-2185.

Verwijst, T. 2001. Willows: an underestimated resource for environment and society. *Forestry Chronicle*, 77(2): 281-285.

Wani, M.S., Ahmad, L. 2013. Estimation of field environment variability for germination and seedling traits in *Madhucaindica* Gmel. *American J. Experimental Agri.*, 3(2): 361-373.

Zobel, B.J., Talbert, J.T. 1984. Applied forest tree improvement, John Wiley and Sons, New York, p 505.

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