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# Genetic variability analysis for growth and yield contributing characters in mulberry germplasm under Jammu region

# Santoshkumar Magadum and Sardar Singh

#### Abstract

The investigation was carried out to study the genetic variability and heritability of growth and leaf contributing characters in 18 mulberry genotypes at Regional Sericultural Research Station, Central Silk Board, Miran Sahib, Jammu during Spring, 2019. Analysis of variance for growth and yield contributing characters showed highly significant differences among the genotypes. Phenotypic coefficient of variation was found higher than the genotypic coefficient of variation for number of new shoots per plant, leaf area, total shoot length, total shoot weight, weight of ten fresh leaves and leaf yield per plant indicated that these traits are governed by genetic factors and existence of greater magnitude of genetic variability among the genotypes. High heritability coupled with high genetic advance as per cent of mean was observed for number of new shoots per plant, leaf area, petiole length, total shoot length, total shoot weight, weight of 10 fresh leaves and leaf yield per plant indicating the prevalence of additive gene action in the expression of these traits and effective progress in improvement through selection could be achieved for leaf yield through successful breeding programmes.

Keywords: Genetic advance, heritability, leaf yield, mulberry, variability

#### Introduction

Mulberry (*Morus* spp.) is a perennial plant which is cultivated in under tropical and temperate climatic conditions. It is the primary and only food plant for silkworm (*Bombyx mori* L.). Mulberry belongs to the genus *Morus* of family Moraceae. Quality and quantity of silk production is directly related with the production high quality mulberry leaves. As leaf productivity is one of the principal factors that decide the sustainability and profitability of sericulture, good quality mulberry leaf increases the cocoon productivity and quality of silk (Doss *et al.*, 2012)<sup>[1]</sup>. Therefore, improvement in mulberry production through development of new varieties with high leaf yield and better adaptability is essential for sustainable growth of sericulture (Vijayan *et al.*, 2012)<sup>[2]</sup>.

Thorough understanding of the genetic variability within a set of germplasm will help in mulberry breeding aiming towards increase in productivity. Genetic variability is the prerequisite for initiation of any crop improvement programme including mulberry and selection acts upon the variability which is present in the genotypes. The precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. The extent of magnitude of genetic variability in the mulberry germplasm helps in the crop improvement through conventional breeding. For making effective selection based on the metric traits estimation of genetic variability generation to generation (Saini *et al.*, 2018) <sup>[3]</sup>. Prior knowledge of genetics on yield contributing traits is very essential to formulate a breeding strategy of mulberry. Therefore, the present study was undertaken to know extent of genetic variability, heritability and genetic advance for different growth and yield contributing characters among 18 mulberry genotypes.

#### Materials and Methods

#### **Experimental site and material**

The present study was conducted at Regional Sericultural Research Station (RSRS), Central Silk Board, CSB Complex, Miran Sahib, Jammu during Spring, 2019. The experimental material comprised of 18 mulberry genotypes *viz.*, V-1, K-2, Sujanpur local, TR-10,

Chak Majra, Chinese white, S-146, C-4, BR-2, AR-14, AR-12, AR-10, S-41, S-13, BC-259, S-1, MS-9404 and S-1635 maintained at a spacing of 90 cm x 90 cm as bush plantation at mulberry germplasm block of the station and managed by following the recommended agronomic package of practices.

# Experimental data

The data on quantitative traits like number of new shoots per plant, longest shoot length (cm), number of leaves per meter of shoot length, internodal distance (cm), leaf area (cm<sup>2</sup>), petiole length (cm), diameter of shoot (cm), total shoot length per plant (cm), total shoot weight (kg), weight of 10 fresh leaves (g) and leaf yield per plant (kg) were recorded from randomly sampled three replications. Leaf length and width was measured with measuring scale and actual leaf area was determined by graphical analysis.

# Statistical analysis and estimation of genetic parameters

The mean data of the above mentioned traits were statistically analyzed, using the standard method suggested by Clewer and Scarisbrick (2001)<sup>[4]</sup>, using TNAUSTAT statistical package. Analysis of variance (ANOVA) was done by the method suggested by Panse and Sukhatme (1985)<sup>[5]</sup>. The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) was estimated as suggested by Burton and De vane (1953)<sup>[6]</sup>. Heritability and genetic advance were calculated by following Lush *et al.* (1945)<sup>[7]</sup> and Johnson *et al.* (1955)<sup>[8]</sup> respectively.

# **Results and Discussion**

Genetic variability in any crop is a pre-requisite to initiate the breeding programme for the selection of superior entries over the existing cultivars. In addition to maintaining the pure stocks of the entries, it is also essential to make a systematic assessment of the extent of variability present for various yield components for effective selection of genotypes to bring about improvement in the desired direction (Saini *et al.*, 2018) <sup>[3]</sup>.

The analysis of variance among 18 mulberry genotypes indicated highly significant differences among them for all the growth and yield contributing characters indicating presence of sufficient amount of variability in respect of all the traits studied (Table 1). The genotypic differences were significant at P=0.01. Similar results are reported by Doss *et al.* (2006) <sup>[9]</sup>, Banerjee *et al.* (2007) <sup>[10]</sup>, Mallikarjunappa *et al.* (2008) <sup>[11]</sup>, Vijayashekara (2009) <sup>[12]</sup>, Biradar *et al.* (2015) <sup>[13]</sup>, Saini *et al.* (2018) <sup>[3]</sup> and Chanotra *et al.* (2019) <sup>[14]</sup>.

The variability and genetic estimates for growth and yield contributing characters are presented in Table 2. Analyzed data indicated the presence of wide range of variability for all the characters studied. Maximum range of variation was observed for total shoot length (1147 cm to 7002 cm) followed by leaf area (123.92 cm<sup>2</sup> to 386 cm<sup>2</sup>) and longest shoot length (186 cm to 315 cm). Similar results were reported by Murthy *et al.* (2010) <sup>[15]</sup> and Saini *et al.* (2018) <sup>[3]</sup>. The wide range of variation obtained may be due to divergent genotypes included in the study. The presence of such wide variability in mulberry with respect to all the traits indicating that significant variation existed among the genotypes.

The genotypic variance measures the magnitude of genetic variability present in the crop and phenotypic variance indicates the amount of variation which is due to the phenotypic values. The estimated phenotypic variance for all the traits was higher than genotypic variance. Higher variance was observed for total shoot length followed by leaf area and longest shoot length which indicates the presence of high environmental influence on these characters. Similar kinds of results were also reported by Mallaikarjunappa *et al.* (2008)<sup>[11]</sup>, Murthy *et al.* (2010)<sup>[15]</sup>, Suresh *et al.* (2017)<sup>[16]</sup> and Saini *et al.* (2018)<sup>[3]</sup>.

Yield being a quantitative character is influenced by many genes and are highly controlled by environmental factors. Observed variability is the sum total of hereditary effects from concerned genes as well as the environment. Hence the variability is partitioned into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (GCV), heritability (h<sup>2</sup>) and genetic advance (GA). These genetic parameters help the breeders in selection of genotypes and crop improvement (Murthy *et al.*, 2010) <sup>[15]</sup>.

The phenotypic coefficient of variation was also found to be higher than genotypic coefficient of variation for all the characters studied. High level of phenotypic and genotypic coefficient of variation (>20%) was observed for number of new shoots per plant, leaf area, total shoot length, total shoot weight, weight of 10 fresh leaves and leaf yield per plant indicated that these traits are governed by genetic factors and existence of greater magnitude of genetic variability among the genotypes and selection will be rewarded for the improvement of these traits. Whereas, moderate PCV and GCV (<20%) was recorded for longest shoot length, number of leaves per meter of shoot length, internodal distance, petiole length and diameter of shoot indicated high influence of environment than genetic factors and selection for these traits will be less effective. These result are in agree with the observation made by Banerjee et al. (2007) [10] Mallikarjunappa et al. (2008) [11], Doss et al. (2012) [1], Biradar et al. (2015)<sup>[13]</sup>, Suresh et al. (2017)<sup>[16]</sup> and Saini et al. (2018)<sup>[3]</sup>.

The selection efficiency was higher when the parameters had higher heritability. The heritability estimates (broad sense) was ranged from 51-95%. All the characters studied had high heritability estimates (65-95%) except longest shoot length and diameter of the shoot which exhibit moderate level of heritability. Occurrence of high heritability for all the characters studied suggests the influence of additive gene effects and indicated high rate of trait transmissibility into the future generations. Hence, simple phenotypic selection for these characters may lead to fast genetic improvement. These findings are in line with results of Tikader *et al.* (2004) <sup>[17]</sup>, Banerjee *et al.* (2007) <sup>[10]</sup>, Murthy *et al.* (2010) <sup>[15]</sup>, Biradar *et al.* (2015) <sup>[13]</sup>, Suresh *et al.* (2017) <sup>[16]</sup> and Saini *et al.* (2018) <sup>[3]</sup>

For heritability estimates to be reliable, it must be in conjunction with high genetic advance as a reliable index for selection of traits. Johnson *et al.* (1955) <sup>[8]</sup> have proved that heritability estimates along with genetic gain is more useful than heritability alone in predicting the resultant effects of selection. Earlier studies in mulberry also stated that certain quantitative traits having high heritability as well as genetic advance respond better to simple phenotypic selection as they contribute to additive gene action, which will aid in effective selection for aiding genetic improvement of quantitative traits in mulberry (Masilamani *et al.*, 2000 and Doss *et al.*, 2012) <sup>[18, 1]</sup>.

High heritability coupled with high genetic advance as per cent of mean (>80%, >20%) was observed for number of new

shoots per plant, leaf area, petiole length, total shoot length, total shoot weight, weight of 10 fresh leaves and leaf yield per plant indicating the prevalence of additive gene action in the expression of these traits and effective progress in improvement through selection could be achieved for leaf yield. Whereas, moderate heritability coupled with high genetic advance as per cent of mean was observed for longest shoot length, number of leaves per meter, internodal distance and diameter of shoot indicated the presence of intra and inter allelic interactions in the expression of these characters. These results are in agreement with the findings of Doss (2006) <sup>[9]</sup>, Tikader and Kamble (2008) <sup>[19]</sup>, Maji (2009) <sup>[20]</sup>, Murthy *et al.* (2010) <sup>[15]</sup>, Biradar *et al.* (2015) <sup>[13]</sup>, Suresh *et al.* (2017) <sup>[16]</sup> and Saini *et al.* (2018) <sup>[3]</sup> in mulberry.

Source of variation	df	Number of new shoots/ plant	Longest shoot length (cm)		Internodal distance (cm)	Leaf area (cm <sup>2</sup> )	Petiole length (cm)	Diameter of shoot (cm)	Total shoot length (cm)	Total shoot weight (kg)	Weight of 10 fresh leaves (g)	Leaf yield/plant (kg)
Replication	2	4.46	11.43	2.72	0.15	113.30	0.22	0.07	324576.0	0.34	0.02	0.25
Treatments	17	102.52**	1516.06**	12.35**	0.91**	12056.07**	2.46**	0.55**	5820628.0**	11.61**	295.75**	2.74**
Error	34	4.91	366.76	1.78	0.14	448.23	0.14	0.10	206726.8	0.38	4.37	0.10
CV (%)		13.73	7.39	7.02	7.09	8.46	7.42	6.21	13.09	13.15	6.39	15.70
CD at 5%		3.64	31.43	2.19	0.62	34.74	0.60	0.53	746.18	1.02	3.43	0.53

\*\* Significant at 1% level of probability

 Table 2: Genetic parameters for growth and yield contributing characters in mulberry germplasm

Sl.	Chanastan	Mean±SEm	Range		-2	-2-2	σ²e	PCV	GCV	h <sup>2</sup>	Genetic	GA as %
No.	Characters		Minimum	Maximum	σ²p	$\sigma^2 g$	σ-e	(%)	(%)	(%)	advance	of mean
1	Number of new shoots/ plant	16.15±1.28	5	29	37.45	32.53	4.91	37.90	35.32	86.88	10.95	67.82
2	Longest shoot length (cm)	258.93±11.05	186	315	749.86	383.10	366.76	10.58	7.56	51.09	28.82	11.13
3	Number of leaves/ meter	19.00±0.77	14	25	5.30	3.52	1.78	12.12	9.88	66.43	3.15	16.59
4	Internodal distance (cm)	5.34±0.22	4	7.14	0.40	0.26	0.14	11.86	9.50	64.24	0.84	15.69
5	Leaf area (cm <sup>2</sup> )	250.23±12.22	123.92	386	4217.51	3869.26	448.25	26.26	24.86	89.62	121.31	48.48
6	Petiole length (cm)	4.99±0.21	3.2	7.2	0.91	0.77	0.13	19.17	17.67	84.99	1.67	33.56
7	Diameter of shoot (cm)	5.23±0.19	4.2	6.2	0.25	0.15	0.10	9.63	7.35	58.28	0.61	11.56
8	Total shoot length (cm)	3472.07±262.50	1147	7002	2078025.44	1871299.36	206726.07	41.52	39.40	90.05	2674.15	77.02
9	Total shoot weight (kg)	4.73±0.36	1.129	10.178	4.13	3.74	0.39	42.95	40.89	90.62	3.79	80.18
10	Weight of 10 fresh leaves (g)	32.71±1.21	16.15	49.83	101.50	97.13	4.37	30.80	30.13	95.69	19.86	60.71
11	Leaf yield/plant (kg)	2.07±0.19	0.418	4.282	0.98	0.88	0.10	47.91	45.26	89.26	1.83	88.10

 $\sigma^2 p$  = Phenotypic variance;  $\sigma^2 g$  = Genotypic variance;  $\sigma^2 e$  = Environmental variance; PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation;  $h^2$  = Heritability (Broad sense); GA = Genetic advance

# Conclusion

The present study indicated that there is adequate genetic variability present in the genotypes studied. High heritability along with high genetic advance as per cent of mean was observed for number of new shoots per plant, leaf area, petiole length, total shoot length, total shoot weight, weight of 10 fresh leaves and leaf yield per plant suggested that these characters can be considered as selection criterion during selection of parents for improvement and development of promising mulberry genotypes through successful breeding programmes.

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