

Original Research Article

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Estimation of Genetic Variability and Heritability in Selected Mulberry Germplasm Accessions (*Morus* spp.)

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ABSTRACT

Keywords

Mulberry, PCV, GCV, Variability, Heritability, Characterization

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Genetic variability analysis and heritability of different yield contributing characters were investigated in 44 mulberry genotypes for six morphological and eight physiological traits to understand the available genetic variability for future improvement of mulberry. Phenotypic coefficient of variation (PCV %) was found to be higher than the respective genotypic coefficient of variation (GCV %) for all the characters denoting variability among genotypes. Estimates of phenotypic and genotypic coefficient of variation were high for fresh leaf weight (39.72, 35.06%) moderate for other traits (10-30%) and least in moisture percentage (9.24, 6.81% respectively). High genetic advance coupled with heritability was observed in the characters namely, fresh leaf weight (77.9 %), followed by number of leaves per meter twig (68.6%), internodal distance (64.4%), leaf length (61.4%), dry leaf weight, moisture percentage (54.3%) and actual leaf area (48.2%) and least in leaf width (36.7%). High genetic advance coupled with high heritability revealed significant contribution of fresh leaf weight among studied components. The study revealed importance of agro-morphological traits in characterization of germplasm accessions and in selection for future breeding programmes.

Introduction

Mulberry is the primary host of silkworms (*Bombyx mori* L.), which belongs to family Moraceae and it is exploited on a commercial scale for silk production. It is a perennial plant belonging to the genus *Morus* of family Moraceae, division Magnoliophyta, class Magnoliopsida falling under order Urticales. The origin of mulberry is Asia. The original home of the genus is lower Himalayan belt of Indo-China. Genus *Morus* has 68 recognized species available in different parts of the

world, of which 35 species are found in Asia and 14 in continental America. Sericulture and silk production is directly correlated with production of high quality mulberry leaves. Hence, development of improved mulberry varieties with high leaf productivity and quality is essential for horizontal and vertical growth of sericulture in the country.

Breeding activities aiming towards increase in productivity can benefit from a thorough understanding of the genetic variability and diversity within a set of germplasm

accessions. 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. Genetic variation is also fundamental for species conservation to meet present and future requirement. 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 parameters heritability and genetic advance indicates the extent of trait transmissibility generation to generation. Hence, in the present investigation foliage yield and some important growth traits of indigenous and exotic accessions of mulberry was carried out to determine genetic variability among 44 mulberry genotypes conserved in the germplasm bank of SKUAST-J.

Materials and Methods

Experimental site and material

The present study was conducted at the Mulberry Germplasm Bank, Udheywalla campus, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu. The experimental material comprised of 44 mulberry genotypes (Table 1) maintained at of 1 x 1 meter spacing as bush plantation.

Experimental data

60 days mature leaves were picked up randomly for three replications for recording data. Eight quantitative traits viz., leaf length (cm), leaf width (cm), actual leaf area (cm²), fresh leaf weight in g (100 leaves), dry leaf

weight in g (100 leaves), moisture percentage, internodal distance and number of leaves per meter twig were recorded from randomly sampled replications. Leaf length and width was measured with measuring scale and actual leaf area was determined by graphical analysis. For obtaining fresh leaf weight 100, leaves were picked up randomly from selected replications and weighed immediately on electronic balance and same leaves were oven dried at 70°C till constant weight was achieved and again weighed on electronic balance to determine the oven dry weight. For determining number of leaves per meter twig, one meter length of each branch was measured and total number of leaves counted. Moisture content and internodal distance was calculated in percentage by using the formulas given below:

Moisture percentage=

$$\frac{\text{Fresh leaf weight} - \text{Oven dry weight}}{\text{Fresh leaf weight}} \times 100$$

$$\text{Internodal distance} = \frac{100 \text{ cm}}{\text{Number of nodes}}$$

Statistical analysis and estimation of genetic parameters

The mean data of the above mentioned traits were statistically analyzed using R software version 3.5.1 2018 for estimation of mean square treatment, environmental variance, genotypic variance, phenotypic variance, heritability percentage, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and genetic advance.

Results and Discussion

Results obtained for studied parameters are presented in Table 2. The extent of variability present among the yield and yield attributes is

presented in Table 3. A perusal of data indicated that the characters were greatly influenced by phenotypic variances and reflected impact on genotypic variances also. The analysis of genetic parameters for various quantitative traits revealed significant mean square estimates for all the characters indicating sufficient diversity among the genotypes. Mean square treatment revealed maximum value for fresh leaf weight (24071) and minimum for leaf width (5.5). This variation in genotypes is helpful in selection of superior parental material for development of promising genotypes.

Phenotypic variations were high as compared to genotypic variation for all traits under study. Genotypic variance was maximum in fresh leaf weight (7329.7) followed by actual leaf area (1781.8), dry leaf weight and moisture percentage (29.8), number of leaves per meter twig (12.1), leaf length (5.9) and internodal distance (1.7), while leaf width (1.1) showed least genotypic variance and phenotypic variations was maximum in fresh leaf weight (9411.1) followed by actual leaf area (3697.7), dry leaf weight and moisture percentage (54.9), number of leaves per meter twig (17.7), leaf length (9.7) and leaf width (3.2), while least phenotypic variance was recorded in internodal distance (2.7).

All parameters studied recorded high heritability estimates and showed high genotypic variance also. Maximum heritability percentage was observed for fresh leaf weight (77.9) whereas least heritability percentage was recorded for leaf width (36.7%) distance indicating their reliability for effecting selection for high leaf yield parameters. Results depicted significant correlation of heritability percentage with that of genetic variance. Phenotypic coefficient of variation was more than genotypic coefficient of variation for all studied parameters. The phenotypic and genotypic coefficient of variation was high for fresh leaf weight (39.7,

35.0 %), actual leaf area (30.2, 20.9%), internodal distance (29.5, 23.6 %), number of leaves per meter twig (27.7, 22.9%), leaf width (16.9, 10.2 %), leaf length (16.7, 13.1%) and dry leaf weight (15.8, 11.7%). Lowest PCV and GCV values were recorded in moisture percentage (9.2 and 6.8%) respectively. High genetic advance was recorded for fresh leaf weight (63.7) followed by actual leaf area (30.0), leaf length (21.2), dry leaf weight (17.8), leaf width (12.8), moisture percentage (10.3), number of leaves per meter twig (3.9) and internodal distance (0.3).

These findings for genetic analysis of genotypes suggested greater phenotypic and genotypic variability among the accessions and sensitiveness of the attributes for making future improvement through selection. Wide differences between GCV and PCV for actual leaf area and leaf width implied its susceptibility to agro-climatic fluctuations and genetic constitution attributed for internodal distance, whereas narrow difference between GCV and PCV for other characters suggests their relative resistance to environmental alterations. PCV was higher than the respective GCV for all the characters denoting environmental factors influencing their expression to some degree or other. High estimates of genetic gain coupled with high values of GCV portrayed that these are controlled by additive genes and phenotypic selection for their improvement could be achieved by simple selection.

PCV was found to be higher than the respective GCV for all the characters denoting variability among genotypes. Estimates of phenotypic and genotypic coefficient of variation were high for fresh leaf weight (39.72, 35.06%) moderate for other traits (10-30%) and least in moisture percentage (9.24, 6.81% respectively) (Fig. 1).

Table.1 Pedigree record of genotypes used for analysis

S.No.	Name of genotype	Donor Name	Origin
1.	Asayuki	CSR & TI, Mysore	Cross Pollinated Hybrid
2.	Enshutukasuka	CSR & TI, Mysore	Collection
3.	Fukushima	CSR & TI, Berhampore	Collection
4.	Goshyerami	CSR & TI, Mysore	Selection
5.	Ichinose	RSRS, Kodathi	Cross Pollinated Selection
6.	Kairyoroso	CSR & TI, Mysore	Cross Pollinated Hybrid
7.	Kamabori	CSR & TI, Mysore	Cross Pollinated Hybrid
8.	Kokuso-20	CSR & TI, Mysore	Mutation
9.	Kokuso-27	CSR & TI, Mysore	Cross Pollinated Hybrid
10.	Limencina	CSR & TI, Mysore	Collection
11.	Miuraso	CSR & TI, Mysore	Collection
12.	Rokokyoso	RSRS, Kodathi	Clonal Selection
13.	Shimanouchi	CSR & TI, Mysore	Cross Pollinated Hybrid
14.	BC-259	CSR & TI, Berhampore	Back Cross Selection
15.	Bhrem C-776	CSR & TI, Pampore	Cross Pollinated Selection
16.	Behrampur	CSR & TI, Berhampore	Clonal Selection
17.	C-763	CSR & TI, Mysore	Cross Pollinated Hybrid
18.	Chakmajra	DOS, J&k Govt.	Natural Selection
19.	Chinese white	CSR & TI, Mysore	Collection
20.	Dhar local	DOS, J&k Govt.	Open Pollinated Hybrid
21.	Kanva-2	CSR & TI, Mysore	Cross Pollinated Hybrid
22.	KNG	CSR & TI, Mysore	Clonal Selection
23.	LF-1	CSR & TI, Mysore	Clonal Selection
24.	LF-2	CSR & TI, Mysore	Clonal Selection
25.	NS-1	Div. of Sericulture, SKUAST-J.	Open Pollinated
26.	NS-2	Div. of Sericulture, SKUAST-J.	Open Pollinated
27.	NS-3	Div. of Sericulture, SKUAST-J.	Open Pollinated
28.	S-1	CSR & TI, Mysore	Clonal Selection
29.	S-30	CSR & TI, Mysore	Mutation
30.	S-36	CSR & TI, Mysore	Mutation
31.	S-41	CSR & TI, Mysore	Mutation
32.	S-54	CSR & TI, Mysore	Mutation
33.	S-146	RSRS, Kodathi	Open Pollinated Selection
34.	S-799	CSR & TI, Mysore	Open Pollinated Hybrid
35.	S-1531	CSR & TI, Mysore	Open Pollinated Selection
36.	S-1608	CSR & TI, Berhampore	Open Pollinated Hybrid
37.	S-1635	CSR & TI, Berhampore	OPH Selection
38.	S-1708	CSR & TI, Berhampore	Open Pollinated Selection
39.	Sujanpur	DOS, J&K Govt.	Open Pollinated Collection
40.	Tr-1	CSR & TI, Berhampore	Colchiploid
41.	Tr-4	RSRS, Kodathi	Polyploid
42.	Tr-8	RSRS, Kodathi	Polyploid
43.	Tr-10	RSRS, Kodathi	Polyploid
44.	V-1	CSR & TI, Mysore	Cross Pollinated Hybrid

Table.2 Pooled mean values of eight quantitative traits of mulberry genotypes for the year 2017-18

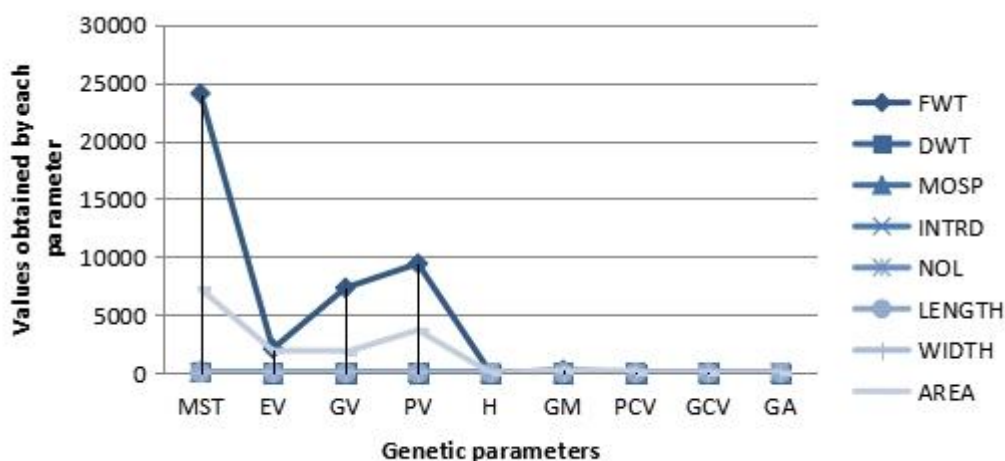
S.No.	Genotype	Leaf length (cm)	Leaf width (cm)	Leaf area (cm ²)	Fresh weight 100 leaves (g)	Dry weight 100 leaves (g)	Leaf moisture (%)	Internodal distance (cm)	Leaves/ meter twig (no.)
1.	Asayuki	16.8	11.2	191.7	141.4	22.8	83.8	4.0	23
2.	Enshutukasuka	15.1	08.1	123.9	156.7	21.9	86.0	4.6	19
3.	Fukushima	19.1	11.1	213.0	177.5	20.4	88.5	3.8	17
4.	Goshyerami	21.8	12.6	278.0	240.3	52.4	78.1	4.6	17
5.	Ichinose	16.2	09.6	156.5	205.4	35.2	82.8	4.3	17
6.	Kairyoroso	4.8	09.6	141.0	102.9	24.2	76.4	4.5	18
7.	Kamabori	17.5	10.6	188.9	133.1	26.4	80.1	4.7	18
8.	Kokuso-20	18.1	10.9	197.5	155.4	30.2	80.5	5.0	17
9.	Kokuso-27	11.4	6.9	80.1	98.3	14.1	85.1	3.2	30
10.	Limencina	14.8	09.8	147.5	125.8	22.4	82.1	4.7	19
11.	Miuraso	19.3	09.3	181.1	362.4	69.6	80.7	6.3	14
12.	Rokokyoso	18.0	8.8	159.4	161.7	37.3	77.0	5.1	18
13.	Shimanouchi	17.6	12.1	215.7	149.9	26.2	82.5	3.4	19
14.	BC-259	16.0	10.9	175.9	235.3	44.2	81.2	5.4	12
15.	Bhrem C-776	19.6	09.7	190.6	306.8	42.6	86.1	9.0	10
16.	Behrampur	21.1	13.0	276.0	216.7	24.9	88.5	4.7	11
17.	C-763	21.8	10.7	237.0	217.2	32.7	85.0	6.9	12
18.	Chakmajra	22.0	11.8	261.5	258.6	36.7	85.8	3.9	11
19.	Chinese white	19.5	11.1	222.3	356.9	64.4	82.0	7.0	11
20.	Dhar local	16.6	10.3	172.5	346.0	63.7	81.5	6.6	12
21.	Kanva-2	18.5	10.4	195.4	243.5	77.2	68.2	5.0	12
22.	KNG	15.0	08.2	125.6	191.7	29.5	84.6	4.1	19
23.	LF-1	16.5	09.9	163.7	306.1	84.8	72.2	4.7	18
24.	LF-2	20.6	10.5	216.8	208.1	63.7	69.3	6.8	12
25.	NS-1	23.2	11.5	271.6	232.1	30.5	86.8	4.8	12
26.	NS-2	22.9	12.5	288.4	244.6	38.9	84.0	9.7	12
27.	NS-3	18.1	12.0	218.4	279.1	48.6	82.5	5.8	13
28.	S-1	17.5	09.1	161.4	178.9	31.3	82.5	5.6	14
29.	S-30	18.1	10.4	191.8	266.3	60.0	77.4	4.7	15
30.	S-36	16.8	09.3	158.3	233.4	72.2	69.0	4.9	15
31.	S-41	21.7	11.6	253.4	322.9	54.7	83.0	5.2	13
32.	S-54	23.3	12.5	295.0	400.6	64.1	84.1	5.1	17
33.	S-146	22.2	12.5	272.6	299.1	79.8	73.3	5.6	14
34.	S-799	34.8	08.4	122.4	126.6	38.6	69.5	5.0	13
35.	S-1531	19.3	10.1	194.6	225.3	57.8	74.3	6.5	12
36.	S-1608	21	09.8	206.6	341.4	76.2	77.6	7.1	13
37.	S-1635	19.6	11.6	227.7	376.6	81.3	78.4	6.7	14
38.	S-1708	19.6	11.7	233.1	320.1	31.4	90.1	7.0	13
39.	Sujanpur	20.6	11.2	232.0	246.2	24.9	89.8	5.6	11
40.	Tr-1	17.1	09.6	164.7	216.7	28.0	87.0	8.0	14
41.	Tr-4	18.8	12.1	228.5	494.8	91.9	81.4	7.4	13
42.	Tr-8	18.5	11.8	223.4	358.1	75.8	78.8	8.4	12
43.	Tr-10	16.0	10.7	172.3	153.8	52.6	65.7	5.8	13
44.	V-1	20.4	10.3	212.1	333.2	47.7	85.6	6.4	14
Mean		18.6	10.6	201.0	224.1	46.7	80.2	5.6	15.2
S.D.		3.09	1.78	60.41	96.36	22.16	7.41	1.67	4.20

Table.3 Coefficient of variations (PCV and GCV), heritability percentage and genetic advance for eight quantitative traits of 44 mulberry genotypes

S.No.	Character	Range		MST	EV	GV	PV	H ² (%)	PCV (%)	GCV (%)	GA
		Min.	Max.								
1.	Fresh leaf weight (g)	98.3	494.8	24071	2081	7329.7	9411.1	77.9	39.72	35.06	63.7
2.	Dry leaf weight (g)	4.1	91.9	114.7	25.1	29.8	54.9	54.3	15.87	11.70	17.8
3.	Moisture content (%)	65.7	90.1	114.7	25.1	29.8	54.9	54.3	9.24	6.81	10.3
4.	Internodal distance (cm)	3.2	9.7	6.3	0.9	1.7	2.7	64.4	29.50	23.68	0.3
5.	Leaves/m (no.)	10.0	30.0	42.1	5.5	12.1	17.7	68.6	27.72	22.95	3.9
6.	Leaf length (cm)	4.8	34.8	21.6	3.7	5.9	9.7	61.4	16.75	13.13	21.2
7.	Leaf width (cm)	6.9	13.0	5.5	2.0	1.1	3.2	36.7	16.92	10.25	12.8
8.	Actual leaf area (cm ²)	80.1	295.0	7261	1916	1781.8	3697.7	48.2	30.24	20.99	30.0

Note: MST: Mean square treatment, EV: environmental variance, GV: genetic variance, PV: phenotypic variance, H²: heritability percentage, PCV: phenotypic coefficient of variance, GCV: genotypic coefficient of variance and GA: genetic advance

Fig.1 Genetic parameters for eight quantitative traits of 44 mulberry genotypes



Tikader and Rao (2002) supported the current observations and highlighted the important of variability estimates for selection of parents in breeding programme. Similar results were also

obtained by Puttarama *et al.*, (2000), Siddiqui *et al.*, (2003), Tikader *et al.*, (2004), Banerjee *et al.*, (2007) and Murthy *et al.*, (2010) and stated that phenotypic variations were high as compared to

genotypic variation. Maximum heritability percentage was observed for fresh leaf weight (77.9) whereas least for leaf width (36.7%) which supports the earlier observations made by Tikader and Roy (1999) and Chikkalingaiah *et al.*, (2008). High genetic advance was recorded for fresh leaf weight (63.7) followed by actual leaf area (30.0), leaf length (21.2), dry leaf weight (17.8), leaf width (12.8), moisture percentage (10.3), number of leaves per meter twig (3.9) and internodal distance (0.3). Similar kinds of results were also reported by Banerjee *et al.*, (2008), Mallaikarjunappa *et al.*, (2008) and Suresh *et al.*, (2017).

High estimates of genetic gain coupled with high values of GCV depicted that these traits are under the control of additive genes and therefore phenotypic selection plays significant role in selection of parental material for improvement and development of promising genotypes by simple selection procedures.

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