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Genetic variability studies for yield and yield attributing traits in mulberry (*Morus* spp.) genotypes under temperate conditions of Kashmir

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Abstract
The present study was carried out with 25 genotypes of mulberry (*Morus* spp.) under temperate conditions. Estimation of the genetic variability, heritability, genetic advance and correlation analysis in the set of twenty five (25) mulberry genotypes revealed that all the characters exhibited large amount of variability. The high amount of GCV and PCV was observed for fruit yield plant^{-1}, followed by leaf yield plant^{-1}. High heritability coupled with high genetic advance was recorded for the character fruit yield plant^{-1}, followed by leaf size (sq.cm) suggesting the higher genetic control over these traits. The correlation studies indicated that the leaf yield plant^{-1} had positive correlation with all the traits. However, significant positive correlation was observed between inter-nodal distance, fruit length, fruit width and shoot thickness. The genetic variability present in the set of breeding material shall not only provide a basis for selection but also provide some valuable information regarding selection of diverse parents to be used in the hybridization programme. Hence, In the present study, significant number of differences were observed in the studied genotypes for all the characteristics which gave an insight into the existence of genetic variation in the available genotypes and thus there is a great scope for selection and further improvement of *Morus* spp. In terms of quality and quantity.

Keywords: Genetic, genotypes, Kashmir, mulberry, *Morus* spp., temperate, variability, yield

Introduction
Mulberry is a fast growing deciduous, perennial and highly heterozygous plant which exhibit sexual polymorphism. It is believed to have originated in the Northern hemisphere, particularly in the Himalayan foothills and spreads to the tropics of southern hemisphere. It can be grown in the diverse edapho-climatic conditions which require more productive hybrids for acclimatization in particular area (Tikader *et al.*, 2004) [16]. It is the primary food plant of silkworm (*Bombyx mori* L.); hence, availability of good quality leaf has great impact on the sustainability and profitability of sericulture industry (Vijayan *et al.*, 2010) [17]. Increased production of silk to a very large extent depends upon the quality of cocoons which in turn has a direct relation with the quality of feed i.e. mulberry leaf (Sarkar *et al.*, 1987) [12].
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 pre-requisite for initiation of any crop improvement programme including mulberry and selection acts upon the variability which is present in the genotypes (Saini *et al.* 2018) [11]. 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 basing upon the metrictraits estimation of genetic variability parameters heritability and genetic advance as per percent of mean (GAM) indicates the extent of trait transmissibility generation to generation. In view of the above facts the study was aimed to evaluate the mulberry (*Morus* spp.) genotypes

through genetic variability, heritability, and genetic advance estimation and correlation analysis.

Materials and Methods

The experiment was conducted at the mulberry germplasm bank of College of Temperate Sericulture, SKUAST-Kashmir, Mirgund during 2021. The experimental material comprised of twenty five (25) mulberry genotypes including nine (9) indigenous and sixteen (16) exotic (Table 1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Nine plants were selected from each plot for collection of data for various yield contributing charactersviz; Shoot thickness (cm), Petiole length (cm), Petiole thickness (cm), Leaf lamina length (cm), Leaf lamina width (cm), Leaf size (sq.cm), Inter-nodal distance (cm), Leaf yieldplant^{-1}(kg), Fruit length (cm), Fruit width (cm), and Fruit yieldplant^{-1}(g). The average values of all the observations were used for statistical analysis. Genotypic and phenotypic coefficients of variation were calculated according to the formula given by Burton and De-Vane (1953) [5]. Heritability was calculated according to the formula given by Hanson *et al.*, (1956). From the heritability estimates the genetic advance was estimated as per Johnson *et al.*, (1955). Correlation coefficient were estimated using the formula given by Miller *et al.*, (1958).

Table 1: List of selected mulberry genotypes studied

S. No.	Genotype	Species	Indigenous/Exotic
1.	Enshutakasuke	*M. bombycis*	Exotic
2.	KNG	*M. alba*	Exotic
3.	Kokuso-21	*M. alba*	Exotic
4.	Kokuso-20	*M. alba*	Exotic
5.	Kairiyoroso	*M. multicaulis*	Exotic
6.	Kanva-2	*M. indica*	Indigenous
7.	Kasuga	*M. multicaulis*	Exotic
8.	Zust	*M. alba*	Exotic
9.	Mandaliya	*M. alba*	Exotic
10.	Tomeiso	*M. alba*	Exotic
11.	Francee	*M. alba*	Exotic
12.	Rokokuyaso	*M. multicaulis*	Exotic
13.	Obawase	*M. bombycis*	Exotic
14.	Robeshsarnal	*M.indica*	Indigenous
15.	Chinese-white	*M. alba*	Exotic
16.	Serpentina	*M. alba*	Exotic
17.	Sujanpur	*M. alba*	Indigenous
18.	V-1	*M. indica*	Indigenous
19.	Tr-10	*M. alba*	Indigenous
20.	S-1531	*M. alba*	Indigenous
21.	Botatul	*M. alba*	Indigenous
22.	Chatatul-Mirgund	*M. alba*	Indigenous
23.	Goshoerami	*M. multicaulis*	Exotic
24.	Ichinose	*M. alba*	Exotic
25.	Cherry	*M. indica*	Indigenous

Results and Discussion

The presence of variability in any crop population is essential for improvement in breeding program of a crop (Hasan *et al.*, 2006). The analysis of variance for eleven (11) quantitative traits of twenty five (25) mulberry genotypes presented in Table 2 depict that the mean total of squares due to genotypes was found to be highly significant in all the traits *viz*; Shoot thickness (cm), Petiole length (cm), Petiole thickness (cm), Leaf lamina length (cm), Leaf lamina width (cm), Leaf size (sq.cm), Inter-nodal distance (cm), Leaf yieldplant^{-1}(kg), Fruit length (cm), Fruit width (cm) and Fruit yieldplant^{-1}(g). This suggests a significant amount of genetic variation among the genotypes for all the characters under investigation and offers an opportunity for further study and assessment of variability parameters. Similar results of significant mean sum of squares due to genotypes were carried out by many workers *viz*: Banerjee *et al. (*2007) [1]. Doss *et al.* (2006) [7], Tikader and Kamble (2008) [15], Mallikarjunappa *et al.* (2008) [8], Vijayashekara (2009) [19] and Biradar *et al.* (2015) [3].

The coefficient of variation was measured at genotypic and phenotypic rates. Usually, the phenotypic coefficient of variation was greater in magnitude than the coefficient of variation in the genotypes signifying that the variability is not only due to genotypes but also due to the influence of climate. In the current study (Table 3 and 4) the moderate value of genotypic coefficient of variation (GCV) was recorded forShoot thickness (16.49%) followed by Petiole length (16.49%), Petiole thickness (15.26%), Leaf lamina length (15.42%), Leaf lamina width (15.36%), Leaf size (19.97%), Inter-nodal distance (19.02%), Leaf yieldplant^{-1}(25.90%), Fruit length (20.64%), Fruit width (14.85%) and Fruit yieldplant^{-1}(31.42%). The moderate value of phenotypic coefficient of variation (PCV) was recorded for Shoot thickness (18.37%) followed by Petiole length (16.89%), Petiole thickness (21.18%), Leaf lamina length (15.53%), Leaf lamina width (15.44%), Leaf size (19.97%), Inter-nodal distance (19.37%), Leaf yieldplant^{-1}(25.91%), Fruit length (20.67%), Fruit width (15.90%) and Fruit yieldplant^{-1}(31.43%).Similar kinds of results were also reported by Mallaikarjunappa *et al.* (2008) and Suresh *et al.* (2017) [13]. Heritability was recorded maximum in fruit yield per plant (0.99%), followed by leaf yield per plant (0.99%) and leaf size (sq.cm) i.e, 0.99%. These results of the present study are in line with the findings of Das and Krishnaswami (1969) [6] and Tikadar (1997). While as Genetic advance was recorded maximum in fruit yield per plant (310.68%), followed by leaf size (sq.cm) i.e, 70.57%. These results are in conformity with the studies of Doss *et al.* (2006) [7]. Low estimates of heritability and genetic advance obtained for petiole thickness, fruit width, fruit length and shoot thickness showed the influence of environment on the expression of these characters. Therefore, direct selection based on these characters alone would be less effective.

Burton (1952) [4] has suggested that the study of GCV% together with H^2 estimates would give the best picture of progress to be expected from selection. Genetic advance provides information about the extent of genetic gain which is possible to achieve through selection, while heritability indicates how much of the phenotypic variability is heritable. Heritability estimates enable a plant breeder to base his selection on the phenotypic performance for further improvement of specific traits. High value of heritability indicates the possible control of additive gene action in expression of the traits (Panse, 1957) [9].

Table 2: Analysis of variance (mean squares) for agro-morphological traits in mulberry genotypes

Source of variation	Degree of freedom	Shoot thickness (cm)	Petiole Length (cm)	Petiole thickness (cm)	Leaf lamina length (cm)	Leaf lamina width (cm)
Replication	2	0.94	0.45	0.01	0.75	1.33
Genotypes	24	0.77**	1.24**	0.01**	17.42***	10.01**
Error	48	0.05	0.02	0.002	0.08	0.03

Source of variation	Degree of freedom	Leaf size (sq.cm)	Inter-nodal distance (cm)	Leaf yield plant^{-1} (kg)	Fruit length (cm)	Fruit width (cm)	Fruit yield plant^{-1} (g)
Replication	2	20.89	0.91	0.24	0.04	0.02	12.59
Genotypes	24	3522.07**	2.50**	1.54**	0.52**	0.07**	68267.87**
Error	48	0.07	0.0308	0.0002	0.0004	0.0032	5.451

**Significant at 0.01 level of significance

Table 3: Genetic parameters of variation for agro-morphological traits in mulberry (*Morus* spp.) genotypes

S. No.	Characters	Range	Mean	GCV	PCV	h^2	Genetic advance	Genetic Adv as % of mean 5%
1.	Shoot thickness (cm)	1.56-3.60	2.96	16.49	18.37	0.80	0.90	30.51
2.	Petiole length (cm)	2.70-5.30	3.89	16.49	16.89	0.94	1.27	32.79
3.	Petiole thickness (cm)	0.19-0.43	0.34	15.26	21.18	0.51	0.07	22.65
4.	Leaf lamina length (cm)	11.50-21.30	15.59	15.42	15.53	0.98	4.91	31.54
5.	Leaf lamina width (cm)	8.46-16.23	11.87	15.36	15.44	0.98	3.73	31.47
6.	Leaf size (sq.cm)	121.56-350.0	171.56	19.97	19.97	0.99	70.57	41.13
7.	Inter-nodal distance (cm)	3.26-6.40	4.77	19.02	19.37	0.96	1.83	38.47
8.	Leaf yield plant^{-1} (kg)	1.62-4.08	2.76	25.90	25.91	0.99	1.47	53.34
9.	Fruit length (cm)	1.33-2.83	2.02	20.64	20.67	0.98	0.85	42.46
10.	Fruit width (cm)	0.76-1.24	1.01	14.85	15.90	0.87	0.28	28.58
11.	Fruit yield plant^{-1}(g)	350.40-893.70	479.99	31.42	31.43	0.99	310.68	64.73

Table 4: Genotypic correlation coefficients for agro-morphological traits in mulberry (*Morus* spp.) genotype

	St	Pl	Pt	Lflmln	Lflmw	Lfsize	Intd	Lfyld	Frtln	Frtw	Frtyld
St	1.0000	0.0829	0.3503*	0.2668*	0.1562	0.1751	-0.0906	0.2678*	-0.0827	-0.0819	0.4137**
Pl		1.0000	0.2107	0.4721**	0.4238**	0.1078	0.5411**	0.0566	-0.0448	0.3155*	0.0723
Pt			1.0000	0.7885**	0.5671**	0.3185*	0.2605*	0.0881	-0.3080	0.0644	0.0939
Lflmln				1.0000	0.6812**	0.2633*	0.3913**	0.0203	-0.3369	0.0522	-0.0338
Lflmw					1.0000	0.3306*	0.2540*	0.0885	-0.1925	0.1411	-0.1067
Lfsize						1.0000	0.1309	0.1651	0.0023	-0.1543	0.0442
Intd							1.0000	0.3809**	0.1555	0.5546**	0.1792
Lfyld								1.0000	0.2907*	0.6479**	0.0105
Frtln									1.0000	0.3177*	0.3118*
Frtw										1.0000	0.0215
Frtyld											1.0000

**Significant at 0.01 level of significance

*Significant at 0.05 level of significance

St=Shoot thickness (cm), Pl=Petiole length (cm), Pt=Petiole thickness (cm), Lflmln=Leaf lamina length (cm), Lflmw= Leaf lamina width (cm), Lfsize= Leaf size (sq.cm), Intd=inter-nodal distance (cm), Lfyld=Leaf yield plant^{-1}(kg), Frtln=Fruit length (cm), Frtw=Fruit width (cm), Frtyld=Fruit yield plant^{-1} (g).

Association studies between yield and yield contributing characters

The correlation studies among eleven (11) yield attributing characters revealed significant correlation between the traits which is described here under in detail and presented in Table 4.Shoot thickness showed positive correlation for all traits expect inter-nodal distance (-0.0906), fruit length (-0.0827) and fruit width (-0.0819), but showed positive significant correlation with fruit yield plant^{-1} (0.4137**), leaf yield plant^{-1} (0.2678*), leaf lamina length (0.2668*) and petiole thickness (0.3503*). Petiole length had positive association with petiole thickness (0.2107), leaf size (0.1078), leaf yieldplant^{-1} (0.0566) and fruit yieldplant^{-1} (0.0723), but showed positive significant correlation with leaf lamina length (0.4721**), leaf lamina width (0.4238**), inter-nodal distance (0.5411**) and fruit width (0.3155*), while exhibited a negative correlation with fruit length (-0.0448). Petiole thickness exhibited a positive correlation with fruit width (0.0644), leaf yieldplant^{-1} (0.0881) and fruit yield plant^{-1}(0.0939) but showed positive significant correlation with leaf lamina length (0.7885**), leaf lamina width (0.5671**), leaf size (0.3185*) and inter-nodal distance (0.2605*), while exhibited a negative correlation with fruit length (-0.3080). Leaf lamina length exhibited a positive correlation with fruit width (0.0522) and leaf yieldplant^{-1} (0.0203) but showed positive significant correlation with leaf lamina width (0.6812**), leaf size (0.2633*), inter-nodal distance (0.3913**), while exhibited a negative correlation with fruit length (-0.3369) and fruit yield plant^{-1} (-0.0338). Leaf lamina width showed positive correlation with fruit width (0.1411) and leaf yieldplant^{-1} (0.0885) but showed positive significant correlation with leaf size (0.3306*), inter-nodal distance (0.2540*), while exhibited a negative correlation with fruit length (-0.1925) and fruit yield plant^{-1} (-0.1067). Leaf size showed positive correlation with inter-nodal distance (0.1309), leaf yieldplant^{-1} (0.1651), fruit length (0.0023) and fruit yield plant^{-1} (0.0442), but showed negative correlation with fruit width (-0.1543). Inter-nodal distance exhibited a positive correlation with fruit length (0.1555) and fruit yield plant^{-1} (0.1792), but showed positive significant correlation with fruit width (0.5546**) and leaf yieldplant^{-1} (0.3809**). Leaf yieldplant^{-1} exhibited a positive correlation with fruit yieldplant^{-1} (0.0105) but showed positive significant correlation with fruit length (0.2907*) and (0.6479**). Fruit length exhibited a positive correlation with fruit width (0.3177*) and fruit yield plant^{-1} (0.3118*). Fruit width exhibited a positive correlation with fruit yield plant^{-1} (0.0215).The results of the present study are also in agreement with the findings of Vijayan *et al*. (1997) [18].

In conclusion study with twenty five (25) mulberry genotypes of mulberry (*Morus* spp.) revealed significant amount of differences among the genotypes for all the characteristics which gives an insight into the existence of genetic variation in the available genotypes reflecting that there is a great scope for selection. Traits like fruit yield plant^{-1} and leaf size (sq.cm) have high heritability as well as high genetic advance and selection can be based on these traits.The correlation studies indicated that the leaf yield plant^{-1} had positive correlation with all the traits. Therefore, selection of these characters would be more effective for the improvement of the crop.

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