RESEARCH ARTICLE

GENETIC VARIATION, HERITABILITY, CORRELATION AND PATH ANALYSIS FOR LEAF YIELD IN CLONALLY SELECTED MULBERRY GENOTYPES (*MORUS* SPP.)

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Abstract - Fourteen clonally selected mulberry genotypes were evaluated to estimate the genetic variability, correlation, and path analysis for important leaf yield contributing characters. Analysis of variance revealed significant differences for all the traits under study. In general, PCV estimates were higher than GCV estimates for all the eleven characters studied. High heritability (>60%) accompanied by high genetic advance (>20%) recorded in number of branches/plant, petiole length, leaf area, stem girth, leaf specific weight, leaf moisture retention, leaf thickness, and leaf yield/plant is due to additive gene effects and selection based on these may be effective. correlation studies indicated that total leaf yield/plant had a positive and significant association with all the studied characters except petiole length. Path coefficient analysis revealed that leaf thickness had the highest positive direct effects on leaf yield/plant, suggesting their importance while imposing selection for correlation of leaf yield in mulberry.

Keywords: Correlation, Genetic variability, Heritability, Mulberry, Path analysis

INTRODUCTION

Mulberry (*Morus* spp.) is a perennial, cross-pollinated, highly heterozygous, and vegetatively propagated plant that belongs to the family Moraceae, under the order Rosales. Its world-wide distribution shows this adaptability to various environmental situations. The leaf is the only economically important part of the plant in the sericulture industry for rearing monophagous silkworms (*Bombyx mori* L.) and obtaining cocoons, which in turn leads to silk production. The quantity and quality of leaves produced by mulberry have a direct influence on silkworm cocoon production. The leaves vary in shape and size depending on the variety and environmental conditions. Thus, the objectives of mulberry breeding are mainly focused on the enhancement of quantitative and qualitative characteristics of the leaf. Since mulberry leaf yield is a complex characteristic and is highly influenced by the environment, the yield, as such, may not be the best criterion for selection. Therefore, it is important to study the genetics of yield components and their degrees of association with yield. These characters need to be integrated and then selection could be affected to get better results (Rahman *et al.*, 2004). Evaluation of the mulberry gene pool for important leaf yield-contributing traits is a pre-request for mulberry improvement. Heritability estimation and genetic advancement in mulberry genotypes revealed high heritability (> 70%) in leaf area, plant height, number of leaves per meter, length of a branch, and weight of 100 leaves per plant (Masilamani *et al.*, 2000). Genetic analysis of different morphological quantitative characters such as total shoot length, length of longest shoot, nodes per shoot, leaf lamina, leaf weight, leaf yield, etc., has wide variations among the mulberry germplasm of diverse origins. The highly heritable characters are leaf lamina area, leaf weight, and petiole characteristics, which have a positive correlation with leaf yield (Banerjee *et al.*, 2007). Hence, the present study was conducted to assess the genetic variability, heritability, genetic advance, correlations, and path analysis for yield contributing traits in 14 clonally selected mulberry genotypes for future exploitation.

MATERIALS AND METHODS

The experiment was conducted on fourteen clonally selected mulberry genotypes that were grown in the field gene bank of the Dept. of Sericulture Science, University of Mysore, Mysuru, in a randomized block design with three replications during 2017-2020. Recommended doses of fertilizer and cultural practices were adopted. The observations were recorded on six randomly selected plants for eleven economically important leaf yield attributing traits, viz., number of branches/plant, average branch length, stem girth, inter-nodal length, petiole length, leaf area, leaf thickness, leaf specific weight, leaf moisture content and its retention capacity, and leaf yield/plant. The mean data of eleven traits, covering three seasons over three years, was used. Analysis of variance was done for partitioning the total variation due to treatments and replications according to the procedure given by Panse and Sukhatme (1967). The genotypic and phenotypic coefficients of variance were arrived at according to AI-Jibouri *et al.* (1958). The genotypic and phenotypic coefficients of variation as suggested by Burton and Devane (1953).

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Heritability and genetic advance were computed according to Johanson *et al.* (1955). Path coefficient analysis was carried out following the procedure employed by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance

Analyzing mean data for 11 characters was subjected to an analysis of variance for experimental design. The mean sum of squares values for all the eleven characters is presented in Table-1. The mean sum of squares due to 14 genotypes was significant for all the characters studied, suggesting that the clonally selected genotypes were genetically divergent from each other. This indicates that there is ample scope for selection of promising lines for the present gene pool for yield and its components. These findings of mean sum of squares are in accordance with the findings of Mallikarjunappa *et al.* (2008), who also observed significant variability for leaf yield components in mulberry.

Variability and genetic components of variation

The genetic variability estimates, including genotypic mean, range, genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (broad sense), and genetic advance as a percent of mean (Table 2), were estimated for each trait under study, and the comparative performance of all the genotypes under study has been described as follows. Higher phenotypic co-efficient of variation (PCV) values than the corresponding genotypic co-efficient of variation (GCV) values observed for all characters with a narrow difference indicate that environmental influence was minimal and that genetic factors dominated in controlling variability in these traits. The magnitude of the coefficient of variation was divided into three categories: high (> 20%), moderate (10–20%), and low (10%). A wide range of PCV was observed for traits ranging from 3.05% for leaf moisture content to 37.61% for leaf yield. Similarly, GCV ranged from 0.93% for leaf moisture percentage to 35.06% for leaf yield. High GCV and PCV were recorded for the number of branches/plant, leaf area, leaf thickness, and leaf yield/plant. The magnitude of GCV and PCV for the above traits suggested the presence of a high degree of variability and, therefore, better scope for improvement through simple selection. Low GCVs and PCVs (10%) were found for the leaf moisture content and leaf specific weight characters. The lower GCV and PCV indicate a narrow genetic base for these traits. Improvement in these characters can be brought about by hybridization or induced mutagenesis to widen the genetic base. While branch length, inter-nodal distance, petiole length, stem girth, and leaf moisture retention capacity have moderate GCVs and PCVs (10-20%), this indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement through selection in advanced generations.

Heritability and genetic advance

Heritability in a broad sense includes both fixable (additive) and non-fixable (dominant and epistatic) variations and also provides a good indication of the repeatability of the traits. The estimates of heritability for different characters ranged from 9.26% to 98.01%, respectively. Although the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals, which is possible by using the estimate of genetic advance. Heritability estimates (above 60%) along with genetic advance (above 20%) would be more helpful in predicting gain under selection than heritability estimates alone (Jhonson *et al.*, 1955). In the present study, high heritability coupled with high genetic advance was observed for characters viz., number of branches/plant, petiole length, leaf area, stem girth, leaf thickness, and leaf yield, indicating the predominance of additive gene action and being expected to respond to direct selection (Panse, 1957). High heritability with moderate genetic advance was observed for leaf specific weight and leaf moisture retention capacity, indicating the predominance of both additive and non-additive gene action (Liang and Walter, 1968).

Correlation Coefficients

In plant breeding, correlations are important as they measure the degree of association between two or more traits and give an indication of the traits that could be used for a particular selection programme. In the present study, eleven quantitative characters were considered for working out character associations between different characters (Table 3). Leaf yield per plant had a significant positive correlation with the number of branches per plant (r = 0.323), branch length (r = 0.616), inter-nodal distance (r = 0.631), leaf area (r = 0.355), leaf specific weight (r = 0.691), moisture content (r = 0.539), moisture retention capacity of leaves (r= 0.343), and leaf thickness (r = 0.343), while petiole length (r = -0.308) was negatively correlated with the leaf yield. Similar findings were also reported by Rahman *et al.* (2004) and Mallikarjunappa *et al.* (2008) in the mulberry.

Path Coefficient analysis

Path analysis provides more quality and complete insight into the relationships that exist among the studied traits, allows for more precise establishment of cause-effect connections among them, and allows separation of direct from indirect effects of any particular trait on any dependent variable (Wright 1921), which in this case is total leaf yield/plant (Table 4). The nine characters were considered as casual variables of leaf yield (dependent trait) in mulberry. Leaf thickness had the maximum positive direct effect (+0.566) on leaf yield per plant, followed by leaf specific weight (+0.511), number of branches per plant (+0.457), leaf moisture content (+0.391), branch length (+0.211), stem girth (0.126), and leaf moisture retention capacity (+0.169). Leaf thickness and leaf yield are due to the direct effect of a character, which reveals the true relationship between them, and direct selection for yield is rewarding.

Table 1. ANOVA for 11 traits in 14 clonally selected mulberry genotypes.

Sl. No.	Characters	Mean sum of squares		
		Replications (df : 5)	Treatments (df : 13)	Error (df : 26)
1	**Number of branches/plant**	264.36	18.88**	13.36
2	**Average branch length (cm)**	13722.19	980.15 **	8.55
3	**Inter-nodal length (cm)**	29.00	2.07**	4.60
4	**Petiole length (cm)**	33.43	2.38**	14.81
5	**Leaf area (cm^2)**	503160.02	35940.00**	60.09
6	**Stem girth (cm)**	2.56	0.18**	31.76
7	**Leaf specific weight (mg/ cm^2)**	161.60	11.54 **	28.30
8	**Leaf moisture content (%)**	108.99	7.78**	1.61
9	**Leaf moisture retention capacity (%)**	4778.60	341.32**	25.91
10	**Leaf thickness (µm)**	68305.33	4878.95**	296.84
11	**Leaf yield/plant (g)**	1203483.23	85963.08**	40.78

** Significant at 1% level.

Table 2. Estimates of mean, range, components of variance, heritability and genetic advance for leaf yield attributing traits in mulberry

Characters	Range	Mean	Co-efficient of Variation		Variance		Heritability (broad sense)	GA (%) Mean
			Genotypic	Phenotypic	Genotypic	Phenotypic		
Number of branches/plant	5.55-11.65	8.32±0.48	20.5	24.99	2.91	4.32	67.33	34.64
Average branch length (cm)	80.01-132.01	99.43±4.36	12.07	16.18	144.26	258.82	55.73	18.57
Inter-nodal length (cm)	4.68-6.64	5.49±0.27	9.47	15.45	0.27	0.71	37.55	11.87
Petiole length (cm)	3.78-5.95	4.93±0.16	12.33	14.77	0.37	0.53	69.72	21.21
Leaf area (cm^2)	143.24-379.62	234.66±9.98	32.7	34.32	5890.33	6488.33	90.78	64.19
Stem girth (cm)	0.53-1.30	0.88±0.03	19.37	21.18	0.02	0.03	83.68	33.92
Leaf specific weight (mg/ cm^2)	14.23-20.09	16.15±0.26	8.43	9.31	1.85	2.26	81.98	15.72
Leaf moisture content (%)	72.78-77.34	75.40±0.89	0.93	3.05	0.49	5.31	9.26	0.58
Leaf moisture retention capacity (%)	55.32-80.70	71.75±1.48	10.21	11.37	54.69	67.86	80.59	19.06
Leaf thickness (µm)	53.83-173.50	94±1.65	30.28	30.59	810.41	826.85	98.01	61.76
Leaf yield/plant (g)	101.71-648.24	337.16±18.74	35.06	37.61	13975.85	16083.82	86.89	67.32

Table 3. Simple correlation matrix for important leaf yield attributing characters

Characters	LY	NB	ABL	ID	PL	LA	SG	LSW	LM	LMR	LT
LY	1.000										
NB	0.323**	1.000									
ABL	0.616**	0.719**	1.000								
ID	0.631**	-0.529**	0.423**	1.000							
PL	-0.308**	0.303**	0.582**	0.109 ^{NS}	1.000						
LA	0.355**	0.409**	0.318**	0.606**	0.558**	1.000					
SG	0.227 ^{NS}	0.089 ^{NS}	0.563**	0.041 ^{NS}	0.737**	0.092 ^{NS}	1.000				
LSW	0.691**	0.341**	-0.116 ^{NS}	-0.013 ^{NS}	0.394**	0.266*	0.147 ^{NS}	1.000			
LM	0.539**	-0.065 ^{NS}	-0.111 ^{NS}	-0.277*	-0.675**	0.382**	-0.613**	0.583**	1.000		
LMR	0.453**	-0.199*	-0.239*	-0.115 ^{NS}	0.267*	0.734**	0.387**	0.583**	0.047 ^{NS}	1.000	
LT	0.343**	0.301**	0.515**	0.195 ^{NS}	0.916**	0.442**	0.551**	0.361**	0.572**	0.331**	1.000
*Significant at 5% level ; ** Significant at 1% level.											

LY= Leaf yield/plant, NB= Number of branches/plant, ABL=Average branch length, ID= Inter-nodal length, PL=Petiole length, LA=Leaf area, SG=Stem girth, LSW=Leaf specific weight, LM=Leaf moisture content, LMR=Leaf moisture retention capacity, and LT=Leaf thickness.

Table 4. Path co-efficient analysis with dependent variables for leaf yield

Characters	NB	ABL	ID	LA	SG	LSW	LM	LMR	LT	Correlation with leaf yield
NB	**0.457**	-0.051	0.008	-0.002	-0.373	-0.062	0.019	-0.224	-0.024	**0.323**
ABL	-0.171	**0.211**	0.200	0.000	-0.060	0.119	-0.117	0.034	-0.205	**0.616**
ID	-0.006	-0.050	**-0.851**	-0.005	0.020	0.025	0.071	0.423	0.025	**0.631**
LA	-0.052	-0.002	0.153	**0.030**	-0.083	-0.011	0.002	-0.228	0.269	**0.155**
SG	-0.316	-0.015	-0.020	-0.003	**0.126**	0.055	0.001	0.027	-0.188	**0.227**
LSW	0.155	-0.089	0.076	0.001	-0.162	**0.511**	0.073	-0.108	0.045	**0.691**
LM	-0.069	0.131	0.319	0.000	-0.002	0.107	**0.391**	-0.222	-0.074	**0.539**
LMR	-0.221	0.010	-0.502	-0.009	0.031	0.043	0.059	**0.169**	-0.127	**0.453**
LT	-0.030	-0.077	-0.038	0.014	-0.277	-0.022	0.025	-0.161	**0.566**	**0.343**
Residual = 0.096										

LY= Leaf yield/plant, NB= Number of branches/plant, ABL=Average branch length, ID= Inter-nodal length, LA=Leaf area, SG=Stem girth, LSW=Leaf specific weight, LM=Leaf moisture content, LMR=Leaf moisture retention capacity, and LT=Leaf thickness

CONCLUSIONS

The phenotypic value of a clone is due to its genotype (G), the environment (E) and the genotype x environment interaction (GE). Of these, only the G effects are heritable and stable. In the present investigation, it is shown that in general, estimates of phenotypic coefficient of variation were found to be higher than their corresponding genotypic coefficients of variation, indicating that there is little influence of the environment on the expression of these characters. However, good correspondence was observed in terms of genotypic coefficient of variation and phenotypic coefficient in all characters.

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