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Assessment of genetic variability in polycross hybrids of mulberry for growth and yield contributing characters under sub-tropical conditions of Jammu

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Abstract

The present study was carried out to estimate the genetic variability, heritability and genetic advance of growth and yield contributing characters among 916 polycross hybrids of mulberry at Regional Sericultural Research Station, Central Silk Board, Miran Sahib, Jammu during Autumn, 2024. Phenotypic coefficient of variation was found to be higher than the corresponding genotypic coefficient of variation for all the characters indicating the role of environment in the expression of characters. High phenotypic and genotypic coefficient of variation was observed for number of new shoots per plant, longest shoot length, leaf area, total shoot length and leaf yield per plant indicated that these traits are governed by genetic factors and existence of greater magnitude of genetic variability in the population, thus provide ample scope for improvement through selection. High heritability coupled with high genetic advance as per cent of mean was observed for number of new shoots per plant, longest shoot length, number of leaves per meter, internodal distance, leaf area, total shoot length, weight of 10 fresh leaves, leaf moisture retention capacity and leaf yield per plant indicating that variation in these traits was most likely due to additive gene effect. The directional selection would be effective to improve these characters. Therefore, number of new shoots per plant, longest shoot length, number of leaves per meter, internodal distance, leaf area, total shoot length, weight of 10 fresh leaves, leaf moisture retention capacity and leaf yield per plant can be considered as selection criterion during mulberry improvement for leaf productivity.

Keywords: Heritability, mulberry, genetic advance, variability, leaf yield

Introduction

Mulberry is a perennial, fast growing, deciduous plant which is cultivated as bush or dwarf tree mainly to utilize leaves for silkworm rearing. Mulberry is cross-pollinated and highly heterozygous in nature which contributes to wide range of diverseness in the mulberry genetic stocks. Improved mulberry varieties play a vital role in increasing silk productivity and profitability of sericulture. Superior mulberry varieties need to be developed due to new silkworm hybrids, more number of silkworm crops per year and increased demand of high quality silk. Therefore, creation of genetic variability is essential for development of superior mulberry varieties.

Development of mulberry varieties through conventional hybridization breeding method is mainly dependent on generation of hybrid seeds from several crosses. Cross hybridisation is a time consuming and tedious process because it involves emasculation, bagging and pollination, needs more labor and resources. In mass or OPH selection, pollen source of hybrid is unknown and several OPH varieties thus developed may have some undesired traits. To overcome such limitation, polycross breeding is being practiced since long time especially for obligate cross pollinators in particular those that can be propagated vegetatively (Frandsen and Frandsen, 1948) [3]. A polycross is a mating arrangement for inter pollinating a group of cultivars or clones using natural hybridization in an isolated crossing block (Klein *et al.*, 1973) [6]. Progeny from each entry have a common parent in a polycross design. Thus, half sib families are generated and these are frequently used for evaluating general combining ability. Purpose of polycross breeding is to provide equal opportunities for each entry to be crossed with other entry. Thus, the polycross mating creates greater amount of genetic variability and consequently generates

large number of segregating population with least manpower and resources, offering greater scope for selection of superior genotypes.

Mulberry leaf yield is a complex character jointly contributed by a good number of component characters and is highly influenced by different genotypes. The extent of magnitude of genetic variability in the mulberry helps in the crop improvement. Genetic variability is the pre-requisite for initiation of any crop improvement programme and selection acts upon the variability which is present in the genotypes. The precise information on the nature and degree of genetic variability helps the plant breeder in choosing the diverse parents for purposeful hybridization (Magadum and Singh, 2022) [8]. Prior knowledge of genetics on yield contributing traits is very essential in 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 polycross hybrids of mulberry under sub-tropical conditions of Jammu.

Materials and Methods

A polyclonal seed orchard was established at CSR&TI, Berhampore by using 29 superior divergent parents (16 female and 13 male parents). After natural pollination during flowering season in 2022 & 2023, polyclonal hybrid fruits were harvested from individual female parents of seed orchard and seeds were extracted by water soaking method (Barbour *et al.*, 2008) [1]. Polycross hybrid seeds were collected from 16 female parents and were sown in controlled condition at CSB-RSRS, Jammu. The seedlings nursery was raised with more than 5000 seedlings and was characterized for visual observations of leaf and growth parameters after 8 months of establishment. Out of which, a total of 916 promising polycross hybrid progenies were selected for further evaluation under progeny row trial in main field. The present study was conducted at Regional Sericultural Research Station, Central Silk Board, Miran Sahib, Jammu during Autumn, 2024. The experimental material comprised of 916 polycross hybrids of mulberry maintained at a spacing of 90 cm x 90 cm as bush plantation. All the hybrid progenies were maintained by following the recommended agronomic package of practices.

All the polycross hybrids were evaluated for growth and yield contributing traits and data was recorded on number of new shoots per plant, longest shoot length (cm), number of leaves per meter of shoot length, internodal distance (cm), leaf area (cm²), total shoot length per plant (cm), weight of 10 fresh leaves (g), leaf moisture content (%), leaf moisture retention capacity (%) and leaf yield per plant (kg). The experimental data were analyzed statistically following the method of analysis of variance for single factor (Gomez and Gomez, 1984) [4]. Mean, Variance components (*viz.*, PV, GV, EV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were estimated as per Singh and Chaudhary (1979) [12]. The broad sense heritability, genetic advance and genetic advance as percent of mean were calculated as suggested by Johnson *et al.* (1955) [5].

Results and Discussion

Identification of high yielding genotypes among the segregation progenies is essential to overcome the problem of low productivity in mulberry. Identification of these better genotypes, their introduction in clonal evaluation trials coupled with establishment of suitable selection criteria will be helpful for successful mulberry improvement programme.

The results revealed highly significant differences among the hybrid progenies for all the characters indicating presence of sufficient amount of variability and thus providing the scope for selection of progenies to improve the leaf productivity. Similar results are reported by Biradar *et al.* (2015) [2], Suresh *et al.* (2017) [13], Saini *et al.* (2018) [11], Magadum and Singh (2021) [9], Magadum and Singh (2022) [8], Kumara and Ramesh (2022) [7]. The variability and genetic estimates for growth and yield contributing characters are presented in Table 1. 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 (348 cm to 4280 cm) followed by longest shoot length (85 cm to 228 cm), leaf area (143.5 cm² to 347.4 cm²), weight of 10 fresh leaves (18 g to 48 g) and leaf yield per plant (0.182 kg to 2.160 kg). Similar results were reported by Murthy *et al.* (2010) [10], Suresh *et al.* (2017) [13], Saini *et al.* (2018) [11] and Magadum and Singh (2021) [9], Magadum and Singh (2022) [8]. The wide range of variation obtained may be due to divergent progenies 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 progenies. The genetic analysis of metric traits is a prerequisite for plant breeding programmes, which can lead to the appropriate planning of plant breeding strategies. 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 kind of results were also reported by Murthy *et al.* (2010) [10], Suresh *et al.* (2017) [13], Saini *et al.* (2018) [11], Magadum and Singh (2021) [9], Magadum and Singh (2022) [8], Kumara and Ramesh (2022) [7].

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 (PCV), heritability (*h*²) and genetic advance (GA). These genetic parameters help the breeders in selection of genotypes and crop improvement (Magadum and Singh, 2021) [9].

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, longest shoot length, leaf area, total shoot length and leaf yield per plant indicated that these traits are governed by genetic factors and existence of greater magnitude of genetic variability in the population, thus provide ample scope for improvement through selection. These results are in line with the observations made by Biradar *et al.* (2015) [2], Suresh *et al.* (2017) [13], Saini *et al.* (2018) [11] and Magadum and Singh (2021) [9], Magadum and Singh (2022) [8]. Whereas, moderate PCV and GCV (<20%) was recorded for number of leaves per meter of shoot length, internodal distance, leaf weight of 10 fresh leaves, leaf moisture content and leaf moisture retention capacity indicated high influence of environment than genetic factors and selection for these traits will be less effective.

The selection efficiency was higher when the parameters had

higher heritability. The heritability estimates (broad sense) was ranged from 66.75-86.84%. All the characters studied had high heritability estimates (66-86%). 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 conformity with results of Biradar *et al.* (2015)^[2], Suresh *et al.* (2017)^[13], Saini *et al.* (2018)^[11] and Magadum and Singh (2021)^[9], Magadum and Singh (2022)^[8].

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)^[5] 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 responded 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 (Magadum and Singh, 2021)^[9]. Thus a trait possessing high heritability along with high GAM will be useful for selection in segregation population.

High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was observed for number of new shoots per plant, longest shoot length, number of leaves per meter, internodal distance, leaf area, total shoot length, weight of 10 fresh leaves, leaf moisture retention capacity 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. These results are in agreement with the findings of Biradar *et al.* (2015)^[2], Suresh *et al.* (2017)^[13], Saini *et al.* (2018)^[11] and Magadum and Singh (2021)^[9], Magadum and Singh (2022)^[8] in mulberry. Whereas, high heritability coupled with low genetic advance as per cent of mean was observed for leaf moisture content indicated the presence of intra and inter allelic interactions in the expression of the character.

Table 1: Genetic parameters for growth and yield contributing characters in polycross hybrids of mulberry

Sl. No.	Characters	Mean±SEm	Range		σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h^2 (%)	Genetic advance	GA as% of mean
			Minimum	Maximum								
1	Number of new shoots/ plant	12.31±1.96	4	25	35.75	24.28	11.47	48.57	40.03	67.92	8.37	67.95
2	Longest shoot length (cm)	148.32±18.94	85	228	1580.37	1162.15	418.22	26.80	22.98	73.54	60.22	40.60
3	Number of leaves/ meter	18.61±0.54	14	27	7.87	6.83	1.04	15.07	14.04	86.79	5.02	26.95
4	Internodal distance (cm)	5.48±0.12	3.71	7.14	0.38	0.33	0.05	11.25	10.48	86.84	1.10	20.12
5	Leaf area (cm ²)	218.42±12.81	143.5	347.4	2377.12	1791.49	585.63	22.32	19.38	75.36	75.69	34.65
6	Total shoot length (cm)	2487.63±325.74	348	4280	2381336	1783471	597864	62.03	53.68	74.89	2380.8	95.71
7	Weight of 10 fresh leaves (g)	33.86±1.53	18	48	45.89	35.17	10.72	20.01	17.51	76.64	10.69	31.59
8	Leaf moisture content (%)	70.23±1.04	63.91	78.16	11.49	7.67	3.82	4.83	3.94	66.75	4.66	6.64
9	Leaf moisture retention capacity (%)	67.49±2.09	43.84	88.35	134.45	112.61	21.84	17.18	15.72	83.76	20.01	29.64
10	Leaf yield/plant (kg)	1.09±0.13	0.182	2.16	0.46	0.32	0.14	62.22	51.90	69.57	0.97	89.17

σ^2_p = Phenotypic variance; σ^2_g = Genotypic variance; σ^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 among the polycross hybrids studied. High phenotypic and genotypic coefficient of variation was observed for number of new shoots per plant, longest shoot length, leaf area, total shoot length and leaf yield per plant indicating the existence of greater magnitude of genetic variability in the population. High heritability along with high genetic advance as per cent of mean was observed for number of new shoots per plant, longest shoot length, number of leaves per meter, internodal distance, leaf area, total shoot length, weight of 10 fresh leaves, leaf moisture retention capacity and leaf yield per plant suggested that these characters can be considered as selection criterion for improvement and development of promising mulberry genotypes through successful breeding programmes.

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