

## GENETIC DIVERSITY AND RELATEDNESS IN EXOTIC MULBERRY (*MORUS*) GERMPLASM ACCESSIONS

Syed Said Badshah Bukhari<sup>1</sup>, Ghulam Ali Bajwa<sup>2</sup> and Miskeen Ali<sup>3</sup>

### ABSTRACT

Nine agronomic traits were used for assessing genetic variability and interrelationship in ten exotic mulberry germplasm accessions. The results showed highly significant ( $p < 0.01$ ) variation in all agronomic traits. Both direct and indirect interactions were found among the traits. The highest genetic coefficient of variation (GCV) was 48.18% in total shoot length (TSL), while the lowest GCV was 3.27% in number of branches per plant (NB). The highest phenotypic coefficient of variation (PCV) was 48.19% in TSL, and the lowest PCV was 4.01% in moisture content. The PCV was slightly greater than GCV in all the traits. The heritability ( $h^2$ ), in broader sense, was ranged between 0.50% and 1.0%. Seven agronomic traits have  $h^2 > 0.80\%$ . The highest genetic advance (GA) was in TSL (75.95%) and the lowest in inter-nodal distance (0.78%). Cluster analysis showed different levels of linkage among accessions. There were two main clusters and each cluster was divided into subgroups. The linkages among accessions were independent of their geographical origins and sprouting behaviour. Heritability combined with genetic advance showed both additive gene action and intra- and inter allelic interactions in the expressions of the traits. Based on these findings, it is recommended that for improving leaf yield, growth traits which have significant positive effect on leaf yield, such as, TSL, longest shoot length and NB should be considered for mulberry breeding programme. The breeding programme is suggested to be based on hybridization followed by selection method.

**Key words:** Genetic variability, phenotypic variation, heritability, genetic advance, genetic linkage, mulberry, breeding

### INTRODUCTION

Originated from China, mulberry, an exclusive source of food for the domesticated silkworm, *Bombyx mori* L., is a heterozygous perennial plant (Vavilov, 1926). It grows naturally across Asia, Europe, North and South America, and Africa, both in temperate and tropical conditions. Mulberry, however, is extensively cultivated in east, central, and south Asia for silkworm rearing. Apart from diverse climatic adaptability, mulberry is hybridized easily, both naturally and artificially. Frequent hybridization makes genetic background of mulberry more complicated and highly heterozygous (Dwivedi, *et al.*, 1989; Dandin, 1998), which creates a wide range of variability in the gene pool (Zhao, *et al.*, 2006). Several studies have highlighted genetic variability of mulberry germplasm (Thangavelu, *et al.*, 2000; Tikader and Rao, 2002). The easy hybridization and genetic variability has resulted in abundant mulberry germplasm worldwide. Only in China, more than 3,000 mulberry germplasm sources comprising 15 species and four varieties have been reported (Pan, 2000).

Genetic variation is fundamental for species conservation for present and future uses (Gilpin and Soule, 1986; Quedraogo, 2001). Apart from conservation, distantly related parents provide a broad spectrum of variability to ensure the efficiency of

---

<sup>1</sup> Director General, Pakistan Forest Institute, Peshawar

<sup>2</sup> Coordinator Sericulture, Pakistan Forest Institute, Peshawar

<sup>3</sup> Forest Ranger, Pakistan Forest Institute, Peshawar

selection for better type, in terms of improved yield, quality and resistance to diseases (Banerjee, 2007). High degree of genetic variability in mulberry is benign for mulberry conservation and genetic improvement through breeding. Characterization and evaluation of genotype is the first step for any crop improvement programme. There are different methods of genotype analysis, however, agronomic (growth and yield) traits are reliable practical indicators of genetic diversity. Variation and association among different agronomic traits indicate nature and magnitude of genetic variability. This information can be utilized in mulberry breeding and improvement programme (Vijayan, *et al.*, 1997; Tikader and Roy, 1999). Among agronomic traits, leaf yield is an important quantitative trait of crop improvement measure which is affected, directly or indirectly, by several other agronomic traits. Thorough knowledge of such traits is very important for selecting genotype for a breeding programme.

Sericulture cottage industry demands high yielding mulberry varieties, suitable for different climatic zones. Moreover, efficiency and viability of sericulture industry depends largely on availability and quality of mulberry leaf, since 60% of total cost of silkworm cocoon production is incurred on mulberry cultivation (Das and Krishna, 1965; Zhao, *et al.*, 2009). Pakistan Forest Institute, Peshawar, introduced high yielding exotic germplasm of mulberry in 1980s from sericulturally advanced countries, such as, China, Japan and South Korea, to fulfill mulberry leaf demand in the country. The germplasm has been maintained and propagated under sub-tropical conditions. The genetic diversity and its relatedness have not been assessed, therefore, present study was conducted to assess: (i) the magnitude of genetic variability, (ii) association among agronomic traits, and (iii) relatedness among accessions.

## MATERIALS AND METHODS

Ten exotic mulberry accessions, i.e., early sprouting Kanmasi (KME), late sprouting Kanmasi (KML), early sprouting *Morus latifolia* (MLE), late sprouting *M. latifolia* (MLL), early sprouting Karyansubhan (KSE), late sprouting Karyansubhan (KSL), early sprouting Qumjee (QJE), late sprouting Qumjee (QJL), early sprouting Husang (HUE) and late sprouting Husang (HUL) were used to assess genetic diversity and their relatedness. Four accessions were Japanese (Kanmasi and *M. latifolia*), four Korean (Karyansubhan, Qumjee) and two Chinese (Husang). The study was conducted in July-August 2010 at Pakistan Forest Institute, Peshawar (34° 0' 28" North, 71° 34' 24" East, and at 510 m altitude). Mulberry accessions were planted at 2x2 m<sup>2</sup> (plant to plant and row to row) distance and irrigated at fortnightly interval. The plants were pollarded in December 2009 for bush type growth

Nine agronomic traits, number of branches per plant (NB), total shoot length (TSL), longest shoot length (LSL), single leaf weight (SLW), number of leaf per branch (NLB), inter-nodal distance (IND), moisture content (MC), moisture retention capacity (MRC) and leaf yield per plant (LYP) were assessed. Fresh single leaf weight was recorded at 5<sup>th</sup> to 9<sup>th</sup> leaf position in descending order. A total of 120 leaves per replication (24 branches) were plucked at 1000 hrs. Freshly plucked leaves were weighed and placed in polythene bags. The bags were kept at room temperature and leaves for six hours. The leaves were again weighed after six hrs and placed in oven at 80°C for 48 hours for drying.

The leaf moisture content and leaf moisture retention capacity were calculated through following methods as described by Tikader and Roy, (1999) and Vijayan, *et al.* (1996):

$$\text{MC (\%)} = \frac{\text{Fresh leaf weight} - \text{Oven dry leaf weight}}{\text{Fresh leaf weight}} \times 100$$

$$\text{MRC (\%)} = \frac{\text{Leaf weight after 6 hours} - \text{Oven dry leaf weight}}{\text{Fresh leaf weight} - \text{Oven dry leaf weight}} \times 100$$

Genetic diversity was estimated on basis of genetic variance ( $\sigma^2_g$ ), environmental variance ( $\sigma^2_e$ ) and phenotypic variance ( $\sigma^2_p$ ), calculated using 1-Way analysis of variance. Based on variance, genotypic coefficient of variation and phenotypic coefficient of variation in different agronomic traits were calculated using following formulae as described by Poehlman and Sleper (1995):

$$\text{— GCV(\%)} = \left( \frac{\sqrt{\sigma^2_g}}{\bar{X}} \right) \times 100$$

$$\text{— PCV(\%)} = \left( \frac{\sqrt{\sigma^2_p}}{\bar{X}} \right) \times 100$$

Where:

$$\begin{aligned} \sigma^2_g &= \{MS_{(Acc)} - MS_{(E)}\} / R \\ \sigma^2_p &= \sigma^2_g + \sigma^2_e \\ \sigma^2_e &= MS_{(E)} \end{aligned}$$

$MS_{(Acc)}$  = Accession Mean Square;  $MS_{(E)}$  = Error Mean Square; R= No. of Replications; g = Genetic; p = Phenotypic; e = Environmental

The heritability ( $h^2$ ), in broader sense, afterward written as heritability, was estimated from total genetic variance, without taking into consideration the components of genetic variance. Following formula was used to estimate heritability of each agronomic trait:

$$h^2 (\%) = \left( \frac{\sigma^2_g}{\sigma^2_p} \right) \times 100$$

The expected gain or genetic advance estimated at 20% selection intensity ( $i=1.40$ ; a constant based on selection intensity in standard deviation units) was calculated as follow:

$$GA = (i)(\sqrt{\sigma^2_p})(h^2)$$

Genetic relatedness among accessions was assessed by Ward Linkage Cluster Variable Analysis using the nine agronomic traits.

## EXPERIMENTAL DESIGN AND ANALYSES

The study was conducted in a randomized complete block design with four replications. There were five plants, selected at random, per replication. The growth and yield traits data were analyzed using Minitab Statistical Software version 15. The overall variation in agronomic traits was assessed using 1-Way analysis of variance while individual difference in the traits was subjected to Tukey's honestly significant difference (HSD) test. The correlation matrix among the agronomic traits was established using Pearson Correlation Matrix.

## RESULTS

The results showed a highly significant variation in leaf yield per plant ( $F_{9, 30} = 263.5$ ;  $p < 0.01$ ), total shoot length ( $F_{9, 30} = 54430.1$ ;  $p < 0.01$ ), longest shoot length ( $F_{9, 30} = 1201.2$ ;  $p < 0.01$ ), number of branches/plant ( $F_{9, 30} = 8380.5$ ;  $p < 0.01$ ), single leaf weight ( $F_{9, 30} = 1361.5$ ;  $p < 0.01$ ), number of leaf per branch ( $F_{9, 30} = 456.8$ ;  $p < 0.01$ ), inter-nodal distance ( $F_{9, 30} = 248.7$ ;  $p < 0.01$ ), moisture content ( $F_{9, 30} = 22.2$ ;  $p < 0.01$ ) and moisture retention capacity ( $F_{9, 30} = 5.07$ ;  $p < 0.01$ ). Leaf yield was ranged between 3.16 kg/plant and 5.90 kg/plant with the highest LYP in late sprouting Chinese accession, HUL ( $5.90 \pm 0.03$  kg/plant) followed by Korean accession, KME. The lowest LYP ( $3.16 \pm 0.05$  kg/plant) was recorded in early sprouting Chinese accession, HUE (Table 1). The LYP did not differ significantly ( $CV = 0.31$ ;  $p = 0.05$ ) among HUL, KML and KME. Similarly there was not significant difference in LYP among KSE, QJE and QJL. The highest TSL was in KME ( $219.58 \pm 0.61$  m), while the lowest TSL was in KSL ( $50.43 \pm 0.12$  m). The longest shoot length ( $361.13 \pm 2.27$  cm) and highest NB ( $222.71 \pm 0.98$ ) was found in KSE. The shortest shoot length ( $237.71 \pm 2.14$  cm) was observed in QJE. The heaviest leaf ( $6.21 \pm 0.06$  g) was recorded in QJE and the lightest leaf ( $3.07 \pm 0.01$  g) was of KME. The difference in SLW between QJE and HUL was not significant ( $CV = 0.16$ ,  $p = 0.05$ ). Significantly greater NLB was observed in HUL ( $21.89 \pm 0.37$ ) and the least NLB ( $11.67 \pm 0.02$ ) were in HUE. The longest inter-nodal distance ( $4.82 \pm 0.08$  cm) was found in KSE while the shortest IND ( $2.95 \pm 0.03$  cm) was in HUL. The highest leaf MC ( $76.05 \pm 0.41\%$ ) and Leaf MRC ( $70.29 \pm 0.53\%$ ) were found in QJE. The lowest leaf MC was  $69.08 \pm 0.45\%$  in KME while the lowest MRC was  $62.60 \pm 1.35\%$  in KSL.

The Korean accessions showed superiority in six tested agronomic traits (LSL, NB, IND, SLW, MC, MRC) followed by Chinese (LYP, NLB) and Japanese (TSL). The Chinese accessions resulted in lowest response in four traits (LYP, NLB, NB, and IND), Korean accessions in three traits (TSL, LSL, MRC) and the Japanese in two traits (SLW, MC). The early sprouting accessions performed relatively better in most of the traits as compared to late sprouting accessions. Early sprouting accessions excelled in seven traits in contrast to two traits of late sprouting accessions. There was a significantly greater LYP in HUL, KSL and MLL as compared to their corresponding early sprouting accessions. The difference in LYP of early and late accessions, QJ and KS was not significant. The differences in other agronomic traits of early and late sprouting accessions were mixed.



The genetic coefficient of variation (GCV) was ranged between 3.27% and 48.18% (Table 2). The highest GCV was in TSL followed by NBP, while the lowest GCV was in MRC. The difference in GCV between MC and MRC was marginal. The GCV was slightly higher in SLW as compared to LYP. The phenotypic coefficient of variation was ranged between 4.01% and 48.19%. The highest PCV was estimated in TSL, while the lowest PCV was in MC. The highest increase in PCV over GCV was 40.98% in MRC followed by 16.97% increase in MC. The least increase in PCV was observed in TSL and NB (0.02%). The least difference in GCV and PCV between TSL and NB; MC and MRC, and among SLW, NLB and LYP indicated their close relatedness. The PCV was relatively greater as compared to corresponding GCV in all the agronomic traits. Based on GCV and PCV values, the agronomic traits were classified into four groups, i.e.: (i) GCV and PCV <10% (MRC, MC), (ii) GCV and PCV >10% and <20% (LSL, IND), (iii) GCV and PCV >20% and <30% (NLB, LYP, SLW), and (iv) GCV and PCV >40% and <50%.

Table 2. Genetic variation and heritability estimates in the agronomic traits of exotic mulberry accessions

Trait	$\sigma^2_g$	$\sigma^2_e$	$\sigma^2_p$	GCV (%)	PCV (%)	$h^2$ (%)	GA (%)
TSL (m)	2943.60	0.22	2943.81	48.18	48.19	1.00	75.95
LSL(cm)	1579.65	15.27	1594.91	13.49	13.56	0.99	55.38
NB (#)	2905.65	1.39	2907.04	41.47	41.48	1.00	75.45
SLW (g)	1.44	0.04	1.48	26.39	26.76	0.97	1.66
NLB (#)	9.13	0.08	9.21	20.05	20.14	0.99	4.21
IND (cm)	0.31	0.01	0.32	15.25	15.37	0.98	0.78
MC (%)	6.26	2.23	8.49	3.44	4.01	0.74	3.01
MRC (%)	4.61	4.53	9.14	3.27	4.61	0.50	2.13
LYP (kg)	1.06	0.02	1.08	22.35	22.56	0.98	1.43

GCV= genetic coefficient of variation; PCV= phenotypic coefficient of variation;  $h^2$ = heritability (broader in sense); GA= Genetic advance,  $\sigma^2_e$ = total environmental variance;  $\sigma^2_g$ = total genetic variance;  $\sigma^2_p$ = total phenotypic variance

The heritability ( $h^2$ ) varied between 0.50% and 1.0% in the agronomic traits. The highest  $h^2$  was estimated in TSL and NB, while the lowest  $h^2$  estimated was in MRC. Seven agronomic traits showed very high heritability (>0.80%), while the rest showed high heritability ( $\geq 0.5\%$ ). Apart from TSL and NB, the  $h^2$  level between LSL and NLB was same (0.99%). It was also of same level between IND and LYP (0.98%). The difference in  $h^2$  among TSL, LSL, NB, SLW, NLB, IND and LYP was marginal (0-3.1%). The genetic gain or genetic advance (GA) expressed in percentage of mean was ranged between 0.78% and 75.95%. The highest GA was assessed in TSL followed by NB. The lowest GA was in IND. There was a marginal difference in GA between TSL and NB; SLW and LYP. The genetic gain decreased considerably in SLW (1.66%) and LYP (1.43%) as compared to GCV and PCV, while it increased in LSL.

The correlation analysis showed both direct and indirect relationships among the agronomic traits. The LYP positively correlated with TSL, LSL and NLB while it was negatively correlated with rest of the agronomic traits (Table 3). The correlation between LYP and TSL; LYP and NLB was highly significant ( $p < 0.01$ ). The LYP was correlated significantly but negatively ( $p < 0.05$ ) with MC and MRC. There was a positive and highly significant ( $p < 0.01$ ) correlation between MC and SLW as well as MRC and SLW. This positive and highly significant correlation and subsequent positive correlation between SLW and NLB may also have contributed indirectly to LYP. The moisture content and moisture retention capacity was correlated negatively with other traits but were positively and significantly correlated with each other. The correlation between TSL and LSL was though positive but not significant ( $p > 0.05$ ).

Table 3. Correlation matrix among different agronomic traits of exotic mulberry accessions

	LYP	TSL	LSL	NB	SLW	NLB	IND	MC	MRC
LYP	....								
TSL	0.425**	....							
LSL	0.066	0.04	....						
NB	-0.296	0.091	0.632**	....					
SLW	-0.027	-0.392*	-0.536**	-0.568**	....				
NLB	0.497**	-0.370*	-0.237	-0.376*	0.007	....			
IND	-0.396	0.383*	0.602**	0.640**	-0.376*	-0.463**	....		
MC	-0.357*	-0.284	-0.055	-0.188	0.643**	-0.259	-0.204	....	
MRC	-0.313*	-0.193	-0.211	-0.227	0.411**	-0.268	0.022	0.397*	....

LYP = leaf yield per plant; TSL= total shoot length; LSL= longest shoot length; NB = number of branches/plant; SLW = single leaf weight; NLB = number of leaf/branch; IND = inter-nodal distance; MC = moisture content; MRC = moisture retention capacity; \*significant ( $p < 0.05$ ); \*\* highly significant ( $p < 0.01$ )

The dendrogram, obtained using nine agronomic traits indicated different levels of linkage among accessions. The results further manifested independence of genetic linkages from geographical origin of accessions. The cluster analysis of coefficient showed a distance ranged between 0.0 and 0.19; indicating a similarity coefficient between 92.52 and 100.0% (Figure 1). There were two clusters and each cluster was divided into subgroups. Six accessions, including both early and late sprouting Chinese, Japanese and Korean accessions, constituted cluster I which was further divided into three subgroups, viz. AI, AII and AIII. Cluster I was dominated by early sprouting accessions, while cluster II was dominated by late sprouting accessions. The subgroup-AI included accessions: HUE, MLE and KSL, while subgroup-AII contained Korean accession QJL. Subgroup-AIII has had Japanese and Korean accessions, KME and KSE. Accessions: HUE and KSE were most distantly related in cluster I as compared to other accessions. The cluster II consisted of four accessions which were grouped into two subgroups. The subgroup-BI included Chinese and Korean accessions: QJE and

HUL, while subgroup-BII was consisted of Japanese accessions: KML and MLL. Accessions: QJE and HUL were most distantly related in cluster II. The least similarity (92.52%) was between cluster I and II.

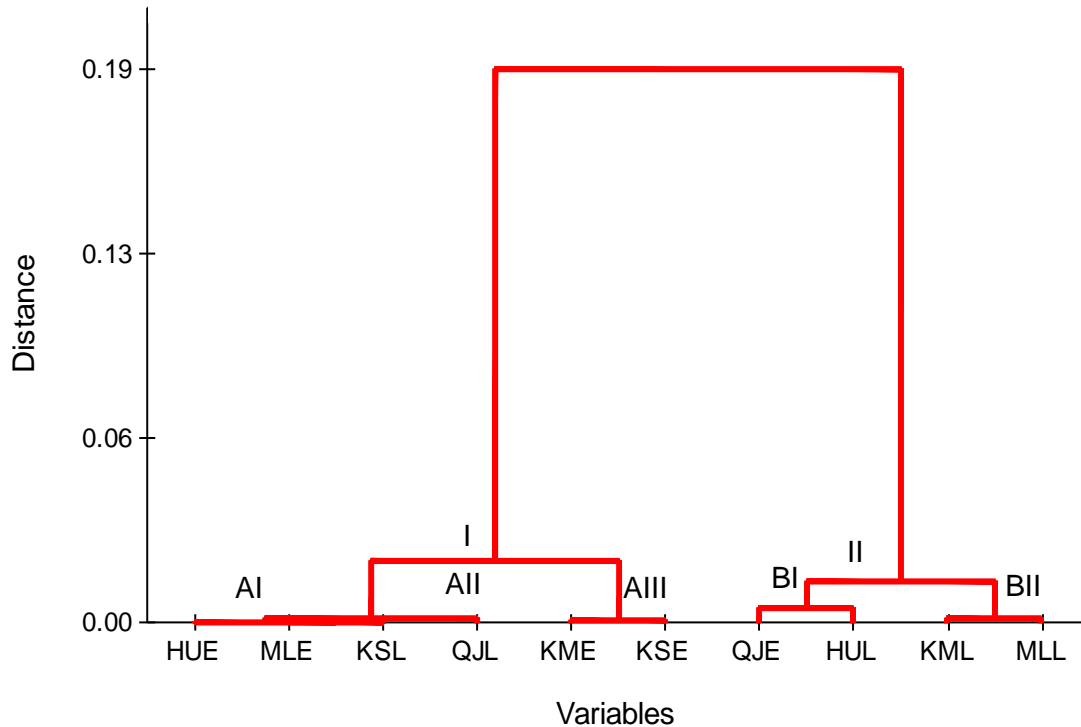


Fig. 1. Dendrogram obtained using Ward's minimum variance cluster analysis demonstrating relatedness in ten exotic mulberry accessions

## DISCUSSION

Mulberry genetic resources are the backbone of crop improvement. Collection, introduction and exchange enrich existing gene pool as well as provide breeders a great scope for further improvement. The present results show a highly significant phenotypic variability in growth and yield traits of ten exotic mulberry accessions. Some accessions were superior to other accessions in some traits and vice versa. The growth traits, such as, total shoot length, longest shoot length, number of branches and inter-nodal distance was found relatively greater in early sprouting Korean accessions: Karyansubhan, while leaf traits, such as, single leaf weight, moisture content and moisture retention capacity were higher in early sprouting Korean accession: Qumjee. The leaf yield was superior in late sprouting Chinese accession: Husang. These findings of phenotypic variation in agronomic traits are in corroboration with findings reported earlier by several workers (Banerjee, *et al.*, 2007; Tikader and Kamble, 2009; Murthy, *et al.*, 2010; Ghosh, *et al.*, 2009).



The present growth and yield performance of exotic mulberry accessions indicate adaptation of the accessions under sub-tropical conditions of Peshawar-Pakistan. The adaptation of an accession in a habitat requires adaptive changes in response to climatic, edaphic, biological and cultural factors (Bradshah, 1972; Williams, 1987). Furthermore, adaptation is an adjustment where the ability to survive and reproduce are more important than competitive ability (Heide, 1985; Tigerstedt, 1994). The present growth and yield performance show a varying degree of adaptability of the accessions which may be explained in terms of their genetic variability.

The present study showed mixed relatedness response among agronomic traits. Some traits were correlated directly while the others indirectly. Direct positive correlation among leaf yield, total shoot length, the longest shoot length, number of leaf/branch shows a direct impact of these traits on leaf yield. A positive and highly significant correlation between SLW and MC; SLW and MRC, and subsequent positive correlation between SLW and NLB indicate an indirect impact of SLW on LYP. Such direct and indirect impacts of agronomic traits on leaf yield have been reported earlier in mulberry accessions (Sahu, *et al.*, 1995; Singhvi *et al.*, 1998). Apart from mulberry, such correlations between yield and other agronomic traits have also been reported in several other crops (Singh and Banerjee, 1986). This positive correlation among different selected agronomic traits would be useful for selecting plants from diverse accessions for future breeding programme.

The phenotypic coefficients of variation in the agronomic traits were slightly greater as compared to genotypic coefficients of variation. This highlights consistency in expression of the traits irrespective of growing conditions and geographical origin. The results, further, indicate overwhelming genotypic control of the traits with small effect of environment. Earlier, the strong genotypic control of agronomic traits in mulberry has also been found by Murthy, *et al.* (2010) and Banerjee, *et al.* (2007). Apart from GCV and PCV, heritability ( $h^2$ ) was higher in all selected agronomic traits ( $\geq 0.50$ ). The genetic advance varied from very low (0.78%) to very high (75.95%). High heritability combined with genetic advance was recorded in the total shoot length, longest shoot length and number of branches/plant. This shows probable additive gene action and low environmental effect on these traits. While high heritability and moderate genetic advance in number of leaf/branch, moisture content, moisture retention capacity, single leaf weight and leaf yield show presence of intra- and inter allelic interactions in the expressions of these traits. Johnson, *et al.* (1955) have also found heritability estimates combined with genetic advance more expressive than heritability estimates alone in predicting the resultant effects of gene action. The heritability estimates combined with genetic advance thus more useful for determining type of gene action and subsequently for selecting breeding protocol.

Constitution of different clusters, based on agronomic traits, helps in gaining clarity about the origin, evolutionary trends and potential for crop improvement (Rajan, *et al.*, 1997; Fotedar and Dandin, 1998). The present findings show mixed genetic linkages, both intra- and inter geographical origin, and sprouting behaviour. The early sprouting Chinese accession: Husang was genetically closer to early sprouting Japanese accession: *M. latifolia* and late sprouting Korean accessions: Karyansubhan and Qumjee. Similarly, early sprouting Korean accession: Qumjee showed close genetic relatedness

with late sprouting Chinese accession: Husang and late sprouting Japanese accessions: Kanmasi and *M. latifolia*. These findings of genetic variability and relatedness of accessions from diverse origin would help to plan efficient management and utilization of exotic mulberry germplasm. The present findings show that the agronomic traits are either under control of additive gene action or intra- and inter allelic action. This signifies ineffectiveness of breeding method based only on simple selection. The present gene action pattern suggests hybridization followed by selection method for evolving mulberry accessions with superior growth and yield traits. Earlier similar observations have been made by Tikadar (1997) and Masilamani, *et al.* (2000) for enhancing growth and yield performance of mulberry accessions.

## CONCLUSION

The results showed a highly significant variability in agronomic traits. The most important quantitative trait, leaf yield was ranged between 3.16 kg/plant and 5.90 kg/plant with the highest in late sprouting Chinese accession: HUL. The Korean accessions showed better performance in most of the agronomic traits. The genetic coefficient of variation (GCV) was ranged between 3.27% and 48.18%. The phenotypic coefficient of variation was ranged between 4.01% and 48.19%. The marginal difference between the phenotypic and genotypic coefficients of variation indicated least environmental effect on the agronomic traits. The estimates of heritability and genetic advance also indicated consistent genetic control of these traits. The minimum variance distance ranged between 0.0 and 0.19 which indicates overall genetic diversity among the accessions and close relatedness of some accessions. Based on these findings, it is concluded that the exotic mulberry accessions have enough genetic diversity for further breeding. The nature of gene action, however, suggests breeding programme based on hybridization followed by selection method.

## REFERENCES

- Banerjee, R., Roy, C.S., Sau, H., Das, B.K., Gosh, P. and Saratchandra, B. 2007. Genetic diversity and interrelationship among Mulberry genotypes. *J. Genet. & Genom.* 34: 691-697.
- Bradshah, A.D. 1972. Some of the evolutionary consequences of being a plant. *Evolutionary Biol.*, 5: 25-47.
- Cappelozza, L., Corradazzi, A.T., Cappelozza, S., Baladau, B. and Mariani, P, 1996. Studies on phenotypic variability of seven cultivars of *M. alba* L. and three of *M. multicaulis* (Moraceae) Part II. *Sericologia* 36: 91-102.
- Cappelozza, L., Corradazzi, A.T. and Tornadore, N. 1995. Studies on phenotypic variability of seven cultivars of *Morus alba* L. and three of *M. multicaulis* P. (Moraceae) Part I. *Sericologia* 35: 257-270.
- Dandin, S.B. 1998. Mulberry a versatile bio-source in the service of mankind. *Acta Sericologia Sin.* 24: 109-113.

- Das, B.C. and Krishnaswami, S. 1965. Some observations on inter-specific hybridization in mulberry. *India J. Seric.* 4:1-8.
- Dwivedi, N.K., Suryanarayana, N., Susheelamma, B.N., Sikdar, A.K. and Jolly, M.S. 1989. Inter-specific hybridization studies in mulberry. *Sericologia* 29: 147-149.
- Fotedar, R.K. and Dandin, S.B. 1998. Genetic divergence in mulberry. *Sericologia* 38: 115-125.
- Ghosh, M.K., Sahu, P.K., Roy, C.S., Sil, S.K., Chakrabarti, S. and Bajpal, A.K. 2009. Genetic diversity evaluation in exotic mulberry germplasm. *J. New Seeds* 10: 41-50.
- Gilpin, M.E. and Soule, M.E. 1986. Minimum viable population processes of species extinction. In: *Conservation Biology, the Science of Scarcity and Diversity*, Soule, M.E. (Eds.). Sunderland: MA Sinauer Associates, Pp: 19-34.
- Heide, O. 1985. Physiological aspects of climatic adaptation in plants with special reference to high latitude environments. Pp: 1-22. In: *Plant Production in the North*. Kaurin, A., Junttila, O. and Nilson, J. (Eds.). Oslo: Norwegian Univ. Press.
- Johnson, H.W., Robinson, H.F. and Comstock, R.F. 1955. Genotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J.* 47: 477-483.
- Masilamani, S., Reddy, A.R., Sarkar, A., Sreeniva, B.T. and Camle, C.K. 2000. Heritability and genetic advance of quantitative traits in mulberry (*Morus* spp.). *Indian J. Seric.* 39: 16-20.
- Murthy, B.C.K., Puttaraju, H.P. and Hittalmani, S. 2010. Genetic variability and correlation studies in selected mulberry (*Morus* spp.) germplasm accessions. *J. Plant Breed.* 1: 351-355.
- Pan, Y.L. 2000. Progress and prospect of germplasm resources and breeding of mulberry. *Acta Sericologia Sin* 26:1-8.
- Poehlman, J.M. and Sleper, D.A. 1995. *Breeding Field Crops*. New Delhi: Panima Publishing Corporation. Pp: 60-82.
- Quedraogo, A.S. 2001. Conservation, management and use of forest genetic resources. Proceed: *Training Workshop on the Conservation and Sustainable Use of Forest Genetic Resources in Eastern and Southern Africa*. Kenya: Nairobi, Pp 1-14.
- Rajan, M.V., Chaturvedi, H.K. and Sarkar, A. 1997. Multivariate analysis as an aid to genotypic selection for breeding in mulberry. *Indian J. Seric.* 36: 111-115.
- Sahu, P.K., Yadav, B.R. and Saratchandra, B. 1995. Evaluation of yield component in mulberry germplasm varieties. *Acta Bot.* 23: 191-195.

- Singh, M.K. and Banerjee, S.P. 1986. Path analysis of yield components in rice. *Nat. Sci.* 21: 876-892.
- Singhvi, N.R., Chakraborty, S., Singhal, B.K., Rekha, M., Sarkar, A. and Datta, R.K. 1998. Character association of leaf yield traits in mulberry. *Bull. Sericult. Res.* 9: 83-84.
- Thangavelu, K., Tikader, A., Ramesh S.R., Rao, A.A., Naik, V.G., Sekar, S. and Deole, A.L. 2000. Catalogue on mulberry (*Morus* spp) germplasm 2: 1-225.
- Tigerstedt, P.M.A. 1994. Adaptation, variation and selection in marginal areas. In: *Breeding fodder crops for marginal conditions*. Rongli, O.A., Solborg, E.T. and Schjelderup, I. (Eds.). Proceed. 18<sup>th</sup> Fodder Crop Section Meeting. Loen Norway, 25-28 August 1993. *Development in Plant Breeding* 2: 13-19.
- Tikadar, A. 1997. Studies on heritability, genetic parameters and response to selection in mulberry. *Bull. Seric. Res.* 8: 19-22.
- Tikader, A. and Kamble, C. 2009. Performance of exotic mulberry (*Morus* spp.) germplasm on growth and yield traits in Indian conditions. *African J. Plant Sci.* 3: 30-36.
- Tikader, A. and Rao, A.A. 2002. Phenotypic variation in mulberry (*Morus* spp.) germplasm. *Sericologia* 42: 221-233.
- Tikader, A. and Roy, B.N. 1999. Genetic variability and character association in mulberry germplasm (*Morus* spp.). *Indian J. Forest.* 22: 26 –29.
- Vavilov, N.I. 1926. Studies on the origin of cultivated plants. *Bull. Appl. Bot.* 16: 139-248.
- Vijayan, K., Raghunath, M.K., Das, K.K., Tikader, A., Chakraborti, S.P., Roy, B.N., and Qadri, S.M.H. 1997. Studies on leaf moisture of mulberry germplasm varieties. *Indian J. Seric.* 36:155-157.
- Vijayan, K., Tikader, A., Das, K.K., Roy, B.N. and Pavan, K.T. 1996. Genotypic influence on leaf moisture content and moisture retention capacity in mulberry (*Morus* spp.). *Bull Seric. Res.* 7:95-98.
- Williams, W.M. 1987. Adaptive variation. In: *White Clover*. Baker, M.J. and Williams, W.M. (Eds.). Walling Ford: CAB International. Pp: 299-321.
- Zhao, W., Fang, R., Pan, Y., Yang, Y., Chung, J.W., Chung, M. and Park, Y.J. 2009. Analysis of genetic relationships of mulberry (*Morus* L.) germplasm using sequence-related amplified polymorphism (SRAP) markers. *African J Biotechnol.* 8: 2604-2610.
- Zhao, W., Zhou, Z.H., Mia, X.X., Wang, S.B., Zhang, L., Pan, Y. L. and Huang, Y.P. 2006. Genetic relatedness among cultivated and wild mulberry (Moraceae: *Morus*) as revealed by inter simple sequence repeat (ISSR) analysis in China. *Can. J. Plant Sci.* 86: 251-257.

Table 1: Phenotypic variability in selected traits of different exotic mulberry accessions

Accession	Agronomic traits								
	LYP±SE (kg)	TSL±SE (m)	LSL±SE (cm)	NB±SE (#)	SLW±SE (g)	NLB±SE (#)	IND±SE (cm)	MC±SE (%)	MRC±SE (cm)
HUE	3.16±0.05e	132.33±0.27d	291.87±1.20e	147.21±0.23d	3.96±0.05e	11.67±0.02g	3.99±0.04bc	72.27±0.45bc	68.70±0.65ab
KME	5.87±0.08a	219.58±0.61a	300.92±0.70d	190.50±0.29b	3.07±0.01h	15.07±0.02de	3.69±0.04d	69.08±0.45d	63.50±1.30c
KSE	4.14±0.05d	52.0±0.14i	361.13±2.27a	222.71±0.98a	4.82±0.02c	12.84±0.12f	4.82±0.08a	74.22±0.85ab	66.61±0.50abc
MLE	3.29±0.03e	92.15±0.03g	275.41±0.21f	137.46±0.74e	4.64±0.02c	14.74±0.06e	3.83±0.02cd	73.59±0.58ab	64.41±2.19bc
QJE	4.01±0.01d	61.62±0.08h	237.71±2.14i	69.67±0.61g	6.21±0.06a	13.50±0.17f	3.41±0.05e	76.05±0.41a	70.29±0.53a
HUL	5.90±0.03a	156.05±0.06c	249.42±0.66h	51.58±0.60h	6.06±0.02ab	21.89±0.37a	2.95±0.03g	72.47±0.24bc	66.11±0.70abc
KML	5.73±0.07a	101.72±0.24f	339.67±0.58b	93.71±0.31f	3.15±0.02g	16.20±0.07c	4.15±0.00b	69.89±0.32cd	64.51±0.56bc
KSL	4.50±0.14c	50.43±0.12j	262.66±0.30g	136.50±0.52e	4.16±0.00d	15.49±0.07d	3.68±0.01d	69.13±0.34d	62.60±1.35c
MLL	5.31±0.07b	102.86±0.02e	300.25±0.72d	90.88±0.24f	5.98±0.01b	11.94±0.01g	3.12±0.01fg	75.86±0.44a	65.49±1.35abc
QJL	4.16±0.04d	157.35±0.02b	326.64±0.32c	159.46±0.83c	3.45±0.06f	17.41±0.06b	3.15±0.01f	74.45±0.99ab	63.95±1.04bc
Max	5.90	219.58	361.13	222.71	6.21	21.89	4.82	76.05	70.29
Min	3.16	50.43	237.71	51.58	3.07	11.67	2.95	69.08	62.60
Mean ±SE	4.61±0.33	118.27±17.19	294.57±12.58	129.97±17.06	4.55±0.38	15.08±0.96	3.68±0.18	72.70±0.83	65.62±0.76
CV	0.31	1.12	5.53	2.84	0.16	0.68	0.17	2.67	5.13

\*\*highly significant ( $p < 0.01$ ); Figures in a column with same alphabet(s) are not significant with each other ( $p = 0.05$ ); LYP= leaf yield/plant; TSL= total shoot length; LSL= longest shoot length; NB= number of branches/plant; SLW= single leaf weight; NLB= number of leaf/branch; IND= inter-nodal distance; MC= moisture content; MRC= moisture retention capacity