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Multivariate Analysis of Indigenous and Exotic Mulberry (*Morus Spp*.) Germplasm for Identifying Diverse Genotypes under Humid Subtropical Region

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ABSTRACT

Mulberry genetic resource is increasingly being recognized as one of the basic key material for sustainable silk production under changing climatic scenario. In this investigation, multivariate analysis was done to assess the diversity in 247 mulberry accessions (includes indigenous, exotic, improved and tetraploid clones/lines) for foliage yield and its growth attributes during 2014 to 2016. The analysis of variance (ANOVA) showed the presence of significant variation among accessions for the parameters measured. Wide range and variance among the accessions indicated the presence of variability for the traits on which selection can be practised. Primary branches per plant and inter nodal distance exhibited high genotypic (38.65, 25.99) and phenotypic (40.71, 26.99) coefficient of variance, respectively. Simple correlation coefficients revealed that foliage yield had significantly positive relationship with primary branches, while negatively correlated with inter-nodal distance. Principal component (PC) analysis showed first two PCs having eigen value >1 explained more than 78% of the genotypic variations. Cluster analysis classified 247 accessions into eight divergent groups and greater genetic distance was detected among the members of cluster III and cluster VIII and cluster VI and VIII. The members of these divergent clusters may be combined in future breeding programmes to obtain genotypes with combined foliage yield and more branches per plant. The results showed that the germplasm having a wide genetic diversity thus the accessions viz., ME – 0042, ME – 0011, ME - 0084, MI – 0222, MI – 0092 and ME – 0006 can serve as a promising donors for improving the foliage productivity.

Key words: *Mulberry Accessions, Variability, Principal Component and Cluster Analysis*

INTRODUCTION

Mulberry (*Morus spp.*) is an economically important tree used for sericulture and it is the sole food plant for the domesticated silkworm, *Bombyx mori*. Mulberry plant bears male or female unisexual flowers on different plants (dioecious) and also on the same plant (Monoecious) with expression of sexual characters often depending on several physiological, biochemical and environmental factors[5].

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Initially, genus *Morus* was divided the into seven species: *Morus alba* L; *Morus nigra* L; *Morus rubra* L; *Morus tarterica* L; *Morus indica* L; *Morus papyrifera* and *Morus tinetoria*[11]. The confusion over the classification of *Morus* into different species remains a major bottleneck for appropriate characterization and utilization in breeding programs. A few species of mulberry are also valued for their leaf (*M. alba, M. indica, M.multicaulis* and *M.latifolia*), edible fruit (*M. alba, M. indica* and *M. laevigata*) and timber (*M. laevigata* and *M. serrata*)[2]. The species such as *Morus alba, M. indica, M. serrata* and *M. laevigata* are native to India and found wildly in the Himalayas[13]. The genus *Morus*, which is widely distributed in all the continents or climatic condition and is cultivated extensively in East, Central and South Asia for silk production. The major area of mulberry cultivation in India belongs to tropical zone (Karnataka, Andhra Pradesh, Tamil Nadu states), sub tropical zone (West Bengal, Himachal Pradesh and the North-Eastern states) and temperate zone (Jammu and Kashmir, Utharakand). Mulberry is propagated asexually by cuttings, grafting, and layering or mainly through saplings from cuttings. 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 further horizontal and vertical growth of sericulture in the country. Development of suitable mulberry variety is one of the focal points in mulberry research. Breeding activities aiming towards increase in productivity can benefit from a thorough understanding of the genetic variability and diversity within a set of elite and wild germplasm accessions. The precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization[22]. Genetic variation is also fundamental for species conservation to meet present and future requirement[16]. Several methods like principal component analysis, factor analysis and cluster analysis are presently available for the selection of parent and detection of genetic variability[10]. Several authors discussed importance of variability and diversity in selection of parents in mulberry[18,35,23,26]. Hence, in the present investigation foliage yield and some important growth traits of indigenous and exotic accessions of mulberry was carried out to examine the magnitude of genetic diversity and also to identifying parents to initiate a hybridization programme.

MATERIAL AND METHODS

Two hundred and forty seven germplasm constitute of indigenous and exotic accessions, tetraploids and improve lines, established in field gene bank were evaluated during September crop seasons for a period of three years 2014-2016. The experimental plot is located at Central Sericultural Research and Training Institute which is situated at 34° 0’ 28" North, 71° 34' 24" East, at altitude of 19 m above mean sea level with humid sub-tropical climate. The genotypes were planted in augmented design with spacing 150 ×150 cm, maintained as high bush plantation pollarded at 5 foot height. All the recommended package of practices was followed to raise healthy crop. Observation were recorded on one year old shoots of 30 year old plantation for foliage yield and two growth traits such as primary branches per plant and inter nodal distance for 3 years. The mean data recorded from randomly selected plants over the years were averaged and used to compute pooled mean values. Descriptive statistics was estimated in excel sheet such as mean, standard deviation (SD), range and trait wise analysis of variance[20]. Genotypic and phenotypic coefficient of variation was determined as suggested by Singh and Chaudhary[20]. Broad sense heritability and genetic advance (GA) was determined as suggested by Johnson. Pearson’s correlation coefficients were worked out between the traits following Snedecor[21] with the help of SPSS 10.1. Multivariate techniques including K-mean cluster analysis was done by SPSS version 10.1. The cluster analysis as a nonparametric multivariate

method classifies genotypes into categories and data were analyzed to determine Euclidean distance based on paired group method to determine dissimilar groups of the accessions. Principle component analysis (PCA) was done using software XLSTAT[7]. The pooled data were subjected to PCA[14] and the number of components was extracted using scree plot of eigen values and Biplots was developed from first two principal components (PRN1 and PRIN2). The PCs with eigen value >1.0 were considered as inherently more informative than any single variable alone[9]. The dimensionality of dataset reduced using PCA analysis was used to assess the multiple traits and to identify accessions that exhibit different foliage yield potential.

RESULTS AND DISCUSSION

Genetic variability and correlation

It is clear from the Table 1, that significant variation present among the accessions for all the traits studied. Mulberry a perennial deciduous tree is reported to have originated in China[33] and distributed throughout the world up to an elevation of 2,100 m. Further it consists of more than 14 species of which 4 species viz. *M. indica, M. alba, M. laevigata and M. serrata* reported to occur in India. The horizontal expansion of sericulture in different states has made it necessary to develop mulberry varieties specific to different agro-climatic zones. Similar results were reported by Tikader and Kamble[29] with highly significant differences of growth and yield traits of mulberry. Phenotypic variability of mulberry germplasm has been detected by Thangavelu *et al.*[23] and Tikader and Rao[32].

The information provided in the Table 2 clearly signifies the presence of wide variation in different mulberry species. The accessions within the species *viz., M. indica. M. alba* & *M.latifolia* contained wide range of variability for characters studied. However, Sharma *et al.*[19] reported no significant morphological differences among genotypes of *M. alba* and *M. indica* species. In developing improved mulberry varieties, a large number of germplasm is required for characterization and evaluation. Among the different Sericulture advanced countries like Japan, China and Italy have evaluated mulberry accessions originated in temperate region[12] to suite their climatic condition. However, many exotic mulberry germplasm of tropical, subtropical and temperate origin were introduced in India and used as parent material for crop improvement[24]. The maximum and minimum mean, standard deviation of the traits studied indicated that significant variation exists among germplasm in different species and also within the exotic and indigenous accessions. The temperate and subtropical accessions showed higher values in respect of number of primary branches per plant and foliage yield (Table 3.). The exotic accessions showed higher values for all the traits studied. The foliage yield ranged from 0.378- 11.696 kg (in exotic accessions), 0.424-12.756 kg (indigenous), 0.388- 11.781kg (improved lines) and 0.518 -11.611kg (tetraploids), indicated wide variation for foliage yield. Thus utilization of these genetic resources would be useful in future breeding programme. The presence of wide variation for foliage yield was corroborated with the findings of earlier workers in mulberry [26, 5] and [29].The coefficient of phenotypic and genotypic variance was calculated for all the traits under study (table no shown). Foliage yield exhibited the highest genotypic and phenotypic variance i.e 81.68 and 96.01 respectively, followed by the primary branches per plant and inter- nodal distance that signifies selection can be applied to isolate more promising line. Among the different types of genetic resources, exotic germplasm and improved lines recorded higher genotypic and phenotypic variance. In the present study close correspondence between phenotypic and genotypic coefficient of variation was recorded for inter-nodal distance and primary branches per plant indicating less influence of environment in expression of these traits. The observed variation in the germplasm was due to genetics and environmental, where as genetic variability is the only heritable from generation to the next generation. Since

heritability alone does not give an idea about the expected genetic gain in the next generation, so traits with high heritability and genetic advance were used as powerful tool in selection process as such traits are controlled by the additive genes and less influenced by the environment. The broad sense heritability was higher for inter-nodal distance (92.75%) and primary branches per plant (89.75) but moderated for leaf yield per plant (72.00%). The combination of high heritability with high genetic advance will provide a reliable measure of particular trait and primary branches per plant recorded highest valued followed by inter-nodal distance. These results are in agreement with the findings of Tikader and Roy[31] and Tikader and Dandin[30]. The association among traits were analysed through Pearson simple correlation matrix. The relationship of different traits indicated that all the traits are associated directly or indirectly with foliage yield. Foliage yield per plant showed significant positive association with primary branches per plant (0.700**) and non-significant positive association with inter-nodal distance (0.072) (Table 2.). Similar observations on association of different traits with foliage yield were also reported by several workers [31, 25, 30 and 34]. Foliage yield is an important economical trait influenced by many associated traits and hence the highly correlated trait such as number of primary branches should be taken into consideration during selection for their high yields since the mulberry leaves are of economic importance in the sericulture industry.

K-mean Cluster analysis

Distribution of germplasm accessions into 8 different clusters by Ward's method for foliage yield traits is presented in Table 6. Mulberry (*Morus spp*.) is cultivated under varied climatic conditions ranging from temperate to tropical. The mulberry accessions investigated in this study were grown humid subtropical environment over different years. Cluster I contained forty four accessions, which includes accessions from exotic, indigenous, improved lines and tetraploids. Cluster II had 88 members with highest mean value among the clusters for foliage yield. This cluster included most of the exotic & improved lines and varieties like S1635, Kanva-2(MI 0014) and Mysore local (MI 0052). Cluster III and IV contained fourteen each from India and other countries. The varieties of stress tolerance such as C-776 (salinity tolerant) and Kosen(ME-0066) for acidic soils of hilly areas of Eastern India are grouped in these clusters. Cluster V contained thirty eight accessions, ten from India and others from china, Japan, Italy, Turkey, France, Portugal, Paraguay and Bangladesh. Cluster VI contained twenty three accessions, which includes accessions mostly from India and Japan contained KNG a popular variety for temperate region of Jammu and Kashmir. Cluster VII contained twenty five accessions, which includes all type of germplasm of indigenous and exotic origin. Cluster VIII includes only one accession ME – 0042(China white), which is a good combining ability parent originated in China. Amurrio *et al*.[1] and Rabbani *et al.*[17] reported a lack of relationship between various clusters based on agronomic traits and origins of genotype in peas (*Pisumsativum*) and mustard (*Brassica juncea*) respectively. The occurrence of this wide variation between the clusters is of great genetic value in providing genotypes aimed at mulberry selection for adaptation to subtropical humid areas. A similar kind of results related to germplasm grouping has been reported by several workers [6,26,] Tikader *et al*., 2003 and [15].The cluster mean values are shown in Table 4. Cluster III had the highest mean value for primary branches per plant with shorter inter nodal distance. Cluster VIII showed highest mean values for foliage yield but lowest value for primary branches per plant. These genotypescan be utilized to induce more primary branches and higher foliage weight in breeding populations. The inter cluster distances are presented in Table 5. Maximum and minimum inter-cluster distance was recorded between clusters III and clusters VIII (20.15), and between clusters I and V (2.90) indicated that the accessions grouped in these clusters are genetically divergent and

similar. The second most diverse clusters having highest genetic distance was cluster VI and VIII with the distance of 19.04. Members of these divergent clusters can be utilized in transgressive breeding programmes. The accessions are distributed equally in different clusters except cluster VIII. The entire cluster group have both exotic and indigenous accessions except VIII where only one exotic accession was grouped. Clustering analysis based on morphological traits and foliage yield grouped 237 mulberry genotypes into eight different clusters (Table 6) and indicates that these genotypes exhibited notable genetic divergence in terms of morphological traits. Therefore, classification in this study based on morphological traits is in agreement with previous report. Earlier reports on clustering in mulberry by various authors also indicated that the exotic and indigenous accessions could be grouped in same cluster[18, 6, 28] and the present study also supports the earlier findings. The clustering pattern clearly indicates that genetic diversity and geographical distribution possess no relation, and the mulberry accessions collected from different sources grouped as per their performance based on agronomical traits. In all the clusters other than cluster VIII, the combination of accessions joined with each other based on close affinity and genetic value. The breeders have the opportunity to select suitable accessions for further utilization. In India, most of the improved variety developed by involving exotic accession as one of the parents is where the importance of using exotic germplasm[24] lines. Tikader and Kamble[29] studied the genetic diversity of indigenous and exotic accessions using Mahalanobis's D^2 - technique for leaf yield and eight agronomic traits. By using Ward's minimum variance cluster analysis they grouped the fifty indigenous and exotic accessions into 9 clusters.

The role of exotic accession is very essential and the result revealed that a good number of exotic accessions performed well with indigenous accessions. The introduced exotic accessions have been used for development of sericulture, and presently the important commercial variety has been developed by using it as one of the parents in hybridizations. Hence, the indigenous x exotic derivatives from cluster III should be crossed with the accessions of cluster VIII to increase the number of primary branches. High yielding accessions from cluster VIII could be further tested for their combining ability. Thus the accessions present in different clusters can be hybridized to assemble desirable traits with higher heterotic potential.

Principal Component Analysis (PCA)

PCA analysis was done to assess the multiple traits to screen genotypes that exhibit high foliage yield. The evaluation of germplasm through principal component analysis is a robust tool to reduce the large number of correlated variables and germplasm into smaller components of uncorrelated variables. A scree plot (Fig.1) displayed the eigen values associated with a component in descending order versus the number of the components. In this study, two principal components (PCs) extracted had Eigen value more than one. The first two principal components, PC1 to PC2 obtained from original data accounted for 78.73% of total variation. Principal components and their respective proportion of the variation explained by eigen values and eigen vectors are presented (Table 7). Among all principal components, PC1 contributed maximum (45.36%) to the total variation. The traits with largest absolute value greater or closer unity within the first principal component influences the clustering more than those with lower absolute value closer to zero[4]. Accordingly, the major contributing traits for diversity in first principal component were foliage yield and primary branches per plant. Presence of positive and negative correlation trends between the components and the variables are interpreted by positive and negative loading. Similarly, for second principal component (PC2) inter-nodal distance was the major contributor for the diversity. The traits studied showed considerable positive factor loadings on PC I. The 2nd PC was related to diversity among mulberry accessions due to inter-nodal

distance and foliage yield with their positive loadings and primary branches per plant with negative loadings. Customary, one variable is selected from these identified groups depending on respective loadings. Hence, for the first group foliage yield is the best choice, which had the largest loading from PC1 followed by primary branches per plant. While, inter-nodal distance for the PC2 had the largest loading.Biplots of PCA analysis with first two principal components are presented (Figure 1). The graph clearly demarcated the distinct genotypes that dispersed along two principal components axis which emphasized on the extent of phenotypic variation explained by these clusters. Genotypes that positively correlated and performed best in respective foliage yield are on the upper right side of the quadrant. The distance of each variable with respect to PC-1 and PC-2 showed the contribution of these variables in the variation of genotypes used. The biplot showed that primary branches per plant and foliage yield as a whole contributed maximum towards variability in mulberry germplasm. These results indicated the importance of the morphological traits and their positive influence on foliage weight. Based on these results morphological traits may be recommended as an indirect measure to enhance foliage yield. Banerjee *et al*.[3] used PCA to categorize traits of that accounted for most of the variance in the data.

Table 1: Analysis of variance for foliage yield and morphological traits

Source of variation	Shoots per plant	Inter-nodal distance	Foliage yield
Accessions	574.22	14.65	268.74
Error	2.16	1.45	2.20
F-test	265.52**	10.09**	122.15**

Table 2: Descriptive statistics of foliage yield and morphological traits of different accessions based on species

SN	Species	No. of accessions	Shoots per plant		Inter-nodal distance		Foliage yield	
			Range	SD.	Range	SD	Range	SD
1	*M.alba*	48	4-26	5.06	1.80 -7.21	1.20	0.512 -12.756	3.85
2	*M.indica*	50	3-22	3.65	2.37- 9.27	1.40	0.491 - 12.691	2.96
3	*M.bombycis*	14	5-19	4.52	1.75 - 5.25	1.00	0.747 - 5.650	1.90
4	*M.latifolia*	20	5-23	5.03	3 - 6.18	1.02	0.548 -11.180	3.23
5	Other sps	10	6-19	4.50	3.61- 7.00	0.98	0.585 - 7.219	2.35
6	unknown	11	4-15	3.27	2.00- 7.21	1.54	0.420 - 10.752	3.12
7	Improved lines	30	4-21	3.74	2.60- 8.00	1.16	0.388 - 11.781	2.80
8	Tetraploids	30	5-24	5.00	2.80- 8.50	2.80	0.518 - 11.611	0.52

Table 3: Descriptive statistics of yield and morphological traits of different accessions based on climatic origin

Region	No. of accessions	Country/ region	Shoots per plant		Inter-nodal distance		Foliage yield	
			Range	SD.	Range	SD.	Range	SD
Tropical	16	India	4- 13	2.31	2.37- 7.73	1.27	0.491- 12.673	3.73
Subtropical	45	India	3- 22	3.57	2.30- 7.21	1.22	0.603-12.691	2.74
	24	Asia	4- 21	5.12	2.60- 9.27	1.50	0.647- 12.756	4.17
Temperate	08	India	7- 15	2.45	3.09- 7.21	1.23	0.953- 10.752	3.21
	38	Japan	4- 26	5.35	1.75- 6.20	1.11	0.420- 11.180	2.90
	21	Europe	4- 22	5.05	3.00- 7.00	1.21	0.512- 10.278	3.14
	02	America	7- 15	5.66	3.30- 5.00	1.20	0.728- 7.219	4.59

Table 4: Mean value of the traits in the 8 clusters

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Shoots per plant	10.25	6.83	20.93	15.11	12.54	16.09	8.56	4.00
Inter-nodal distance	5.94	4.25	4.19	4.75	4.19	4.75	4.82	6.18
Foliage yield	2.34	1.34	7.01	9.52	2.65	3.11	7.98	11.76

Table 5: Inter Cluster distance values among eight clusters for

	I	II	III	IV	V	VI	VII	VIII
Cluster I		3.951	11.784	8.747	2.902	6.008	5.991	**16.633**
Cluster II			15.197	11.647	5.861	9.442	6.883	**16.765**
Cluster III				6.365	9.454	6.238	12.423	**20.152**
Cluster IV					7.356	6.480	6.726	**13.902**
Cluster V						3.622	6.683	**17.468**
Cluster VI							8.963	**19.041**
Cluster VII								**10.873**

Table 6: Distribution of 247 mulberry germplasm accessions into 8 different clusters

Cluster	No. of accessions	Accession name
I	44	ME – 0062, ME - 0028, ME - 0105, ME – 0077,ME - 0123, ME – 0004, ME - 0084, MI – 0205, MI – 0116, MI – 0087, MI – 0084, MI – 0108, MI – 0056, MI – 0088, MI – 0060, MI – 0092, MI – 0075, MI – 0078, MI – 0097, MI – 0004, MI – 0207, ME – 0119, ME – 0007, MI – 0167, MI – 0092, MI – 0026, MI -0523, ME – 0006, MI – 0003, C1614, C1624, C1657, C1778, C1721, C1723, S1618, S1676, S1679, S1695, MI – 0180, MI – 0224, MI – 0228, MI – 0219 and MI – 0231.
II	88	ME-0079, ME – 0046, ME – 0102, ME – 0078, ME - 0072, ME - 0064, ME-0120, ME – 0074, ME – 0106, ME – 0107, ME – 0116, ME – 0092, ME – 0093, ME – 0086, ME- 0267, ME – 0047, ME – 0034, ME – 0109,ME – 0114, ME – 0111, ME – 0096, ME – 0088, ME – 0097, ME – 0126, ME – 0115, ME – 0113, MI – 0179, MI – 0102, MI – 0564, MI – 0024, MI – 0101, MI – 0098, MI – 0095, MI – 0100, MI – 0093, MI – 0163, MI – 0222, MI – 0109, MI – 0014, MI – 0064, MI – 0562, MI - 0164, ACC NO.1190, MI – 0052, ME – 0125, MI – 0522, MI – 0005, ME – 0057, C1540, C1568, C1572, C1592, C1601,C1603,C1612,C1627,C1647,C1649,C1667,C1668,C1670,C1853,C1810, C1700,C1726,S146,S162,S1635,S1662,S1680,S1681,S1682,S1686,S1687,S1688,S1696,S1700,S17 11,MI – 0181,MI – 0182,MI – 0184,MI – 0233,MI – 0214,T 19,MI – 0230,MI – 0220, MI – 0217 and MI – 0221.
III	14	ME – 0089, ME – 0094, ME – 0165, ME – 0037, ME – 0006, ME- 0002, ME- 0226, ME – 0055, ME – 0032, MI – 0105, ME – 0008, C530, C776 and MI – 0227.
IV	14	ME – 0066, ME -0045, ME – 0036, ME – 0110, ME - 0121, ME – 0051, MI – 0144, MI – 0171, MI – 0008, S1, S1573, S1704, MI – 0225 and MI – 0223.
V	38	ME – 0098, ME – 0085, ME – 0017, ME- 0124, ME – 0087, ME – 0104, ME – 0095, ME- 0019, ME – 0117, ME – 0099, ME – 0083, MI – 0068, ME – 0099, MI – 0208, MI – 0085, MI – 0117, MI – 0300, MI – 0017, ME – 0122 ME – 0041, ME – 0003, ME -0075, MI – 0083, MI – 0077, MI - 0001, ME – 0021, C1552, C1690, C1730 S799. S1562, S1574, S1694, S1708, MI – 0232, MI – 0243, MI – 0226 and MI – 0236.
VI	23	ME – 0039, ME – 0035, ME – 0148, ME – 0118, ME – 0011, ME – 0020, ME – 0112, MI – 0089, MI – 0627, MI – 0091, MI – 0169, ME – 0023, ME – 0018, C741, C1679. C1776. C1729. S1684. S1703, MI – 0183, MI – 0229, MI – 0628 and MI – 0213.
VII	25	ME-0027, MI – 0094, MI – 0054, MI – 0050, ME – 0090, MI – 0099, MI – 0057, MI – 0066, ME – 0090, MI – 0035, MI – 0118, MI – 0038, MI – 0015, MI – 0133, MI – 0253, MI -0248, ME – 0001, C1608, S642, S1301, S1622, MI – 0234, MI – 0218, MI – 0235 and MI – 0237.
VIII	1	ME – 0042

Table 7: Vector loadings and percentage explained variation by the first 3 PCs

Traits	PC1	PC2	PC3
Primary branches per plant	0.818	-0.131	-0.560
Inter-nodal distance	0.100	0.992	-0.080
Foliage yield	0.825	0.010	0.564
Loadings			
Eigen value	1.361	1.001	0.638
Variability (%)	45.36	33.37	21.26
Cumulative %	45.37	78.73	100.00

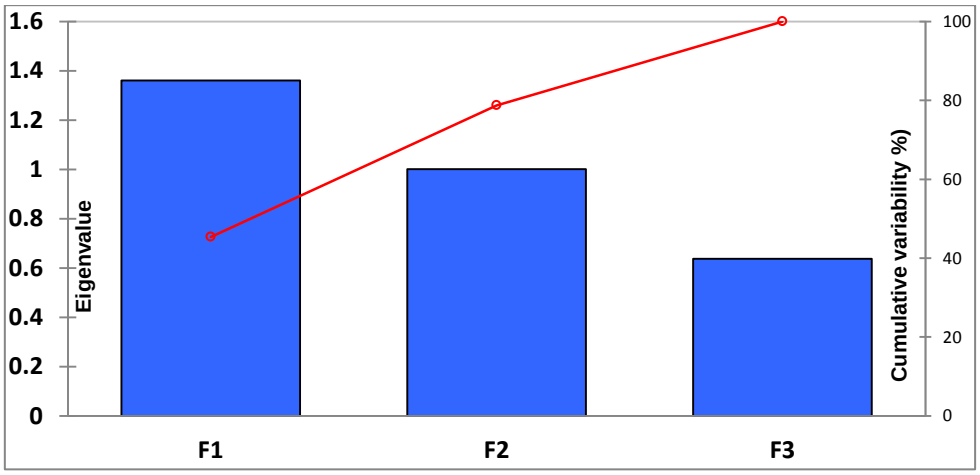

Fig. 1: Scree plot between Eigen values and number of principal components

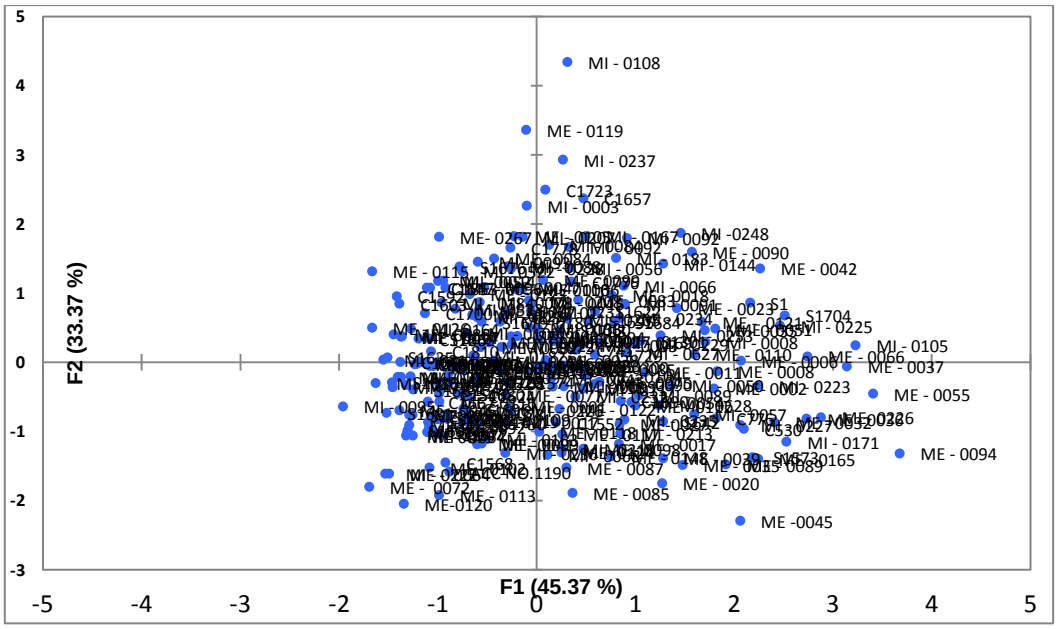

Fig. 2: Biplot between PCs 1 and 2 showing distribution of germplasm accessions

CONCLUSION

Adequate variability exists in the Mulberry gene pool studied to initiate a breeding programme. Primary branches, inter-nodal distance and foliage yield per plant had the highest contributions towards variability. Foliage yield per plant is strongly associated with primary branches. The greatest genetic distance was detected among cluster III and cluster VIII and cluster VI and VII, hence members of these clusters could be exploited in transgressive breeding. On the basis of their

greater inter-cluster distance of germplasm lines, high value of cluster mean according to the trait to be improved and performance of the individual accessions for the trait, the lines could be used in hybridization programme for improvement of different plant traits. The genotypes superior in some clusters might be usefully involved in multiple crossing programmes to recover transgressive segregants with high genetic yield potential. From the principal component analysis (PCA) the first two principal components explained 78.73% of the total variation, suggesting that traits such as primary branches per plant and foliage yield are the principal discriminatory traits in the germplasm. The diverse indigenous and exotic accessions from various clusters are helpful in broadening the breeding programme by planning the crosses and increased use of genetic diversity especially for foliage yield in our country.

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