

Research Note

Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.)

S. Juliet Hepziba¹, K. Geetha² and S. M. Ibrahim³

¹Regional Research Station, Aruppukottai – 626 107

²Regional Research Station, Paiyur -635 112

³Agricultural College and Research Institute, Madurai – 625 104

Email: hepssy@yahoo.com

(Received: 18 Dec 2012; Accepted: 08 Mar 2013)

Abstract

Maize is an important crop after rice and wheat in terms of acreage and ranks second in terms of total production and productivity. The present investigation was carried out during Kharif 2010, involving 70 diverse inbreds collected from different locations. Genetic diversity, variability, association of yield with other component traits and relative importance of direct and indirect effects of different components on yield were assessed. Grouping of genotypes based on biometrical traits led to the formation of ten clusters. The cluster I consisted of 19 inbreds, cluster II consisted of 12 inbreds, while cluster III consisted of eight inbreds followed by cluster IV to X consisting of 1,2,7,3,6,9 and 7 inbreds respectively. The genotypes studied showed a wide range of variation for all the characters. Among the traits evaluated ,maximum genotypic and phenotypic coefficients of variation were observed for grain yield per plant followed by number of rows per cob and number of kernel per row. The estimates of heritability and genetic advance as per cent of mean was high for grain yield per plant, number of kernels per row and number of rows per cob. Grain yield per plant was positively and significantly correlated with cob weight, hundred kernel weight, number of kernel rows per cob and number of kernels per row. Path coefficient analysis further revealed that number of kernel rows per cob exhibited maximum positive direct effect followed by cob length. The significant association of grain yield per plant with hundred kernel weight and number of kernels per row is due to positive indirect effects through number of kernel rows per cob, days to 50% silking, plant height and cob length.

Key words :

Maize, Genetic diversity, Heritability, Correlation, Path analysis

Maize referred as Queen of cereals is an important crop after rice and wheat in terms of acreage and ranks second in terms of total production and productivity. Among the total maize production in the world, 48% of maize is used as poultry feed, 28 % utilized for human consumption, 11% as feed for animals, 1% for seed production and 12% for starch and oil. India stands in fifth position in the world in terms of corn production. The increasing demand necessitates to explore the genetic diversity present in maize germplasm and to utilize them for the production of hybrids with increased vield. Further, knowledge on genetic parameters such as genotypic coefficient of variation, heritability and genetic advance is a prerequisite in the improvement of any crop. Studies on character association and path analysis become important when a breeder is dealing with quantitative characters. Present study attempts to gather information on genetic diversity, variability, association of yield with other component traits and relative importance of the direct and indirect effects of different components on yield in maize inbreds.

The present investigation was carried out at Agricultural College and Research Institute, Madurai during Kharif 2010. Seventy inbreds consisting of different types of corn were collected from different centres and raised in Randomized Block Design replicated thrice. Each inbreds were sown in two rows of 3 m length. The spacing between and within rows was maintained at 60 x 20 cm, respectively. Biometrical characters such as days to tasseling and days to silking were recorded at plot basis. At maturity, five plants were selected at random from each plot and data were recorded plant height(cm), cob on weight(g), cob length(cm), hundred kernel weight(g), number of kernel rows per cob, number of kernels per row and grain yield per plant(g). All the seventy inbreds were subjected to Un-weighted Paired Group method of Arithmetic Average (UPGMA) for estimation of Euclidian distance. Clustering was done by Sequential Agglomerative Hierarchical Non-overlapping (SAHN) method by using NTSYS pc version 2.02 (Rohlf, 1998). The biometrical data collected from fifty eight normal corn inbreds alone were subjected for variability analysis. The coefficient of variation was estimated as quoted by Singh and Narayanan (1993). Heritability in broad sense was estimated as suggested by Lush (1940). Genotypic and Phenotypic correlations and Path co-efficients were calculated by the formula outlined by Singh and Chaudhary (1977).

The genetic diversity analysis facilitates stratified sampling of breeding population and helps in identification of genotypes for hybridization.



Classification of 70 inbreds consisting of different types of corn led to the formation of ten clusters (Table 1). The cluster I consisted of 19 inbreds, cluster II consisted of 12 inbreds, cluster III consists of eight inbreds followed by clusters IV to X clusters consisted of 1,2,7,3,6,9 and 7 inbreds respectively. The genotypes falling in the same cluster are more closely related and possess narrow genetic diversity.

There were variable mean values for different traits in different clusters (Table 2). Cluster IV possessed lowest mean value (150.17 cm) and cluster VIII bear highest mean value (224.35 cm) for plant height. For days to 50% tasseling, cluster V exhibited lowest mean value (55 days), while cluster II and VII showed maximum mean value (58 days). Among the clusters, maximum mean value was observed in cluster IX for hundred kernel weight (26.82g), kernel rows per cob (16.44) and grain yield per plant (201.29 g). Cluster means of different clusters identify the characters to be chosen for selection of parents in hybridization programme (Syed Mudasir et al., 2012). In the present study, the genotypes of different clusters could be used as parents, as they possess high magnitude of variability to obtain desirable recombinants in maize (Subramanian and Subbaraman, 2010). Sharma *et al.* (2009) suggested that while selecting parents for hybridization on the basis of genetic diversity, it is also advisable to take into consideration their per se performance for the traits to be improved. Selection of parents for hybridization should be done from different clusters having wider intercluster distance, and the parents to be selected from the clusters should also have high per se performance for the traits that are contributing maximum towards the divergence. Hence. combining high yielding potential with wide genetic diversity is emphasised for further selection. Thus, crosses between inbreds of cluster I and cluster X are likely to throw high heterotic hybrids with desirable attributes.

The study of yield and yield contributing traits among the 58 inbreds revealed significant genetic variability among the inbreds (Table 3). The estimated mean, coefficients of phenotypic and genotypic variation, broad sense heritability and expected genetic advance as per cent mean are presented in Table 4. The genotypes showed a wide range for individual characters. The genotypes showed a wide range of variation from 5.07 to 39.51 per cent at genotypic level and 6.34 to 39.69 per cent at phenotypic level for different traits. Considerable range of variation for all the characters indicated that improvement can be brought in maize through appropriate selection procedure. Genotypic co-oefficient of variation was maximum for grain yield per plant (39.51%) followed by number of kernels per row (20.39%) The per cent estimate of heritability was maximum for cob weight (99.3) followed by grain yield per plant (99.1), plant height (98.5) and cob length (89.6). High heritability coupled with high genetic advance as per cent mean for grain yield, cob weight and cob length and number of kernels per row indicated that these characters are controlled by additive gene action and phenotypic selection for these characters will be effective. High heritability and high genetic advance for grain yield was earlier reported by Mahajan *et al.* (2011) and Ojo *et al.*(2006).

Yield is identified as a quantitatively inherited complex character. Effective improvement in yield could be achieved only through the improvement of associated characters. The magnitude of both genotypic and phenotypic correlation coefficients of the character pairs viz., grain yield with days to 50% tasseling (-0.106 and -0.128), days to 50% silking (-0.104 and -0.145), plant height (0.246 and 0.250), cob weight (0.595 and 0.601), cob length (0.424 and 0.450), hundred kernel weight (0.700 and 0.767) and number of kernels per row (0.604 and 0.649) were more or less equal (Table 5), which indicated that the environmental influence on these traits were negligible and the actual genetic correlation was expressed without any marked change in degree. Grain yield showed highly significant and positive correlation with cob weight, hundred kernel weight, number of rows per cob and number of kernels per row. Days to 50% tasseling and days to 50% silking exhibited negative correlation with grain yield. Significant positive correlation between grain yield and number of kernels / row have been given by Ojo et al. (2006), while significant positive correlations between grain yield with cob length, number of kernels per row and hundred seed weight were observed by Kumar et al. (2006) and Harjinder et al.(2006).

The dependent variable grain yield is mostly influenced by the direct effect of an independent variable and its indirect effects via other yield components. Path coefficient analysis showing direct effects of attributes on grain yield is presented in Table 6. Grain yield had direct and positive effect with days to 50% tasseling, plant height, cob length and number of rows per kernel. Similar findings were obtained by Karthigeyan (2003) in maize. The character number of rows per cob had the highest direct effect (2.43)



followed by cob length (0.521) according to Kumar *et al.*(2006). The significant association of grain yield with hundred kernel weight and number of kernels per row is due to the indirect effects through number of rows per cob, days to 50% silking, plant height and cob length. The findings revealed that number of rows per cob, days to 50% tasseling, plant height and cob length are the direct components that influenced the grain yield.

References

- Harjinder, S., Chawla, J. S. and Grewal, M. S. 2006. Correlation and Path coefficient analysis on some elite Maize genotypes, *Crop Improv.*, 33 : 31-33
- Karthigeyan, M. 2003. Studies on Combining ability and Heterosis in maize (*Zea mays* L.) M.Sc Thesis submitted to TNAU, AC&RI, Madurai.
- Kumar S., Shahi J.P., Singh J., Singh S.P. 2006. Correlation and Path Analyis in early generation inbreds of Maize (*Zea mays L.*), *Crop Improv.*, 33: 156-160
- Lush, J.L. 1940. Intra-size Correlation and Regression of offspring on dams as a method of estimating Heritability of characters. *Proc Amer. Soc. Ani. Prod.*, **33** : 293-301
- Mahajan, R. C., Wadikar, P.B., Pole, S.P. and Dhuppe, M.V. 2011. Variability, Correlation and Path

analysis studies in Sorghum, *Research J.* Agrl. Sci., **2**: 101-103

- Ojo, D.K., Omikunle, O.A., Oduwaye, O.A., Ajala, M.O. and Ogunbayo, S.A. 2006 Heritability, Character correlation and Path Co-efficient analysis among six inbred lines of Maize (*Zea* mays L.). World J. of Agrl. Sci., 2: 352 - 358
- Rohlf, F.J. 1998. Numerical taxonomy and multivariate analysis system, Version 2.02i. 100. North Country Road, Setanket, New York.
- Sharma, M.K., Mishra, S. and Rana, N.S. 2009. Genetic divergence in French bean (*Phaseolus vulgaris* L.) pole type cultivars. *Legume Res.*, 32 : 220-223.
- Singh, P. and Narayanan, S.S. 1993. Biometrical techniques in Plant Breeding. Kalyani Publishers, New Delhi.p.43.
- Singh, R.K. and Chaudhary, B.D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. p 50
- Subramanian, A. and Subbaraman. N. 2010. Hierarchical Cluster analysis of genetic diversity in Maize germplasm. *Electron. J. Plant Breed.*,1: 431-436
- Syed Mudasir, Sofi1, P.A., Khan, M.N., Sofi, N.R. and Dar, Z.A. 2012. Genetic diversity, Variability and Character association in local common Bean (*Phaseolus vulgaris* L.) germplasm of Kashmir, *Electron. J. Plant Breed.*, **3**: 883-891.



| Clusters | No of genotypes | Genotypes |
|----------|-----------------|---|
| Ι | 19 | UMI30, QPM 6, QPM 12, UMI 48, UMI 131, UMI 467, QPM 13, UMI 34, UMI 42, UMI 40, UMI 61, UMI 64, UMI 430, UMI 51, UMI 128, UMI 54, UMI 176, UMI 92 and UMI 529 |
| Π | 12 | UMI 37, UMI 113, UMI 412, UPC 5, UMI 136, UMI 138, UMI 226, UMI 414, UMI 141, UMI 189 and UMI 401 |
| III | 4 | UMI 118, UMI 124, UMI 419 and UMI 842 |
| IV | 1 | Amber |
| V | 2 | UMI 35 and UPC 7 |
| VI | 7 | UMI 59, UMI 427, UMI 62, UMI 426, CO Bc 1, SCP 1457-6 and SCP 7853-1 |
| VII | 3 | UPC 1, Bangalore PC and UPC 6 |
| VIII | 6 | UMI 66, UMI 841, UMI 78, UMI 79, UMI 80 and UMI 85 |
| IX | 9 | UMI 86, UMI 87, UMI 88, UMI 830, UMI 99, UMI 420, UMI 726, UMI 116 and UMI 120 |
| Х | 7 | UMI 70, UMI 97, UMI 127, UMI 417, UMI 424, UMI 114 and UMI 122 |

Table 1. Distribution of maize inbreds in various clusters

Table 2. Cluster means for different traits in Maize inbreds

| 1 abic 2 | Table 2. Cluster means for unrerent traits in White moreus | | | | | | | | | | |
|----------|--|-----------|---------|--------|--------|---------|--------|---------|------------|--|--|
| Clust | Plant | Days to | Days to | Cob | Cob | Hundred | No of | No of | Grain | | |
| ers | height | 50% | 50% | weight | length | kernel | kernel | kernels | yield | | |
| | (cm) | tasseling | silking | (g) | (cm) | weight | rows / | / row | /plant (g) | | |
| | | | | | | (g) | cob | | | | |
| Ι | 197.30 | 57 | 61.66 | 100.91 | 18.86 | 20.87 | 12.96 | 23.74 | 97.35 | | |
| II | 198.25 | 58 | 62.96 | 121.41 | 20.81 | 19.75 | 11.83 | 21.72 | 83.40 | | |
| III | 170.85 | 58 | 62.75 | 105.91 | 22.67 | 20.75 | 11.50 | 19.50 | 113.39 | | |
| IV | 150.17 | 57 | 60.50 | 119.90 | 19.14 | 17.90 | 12.34 | 46.67 | 99.06 | | |
| V | 157.05 | 55 | 59.25 | 111.58 | 17.74 | 22.38 | 13.50 | 32.72 | 39.45 | | |
| VI | 186.27 | 56 | 60.06 | 79.95 | 15.69 | 18.30 | 11.71 | 20.49 | 58.15 | | |
| VII | 156.38 | 58 | 61.50 | 71.08 | 18.15 | 16.00 | 11.44 | 32.50 | 58.03 | | |
| VIII | 224.35 | 56 | 61.17 | 126.11 | 20.92 | 25.76 | 16.00 | 30.75 | 175.77 | | |
| IX | 193.24 | 56 | 61.33 | 128.44 | 22.57 | 26.82 | 16.44 | 27.33 | 20129 | | |
| Х | 193.03 | 57 | 62.71 | 119.54 | 20.93 | 24.59 | 15.14 | 23.79 | 144.13 | | |

Table 3. Mean square from analysis of variance of grain yield and other related characters in 58 inbred lines of maize

| | - | | | | | | | | | |
|-------------|-----|-----------|-----------|---------|----------|----------|---------|---------|----------|---------|
| Source of | df | Grain | Days to | Days | Plant | Cob | Cob | 100 | No. of | No. of |
| variation | | yield | 50% | to 50% | height | weight | length | kernel | Kernel | Kernels |
| | | (g/plant) | tasseling | silking | (cm) | (g) | (cm) | weight | Rows/Cob | |
| | | | | | | | | (g) | | |
| Genotype | 57 | 7997.82** | 35.87** | 15.47** | 753.54** | 670.97** | 28.13** | 34.49** | 18.24** | 68.66** |
| Replication | 2 | 29.29 | 21.68 | 5.17 | 23.93 | 6.95 | 2.01 | 0.40 | 8.74 | 16.14 |
| Error | 114 | 8.43 | 5.32 | 5.63 | 6.17 | 1.69 | 1.05 | 2.13 | 4.81 | 4.93 |
| | | | | | | | | | | |

** significant at 1 per cent level



Electronic Journal of Plant Breeding, 4(1): 1067-1072 (Mar 2013) ISSN 0975-928X

Table 4. Mean and related variability parameters of 58 Maize inbreds

| Character | Mean | Range | GCV (%) | PCV (%) | Heritability (%) | GA as per cent mean |
|---------------------------|--------|-------------|------------|------------|---------------------|---------------------------|
| Days to 50% tasseling | 56.79 | 50-67 | 5.64 | 6.89 | 67.0 | 9.52 |
| Days to 50% silking | 62.24 | 55-72 | 5.07 | 6.34 | 63.9 | 8.35 |
| Plant height (cm) | 196.97 | 164.1-242.4 | 8.02 | 8.09 | 98.5 | 16.40 |
| Cob weight (g) | 113.67 | 86.1-140.0 | 13.14 | 13.19 | 99.3 | 26.98 |
| Cob length (cm) | 20.32 | 13.82-25.34 | 14.79 | 15.63 | 89.6 | 28.83 |
| Hundred kernel weight (g) | 22.51 | 17.65-29.1 | 14.59 | 15.97 | 83.5 | 27.47 |
| No.of rows per kernel | 13.52 | 10.0-18.0 | 15.65 | 22.54 | 48.2 | 22.38 |
| No.of kernels per row | 23.33 | 16.0-32.0 | 20.39 | 21.88 | 86.8 | 39.13 |
| Grain yield per plant (g) | 130.9 | 32.0-224.0 | 39.51 | 39.69 | 99.1 | 81.00 |

Table 5. Coefficients of phenotypic and genotypic correlations between different pairs of characters in Maize

| Characters | | Days to 50% tasseling | Days to 50% silking | Plant height (cm) | Cob weight (g) | Cob height (cm) | Hundred kernel weight (g) | No.of rows per kernel | No.of kernel per row |
|----------------------|----------------|-----------------------------|---------------------------|-------------------------|----------------------|-----------------------|---------------------------------|--------------------------|----------------------------|
| Grain yield | r _p | -0.106 | -0.104 | 0.246 | 0.595** | 0.424 | 0.700** | 0.606** | 0.604** |
| (g/plant) | rg | -0.128 | -0.145 | 0.250 | 0.601** | 0.450 | 0.767** | 0.886** | 0.649** |
| Days to | r _p | | 0.731** | -0.164 | -0.072 | -0.046 | -0.164 | -0.198 | -0.165 |
| 50% tasseling | rg | | 0.658** | -0.182 | -0.094 | -0.072 | -0.252 | -0.252 | -0.245 |
| Days to | r _p | | | -0.115 | -0.088 | -0.077 | -0.171 | -0.174 | -0.176 |
| 50% silking | rg | | | -0.149 | 0.111 | -0.092 | -0.243 | -0.266 | -0.220 |
| Plant height | r _p | | | | 0.190 | 0.028 | 0.101 | 0.147 | 0.389 |
| (cm) | rg | | | | 0.194 | 0.030 | 0.115 | 0.205 | 0.423* |
| Cob weight | r _p | | | | | 0.392 | 0.543** | 0.438* | 0.493* |
| (g) | rg | | | | | 0.420* | 0.594** | 0.625** | 0.538** |
| Cob length | r _p | | | | | | 0.176 | 0.113 | 0.093 |
| (cm) | r_{g} | | | | | | 0.218 | 0.121 | 0.083 |
| Hundred | r _p | | | | | | | 0.567** | 0.639** |
| kernel weight (g) | r _g | | | | | | | 0.934** | 0.764** |
| No. of rows | r _p | | | | | | | 1.000 | 0.523** |
| per kernel | rg | | | | | | | 1.000 | 0.858** |



Electronic Journal of Plant Breeding, 4(1): 1067-1072 (Mar 2013) ISSN 0975-928X

| Table 6. Path analysis showing direct and indirect effects of metric traits on grain yield | | | | | | | | | | |
|--|---------|---------|--------|--------|--------|---------|-------|--------|-------------|--|
| | Days to | Days to | Plant | Cob | Cob | Hundred | No.of | No.of | Phenotypic | |
| Channeterr | 50% | 50% | height | weight | length | kernel | rows | kernel | correlation | |

| Characters | 50% tasseling | 50% silking | height (cm) | weight (g) | length (cm) | kernel weight (g) | rows per cob | kernel per row | correlation with Grain yield (g/plant) |
|------------------------------|------------------|----------------|----------------|---------------|----------------|----------------------|-----------------|-------------------|---|
| Days to 50% tasseling | 0.203 | -0.070 | -0.037 | 0.022 | -0.037 | 0.236 | -0.612 | 0.167 | -0.106 |
| Days to 50% silking | 0.235 | -0.060 | -0.030 | 0.026 | -0.048 | 0.228 | -0.646 | 0.150 | -0.104 |
| Plant height (cm) | -0.037 | 0.009 | 0.208 | -0.046 | 0.015 | -0.107 | 0.497 | -0.289 | 0.246 |
| Cob weight (g) | -0.019 | 0.006 | 0.040 | -0.240 | 0.218 | -0.557 | 1.519 | -0.367 | 0.595** |
| Cob length (cm) | -0.014 | 0.005 | 0.006 | -0.101 | 0.521 | -0.204 | 0.294 | -0.057 | 0.424 |
| Hundred kernel weight (g) | -0.051 | 0.014 | 0.023 | -0.142 | 0.113 | -0.938 | 2.270 | -0.522 | 0.700** |
| No.of rows per cob | -0.051 | 0.016 | 0.042 | -0.150 | 0.063 | -0.877 | 2.430 | -0.587 | 0.606** |
| No.of kernel per row | -0.049 | 0.013 | 0.087 | -0.129 | 0.043 | -0.717 | 2.085 | -0.684 | 0.604** |

Residual effect: 0.34