

Research Note

Studies of variability using morphological and quality traits in Quality Protein Maize (*Zea mays* L.)

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(Received: 06 Feb 2014; Accepted:23 May 2014)

Abstract

The study was conducted to assess the magnitude of genetic variability in QPM for morphological and quality traits. Fifty seven genotypes of maize (*Zea maize* L.) were grown in a randomized complete block design with three replications at Barout. In this study seed yield per plot followed by plant height, ear girth, ear height, ear length, 1000 grain weight and number of grain per row had high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Heritability and genetic advance were moderate for Days to 50% silking, protein concentration, tryptophan concentration, lysine concentration, number of row per ear and number of grains per row indicating the predominant role of non additive gene action .Hence environment plays major role in governing these characters and improvement of these characters is complicated . It might be possible through heterosis breeding. Seed yield per plot had expressed high heritability (> 85%) coupled with high genetic advance % of mean indicating genetic variance for these characters and additive gene action playing major role in inheritance of these traits and there is better scope for improvement of these characters through simple selection. Correlation coefficient was positive and significant between grain yield and both plant and ear heights, but negative and significant correlation with ear height.

Key words:

Zea mays, QPM, GC, PCV, heritability and genetic advance.

Maize (Zea mays L.) is the most widely distributed important cereal crop in the world after wheat and rice. Maize being a source of carbohydrate, fat, protein, important vitamins and minerals is a potential source of protein for humans and animals (Bjornson and Vassal, 1992). Quality Protein Maize (QPM) has high concentrations of lysine and tryptophan as compared to non-QPM maize which is desirable in human diet because all the cereals are deficient for these amino acids. Feeding QPM is beneficial in south Asia and Africa where malnutrition of children, lactating mothers and pregnant woman is prevalent. In India, three opaque-2 composites have been released. But the farmers due to poor yield, susceptibility to disease and storage problem, did not favor these composites. Some hybrids of QPM have been released by CCS Haryana Agricultural University and RAU, Dholi but QPM research needs more efforts .Genetic variability is pre-requite and important tool of any breeding programme. It provides not only the basis of selection but also some valuable information regarding selection of diverse parent for use in hybridization programme. The heritability is most important among the parameters as this will provide information whether the trait is genetically inherited or influenced by environment and how this can be improved. Burton (1952) had suggested that the genetic components of variation together with heritability estimates would give the best picture of amount of genetic advance to be expected from the selection. Many reports on estimates of genetic

variability are available in maize; information on released genotypes is limited. Hence the present study was planned to determine the estimates of variability, heritability and genetic advance for yield components from 57 maize inbreed lines and hybrids.

Ten QPM inbred lines viz., HKI-161(L₁), HKI-20-2T-1(L₂) HKI-162(L₃), HKI-163(L₄), HKI-170(L₅), HKI-171(L₆), HKI-172(L₇), HKI-191(L₈), HKI- $192(L_9)$ and HKI-193 (L₁₀) were crossed in diallel mating design. The resulting 45 crosses along with 10 parental lines and two checks (HM 5 non QPM hybrid and Saktiman 2 a QPM hybrid) were evaluated in Randomized Block Design (RBD) with three replications at Baraut during kharif 2006. The experimental material was grown in complete randomized block design with three replications. Each genotype was planted in a single row of 5m length with a row to row and plant to plant spacing of 75 cm and 22 cm respectively. The data were recorded from ten random competitive plant on 10 morphological traits viz., days to 50% silking, days to 50% tasseling, plant height, ear height, ear girth, ear length, grain number of rows per ear, number of grains per row and 1000-grain weight. Grain yield per plot (Kg) was measured on whole plot basis and three important quality characters viz., protein concentration (%), lysine concentration (%) and tryptophan concentration (g/16g N) were recorded on five randomly selected plants in control pollination by bulk sibbing in each replication each plot excluding border plants in



each replication for all the genotypes . Analysis of variance was carried out as per suggested by Panse and Sukhatme (1978). GCV and PCV were carried out as method suggested by Burton (1952) and Singh and Choudhary (1979). Heritability (BS) and Genetic advance were estimated by using formula suggested by Burton and De-Vane (1953) and Lush (1949).

In the present investigation, analysis of variance revealed significant difference among the genotypes for all the traits measured indicating the existence of sufficient variation in the material studied, as sown in Table 1.The variance components derived from further partitioning of genotypic difference into phenotypic, genotypic and environmental coefficient of variation and heritability is a good index of transmission of characters from parents to their offspring (Falconer, 1960). The estimates of heritability along with favorable genetic advance are very useful in predicating the resultant effects on selecting the best individuals. The estimates of coefficient of genotypic variance (GCV), phenotypic coefficient of variance (PCV). Heritability (h^2) in broad sense and genetic advance as per cent of mean were estimated for all the characters and are presented in Table 1.

Genotypic and Phenotypic Coefficient of Variance: The highest estimates of GCV and PCV were observed for seed yield per plot (35.15 and 36.15) followed by plant height, ear girth, ear height, ear length,100 grain weight and number of grain per row. Whereas, the characteristics of tryptophan concentration and number of rows per ear showed a more moderate value of GCV and PCV. However, the lowest values of 6.58 were expressed by protein concentration, lysine concentration. days to 50% silking and days to 50% tasseling. The overall range of GCV was found between 5.95 (days to 50 % tasseling) to 35.15 (grain yield per plot), while the overall range of PCV was found between 6.12 (days to 50 % tasseling) to 36.15 (grain yield per plot).

Heritability in broad sense (%) and Genetic advance as percent over mean: The heritability estimates ranged from 62.33 (number of grain per row) to 97.36 (grain yield per plot). The estimates of genetic advance as per cent over mean were found to vary from 10.56 (protein concentration) to 70.56 (seed yield per plot).

In the present study, heritability and genetic advance were moderate for the characteristic days to 50% silking, protein concentration, tryptophan concentration, lysine concentration, number of rows per ear and number of grains per row indicating that non-additive gene action and the environment plays major roles in governing these characteristics. Improvement of these above listed characters is complicated and it might be possible through heterosis breeding.

High heritability (more than 85 %) along with moderate genetic advance as percent of mean for the characters viz., plant height, ear height, ear girth and 1000 grain weight suggests that careful and restricted selection will be effective for the improvement of these characters.

Seed yield per plot had expressed high heritability (more than 85%) coupled with high genetic advance. This result indicates that the genetic variance for these characters are probably owing to their high additive gene effects (Johnson *et al.*, 1955) and there is an increased possibility for improvement of these characters through simple selection as supported by earlier workers (Mani and Bisht, 1996; Kabbdal *et al*, 2003;Reddy, 2003 and Shanthi *et al*, 2011).

Pearson correlation among traits shows positive and significant correlation between grain yield and days to 50% silking and plant height (Table 2) and negative and significantly with ear height. Correlation observed between grain yield and number of row per ear was negative and non significant. Tryptophan content was positive and significant correlated with days to 50% silking. Protein content was negative and significant correlated with seed yield per plant .The highest correlation of 0.68 was observed between number of grain per row with days to 50 % silking. The close relation among these traits will cause them to response similarly during improvement. The earlier worker (Grzesiak, 2001; Bello et al 2012 and Salami et al 2007) also support the above results.

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Electronic Journal of Plant Breeding, 5(3): 526- 530(Sep 2014) ISSN 0975-928X

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Electronic Journal of Plant Breeding, 5(3): 526- 530(Sep 2014) ISSN 0975-928X

| Characters | Treatment sum of | CV (%) | Mean | GCV (%) | PCV (%) | Heritability (b.s.) | GA as % of mean | |
|--------------------------|------------------|--------|--------|---------|---------|---------------------|--------------------|--|
| | squares | | | | | | | |
| Days to 50% silking, | 28.205** | 2.69 | 55.33 | 6.15 | 7.18 | 74.33 | 12.21 | |
| Days to 50% tasseling | 29.258** | 2.78 | 53.20 | 5.95 | 6.12 | 83.08 | 14.77 | |
| Plant height(cm) | 0.425** | 3.16 | 129.66 | 18.65 | 19.34 | 90.35 | 39.35 | |
| Ear height (cm) | 2.330** | 4.96 | 65.33 | 15.23 | 17.65 | 90.36 | 36.36 | |
| Ear girth (cm) | 8.698** | 5.86 | 14.25 | 14.25 | 16.85 | 86.16 | 26.17 | |
| Ear length (cm) | 2.322** | 5.40 | 16.58 | 18.28 | 20.36 | 90.55 | 32.85 | |
| Number of rows per ear | 6.36** | 2.10 | 14.00 | 8.30 | 11.02 | 66.25 | 22.56 | |
| Number of grains per row | 5.36* | 2.02 | 18.33 | 13.56 | 14.56 | 62.33 | 21.89 | |
| 1000-grain weight (g) | 2.405** | 6.15 | 28.33 | 18.36 | 20.15 | 86.15 | 30.59 | |
| Seed yield per plot (Kg) | 3.008** | 1.69 | 1.86 | 35.15 | 36.15 | 97.36 | 70.56 | |
| Protein (%) | 1.897** | 4.36 | 10.79 | 6.58 | 7.82 | 65.23 | 10.56 | |
| Tryptophan (%) | 0.025** | 3.39 | 0.76 | 10.51 | 11.89 | 66.55 | 18.39 | |

3.26

7.77

8.59

70.59

16.25

** Significant at P=0.01 level and * Significant at P=0.05 level

1.062**

4.35

Lysine concentration(g/16g N)



Electronic Journal of Plant Breeding, 5(3): 526- 530(Sep 2014) ISSN 0975-928X

| Characters | Days to 50% | Days to 50% | Plant height | Ear height | Ear girth | Ear length | Number of rows | Number of grains | 1000- grain | Seed yield per | Protein (%). | Tryptophan (%) | Lysine (g/16g N) |
|---------------------------------|-------------|----------------|-----------------|---------------|--------------|---------------|-------------------|---------------------|----------------|-------------------|--------------|-------------------|---------------------|
| | silking, | tasseling | (cm) | (cm) | (cm) | (cm) | per ear | per row | weight (g) | plot (Kg) | (70). | (70) | (g/10g IV) |
| Days to 50% silking, | - | 0.17 | 0.19 | 0.24 | 0.28 | 0.21 | 0.31 | 0.68** | 0.17 | 0.65** | 0.45 | 0.65** | 0.34 |
| Days to 50% asseling | | - | 0.16 | 0.26 | 0.35 | 0.27 | 0.12 | 0.19 | 0.19 | 0.31 | 0.35 | 0.37 | 0.32 |
| lant eight(cm) | | | - | 0.26 | -0.34 | 0.45 | 0.46 | 0.34 | 0.21 | 0.59** | 0.26 | 0.27 | 0.29 |
| Ear height (cm) | | | | - | -0.35 | 0.28 | 0.36 | 0.29 | -0.55 | -0.55** | 0.45 | 0.25 | 0.32 |
| ar girth (cm) | | | | | - | 0.26 | -0.02 | -0.06 | 0.11 | 0.24 | 0.26 | 0.17 | 0.14 |
| Ear length (cm) | | | | | | - | -0.23 | 0.27 | 0.31 | 0.09 | 0.36 | 0.11 | 0.13 |
| Number of rows per ar | | | | | | | - | 0.39 | -0.07 | -0.05 | 0.09 | 0.26 | 0.24 |
| Number of grains per | | | | | | | | - | 0.24 | 0.23 | .022 | 0.07 | 0.05 |
| 000-grain weight (g) | | | | | | | | | - | 0.35 | 0.23 | 0.11 | 0.11 |
| eed yield per plot Kg) | | | | | | | | | | - | -0.52** | 0.34 | 0.11 |
| Protein (%) | | | | | | | | | | | - | 0.22 | 0.33 |
| ryptophan (%) | | | | | | | | | | | | - | 0.32 |
| Lysine oncentration(g/16g N) | | | | | | | | | | | | | - |

** Significant at P=0.01 level and * Significant at P=0.05 level