**Analysis of genetic variability for grain yield and its attributing traits of maize (*Zea mays* L.) inbred lines**

**Abstract**

Forty-two inbred lines were planted in Randomized Block Design with three replications to check variability, heritability and genetic advance as percent of mean for grain yield and its attributing traits during *Kharif* 2021 at Research Farm, CCS HAU, RRS Uchani, Karnal. Understanding maize variability, heritability and genetic advance is critical for effective plant breeding and genetic improvement program. Analysis of variance revealed highly significant differences for all studied traits. Genotypic and phenotypic coefficient of variation was highest with small difference for grain yield per plant and its component traits indicating higher influence of environment on the expression of the traits. Highest broad sense heritability (%) was reported by lysine percent followed by tryptophan percent, cob diameter, days to silking, shelling percent and days to anthesis. High heritability coupled with high genetic advance as percent of mean was found in lysine percent followed by cob diameter, tryptophan percent, ear height, plant height and 100 grains weight number of grains per cob and number of kernels per row which indicates effectiveness of selection due to preponderance of additive gene action and breeder may consider these traits as primary selection criteria.

***Keywords****: Maize, hybrids, analysis of variance, GCV, PCV, variability.*

**Introduction**

“Maize is regarded as third most important cereal crop after wheat and rice. It is widely utilized and traded as a premier feed and food crop, with a wide range of industrial applications ranging from food processing to the manufacture of industrial products” (Murdia *et al.*, 2016). “Importance of maize is due to its high yield potential, appropriateness for high-density planting, tolerance to a variety of agro-climatic conditions and numerous applications, including feed (61%), food (17%) and industrial starch and fuel (22%)” (IIMR, 2024). “Globally, maize is cultivated on an area of nearly 205.9 million hectares with a production of 1210 million tonnes in about 170 countries contributing 36 % to the global food production” (FAO, 2022). “In India, it occupies an area of about 9.86 million hectares with an average productivity of 31.95 q/ha and production is 31.51 million tonnes” (Agri STAT, 2021). In Haryana, area under *kharif* maize is about 9300 ha with production of about 28000 tonnes with an average productivity 30.1 q/ha (Anonymous, 2022). “The major maize producing states during *kharif* season are Karnataka, Andhra Pradesh, Maharashtra, Madhya Pradesh, Uttar Pradesh, Himachal Pardesh, Jammu and Kashmir, Bihar and Punjab. It is also grown in Bihar, Telangana, Karnataka, Coastal of Andhra Pradesh and West Bengal during *Rabi* season while in Haryana, Punjab and Western Uttar Pradesh during spring season” (Murdia *et al.*, 2016). Maize is highly cross-pollinated crop therefore, many opportunities to take advantage of hybrid vigour, depending on the direction, strength and type of gene action. Genetic diversity among genotypes has a substantial impact on breeding techniques for agricultural improvement (Yali, 2021). “Maize is one crop that requires hybrids to be commercially viable. To develop high yielding hybrids, understanding and utilizing genetic diversity for the identification of potential lines and including them in crop improvement for enhancement of existing germplasm is the important strategy” (Reif *et al.,* 2005; Hallauer *et al.,* 1988).

“Maize inbred lines are important because they provide a core resource for genetics and breeding studies and they are widely used in hybrid maize production”. (Anderson and Brown, 1952, Sumanthi *et al*., 2005). The primary objective of maize breeding program is to increase the production per unit area which can be done by enhancing the inherent yielding ability of the crop, hence any trait that helps to the steady generation of high yielding maize lines would be of interest to plant breeders. Knowledge of genetic diversity and linkages between accessions is required for any increase in economically significant features because it aids in understanding the extent of genetic variability, which serves as the foundation for efficient selection. Knowledge of heritability coupled with genetic advance is most useful in predicting the scope for genetic improvement through selection, because heritability alone provides the basis for selection on phenotypic performance but does not indicate the amount of genetic improvement resulting from individual genotype selection.

**Materials and Methods**

A total of 42 inbred lines of maize were evaluated at the Regional Research Station, CCS HAU, Uchani, Karnal in RBD design with 3 replications during *Kharif* season of 2021. Observed data were recorded for seventeen traits such as days to anthesis,days to silking**,** physiological maturity, plant height (cm), ear height (cm), cob length (cm), cob diameter (cm), number of rows per cob, number of kernels per row, number of grains per cob, 100 grain weight (g),number of cobs per plant, shelling percent (%), protein content, lysine percent (%), tryptophan percent (%), grain yield per plant (g). Representative plants were randomly selected from each plot in each replication for the traits such as plant height and ear height. Data for 100 grain weight, protein content in kernel, lysine content in kernel protein and tryptophan content in kernel protein were taken from the sample of bulk seeds and five plants were selected to estimate the biochemical work. For estimation of variance components *viz*., phenotypic variances (σ2p) and genotypic variances (σ2g) both were estimated using the following formula as suggested by Panse and Sukhatme (1967).

 **Genotypic Variance** = (vMSS – eMSS) x CF

**Phenotypic Variance** = σ2g + EMS

Both genotypic and phenotypic coefficient of variability were computed for each character as per method suggested by Burton and De Vane (1953).

**Genotypic Coefficient of Variation (GCV)** = Genotypic standard deviation divided by grand mean of the character × 100

**Phenotypic Coefficient of Variation (PCV)** = Phenotypic standard deviation divided by grand mean of the character × 100

**Heritability (h2):** It was estimated in broad sense by using following formula as suggested by Lush (1940).

**h2** = Genotypic variances (σ2g) divided by Phenotypic variances (σ2p) × 100

The heritability was categorized as low (0-30%), moderate (30-60%) and high (60 and above) as given by Robinson *et al*., (1949).

**Genetic advance as per cent of mean (GAM)**

GAM (%) = Genetic advance (GA) divided by General mean of population (Gm) × 100

Genetic advance as per cent mean was categorized as low (0-10%), moderate (10-20%) and high (20 and above) as given by Johnson *et al.* (1955).

**Result and Discussion**

Analysis of variance for seventeen traits of 42 inbred lines of maize revealed a highly significant difference for all the traits. The results pointed out that genotypes were differed significantly it means an extension range of variability existing among the genotypes for all the traits. Similar results were also reported by earlier workers Patel *et al.* (2024), Banakara *et al.* (2024) Pavan *et al.* (2011) and Kumer *et al.* (2015). The presence of sufficient variability in the genotypes for grain yield per plant and its attributing traits provides ample scope for selecting superior and desirable inbred lines by the plant breeder for further improvement (Table 1).

Table 1: Analysis of variance for seventeen traits of 42 inbred lines of *kharif* maize

|  |  |  |
| --- | --- | --- |
| **Sr. No.** | **Characters** | **Mean sum of squares** |
| **Replication****Df=2** | **Treatment****Df=41** | **Error****Df=82** |
| 1. | Days to anthesis | 0.738 | 78.530\*\* | 2.350 |
| 2. | Days to silking | 0.187 | 75.619\*\* | 1.966 |
| 3. | Physiological maturity | 1.231 | 53.626\*\* | 2.806 |
| 4. | Plant height (cm) | 28.910 | 1584.120\*\* | 174.19 |
| 5. | Ear height (cm) | 23.500 | 369.810\*\* | 21.62 |
| 6. | Cob length (cm) | 0.228 | 2.670\*\* | 0.140 |
| 7. | Cob diameter (cm) | 0.004 | 0.664\*\* | 0.003 |
| 8. | Number of rows per cob | 1.431 | 2.508\*\* | 0.747 |
| 9. | Number of kernels per row | 0.029 | 17.647\*\* | 2.315 |
| 10. | Number of grains per cob | 384.80 | 4105.50\*\* | 868.20 |
| 11. | 100-grain weight (g) | 1.051 | 21.44\*\* | 2.191 |
| 12. | Number of cobs per plant | 0.002 | 0.010\*\* | 0.001 |
| 13. | Grain yield per plant (g) | 33.535 | 190.626\*\* | 69.13 |
| 14. | Shelling percent (%) | 0.314 | 87.060\*\* | 2.430 |
| 15. | Protein content | 0.003 | 0.579\*\* | 0.064 |
| 16. | Lysine percent (%) | 0.001 | 1.172\*\* | 0.003 |
| 17. | Tryptophan percent (%) | 0.000 | 0.034\*\* | 0.000 |

Phenotypic and genotypic variance were computed for the grain yield per plant along with its component traits under study given in Table 2. Similar findings were also observed by Bello *et al.* (2012) The numerical value of phenotypic variance was higher than their genotypic counterpart for all the traits. This is due to the reasons that some non-genetic factors have played an important role in the development of these traits. In present investigation, the values for genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) found to be nearby each other indicates the little influence by the environment.The magnitude of genotypic and phenotypic coefficient of variance was found to be high for the trait lysine percent followed by cob diameter and plant height. These findings also relate with Al-Rawi *et. al*. (2024), Ahmad *et al*. (2020), Chaurasia *et al.* (2022), Kamal *et al*. (2020), Jagadev *et al.* (2021), Pranay *et al*. (2022) and Reddy *et al.* (2012).

 High broad sense heritability was recorded for lysine percent (99.21) followed by tryptophan percent (99.13), cob diameter (98.44), days to silking (92.59), shelling percent (92.07), days to anthesis (91.66), physiological maturity (85.79), cob length (85.30), ear height (84.30), 100 grains weight (74.55), plant height (72.96) and so on as shown in Table 2. However, the selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, heritability values coupled with high genetic advance would be more reliable and useful on correlating selection criteria. Similar findings were reported by Bhusal *et al.* (2017), Kamal *et al.* (2020), Jagadev *et al*. (2021), Thakur *et al*. (2023), Yadav *et al*. (2023) and Al-Rawi *et. al*. (2024). Highest heritability coupled with high genetic advance as percent of mean was recorded in lysine percent, cob diameter, tryptophan percent, ear height, plant height, 100 grain weight, number of grains per cob and number of kernels per row suggesting the preponderance of additive genetic effect in the determination of these traits which was fixable in subsequent generations (Table 2). Yadav *et al*. (2023) also reported the same in their findings.

Table 2: Genotypic and phenotypic coefficient of variance, heritability and genetic advance as percent of mean for seventeen characters in *kharif* maize

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr. No.** | **Characters** | **Mean** | **σ2G** | **σ2P** | **GCV** | **PCV** | **Heritability** | **GAM** |
| 1. | Days to anthesis | 53.35 | 25.40 | 27.71 | 9.44 | 9.86 | 91.66 | 18.63 |
| 2. | Days to silking | 55.64 | 24.55 | 26.51 | 8.90 | 9.25 | 92.59 | 17.65 |
| 3. | Physiological maturity | 88.77 | 16.93 | 19.74 | 4.63 | 5.00 | 85.79 | 8.84 |
| 4. | Plant height (cm) | 137.40 | 469.97 | 644.16 | 15.17 | 18.47 | 72.96 | 27.76 |
| 5. | Ear height (cm) | 72.00 | 116.06 | 137.68 | 14.96 | 16.29 | 84.30 | 28.29 |
| 6. | Cob length (cm) | 12.19 | 0.84 | 0.98 | 7.52 | 8.14 | 85.30 | 14.31 |
| 7. | Cob diameter (cm) | 1.64 | 0.20 | 0.22 | 28.52 | 28.75 | 98.44 | 58.30 |
| 8. | Number of rows per cob | 12.51 | 0.58 | 1.33 | 6.12 | 9.23 | 44.00 | 8.36 |
| 9. | Number of kernels per row | 18.40 | 5.11 | 7.42 | 12.28 | 14.80 | 68.81 | 20.98 |
| 10. | Number of grains per cob | 231.07 | 1079.10 | 1947.32 | 14.21 | 19.09 | 55.41 | 21.80 |
| 11. | 100-grain weight (g) | 17.56 | 6.41 | 8.60 | 14.42 | 16.70 | 74.55 | 25.65 |
| 12. | Number of cobs per plant | 0.99 | 0.00 | 0.01 | 1.00 | 2.47 | 16.67 | 0.84 |
| 13. | Grain yield per plant (g) | 39.85 | 40.49 | 109.62 | 15.96 | 26.27 | 36.94 | 19.99 |
| 14. | Shelling percent (%) | 66.56 | 28.20 | 30.64 | 7.97 | 8.31 | 92.07 | 15.77 |
| 15. | Protein content | 8.76 | 0.17 | 0.23 | 4.72 | 5.54 | 72.64 | 8.29 |
| 16. | Lysine percent (%) | 2.03 | 0.38 | 0.39 | 30.64 | 30.76 | 99.21 | 62.88 |
| 17. | Tryptophan percent (%) | 0.44 | 0.01 | 0.02 | 24.13 | 24.23 | 99.13 | 49.49 |

**Conclusion**

In conclusion, an extension range of variations was observed for all the studied traits. Genotypes differed significantly for all the traits as evidenced by ANOVA. Phenotypic and genotypic coefficient of variation were computed for all the seventeen traits and observed that PCV was higher than GCV with a small difference for all traits indicating higher influence of environment on the expression of these traits. Highest GCV and PCV for lysine percentage followed by cob diameter, number of grains per cob, 100-grain weight, number of kernels per row proposing adequate variability and indicating that these traits might be further improved through selection. High heritability coupled with high genetic advance as percent of mean was observed for lysine percent, cob diameter, tryptophan percent, ear height, plant height, 100 grain weight, number of grains per cob and number of kernels per row indicating that this is due to additive gene effects where cautious selection may lead towards improvement of these traits.

**Authors’ contributions**

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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**Disclaimer**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, *etc*.) and text-to-image generators have been used during the writing or editing of this manuscript.

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