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

**Abstract**

The F1 hybrids along with parents and 2 standard checks (HM8 and HM11) 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 programme. 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 among all the traits indicating higher influence of environment on the expression of the traits. High heritability was recorded for all the characters. Highest broad sense heritability (%) was reported by cob length followed by number of kernels per row, shelling percent and cob diameter. Highest genetic advance as percent of mean was highest in grain yield per plant followed by cob diameter, number of grains per cob, 100 grains weight and kernels per row indicating 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. 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%) (Erenstein, 2010; 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. Maize is highly cross-pollinated crop therefore, there are many opportunities to take advantage of hybrid vigour, depending on the direction, strength and type of gene action. Utilizing the heterosis or hybrid vigour, the productivity of maize has increased substantially over the years in comparison to other cereals. A lot of resources have been used to develop various commercial cultivars including composites, synthetics, double cross hybrids and single cross hybrids. 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 programme 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 124 entries 80 hybrids along with 42 parents and 2 standard checks (HM8 and HM11) 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. Analysis of variance (ANOVA) for traits, coefficient of variability, genetic advance, broad sense heritability was worked out by Panse and Sukhatme (1967), Burton *et al.* (1953) which was analogous to North Carolina Design II (Comstock and Robinson, 1952), Burton and De vane (1953), Lush (1949), Johnson *et al.* (1955) and Allard (1960) respectively. Grades of Heritability (Broad sense) and Genetic advance as percent of mean as shown in Table: 1.

**Table 1: Grades of Heritability (Broad sense) and Genetic advance as percent of mean**

|  |  |  |
| --- | --- | --- |
| **Category** | **Heritability (Broad sense)** | **Genetic advance as percent of mean** |
| **High** | >60% | >20% |
| **Moderate** | 30- 60% | 10-20% |
| **Low** | <30% | <10% |

**Result and Discussion**

Analysis of variance for seventeen traits of 124 entries (parents, crosses and checks) of maize revealed a highly significant difference for all the traits. The results pointed out that genotypes (parents and crosses) have differed significantly it means an extension range of variability existing among the genotypes for all the traits indicating sufficient variability in the genotypes which provides ample scope for selecting superior and desirable genotypes (parents and crosses) by the plant breeder for further improvement. (Table 2).

Table 2: Analysis of variance for 17 traits of 40 inbred, 2 testers, 80 hybrids and 2 checks of maize

|  |  |  |
| --- | --- | --- |
| **Sr. No.** | **Characters** | **Mean sum of squares** |
| **Replication****Df=2** | **Treatment****Df=123** | **Error****Df=246** |
| 1. | Days to anthesis | 0.03 | 57.01\*\* | 2.30 |
| 2. | Days to silking | 0.13 | 57.07\*\* | 2.06 |
| 3. | Physiological maturity | 1.88 | 46.91\*\* | 2.50 |
| 4. | Plant height (cm) | 130.69 | 1292.84\*\* | 128.56 |
| 5. | Ear height (cm) | 18.72 | 358.53\*\* | 25.32 |
| 6. | Cob length (cm) | 1.06 | 24.27\*\* | 0.18 |
| 7. | Cob diameter (cm) | 0.04 | 1.81\*\* | 0.02 |
| 8. | Number of rows per cob | 0.61 | 3.99\*\* | 0.29 |
| 9. | Number of kernels per row | 2.24 | 130.80\*\* | 1.37 |
| 10. | Number of grains per cob | 1135.45 | 27588.02\*\* | 459.44 |
| 11. | 100-grain weight (g) | 3.93 | 159.90\*\* | 4.08 |
| 12. | Number of cobs per plant | 0.00 | 0.01\*\* | 0.00 |
| 13. | Grain yield per plant (g) | 319.76 | 6582.72\*\* | 129.24 |
| 14. | Shelling percent (%) | 6.09 | 182.31\*\* | 2.14 |
| 15. | Protein content | 0.13 | 0.48\*\* | 0.12 |
| 16. | Lysine percent (%) | 0.02 | 0.42\*\* | 0.01 |
| 17. | Tryptophan percent (%) | 0.00 | 0.01\*\* | 0.00 |

Phenotypic and genotypic variance were computed for the grain yield per plant along with its component traits under study given in Table 2. 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.GCV was found to be high for the characters grain yield per plant (47.02) followed by cob diameter (29.85), number of grains per cob (27.66), 100 grain weight (26.79) and number of kernels per row (24.99). 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) and Pranay *et al*. (2022). It was moderate for cob length (19.23) followed by lysine percentage (18.99), ear height (14.62), tryptophan percentage (14.12), plant height (13.19), shelling percentage (10.14), number of rows per cob (8.53), days to anthesis (7.72), days to silking (7.44) and number of cobs per plant (7.57). Similar results were also reported by Chaurasia *et al.* (2022), It was least for physiological maturity (4.23) and protein content (3.94) (Table 3).Phenotypic coefficient of variance was observed high for the characters grain yield per plant (48.41) followed by cob diameter (30.57), number of grains per cob (28.35), 100 grain weight (27.83), number of kernels per row (25.39). These findings also relate with Ahmad *et al*. (2020), Chaurasia *et al.* (2022), Kamal *et al*. (2020), Jagadev *et al.* (2021) and Pranay *et al*. (2022). PCV was moderate for lysine percentage (19.65) followed by cob length (19.45), ear height (16.21), plant height (15.22) tryptophan percent (14.64) shelling percentage (10.32), number of rows per cob (9.50), days to anthesis (8.19), days to silking (7.84), protein content (5.55) and number of cobs per plant (5.17). These findings were also reported by Chaurasia *et al.* (2022). The lowest phenotypic coefficient of variance was recorded for physiological maturity (4.58) (Table 3).

 High heritability was recorded for all the characters. This is due to the additive gene effects where selection may lead towards improvement of the traits. All the traits considered under present investigation showed significantly high broad sense heritability (%) was reported by cob length (97.75) followed by number of kernels per row (96.91), shelling percent (96.56), cob diameter (95.34), number of grains per cob (95.17), grain yield per plant (94.33), tryptophan percent (94.06), lysine percent (93.51), test weight (92.72), days to silking (89.88), days to anthesis (88.79), physiological maturity (85.51), ear height (81.44), number of rows per cob (80.69), number of cobs per plant (77.98), plant height (75.12) and protein content (50.41) (Table 3). Similar findings were reported by Bhusal *et al.* (2017), Matin 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).

 Among all the characters, genetic advance as percent of mean was recorded to be highest in grain yield per plant (94.08) (Kamal *et al*. (2020)) followed by cob diameter (59.92), number of grains per cob (55.57), 100 grains weight (53.15), kernels per row (50.68), cob length (39.17), lysine percent (37.85), tryptophan percent (28.05), ear height (27.19), plant height (23.55) and shelling percent (20.53). Yadav *et al*. (2023) also reported the same in their findings. It was observed moderate in number of rows per cob (15.79) followed by days to anthesis (14.98) and days to silking (14.52). Least genetic advance as percent of mean was recorded in number of cobs per plant (8.31) followed by physiological maturity (8.06) and protein content (5.77) (Table 3).

Table 3: 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 | 55.32 | 18.23 | 19.00 | 7.72 | 8.19 | 88.79 | 14.98 |
| 2. | Days to silking | 57.58 | 18.33 | 19.02 | 7.44 | 7.84 | 89.88 | 14.52 |
| 3. | Physiological maturity | 90.93 | 14.80 | 15.63 | 4.23 | 4.58 | 85.51 | 8.06 |
| 4. | Plant height (cm) | 149.37 | 388.09 | 430.94 | 13.19 | 15.22 | 75.12 | 23.55 |
| 5. | Ear height (cm) | 72.07 | 111.07 | 119.51 | 14.62 | 16.21 | 81.44 | 27.19 |
| 6. | Cob length (cm) | 14.73 | 8.02 | 8.09 | 19.23 | 19.45 | 97.75 | 39.17 |
| 7. | Cob diameter (cm) | 2.59 | 0.59 | 0.60 | 29.85 | 30.57 | 95.34 | 59.92 |
| 8. | Number of rows per cob | 13.01 | 1.23 | 1.33 | 8.53 | 9.50 | 80.69 | 15.79 |
| 9. | Number of kernels per row | 26.28 | 43.14 | 43.60 | 24.99 | 25.39 | 96.91 | 50.68 |
| 10. | Number of grains per cob | 343.86 | 9042.85 | 9196.00 | 27.66 | 28.35 | 95.17 | 55.57 |
| 11. | 100-grain weight (g) | 26.90 | 57.94 | 53.30 | 26.79 | 27.83 | 92.72 | 53.15 |
| 12. | Number of cobs per plant | 1.02 | 0.00 | 0.00 | 4.57 | 5.17 | 77.98 | 8.31 |
| 13. | Grain yield per plant (g) | 98.64 | 2151.16 | 2194.24 | 47.02 | 48.41 | 94.33 | 94.08 |
| 14. | Shelling percent (%) | 76.42 | 60.05 | 60.77 | 10.14 | 10.32 | 96.56 | 20.53 |
| 15. | Protein content | 8.87 | 0.12 | 0.16 | 3.94 | 5.55 | 50.41 | 5.77 |
| 16. | Lysine percent (%) | 1.96 | 0.13 | 0.14 | 18.99 | 19.65 | 93.51 | 37.85 |
| 17. | Tryptophan percent (%) | 0.45 | 0.00 | 0.00 | 14.12 | 14.64 | 93.06 | 28.05 |

**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 grain yield per plant followed by lysine percentage, 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. Highest heritability coupled with high genetic advance as percent of mean was observed for most of the traits indicating that this is due to additive gene effects where cautious selection may lead towards improvement of these traits.

**REFERENCES**

Ahmad, E. and Ansari, A. M. (2017). Study of combining ability and heterosis analysis for yield traits in maize (*Zea mays* L.). *Journal of Pharmacognosy and Phytochemistry*, 6(6): 924-927.

Al-Rawi, O. H., Bedn, A. A., & Hamed, M. A. (2024). Genetic variability and path coefficient analysis for three-way cross in maize. *SABRAO J. Breed. Genet.*, *56*(1), 204-210.

Anderson, E. and Brown, W.L., “Origin of corn belt maize and its genetic significance”, In: Heterosis - A Record of Researches Directed toward Explaining and Utilizing the Vigor of Hybrids, Gowen, J.W., Ed., Iowa State College Press, Ames, 1952, pp. 124-148.

Anonymous (2022): Statistical abstract of Haryana (2021-22), *Department of Economic and Statistical analysis*, Haryana.

Anonymous (2023): *Indian Institute of Maize Research*, Ludhiana.

Bhusal, T., Lal, G. M., Marker, S. and Synrem, G. J. (2017). Genetic variability and traits association in Maize (*Zea mays* L.) genotypes. *Annals of Plants and Soil Research*, 19(1): 59-65.

Burton GW, De Vane EH. Estimating heritability in tall Fescue (*Festuca aurundinacea*) from replicated clonal material. *Agron.* J., 1953;45:478-481

Chaurasia, N. K., Nirala, R. B. P., Singh, B., and Mandal, S. S. (2020). Trait association and path coefficient analysis in maize (*Zea mays* L.) for grain yield and its attributes. *Journal of Pharmacognosy and Phytochemistry*, 9(6): 527-531.

Hallauer, A.R., Russell W.A. and Lamkey K.R. (1988). *Corn Breeding*. In: Corn and corn improvement. 3rd edn. Agron Monogr 18, ASA-CSSA-SSSA, Madison, Wisconsin, USA. 469-564 pp.

Jagadev, P. N., Kanungo, P., and Lenka, D. (2021). Genetic variability, association and path coefficient studies in quality protein maize inbreds. *The Pharma Innovation Journal*, 10(12): 776-779.

Kamal, N., Khanum, S., Siddique, M. and Ahmed, M. F. (2020). Phenotypic correlation coefficient studies to determine interrelationships among grain yield and related characters in maize. *Haya: The Saudi Journal of Life Sciences*, 5(6): 113-116.

Kempthorne, O. (1957). An introduction to genetic statistics.

Panse VG, Sukhatme PV. Statistical methods for agricultural workers. *Indian Council for Agricultural Research.* New Delhi, Indlca 1967; 4.

Pranay, G., Shashibhushan, D., Rani, K. J., Bhadru, D., and Kumar, C. V. (2022). Correlation and Path Analysis in Elite Maize (*Zea mays* L.) Lines. *International Journal of Plant and Soil Science*, *34*(24): 414-422.

Sedhom, S. A. (2022). Evaluation of combining ability for some new yellow maize inbred lines using line X tester model. *Annuals of Agricultural Science, Moshtohor*, 60(4): 1009-1018.

Sumathi, P., Nirmalakumari, A., Mohanraj, K., “Genetic variability and traits interrelationship studies in industrially utilized oil rich CIMMYT lines of maize (Zea mays L.)”, Agricultural journal, 2005, 92(10-12) pp. 612-617.

Tesfaye K, Gbegbelegbe S, Cairns, JE, Shiferaw B, Prasanna, BM, Sonder K, Boote KJ, Makumbi D, Robertson R (2015). Maize systems under climate change in sub-Saharan Africa: potential impacts on production and food security. *International Journal of Climate Change Strategy Management* 7(3):247-271.

Yadav, P.K., Tripathi, M. K., Tiwari, S., Chauhan, S., Tripathi, N., Sikarwar, R. S. and Singh, A. K. (2023). Genetic components and variability assessment for grain yield and its accrediting traits in maize (*Zea mays* L.). *International Journal of Environmental Climate Change*, 13(9): 772-784.

Yali, W. (2022). Review of the genetic variability in maize genotypes (Zea mays L). Plant, 10(1), 1-7.