

Assessment of Genetic Variability, Heritability, and Genetic advance as a percentage of mean in Maize (*Zea mays* L.) Segregating Generations.

ABSTRACT

The recent experiment aimed to investigate genetic traits for eleven characteristics, namely, Days to 50% tasselling, Days to 50% silking, Plant height (cm), Tassel length (cm), Ear length (cm), Ear diameter (cm), Ear height (cm), Number of kernel rows per cob, Number of kernels per row, Cob weight (gms), and Grain yield (gms) during the Kharif and Rabi seasons of 2023-24. The Alpha Lattice Design was employed. Genotypes were sown in single rows, each 2 meters long in each replication. The analysis of variance revealed significant variations among all traits, with phenotypic coefficients of variation (PCV) generally exceeding genotypic coefficients of variation (GCV). Cob weight and grain yield exhibited the highest phenotypic and genotypic coefficients of variation (PCV and GCV) across both seasons, signifying significant genetic variability in the studied material. Ear diameter showed the highest heritability, with ear height coming in second. This high heritability suggests a strong potential for these traits to be successfully passed on to progeny, facilitating effective selection. Traits such as plant height (cm), tassel length (cm), ear length (cm), ear diameter (cm), ear height (cm), number of kernel rows per cob, number of kernels per row, cob weight (gms), and grain yield (gms) demonstrated high heritability and genetic advancement in both seasons, making them promising candidates for enhancement through selection based on additive genetic factors.

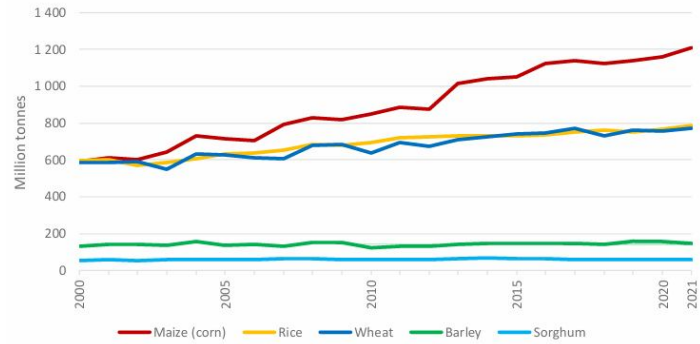
Keywords: *Heritability, Variability, Maize, yield.*

INTRODUCTION

Among the grains, maize (*Zea mays* L.) is the most adaptable crop in terms of kinds and applications. It is the second most popular crop in the world, farmed in temperate, subtropical, and tropical climates. There are several varieties, including field, sweet, and baby corn. Various field corn varieties include high-oil maize, waxy maize, and quality protein maize (QPM). For billions of people, maize is a vital crop that is used for food, feed, and industrial raw materials. Currently, nearly 1137.3 million MT of maize is being produced together by over 170 countries from 197.4 million ha with an average productivity of 5.8 t/ha (FAOSTAT, 2021)(1). In India, the amount of maize produced has grown more than 16 times, from just 2 million tonnes in 1949–1950 to 31.65 million tonnes and it now covers 10.04 million hectares with a mean yield of 3. tons ha⁻¹ making up 9% of the country's food supply. According to 1st Advance Estimates of Production of Food grains for 2022-23, all India Maize production estimate was 23.10 million tonnes. In Telangana, it is grown on around 2.5 lakh hectares, which is 10.04 percent of the total cultivated area with a productivity of 5.178 t ha⁻¹. (IndiaAgriStat.com 2020–21)(2). In maize breeding projects, the goal perpetually is to increase economically essential characteristics while retaining a reasonable level of variety. To promote genetic

variety in germplasm, it is necessary to understand the level of existing genetic variability in the material. Genetic diversity, defined as a heritable variation across genotypes or cultivars, is essential for an efficient long-term breeding effort.

Fig .1 Scenario of crop improvement program



Source: FAO. 2022. FAOSTAT: Production: Crops and livestock products. In: FAO. Rome.

Cited December 2022. <https://www.fao.org/faostat/en/#data/QCL>(1)

The success of any crop improvement program is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection Bello, O.B. *et al*, 2012(3). Variability is the occurrence of differences among individuals due to differences in their genetic makeup or the environment in which they are raised. Wedwesseneet *al*, (4)

MATERIALS AND METHODS

The experiments including selfing in *Kharif* 2023, and further segregating generation in *Rabi*, 2023-24 were carried out at Winter Nursery Centre, Rajendranagar, Hyderabad. Winter Nursery Centre, Hyderabad is in the Southern Telangana agro-climatic zone of Telangana state. Geographically it lies at 17.19 °N latitude, 78.24 °E longitude with an altitude of 542.6 meters above Mean Sea Level (MSL). The rainfall of the Research Station ranged from 606 to 853 mm (long-term range).

The experimental material consists of 54 maize segregating lines in the first season (*Kharif* 2023) and 49 f_{2-3} lines and these were sown in two replications with Alpha Lattice Design. Each genotype was planted in a single row, 2 meters in length in each replication, with a spacing of 60 cm between rows and 20 cm within rows. The crop was cultivated with the recommended agricultural practices. Observations were recorded for eleven quantitative traits *viz.*, Days to 50 percent tasselling, Days to 50 percent silking, Plant height (cm), tassel length (cm), ear length (cm), ear diameter (cm), ear height (cm), Number of kernel rows per cob, Number of kernels per row, cob weight (gms), grain yield (gms).

Johnson et al. [5] developed a method to determine heritability in the broad sense (h^2_{bs}) and genetic progress. Burton's techniques [6] were used to calculate the genotypic and phenotypic coefficients of variation. The PCV and GCV estimations were classified as low (0-10%), moderate (10-20%), and high (>20%) using Sivasubramanian and Madhavamenon's criteria [7]. R 4.4.1-win was used to carry out the analysis.

Statistical analysis:

The analysis of variance (Table 1) was conducted for F2 and F3 generations. Two analyses of variance were conducted. The first was for all genotypes in selected families, and the second was for the chosen families to determine heritability and GCV and PCV.

Coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated using the formulae given by

Burton (1952). **Phenotypic coefficient of variation (PCV %) = $\frac{\sqrt{V_p}}{\bar{X}} \times 100$**

Genotypic coefficient of variation (GCV %) = $\frac{\sqrt{V_g}}{\bar{X}} \times 100$

Where,

V_p = Phenotypic variance

V_g = Genotypic variance

\bar{X} = Mean of the character

- Heritability in a broad sense was estimated as **$H = \sigma_g^2 / \sigma_p^2 \times 100$** .

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance revealed significant differences among genotypes for all traits in both seasons, including Days to 50 percent tasselling, Days to 50 percent silking, Plant height (cm), tassel length (cm), ear length (cm), ear diameter (cm), ear height (cm), Number of kernel rows per cob, Number of kernels per row, cob weight (gms), grain yield (gms). (Table 1), indicating genotypic variation among the evaluated genotypes. There is a chance to choose favorable genotypes with improved yield component qualities, which might perform well and lead to greater yield. These findings are congruent with those of other studies, including Ahmad, M.S.H., 2016. [8]

Variability and Heritability

The variability of eleven quantitative traits in 54 maize segregating lines in the first season (Kharif 2023) and 49 f_{2-3} lines in rabi (2023-24) were assessed using a phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as a percentage of the mean (Table 2).

In this study, the Phenotypic Coefficient of Variation (PCV) was higher than the Genotypic Coefficient of Variation (GCV) for almost all quantitative traits (Table 2) in both the Kharif and rabi seasons of 2023-24. Although the value of the phenotypic coefficient of variation (PCV) for all characters was always found to be higher than the genotypic coefficient variation (GCV) the differences were small in magnitude. This suggests the environment's lower influence on the characters' expression.

UNDER PEER REVIEW

Table 1. Analysis of Variance for Yield and Yield-Contributing Traits in Maize

S.No.	Character/trait	Mean sum of squares							
		Replication (Df:1)		Genotypes (Df:149)		Blocks (Df:14)		Error (Df:135)	
		Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24
1	Daysto50percentsilking	36.75	1.72	49.36**	46.47**	18.43	2.177	5.13	1.517
2	Daysto50percentanthesis	23.14	4.50	50.72**	43.65**	17.65	4.50	4.34	1.429
3	Plantheight(cm)	4.32	38.65	2519.38**	846.96**	35.39	6.38	20.41	35.07
4	Tassel length (cm)	0.106	1.17	84.74**	102.67**	0.461	0.314	0.80	0.46
5	Ear length(cm)	0.451	0.29	56.304**	24.56**	0.148	0.1931	0.58	0.30
6	Ear diameter(cm)	0.48	0.24	643.37**	20.94**	1.17	0.1643	1.17	0.08
7	Ear height (cm)	1.65	0.33	937.19**	389.62**	1.46	2.39	3.73	1.31
8	KernelrowsPer Ear	0.186	11.91*	193.93**	27.439**	0.709	8.038	0.604	2.99
9	Kernel Per Row	0.71	6.22	321.42**	107.376**	1.76	4.097	1.20	1.87
10	Cob weight (gm)	0.02	29.23*	681.56**	2777.7*	6.87	13.94	7.87	9.57
11	Grain yield (gm)	1.03	22.30	320.92**	2105.65**	2.88	7.44	3.52	5.89

**Significantat 1%level

*Significantat 5%level

S. No.	Character	Mean		Range				Coefficient of Variation				Heritability (broad sense) h^2 (bs) (%)		GAM	
				Minimum		Maximum		PCV (%)		GCV (%)					
		K	R	K	R	K	R	K	R	K	R	K	R	K	R
1	DS	68.32	73.80	55	63	79	86	7.72	6.64	6.78	6.41	77	93.3	12.26	12.77
2	DA	65.87	71.98	52	62	77	85	8.05	6.62	7.21	6.35	80.1	92.03	13.29	12.55
3	PH	157.9	145.06	55.8	96.86	217.3	216.32	22.56	14.4	22.37	13.9	98.2	92.83	45.69	27.62
4	TL	32.44	32.02	22.8	12.24	68.2	65.52	20.17	22.42	19.96	22.32	98.19	99.14	40.76	45.78
5	EL	32.97	9.16	20.5	2	38.8	18.21	16.16	38.46	16	38	98.08	97.68	32.66	77.39
6	ED	40.42	7.71	20.4	3.14	90.2	14.65	44.40	42.03	44.32	41.83	99.64	99.07	91.13	85.78
7	EH	70.94	61.65	16.3	31.98	113.37	94.72	30.5	22.68	30.4	22.59	99.34	99.26	62.5	46.37
8	KRPE	36.5	10.93	20.1	4.52	53.77	24.01	26.9	36.05	26.8	31.56	99.2	76.67	55.16	56.94
9	KPR	46.29	14.08	24.2	3.30	67.08	33.02	27.4	52.55	27.32	51.5	99.32	96.07	56.0	104.007
10	CW	25.4	40.96	8.98	5.06	91.5	148.56	72.9	91.14	72.1	90.81	97.7	99.2	146.88	186.39
11	GY	16.27	31.994	5.6	3.01	71.11	125.22	78	101.5	77	101.2	97	99.4	157	208

Table 2. Genetic Variability Parameters for Yield and Yield-Contributing Traits in Maize

PCV=Phenotypic coefficient of variation

GCV=Genotypic coefficient of variation

DA: Day to 50 percent Anthesis, DS: Day to 50 percent Silking, PH: Plant height, TL: Tassel Length, EH: Ear Height, EL: Ear Length, ED: Ear Diameter, KRPE: Kernel Rows Per Ear, KPR: Kernels Per Row, CW: Cob Weight, GY: Grain Yield.

K: Kharif 2023, R: Rabi 2023-2024.

The highest values of phenotypic and genotypic coefficients of variation (PCV and GCV) were recorded for cob weight and grain yield in both seasons, indicating significant genetic variability in the material studied. The segregating population exhibited high PCV and GCV, consistent with findings reported by M. T. Abd EL-Kader et al. in 2022[9], Hassan, A.A., et al in 2018 [10]

Moderate GCV and PCV values were observed for the traits of ear length in Kharif 2023 and for the trait of plant height in rabi 2023-24, which align with similar findings reported by Ram Reddy et al. [11].

Low GCV and PCV were observed for the traits of days to 50% anthesis and days to 50% silking in both seasons. The minimal difference between genotypic and phenotypic coefficients of variation suggests that environmental factors had little effect on the expression of these traits. These findings are consistent with the experimental results of Barathi et al. [12] and Ellandula et al. [13].

A large number of traits had considerably high heritability estimates, indicating that additive gene action predominated. The highest heritability was found in ear diameter, followed by ear height, KPR, KRPE, plant height, tassel length, and others. The least heritability is seen in days to 50% silking in Kharif 2022. Similar high and low heritability values were recorded by Ram Reddy et al. 2012. The highest heritability was found in grain yield followed by ear height and the least in KRPE in rabi 2023-24. Similar high and low heritability values were recorded by Ashutosh Kumar et al. 2017 [14]. However, improving such traits may not be beneficial as broad sense heritability is based on total genetic variance, including additive, dominant, and epistatic variances. Heritability values with high genetic progress are more trustworthy for determining selection criteria. Higher heritability suggests additive gene activity, which allows selection to be successful in early generations.

Genetic advance as a percentage of the mean indicated that additive genetic factors predominantly influence these traits. Utilizing heritability estimates alongside genetic advances enhances the reliability and utility of selection procedures. According to Johnson et al. (1955), the observed GAM values were classified as low (less than 10%), moderate (10–20%), and high (greater than 20%). In the present study, genetic advance was calculated and expressed as a percentage of the mean for all traits (Table 2). High genetic advances were observed for total grain yield, followed by cob weight and ear diameter in the kharif season and KPR in the rabi season. Bharathi et al. [12] reported high genetic advance values for total grain yield. Moderate GAM values were observed in days to 50% silking and days to 50% anthesis in both seasons. Similar values were obtained by Wedwessen et al. [4].

High heritability combined with high genetic advance was observed for all the traits except in days to 50% silking and days to 50% anthesis in both the kharif and rabi seasons. These findings suggest that these traits are promising targets for improvement through selection, likely driven by additive genetic factors. Kinfu and Tsehaye [15] and Bhiusal et al. [16]

CONCLUSION

The analysis of variance revealed significant variation between the inbred lines, with phenotypic coefficients of variation (PCV) greater than genotypic coefficients of variation (GCV) for all traits. This suggests that direct selection will be effective in improving these traits. The highest PCV and GCV traits were total grain yield and cob weight during both seasons, indicating significant variability among the genotypes and indicating that phenotypic selection will be beneficial for improving these traits due to their high heritability and high genetic advance.

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