

ASSESSMENT OF GENETIC PARAMETERS IN MAIZE (*Zea mays* L.) FOR YIELD AND ASSOCIATED TRAITS

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ABSTRACT

The present study was undertaken during the *rabi* season of 2024–25 at the Regional Agricultural Research Station (RARS), Lam, Guntur, Andhra Pradesh, to evaluate the extent of genetic variability, heritability and genetic advance in maize (*Zea mays* L.) inbred lines. A total of 50 inbred lines comprising 48 test entries along with two standard checks (LM 13 and LM 14) are assessed using alpha lattice design with two replications. Data was recorded on thirteen quantitative traits encompassing phenological, morphological and yield-related parameters. Analysis of variance revealed highly significant differences among the genotypes for all the traits studied indicating the presence of considerable genetic variability. The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits, reflecting the influence of environmental factors on trait expression. High estimates of GCV and PCV were observed for ear height, 100-kernel weight and grain yield per plant suggesting the existence of substantial variability within the genetic material. Moderate variability was recorded for plant height, ear length and SPAD chlorophyll meter reading, whereas relatively low variability was observed for days to 50% anthesis, days to 50% silking and days to maturity. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, ear height, number of kernels per row, 100-kernel weight and grain yield per plant indicating the predominance of additive gene effects and the potential effectiveness of direct selection for these traits. Moderate heritability with moderate genetic advance was observed for ear length, ear girth, number of kernel rows per ear and SPAD chlorophyll meter reading, suggesting the involvement of both additive and non-additive gene actions.

Keywords: Maize, Genetic variability, GCV, PCV, Heritability, Genetic advance and inbred lines.

INTRODUCTION

Maize (*Zea mays* L.) is a cereal crop of considerable global importance, contributing significantly to agricultural productivity and food security. It ranks second only to wheat in terms of area under cultivation, while attaining

the foremost position in overall production and productivity. After rice and wheat, maize is the third most widely consumed cereal for human use. The crop originated in South America and is taxonomically classified under the family Poaceae. Cytogenetically, it is a diploid species with a chromosome complement of $2n = 20$ and

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constitutes the sole representative of the genus *Zea* (Korsa *et al.*, 2024).

It is widely regarded to have originated through a process of gradual selection from its ancestral progenitor, teosinte (*Zea mexicana*), a primitive grass indigenous to Mexico and Guatemala. Being a C_4 species, maize possesses a highly efficient photosynthetic system, which underpins its superior grain yield potential and enables its cultivation across a broad spectrum of agro-ecological environments (Khan *et al.*, 2024).

Genetic variability represents a fundamental prerequisite for the success of crop improvement programmes, as it forms the basis for effective selection and facilitates the optimal utilization and expansion of the available gene pool. The magnitude of variability in quantitative traits is commonly evaluated using genetic parameters such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), which also provide insights into the relative contribution of environmental factors to trait expression. Heritability serves as an estimate of the proportion of total phenotypic variance attributable to genetic factors and thereby indicates the potential for transmission of traits to subsequent generations. However, heritability estimates alone may not sufficiently predict the response to selection; hence, the combined assessment of heritability and genetic advance is considered more informative, as it provides a reliable indication of the expected genetic gain and aids in the formulation of effective breeding strategies (Ghorpade *et al.*, 2025).

MATERIAL AND METHODS

The experiment was carried out during the *rabi* season of 2024–25 at the Regional Agricultural Research Station (RARS), Lam, Guntur, Andhra Pradesh (16.180° N latitude,

80.290° E longitude and 31.5 m above mean sea level). The experimental material consisted of 50 maize (*Zea mays* L.) inbred lines, comprising 48 test entries along with two standard checks (LM 13 and LM 14), as presented in Table 1.

The trial was laid out in an alpha lattice design with two replications. Each replication was divided into 10 blocks and within each block, five inbred lines were allocated following appropriate randomization. Each genotype was sown in two rows of 4 m length, maintaining a spacing of 60 cm between rows and 20 cm between plants within rows. All recommended agronomic practices and necessary plant protection measures were uniformly applied throughout the crop growth period to ensure proper crop establishment and maintenance.

Observations on pre- and post-harvest traits were systematically recorded from ten randomly selected plants per entry in each replication. A total of thirteen quantitative characters were evaluated, viz., days to 50% anthesis, days to 50% silking, anthesis–silking interval (days), days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, 100-kernel weight (g), grain yield per plant (g) and SPAD chlorophyll meter reading (SCMR).

The analysis of variance for individual traits was carried out in accordance with the standard statistical methodology prescribed by Panse and Sukhatme (1978). The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated following the approach proposed by Burton (1952). Broad-sense heritability, along with genetic advance expressed as per cent of mean, was computed and categorized based on the criteria suggested by Johnson *et al.* (1955). All statistical analyses were performed using INDOSTAT software (version 9.1).

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance revealed highly significant differences among the inbred lines for all the traits under investigation, indicating the existence of substantial genetic variability that can be effectively exploited in breeding programmes (Table 2).

Genotypic and Phenotypic Coefficients of Variation

Phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) for all the traits evaluated (Table 3), suggesting a considerable influence of environmental factors on trait expression. High values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for ear height, 100-kernel weight and grain yield per plant, indicating the presence of substantial variability among the inbred lines under study. These results are in conformity with earlier findings reported by Reddy *et al.* (2022), Singh *et al.* (2024) and Gogoi *et al.* (2025) for ear height; Khan *et al.* (2024) for 100-kernel weight and Pradhan *et al.* (2022), Rani *et al.* (2022) and Sondarava *et al.* (2025) for grain yield per plant.

Moderate values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for plant height, ear length and SPAD chlorophyll meter reading (SCMR), reflecting a moderate level of variability among the inbred lines evaluated. These results are in agreement with the findings of Damtie *et al.* (2021), Pradhan *et al.* (2022) and Reddy *et al.* (2022) for plant height; Korsa *et al.* (2024), Singh *et al.* (2024) and Gogoi *et al.* (2025) for ear length and Sravani *et al.* (2021) (PCV value) for SPAD chlorophyll meter reading (SCMR).

Low values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for days to 50% anthesis, days to 50% silking and days to maturity, indicating the presence of limited variability among the inbred lines studied. These results are in agreement with earlier findings of Damtie *et al.* (2021), Pradhan *et al.* (2022), Korsa *et al.* (2024), Gogoi *et al.* (2025) and Sondarava *et al.* (2025) for days to 50% anthesis and days to 50% silking and Kinfé and Tsehaye (2015), Reddy *et al.* (2022), Khan *et al.* (2024) and Samskrithi *et al.* (2025) for days to maturity.

Heritability and Genetic Advance

High heritability coupled with high genetic advance as a percent of mean was recorded for traits such as plant height, ear height, number of kernels per row, 100-kernel weight and grain yield per plant. This combination suggests the predominance of additive gene action, indicating that direct selection would be effective for the improvement of these traits. These findings are in agreement with the reports of Singh *et al.* (2024) for plant height; Khan *et al.* (2024) for ear height; Patil *et al.* (2016) for number of kernels per row; Rani *et al.* (2022), Reddy *et al.* (2022) and Veeravishnu *et al.* (2023) for 100-kernel weight and Sondarava *et al.* (2025) for grain yield per plant.

Moderate heritability coupled with moderate genetic advance as a percent of mean was observed for traits such as ear length, ear girth, number of kernel rows per ear and SPAD chlorophyll meter reading (SCMR). This pattern indicates the influence of non-additive gene effects in the expression of these traits. The results obtained in the present study are in conformity with the findings of Reddy *et al.* (2022) for ear length and ear girth; Patil *et al.* (2016) for number of kernel rows per ear and Sravani *et al.* (2021) for SPAD chlorophyll meter reading (SCMR).

Days to 50% silking showed high heritability accompanied by low genetic advance, indicating the involvement of both additive and non-additive gene effects and suggesting limited scope for improvement through direct selection. Comparable results have been reported by Reddy *et al.* (2022), Korsia *et al.* (2024) and Gogoi *et al.* (2025). In contrast, the anthesis–silking interval exhibited

moderate heritability with high genetic advance, reflecting the combined influence of additive and non-additive gene actions in its inheritance. These findings are in accordance with those of Reddy *et al.* (2022) and Khan *et al.* (2024).

Moderate heritability accompanied by low genetic advance as a percent of mean was recorded for days to 50% anthesis and days

Table 1. List of inbred lines evaluated in the study Mean sum of squares

Entry	Inbreds/ Genotypes	Source of the material	Entry	Inbreds/ Genotypes	Source of the material
1	PL 22339	ARS, Peddapuram	26	PL 23030	ARS, Peddapuram
2	PL 22344	ARS, Peddapuram	27	PL 23150	ARS, Peddapuram
3	PL 22348	ARS, Peddapuram	28	PL 23153	ARS, Peddapuram
4	PL 22351	ARS, Peddapuram	29	PL 23239	ARS, Peddapuram
5	PL 22367	ARS, Peddapuram	30	PL 23042	ARS, Peddapuram
6	PL 22373	ARS, Peddapuram	31	PL 23044	ARS, Peddapuram
7	PL 22384	ARS, Peddapuram	32	PL 23058	ARS, Peddapuram
8	PL 22389	ARS, Peddapuram	33	PL 23059	ARS, Peddapuram
9	PL 22390	ARS, Peddapuram	34	PL 23066	ARS, Peddapuram
10	PL 22393	ARS, Peddapuram	35	PL 23077	ARS, Peddapuram
11	PL 22394	ARS, Peddapuram	36	PL 23089	ARS, Peddapuram
12	PL 22406	ARS, Peddapuram	37	PL 23090	ARS, Peddapuram
13	PL 22407	ARS, Peddapuram	38	PL 23091	ARS, Peddapuram
14	PL 22408	ARS, Peddapuram	39	CML 72	CIMMYT
15	PL 22409	ARS, Peddapuram	40	CML 425	CIMMYT
16	PL 22410	ARS, Peddapuram	41	CML 451	CIMMYT
17	PL 22415	ARS, Peddapuram	42	CML 474	CIMMYT
18	PL 22422	ARS, Peddapuram	43	CML 574	CIMMYT
19	PL 22426	ARS, Peddapuram	44	CML 575	CIMMYT
20	PL 22429	ARS, Peddapuram	45	CML 577	CIMMYT
21	PL 22434	ARS, Peddapuram	46	CML 581	CIMMYT
22	PL 22439	ARS, Peddapuram	47	CML 582	CIMMYT
23	PL 22441	ARS, Peddapuram	48	CML 595	CIMMYT
24	PL 22448	ARS, Peddapuram	49	LM 13	PAU, Ludhiana
25	PL 23012	ARS, Peddapuram	50	LM 14	PAU, Ludhiana

Table 2. Analysis of variance for 13 characters under study in 50 inbred lines of maize (*Zea mays* L.)

Source of variation	DF	DFA	DFS	ASI	DM	PH	EH	EL	EG	NKPE	NKPR	HKW	GYPP	SCMR
Replications	1	42.25	7.84	0.25	44.92	597.51	22.49	6.02	2.90	3.42	21.72	16.31	55.25	35.08
Treatments	49	19.58*	20.06**	0.32**	42.08*	1200.20**	381.28**	7.47**	3.80**	3.77**	41.65**	163.42**	1068.19**	55.95**
Blocks within replications	18	8.54	5.69	0.10	25.03	292.20	9.25	3.97	1.39	2.11	15.97	7.74	24.01	18.79
Error	31	10.05	4.90	0.11	19.36	260.81	12.47	2.24	1.29	1.47	7.05	7.26	29.81	15.66
Total	99	80.42	38.48	0.78	131.38	2350.72	425.48	19.70	9.38	10.76	86.39	194.71	1177.25	125.48

DF: Degrees of freedom Where * and ** significant at 5% and 1% level of significance respectively

DFA- Days to 50% anthesis, **DFS**-Days to 50% silking, **ASI**-Anthesis silking interval (days), **DM**-Days to maturity, **PH**-Plant height (cm), **EH**-Ear height (cm), **EL**-Ear length (cm), **EG**-Ear girth (cm), **NKPE**-Number of kernel rows per ear, **NKPR**-Number of kernels per row, **HKW**-100-kernel weight (g), **SPAD** Chlorophyll Meter Reading (SCMR), **GYPP**-Grain yield per plant (g)

to maturity, suggesting the predominance of non-additive gene action in the expression of these traits. The observed moderate heritability is likely attributable to environmental influences rather than inherent genetic variability among the inbred lines, indicating that direct selection may be less effective for their improvement. These findings are consistent with the reports of Pradhan *et al.* (2022) for days to 50% anthesis and Kinfe and Tsehaye (2015) and Patil *et al.* (2016) for days to maturity.

CONCLUSION

The analysis of variance revealed significant differences among the inbred lines, while higher PCV than GCV for all traits indicated environmental influence on their expression. High PCV and GCV values for ear height, 100-kernel weight and grain yield per plant reflected substantial variability, suggesting good scope for improvement through selection. Furthermore, high heritability coupled with high genetic advance for plant height, ear height, number of kernels per row, 100-kernel weight and grain yield per plant indicated the predominance of additive gene action. Hence, these traits are heritable and amenable to effective improvement through direct selection.

REFERENCES

- *Burton, G.W. 1952. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress. 277-283.
- Damtie, Y., Assefa, G. and Mulualem, T. 2021. Genetic variability heritability trait associations and path coefficient analysis of maize (*Zea mays* L.) inbred lines at Pawe North western Ethiopia. Pelagia Research Library, 11 (2): 57-64.

Table 3. Estimates of genetic parameters for 13 characters under study in 50 inbred lines of maize (*Zea mays* L.)

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as % of mean
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50% anthesis	66.15	58.50	72.00	3.30	5.82	32.15	3.85
2	Days to 50% silking	68.46	60.50	74.50	4.02	5.16	60.75	6.46
3	Anthesis silking interval (days)	2.31	2.00	3.00	14.07	20.24	48.29	20.14
4	Days to maturity	119.20	110.50	128.50	2.83	4.65	36.99	3.54
5	Plant height (cm)	135.50	77.33	190.35	15.99	19.95	64.30	26.42
6	Ear height (cm)	53.15	27.27	83.00	25.55	26.40	93.67	50.94
7	Ear length (cm)	13.88	10.15	17.42	11.64	15.87	53.83	17.60
8	Ear girth (cm)	12.06	9.32	14.61	9.29	13.22	49.34	13.44
9	Number of kernel rows per ear	13.80	10.80	16.90	7.78	11.73	43.97	10.62
10	Number of kernels per row	21.75	10.10	29.95	19.12	22.68	71.04	33.20
11	100 kernel weight (g)	28.07	12.66	56.36	31.48	32.91	91.50	62.03
12	Grain yield per plant (g)	58.15	13.38	53.00	39.19	40.30	94.57	78.50
13	SPAD Chlorophyll Meter Reading (SCMR)	39.22	24.91	50.84	11.44	15.26	56.25	17.68

Ghorpade, T.R., Misal, A.M., Umate, S.M., Kalpande, H.V and Rathod, A.H. 2025. Studies on genetic variability, heritability and genetic advance in maize (*Zea mays* L.) inbred lines. International Journal of Advanced Biochemistry Research. 9 (8): 1639-1642.

Gogoi, D., Bordoloi, D., Sarma, A and Barua, N.S. 2025. Correlation and path analysis of early inbred lines of maize (*Zea mays* L.) for yield and yield related traits. Indian Journal of Plant Genetic Resources, 38 (01): 123-130.

Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 47: 314-318.

Khan, S.A., Iqbal, A.M., Shikari, A.B., Dar, Z.A., Wani, M.A., Mahdi, S.S., Waza, S., Ahanger, M.A., Bangroo, S and Islam, N. 2024. Diversity analysis of highland temperate maize (*Zea mays* L.) inbred lines. SKUAST Journal of Research. 26 (1): 38-45.

- Kinfe, H. and Tsehay, Y. 2015. Studies of heritability, genetic parameters, correlation and path coefficient in elite maize hybrids. *Academic Research Journal of Agricultural Science and Research*,3 (10): 296-303.
- Korsa, F., Dessalegn, O., Zeleke, H and Petros, Y. 2024. Genetic variability for the yield and yield related traits in some maize (*Zea mays* L.) inbred lines in the Central Highland of Ethiopia. *International Journal of Agronomy*. 1: 1-13.
- Panse, V. G and Sukhatme, P. V. 1978. *Statistical Methods for Agricultural Workers*, ICAR, New Delhi.
- Patil, S.M., Kumar, K., Jakhar, D.S., Rai, A., Borle, U.M. and Singh, P. 2016. Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.). *International Journal of Agriculture, Environment and Biotechnology*, 9 (6): 1103-1108.
- Pradhan, P., Thapa, B., Ghosh, A., Subba, V., Sahu, C.R and Kundagrami, S. 2022. Genetic variability assessment on yield attributing traits in maize (*Zea mays* L.) inbred lines. *The Pharma Innovation Journal*. 11 (5): 1642-1645.
- Rani, M., Anusha, C., Lavanya, G.R and Kiran, M.S. 2022. Genetic variability and interrelationship in maize (*Zea mays* L.) genotypes for grain yield and yield component characters. *International Journal of Environment and Climate Change*,12 (11): 3264-3271.
- Reddy, S.G.M., Lal, G.M., Krishna, T.V., Reddy, Y.V.S and Sandeep, N. 2022. Correlation and path coefficient analysis for grain yield components in maize (*Zea mays* L.). *International Journal of Plant & Soil Science*. 34 (23): 24-36.
- Samskriti, S., Sharma, D and Kandel, B.P. 2025. Genetic parameters estimation of promising maize hybrids in sundarbazar, lamjung. *Agricultura*, 134 (1-2): 133-134.
- Singh, S., Sudan, R.S., Kumar, B., Singh, P and Sharma, M. 2024. Genetic divergence in maize (*Zea mays* L.) inbred lines under subtropical conditions of Jammu region of India. *Plant Archives*, 24 (2): 1829-1836.
- Sondarava, P.M., Patel, M.B., Parmar, D.J., Borkhatariya, T.H., Vadodariya, J.M and Akbari, K.M. 2025. Appraisal of genetic variability, heritability and genetic advance for quantitative traits in maize (*Zea mays* L.). *Horizon*,3 (2): 22-29.
- Sravani, D., Bharathi, D., Reddi Sekhar, M. and Nirmal Kumar, A.R. 2021. Estimation of genetic parameters for quantitative traits in maize (*Zea mays* L.) inbred lines. *The Pharma Innovation Journal*, 10 (8): 501-503.
- Veeravishnu, S., Sudhir Kumar, I., Harish Chanar S.R., Pushpalatha, G and Krishnam Raju, K. 2023. Genetic variability and association studies for grain yield and its component traits in maize (*Zea mays* L.) inbreds. *The Pharma Innovation Journal*,12 (5): 295-299.

Yogitha,S.N., Satish, Y., Pushpa reni, Y. and Vijaya kumar, G. 2026. Assessment of genetic parameters in maize (*Zea mays* L.) for yield and associated traits. *The Journal of Research ANGRAU*,54(2):15-21