DoI: https://doi.org/10.58537/jorangrau.2026.54.1.04

J. Res. ANGRAU 54 (1) 37-45, 2026

GENETIC VARIABILITY, HERITABILITY AND GENETIC GAIN POTENTIAL FOR YIELD TRAITS IN MAIZE (*Zea mays* L.)

P. KIREETI VARMA *, I. SUDHIR KUMAR , K.R. YATHISH and P. MUNIRATNAM

Department of Genetics and Plant Breeding, Agricultural College, Bapatla - 522101
Acharya N.G. Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Date of Receipt : 09-02-2026 Date of Acceptance : 18-03-2026

ABSTRACT

The present study was undertaken to evaluate the extent of genetic variability, heritability, and genetic advance for yield and component traits in seventy maize (*Zea mays* L.) inbred lines. The genotypes were assessed during *rabi* 2024–25 at two locations—ARS, Peddapuram and WNC, ICAR-IIMR, Rajendranagar—using an alpha-lattice design with two replications. The analysis of variance revealed highly significant differences among the inbred lines for all traits investigated, confirming the presence of substantial genetic variability. In the pooled analysis, high genotypic and phenotypic coefficients of variation were recorded for anthesis–silking interval, 100-kernel weight and grain yield per plant, indicating a strong scope for selection and the involvement of both additive and non-additive gene effects. Moderate variability was observed for plant height, ear height, ear length and number of kernels per row, whereas the remaining traits expressed comparatively low variability. Furthermore, high heritability coupled with high genetic advance as a percentage of the mean for plant height, ear height, ear length, number of kernels per row, 100-kernel weight and grain yield per plant suggests the predominance of additive gene action, thereby enabling effective improvement through direct selection. These findings provide a strong foundation for identifying promising parental lines and advancing yield-oriented maize breeding programmes.

Keywords: Genetic Variability, GCV, Genetic Advance, Heritability, Maize and PCV.

INTRODUCTION

Maize (Zea mays L.) is one of the most widely cultivated cereal crops globally, ranking third in production after rice and wheat. Owing to its exceptional yield potential, broad adaptability, and diverse end uses, it is often referred to as the “Queen of Cereals.” Beyond its role as a staple food and an important fodder crop, maize is increasingly utilized for bioethanol production, thereby contributing to sustainable and renewable energy initiatives. As a C_4, day-neutral species, maize demonstrates high photosynthetic efficiency and superior water-use effectiveness, which enable it to maintain productivity across a range of agro-climatic conditions, including stress-prone environments. This resilience underscores its importance in climate-smart and climate-resilient agriculture (Sondarava *et al.,* 2025).

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* Corresponding Author Email: kireetivarma.pusapati@gmail.com

Botanically, maize (2n = 2x = 20) belongs to the family Poaceae, subfamily Panicoideae, and tribe Maydeae. It is believed to have originated in the Central American–Mexico region, from where it spread globally and evolved into a versatile crop capable of thriving in tropical, subtropical and temperate ecosystems. India is a major maize producing country, with Andhra Pradesh contributing 19.04 lakh tonnes and achieving a productivity of 6543 kg/ha, accounting for 5.6% of the national production, which reached 42.23 million tonnes in 2025 (https://apseeds.ap.gov.in/Website/Maize.aspx).

Understanding the genetic parameters underlying variation in maize is essential for designing efficient breeding and selection strategies. The assessment of genotypic and phenotypic coefficients of variation (GCV and PCV) provides insights into the magnitude of inherent variability and the potential for improvement through selection. High estimates of PCV and GCV indicate the presence of considerable genetic variability among traits, which is crucial for effective selection-based enhancement. Similarly, heritability, which quantifies the proportion of phenotypic variation attributable to genetic factors, serves as a key predictor of the success of selection. When high heritability is accompanied by a high genetic advance, it suggests that traits are predominantly governed by additive gene action, enabling substantial improvement through direct selection (Samskriti *et al*., 2025).

Since yield and many agronomically important traits in maize are quantitatively inherited and influenced by multiple genes with strong environmental interactions, evaluating both additive and non-additive genetic components is vital. The combined interpretation of heritability and genetic advance therefore offers a more reliable indication of the expected response to selection and helps identify traits amenable to genetic improvement. In this context, the present study was undertaken to assess the genetic variability, heritability, and genetic advance for grain yield and its related traits in a diverse set of maize inbred lines, with the goal of identifying promising parents for use in future breeding programmes.

MATERIAL AND METHODS

A panel of 70 maize inbred lines was evaluated during *rabi* 2024–25 at two locations: ARS, Peddapuram (Location 1) and WNC, ICAR–IIMR, Rajendranagar, Hyderabad (Location 2). The experiment was laid out in an alpha-lattice design with two replications, comprising seven blocks per replication, each block containing 10 genotypes. Each inbred line was sown in two rows of 3 m length, with a spacing of 60 cm between rows and 20 cm between plants, resulting in a plot size of 3.6 m² at both locations. All recommended agronomic practices were followed as per the standard package of practices for maize.

Observations were recorded on pre and post-harvest traits using data from five plants selected at random from each entry in each replication. The traits evaluated included days to 50% anthesis, days to 50% silking, anthesis–silking interval, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), days to maturity, number of kernel rows per ear, number of kernels per row, 100-kernel weight (g), shelling percentage (%), and grain yield per plant (g).

The data collected for all traits were subjected to analysis of variance (ANOVA) following the standard procedures described by Panse and Sukhatme (1978). Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated using the method proposed by Burton (1952). Broad-sense heritability and genetic advance were computed according to the formulas of Johnson *et al*. (1955). Statistical analyses were carried out using RStudio (Version 2025.05.1+513).

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance (ANOVA) was carried out to partition the total variability into its component sources and to determine the extent of differences among the genotypes. The existence of significant variability within a crop population forms the foundation for effective selection and genetic improvement. The ANOVA results for the 70 maize inbred lines evaluated at two locations and pooled over environments are presented in Tables 1, 2, and 3.

Across both individual locations and the pooled analysis, highly significant differences were observed among the inbred lines for all yield and yield-related traits, indicating the presence of substantial genetic variability that can be exploited in breeding programmes. In the pooled analysis, the genotype × location interaction was significant for days to 50% anthesis, days to 50% silking, days to maturity, 100-kernel weight, and grain yield per plant, suggesting that these traits are influenced by environmental factors and that genotypic performance varied across testing environments.

Phenotypic and Genotypic Coefficients of Variation

The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation for the 13 yield and yield-associated traits are presented in Table 4 and Fig. 1. In the pooled analysis, GCV values exceeded their corresponding PCV values for all traits, indicating that genetic factors were the primary contributors to the observed variability and that environmental influence was relatively limited. This suggests that phenotypic selection would be effective for improving these traits. The magnitude of PCV and GCV across traits ranged from low (<10%), moderate (10–20%), to high (>20%), depending on the nature of the character. High PCV and GCV were recorded for anthesis–silking interval (PCV: 20.10; GCV: 26.30), 100-kernel weight (PCV: 22.00; GCV: 22.80), and grain yield per plant (PCV: 31.70; GCV: 33.80). These findings agree with earlier reports by Rani *et al.* (2022) and Veeravishnu *et al*. (2023) for ASI; Ghosh *et al.* (2014) and Khan *et al*. (2024) for 100-kernel weight; and Antony *et al*. (2024) and Samskrithi *et al*. (2025) for grain yield per plant.

Moderate PCV and GCV were obtained for plant height (PCV: 12.20; GCV: 13.10), ear height (PCV: 18.50; GCV: 19.10), ear length (PCV: 13.80; GCV: 14.90), and number of kernels per row (PCV: 17.30; GCV: 18.40). Similar trends were reported by Gogoi *et al.* (2025) for plant height, ear length and kernels per row and by Banakara *et al.* (2024) and Tesfaye *et al*. (2021) for ear height. Low PCV and GCV values were recorded for days to 50% anthesis (4.69; 4.95), days to 50% silking (4.56; 4.81), ear girth (9.04; 9.74), days to maturity (5.35; 7.08), number of kernel rows per ear (6.84; 7.69), and shelling percentage (6.12; 6.52). These observations corroborate the earlier reports of Samskrithi *et al*. (2025) and other recent studies.

Heritability and Genetic Advance

High broad-sense heritability combined with high genetic advance as percent of the mean (GAM) was recorded for plant height (86.90%; 23.40%), ear height (85.10%; 35.20%), ear length (86.20%; 26.50%), number of kernels per row (88.40%; 33.60%), 100-kernel weight (92.90%; 43.70%), and grain yield per plant (88.00%; 61.30%). Such combinations indicate predominant additive gene action and imply that direct selection would be effective for improving these traits.

Table 1. Analysis of variance for yield and yield attributing traits under study in maize (Zea mays L.) inbred lines at ARS, Peddapuram (L1)

Source of variance	DF	DFA	DFS	ASI	PH	EH	DM	EL	EG	NKPE	NKPR	HKW	SH	GYPP
Replication	1	1.21	0.35	0.26	51.60	134.10	0.26	1.91	2.86	0.62	0.67	0.86	11.81	40.20
Genotype	69	17.02***	16.53***	0.38	1046.5***	483.2***	17.89***	8.63***	3.59***	2.66**	44.67***	64.66***	50.16***	1501.7***
Replication: Block	15	3.66*	3.91*	0.24	234.30	146.10	4.00	4.98*	2.68**	0.41	22.73	0.44	14.23	36.40
Residuals	57	1.50	1.83	0.35	186.40	113.30	2.15	2.50	0.94	1.25	15.59	0.29	19.87	19.20

Table 2. Analysis of variance for yield and yield attributing traits under study in maize (Zea mays L.) inbred lines at WNC, ICAR-IIMR, Rajendranagar (L2)

Source of Variance	DF	DFA	DFS	ASI	PH	EH	DM	EL	EG	NKPE	NKPR	HKW	SH	GYPP
Replication	1	18.56	13.83	0.35	0.60	71.40	13.83	1.00	1.04	0.10	3.04	1.83	28.55	46.20
Genotype	69	36.05***	35.72***	0.36*	852.60***	316.80***	35.72***	7.02***	2.42***	1.86**	40.33***	68.50***	50.54***	822.90
Replication: Block	12	5.13	4.65	0.23	242.70	132.2**	4.65	2.89	0.67	0.70	4.67	0.47	16.71	20.80
Residuals	57	5.39	5.27	0.22	203.60	47.40	5.27	2.27	0.47	0.98	6.75	0.48	16.81	11.90

Table 3. Pooled Analysis of variance for yield and yield attributing traits under study in maize (Zea mays L.) inbred lines at ARS, Peddapuram (L1) and WNC, ICAR-IIMR, Rajendranagar (L2) during rabi 2024-25

Source of variance	df	DFA	DFS	ASI	PH	EH	DM	EL	EG	NKPE	NKPR	HKW	SH	GYPP
Location	1	15009***	14732***	1.28*	2484.1***	11075***	315236***	0.01	9.80***	0.49	0.67	6.00***	0.28	19631***
Genotypes	2	45.00***	45.00***	0.57***	1605.0***	669.00***	466.00***	14.58***	5.34***	4.00***	79.34***	109.00***	99.00***	1715***
Replication: Loc	69	10.00	7.00	0.30	26.10	103.00	0.00	1.45	1.95	0.36	1.86	1.35	20.18	43.00
Genotypes: Location	69	7.00***	7.00***	0.17	274.80	123.00*	404.00***	0.87	0.61	0.47	4.57	22.92***	0.27	593.00***
Loc: Rep: Block	24	4.00	4.00	0.23	238.50	139.00*	123.00	3.93*	1.67**	0.56	13.70	0.45	15.47	29.00*
Residuals	124	3.00	4.00	0.28	195.00	80.00	103.00	2.39	0.70	1.11	11.17	0.39	18.34	16.00

Table 4 . List of genetic parameters for yield and yield attributing traits under study in maize (*Zea mays* L.) inbred lines at ARS, Peddapuram and WNC, ICAR- IIMR, Rajendranagar

Genetic Parameters	Days to 50% anthesis			Days to 50% silking			Anthesis silking interval (ASI)			Plant height (cm)			Ear height (cm)		
	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled
PCV	4.60	5.50	4.69	4.41	5.38	4.56	24.12	20.86	20.10	14.11	13.35	12.20	20.91	21.11	18.50
GCV	4.42	5.20	4.95	4.20	5.10	4.81	10.21	14.82	26.30	13.16	12.12	13.10	18.95	19.58	19.10
Heritability (broad sense)	92.40	89.60	89.70	90.90	89.90	89.60	17.90	50.50	58.50	86.90	82.40	86.90	82.10	86.00	85.10
Genetic advancement 5%	5.45	7.64	6.37	5.26	7.63	6.31	0.14	0.40	0.46	39.68	33.58	36.10	25.19	21.56	22.90
Gen.Adv as % of 5% Mean	8.76	10.14	9.15	8.26	9.96	8.88	8.91	21.68	31.70	25.27	22.65	23.40	35.38	37.41	35.20
General mean	62.24	75.32	69.56	63.75	76.67	71.00	1.51	1.84	1.45	157.04	148.24	154.06	71.21	57.63	64.92
Minimum	53.00	63.00	53.00	54.00	65.00	54.00	0.00	0.00	0.00	90.00	98.00	90.00	30.00	30.00	30.00
Maximum	69.00	86.00	86.00	70.00	87.00	87.00	3.00	2.00	3.00	225.00	203.00	225.00	110.00	90.00	110.00

Table 4 . List of genetic parameters for yield and yield attributing traits under study in maize (*Zea mays* L.) inbred lines at ARS, Peddapuram and WNC, ICAR- IIMR, Rajendranagar

Genetic Parameters	Days to 50% anthesis			Days to 50% silking			Anthesis silking interval (ASI)			Plant height (cm)			Ear height (cm)		
	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled
PCV	4.60	5.50	4.69	4.41	5.38	4.56	24.12	20.86	20.10	14.11	13.35	12.20	20.91	21.11	18.50
GCV	4.42	5.20	4.95	4.20	5.10	4.81	10.21	14.82	26.30	13.16	12.12	13.10	18.95	19.58	19.10
Heritability (broad sense)	92.40	89.60	89.70	90.90	89.90	89.60	17.90	50.50	58.50	86.90	82.40	86.90	82.10	86.00	85.10
Genetic advancement 5%	5.45	7.64	6.37	5.26	7.63	6.31	0.14	0.40	0.46	39.68	33.58	36.10	25.19	21.56	22.90
Gen.Adv as % of 5% Mean	8.76	10.14	9.15	8.26	9.96	8.88	8.91	21.68	31.70	25.27	22.65	23.40	35.38	37.41	35.20
General mean	62.24	75.32	69.56	63.75	76.67	71.00	1.51	1.84	1.45	157.04	148.24	154.06	71.21	57.63	64.92
Minimum	53.00	63.00	53.00	54.00	65.00	54.00	0.00	0.00	0.00	90.00	98.00	90.00	30.00	30.00	30.00
Maximum	69.00	86.00	86.00	70.00	87.00	87.00	3.00	2.00	3.00	225.00	203.00	225.00	110.00	90.00	110.00

Genetic Parameters	**Ear length (cm)**			**Ear girth (cm)**			**Days to maturity**			**No. of kernel rows per ear**		
	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled
PCV	15.22	13.89	13.80	10.38	9.17	9.04	2.46	3.72	5.35	8.16	6.88	6.84
GCV	13.15	12.01	14.90	8.94	8.47	9.74	2.34	3.52	7.08	6.74	5.36	7.69
Heritability (broad sense)	74.60	74.80	86.20	74.10	85.20	86.10	90.50	89.90	57.20	68.10	60.80	79.20
Genetic advancement 5%	3.01	2.72	3.40	1.93	1.87	2.07	5.45	7.63	12.70	1.50	1.11	1.64
Gen.Adv as % of 5% Mean	23.40	21.40	26.50	15.84	16.10	17.30	4.58	6.88	8.34	11.45	8.61	12.50
General mean	12.86	12.71	12.86	12.15	11.58	11.97	118.97	110.95	152.53	13.12	12.84	13.08
Minimum	6.00	7.67	6.00	7.33	9.00	7.30	109.00	100.00	109.00	10.00	10.00	10.00
Maximum	17.67	18.33	18.30	16.33	14.33	16.30	125.00	122.00	238.00	16.67	16.00	17.00
Genetic Parameters	**No. of kernels per row**			**100 kernel weight (g)**			**Shelling %**			**Grain yield per plant (g)**		
	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled	L1	L2	Pooled
PCV	18.16	18.31	17.30	24.44	25.91	22.00	6.09	6.29	6.12	39.14	38.66	31.70
GCV	15.38	17.26	18.40	24.40	25.85	22.80	5.15	5.45	6.52	38.94	38.45	33.80
Heritability (broad sense)	71.70	88.90	88.40	99.70	99.50	92.90	71.50	75.10	87.90	99.00	98.90	88.00
Genetic advancement 5%	6.54	8.01	8.17	11.67	11.99	10.10	6.90	7.33	9.08	55.75	41.22	37.70
Gen.Adv as % of 5% Mean	26.82	33.54	33.60	50.18	53.13	43.70	8.97	9.72	11.80	79.82	78.77	61.30
General mean	24.36	23.88	24.32	23.25	22.56	23.10	76.88	75.41	76.91	69.85	52.32	61.47
Minimum	11.00	12.00	11.00	9.00	13.00	9.00	57.07	58.07	57.10	22.00	20.00	20.00
Maximum	37.00	36.33	37.00	35.00	37.00	37.00	88.06	89.00	89.00	150.00	117.00	150.00

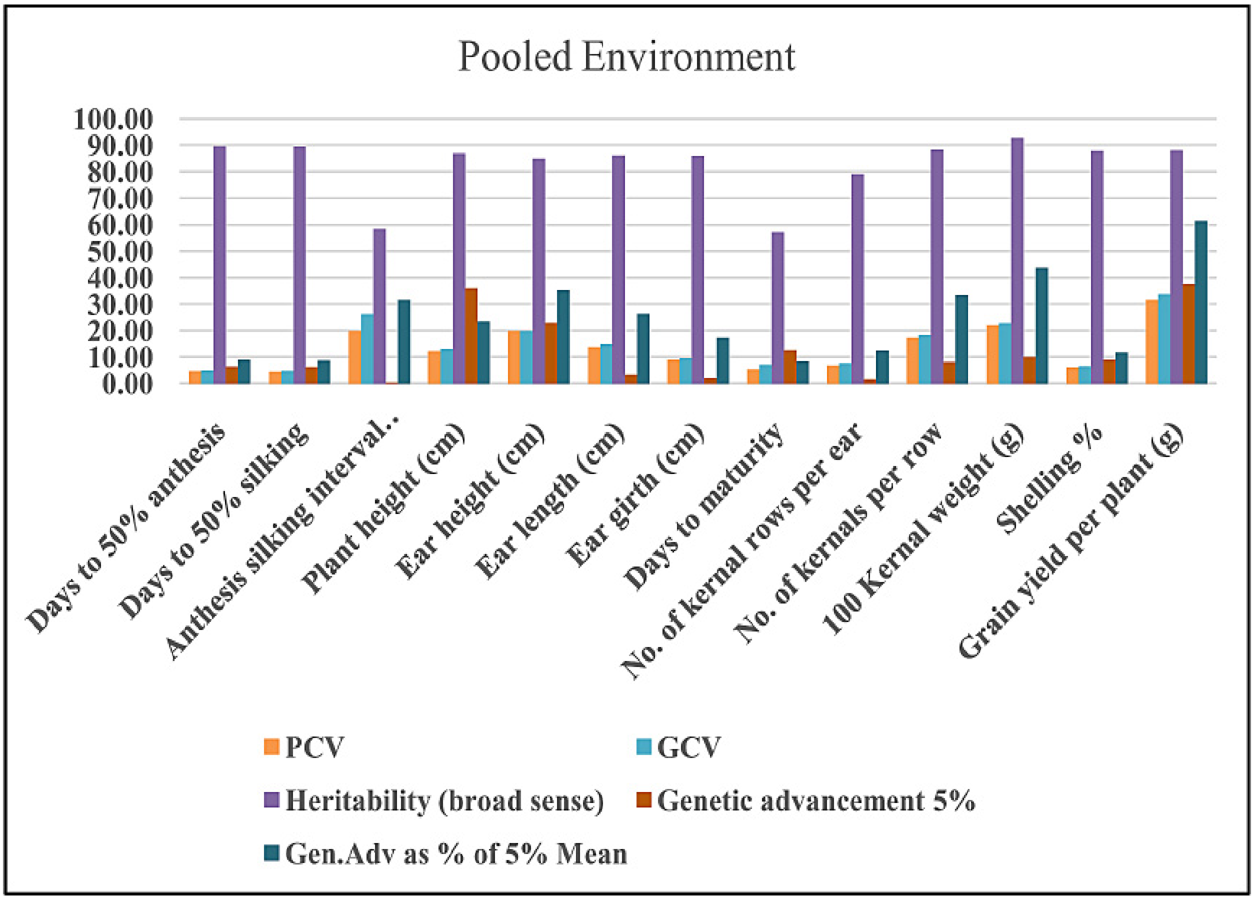

Fig.1. Bar diagram representing the genetic parameters in pooled environment of two locations ARS, Peddapuram and WNC, ICAR-IIMR, Rajendranagar

These results align with the findings of Gogoi *et al*. (2025), Sondarava *et al*. (2025), and other contemporary studies. Traits such as number of kernel rows per ear and shelling percentage exhibited high heritability but moderate genetic advance, suggesting that although these traits are genetically controlled, the response to selection may be moderate and influenced by both additive and non-additive gene effects. Conversely, traits such as days to 50% anthesis and days to 50% silking recorded high heritability but low genetic advance, indicating strong genetic control yet limited improvement potential through simple selection. The narrow GCV–PCV difference for these traits highlights a predominantly genetic influence, although non-additive gene effects may constrain the progress of direct phenotypic selection.

CONCLUSION

The evaluation of 70 maize inbred lines revealed substantial genetic variability for all yield and yield-contributing traits, providing a strong basis for effective parental selection in breeding programmes. The consistently higher genotypic variance over phenotypic variance across traits indicated that most characters were under strong genetic control with minimal environmental influence. High levels of variability observed for anthesis–silking interval, 100-kernel weight, and grain yield per plant highlight their potential for substantial genetic improvement. Moderate variability in plant height, ear height, ear length, and

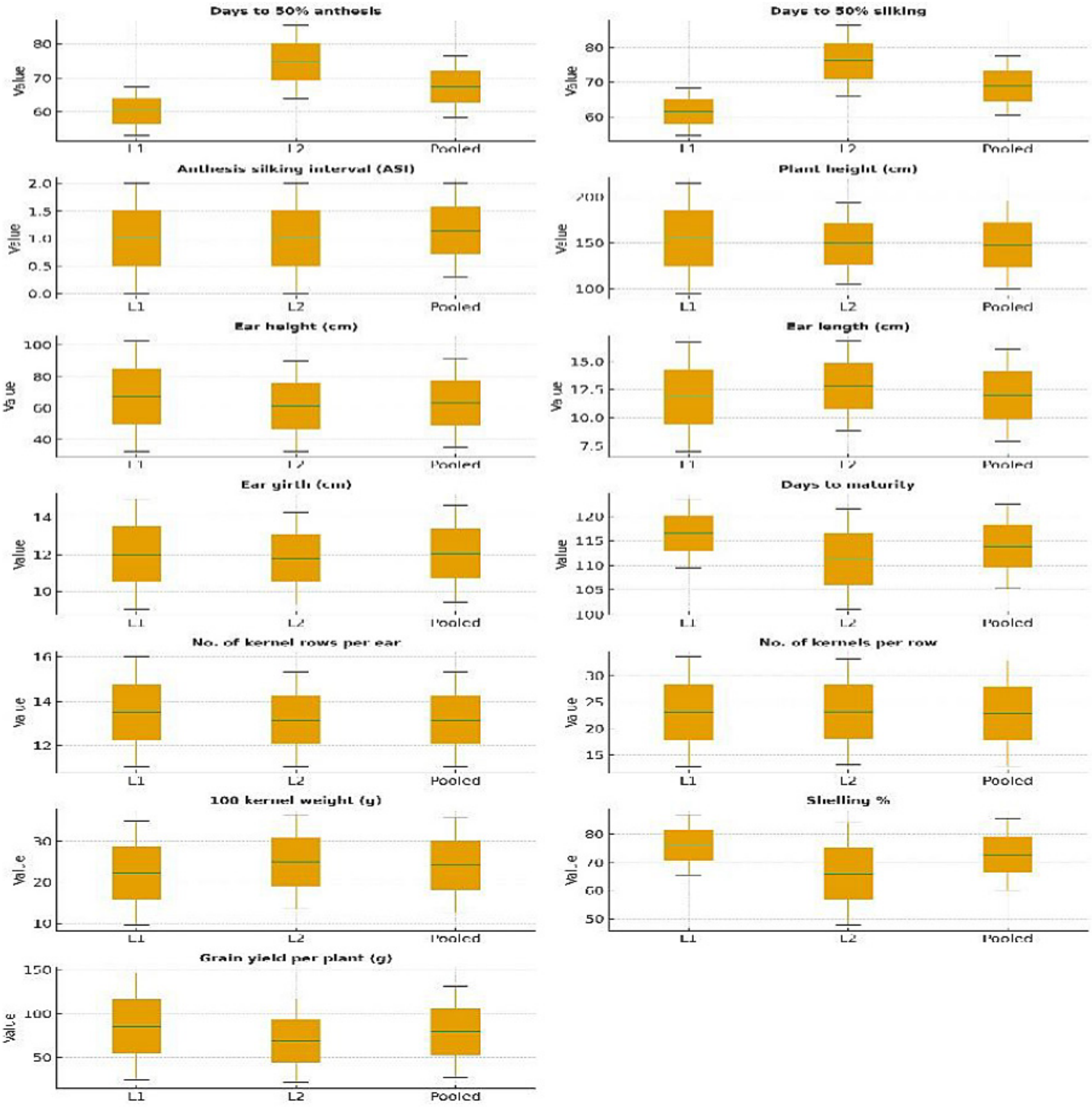

Fig. 2. Box and Whisker plot representation of PCV, GCV, Heritability and Genetic advance at 5% mean for 13 traits over two locations: ARS, Peddapuram and WNC, ICAR-IIMR, Rajendranagar and pooled environment.

number of kernels per row further supports their usefulness in selection programmes. Importantly, the combination of high heritability and high genetic advance for plant height, ear height, ear length, number of kernels per row, 100-kernel weight, and grain yield per plant suggests a predominance of additive gene action governing these traits. This indicates that direct phenotypic selection would be highly effective for improving these characters in subsequent breeding cycles. Overall, the identified inbred lines with favourable genetic attributes provide a valuable resource for strategic parent selection, facilitating the development of superior hybrids aimed at enhancing maize productivity.

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