



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(6): 631-636
Received: 19-04-2026
Accepted: 25-05-2026

Rama Kanth Reddy P
Department of Genetics and Plant
Breeding, College of Agriculture,
Rajendranagar, Professor
Jayashankar Telangana
Agricultural University,
Hyderabad, Telangana, India

MV Nagesh Kumar
Professor Jayashankar Telangana
Agricultural University,
Rajendranagar, Hyderabad,
Telangana, India

V Selvarangam
Pioneer Hi-Bred Pvt. Ltd., Multi-
Crop Research Center, Hyderabad,
Telangana, India

N Sunil
Winter Nursery Centre, ICAR-
Indian Institute of Maize Research,
Rajendranagar, Hyderabad,
Telangana, India

A Dhandapani
National Academy of Agricultural
Research Management,
Rajendranagar, Hyderabad,
Telangana, India

Corresponding Author:
Rama Kanth Reddy P
Department of Genetics and Plant
Breeding, College of Agriculture,
Rajendranagar, Professor
Jayashankar Telangana
Agricultural University,
Hyderabad, Telangana, India

Genetic variability and trait association among yield and related quantitative traits in Maize (*Zea mays* L.) testcross hybrids and parental lines

Rama Kanth Reddy P, MV Nagesh Kumar, V Selvarangam, N Sunil and A Dhandapani

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i6h.5759>

Abstract

The present study was conducted to assess genetic variability, heritability and trait associations among 100 maize (*Zea mays* L.) genotypes comprising 64 testcross hybrids, 34 parental lines and two checks. The experiment was laid out in a randomized complete block design with two replications during Kharif 2023. Analysis of variance revealed significant differences among genotypes for all twelve traits, indicating the presence of substantial genetic variability. Grain yield per hectare ranged from 2.07 to 13.46 t ha⁻¹ with a mean of 8.14 t ha⁻¹. Phenotypic variance was generally higher than genotypic variance for all traits, although the differences were relatively small, suggesting limited environmental influence on trait expression. The highest genotypic and phenotypic coefficients of variation were observed for grain yield per hectare (39.23 and 39.95%), followed by ear height (25.63 and 29.16%) and number of kernels per row (24.23 and 26.49%). High heritability coupled with high genetic advance as percent of mean was recorded for grain yield per hectare (76.42% and 62.90%), number of kernels per row (83.67% and 45.66%), ear height (77.25% and 46.40%), plant height (83.19% and 36.84%) and cob length (82.17% and 35.56%), indicating the importance of additive gene action. Grain yield per hectare showed strong positive correlations with cob length (0.89), number of kernels per row (0.85), cob girth (0.83), plant height (0.81), test weight (0.67) and kernel rows per cob (0.61). The study identified cob length, cob girth, number of kernels per row, kernel rows per cob and test weight as important traits for indirect selection towards yield improvement in maize.

Keywords: Genetic variability, heritability, correlation, maize, testcross hybrids

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops cultivated worldwide and serves as a major source of food, feed, fodder and industrial raw material. Owing to its remarkable adaptability, high yield potential and diverse end uses, maize is often referred to as the “Queen of Cereals.” Globally, maize is cultivated across a wide range of agro-climatic conditions and plays a crucial role in ensuring food and nutritional security. In addition to human consumption, a substantial proportion of maize production is utilized in the livestock and poultry sectors, while its industrial applications include the manufacture of starch, ethanol, corn oil, sweeteners and various value-added products. According to FAOSTAT (2023) [6], maize is grown in more than 160 countries with a global production exceeding 1.2 billion tonnes. In India, maize ranks third after rice and wheat among cereal crops and occupies an area of about 10.04 million hectares with an average productivity of 3.35 t ha⁻¹ (Agricoop, 2023–24).

The growing demand for maize driven by population expansion, rapid urbanization, increasing livestock production and industrial utilization necessitates continuous improvement in productivity. Since the scope for increasing cultivated area is limited, enhancement of grain yield through genetic improvement remains one of the most effective approaches to meet future demand. Hybrid breeding has played a pivotal role in increasing maize productivity worldwide by exploiting heterosis and combining favorable alleles from diverse parental lines. The success of any breeding programme largely depends on the availability and utilization of sufficient genetic variability within the breeding material.

Assessment of genetic variability is therefore an essential prerequisite for the development of superior cultivars and hybrids. The magnitude of variability present in a population determines the effectiveness of selection and the potential for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide valuable information regarding the extent of variability available for selection. However, variability alone is not sufficient to predict the response to selection. Estimates of heritability and genetic advance help breeders understand the proportion of variation that is heritable and the expected improvement achievable through selection (Dudly and Moll, 1969). High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and suggests that selection based on phenotypic performance can be highly effective (Nwangburuka *et al.*, 2012) [11].

Grain yield is a complex quantitative trait governed by several component characters and influenced by environmental factors. Therefore, direct selection for yield alone may not always be effective. Understanding the relationships among yield and its contributing traits through correlation analysis provides an opportunity to identify key characters that can be used as indirect selection criteria. Traits exhibiting strong and positive associations with grain yield can be targeted in breeding programmes to improve selection efficiency and accelerate genetic gain.

The evaluation of hybrids and their parental lines provide valuable insights into the expression of yield and related traits, helping breeders identify superior combinations and important yield determinants. In the present investigation, 100 maize genotypes comprising 64 testcross hybrids, 34 parental lines and 2 commercial checks were evaluated to assess the extent of genetic variability, heritability, genetic advance and trait associations for grain yield and its related characters. The study was undertaken to identify important yield-contributing traits and generate information useful for the development of high-yielding maize hybrids suitable for future breeding programmes.

Material and Methods

The material for the present study comprised of 100 maize genotypes, which include in 64 maize testcross hybrids along with 34 parents and two checks. These genotypes were evaluated in randomized complete block design (RCBD) with two replications during *khari*, 2023 at Maize Research Centre, Rajendranagar. Each entry was raised in two rows of four-meter length with a spacing of 60 cm × 20 cm and following all the recommended package of practices. The observations were recorded from each genotype for twelve quantitative traits viz., days to 50 per cent tasseling (DTT), days to 50 per cent silking (DTS), anthesis-silking interval (ASI), leaf angle (LA), plant height (PH) (cm), ear height (EH) (cm), cob length (CL) (cm), cob girth (CG) (cm), kernel row number (KRN), number of kernels per row (NKPR), hundred grain weight (TW) (g), shelling percentage (SP) and grain yield per hectare (GYPHA) (t/ha). The mean values of the data from these genotypes were subjected to analysis of variance (ANOVA) using variability package (Popat *et al.* 2020) [13] in R-studio Rx643.6.2 and ANOVA was tested for significance. Genotypic and phenotypic variances were determined according to Singh and Chaudhary (1985) [15] using MS-Excel programme. The genotypic coefficient of variation and phenotypic coefficient of variation were computed according to Burton and De vane (1953) [3] using the following formula.

$$GCV = \sqrt{\sigma^2_g} / \bar{X} \times 100$$

$$PCV = \sqrt{\sigma^2_p} / \bar{X} \times 100$$

Where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance and $\bar{X}$ = sample mean. The GCV and PCV were classified according to Sivasubramanian and Menon (1973) [16] as low (less than 10%), moderate (10-20%) and high (more than 20%). Heritability in broad sense (h^2_{bs}) was computed for each character as the ratio of genotypic variance to the total variance as suggested by Hanson *et al.* (1956) [7].

$$\text{Heritability broad sense } (h^2_{bs}) = \frac{\sigma^2_g}{\sigma^2_p}$$

Where, σ^2_g = genotypic variance and σ^2_p = phenotypic variance. It was categorized by Robinson *et al.* (1951) [14] as low (less than 0.30), moderate (0.31 – 0.60) and high (more than 0.60). Genetic advance and genetic advance as percent of mean were estimated according to Johnson *et al.* (1955) [9] using the following formula,

$$GA = i \times h^2_{bs} \times \sigma_p$$

Where, i = 2.06 (selection intensity at 5%), σ_p = Phenotypic standard deviation, h^2_{bs} = Heritability in broad sense.

$$\text{Genetic advance as per cent of mean (GAM)} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

The GAM is grouped as low (less than 10%), moderate (10-20%) and high (more than 20%) respectively, according to Johnson *et al.* (1955) [9]. Karl Pearson's simple correlation coefficients for all the eleven characters were worked out using variability package (Popat *et al.* 2020) [13] and the heatmap of the correlation was made using function *corrplot* in R-studio Rx643.6.2.

Results

The analysis of variance revealed highly significant differences among the 100 maize genotypes for all the twelve quantitative traits studied, indicating the presence of substantial genetic variability within the experimental material (Table 1). The significant genotypic mean squares observed for all traits suggest that the germplasm possesses adequate variability for effective selection and further genetic improvement. Particularly large genotypic mean squares were recorded for plant height (1777.40), ear height (541.85), number of kernels per row (121.12), test weight (63.61) and grain yield per hectare (20.79), indicating considerable divergence among genotypes for these economically important traits. Such significant variation among genotypes forms the basis for successful selection and breeding programmes aimed at yield enhancement in maize.

A wide range of variation was observed for all the traits under study, indicating the existence of substantial phenotypic diversity among the evaluated maize genotypes. Grain yield per hectare varied from 2.07 to 13.46 t ha⁻¹ with a mean value of 8.14 t ha⁻¹ (Table 1). Similarly, considerable variation was observed for flowering traits, plant architecture traits, cob traits and yield-contributing characters. The phenotypic variance was generally higher than the corresponding genotypic variance for all traits, suggesting some degree of environmental influence on trait expression (Table 2). However, the differences between phenotypic and genotypic variances were relatively narrow for

most characters, indicating that the observed variability was predominantly genetic in nature.

Among the traits studied, grain yield per hectare exhibited the highest genotypic coefficient of variation (39.23%) and phenotypic coefficient of variation (39.95%), followed by ear height (25.63% and 29.16%), number of kernels per row (24.23% and 26.49%), plant height (19.61% and 21.50%) and cob length (19.04% and 21.00%) (Table 2). Moderate GCV and PCV values were observed for test weight and cob girth, whereas comparatively lower estimates were recorded for flowering traits, shelling percentage, leaf angle and kernel rows per cob. The relatively higher GCV and PCV estimates for grain yield and major yield-contributing traits indicate the existence of sufficient exploitable variability and greater scope for improvement through selection.

Broad-sense heritability estimates ranged from 36.30% for shelling percentage to 83.67% for number of kernels per row (Table 2). High heritability estimates were recorded for number of kernels per row (83.67%), plant height (83.19%), cob length (82.17%), ear height (77.25%) and grain yield per hectare (76.42%), indicating that the expression of these traits was largely governed by genetic factors. Moderate heritability estimates were observed for days to 50% tasseling, days to 50% silking, cob girth and kernel rows per cob, whereas comparatively lower values were observed for shelling percentage, test weight and leaf angle.

Genetic advance expressed as percentage of mean ranged from 4.66% for shelling percentage to 62.90% for grain yield per hectare (Table 2). High genetic advance as percent of mean was recorded for grain yield per hectare (62.90%), ear height (46.40%), number of kernels per row (45.66%), plant height (36.84%) and cob length (35.56%). Moderate genetic advance was observed for test weight, cob girth and kernel rows per cob, while lower estimates were recorded for flowering traits, shelling percentage and leaf angle. The combination of high heritability and high genetic advance for grain yield per hectare, ear height, number of kernels per row, plant height and cob length suggests the predominance of additive gene action and indicates that improvement through direct phenotypic selection would be effective for these traits.

The correlation analysis revealed several significant associations among grain yield and its component traits (Fig. 1). Grain yield per hectare exhibited strong and highly significant positive correlations with cob length ($r = 0.89$), number of kernels per row ($r = 0.85$), cob girth ($r = 0.83$), plant height ($r = 0.81$), ear height ($r = 0.68$), test weight ($r = 0.67$) and kernel rows per cob ($r = 0.61$). These associations indicate that improvement in these component traits is likely to contribute positively towards grain yield enhancement.

Among the yield-contributing traits, cob length showed strong positive associations with number of kernels per row ($r = 0.92$), cob girth ($r = 0.81$), plant height ($r = 0.82$), ear height ($r = 0.73$), test weight ($r = 0.63$) and grain yield per hectare ($r = 0.89$). Cob girth was positively associated with number of kernels per row ($r = 0.81$), kernel rows per cob ($r = 0.70$), test weight ($r = 0.65$) and grain yield per hectare ($r = 0.83$). Likewise, number of kernels per row exhibited significant positive relationships with cob length, cob girth, kernel rows per cob, test weight and grain yield.

Plant height and ear height displayed a strong positive association ($r = 0.88$), indicating that taller plants generally possessed higher ear placement. Flowering traits, namely days to 50% tasseling and days to 50% silking, showed highly significant positive correlation with each other ($r = 0.96$),

reflecting the synchronized nature of flowering in maize. However, both flowering traits exhibited significant negative correlations with grain yield per hectare, suggesting that earlier flowering genotypes tended to be more productive under the experimental conditions. Shelling percentage also showed a negative association with several yield-contributing traits and grain yield. Overall, the correlation analysis identified cob length, cob girth, number of kernels per row, kernel rows per cob and test weight as major contributors to grain yield improvement.

The comparative distribution analysis between the 64 testcross hybrids and the parental lines revealed clear differences in the expression of agronomic and yield-related traits (Fig. 2). Hybrids generally exhibited superior performance for plant height, ear height, cob length, cob girth, kernel rows per cob, number of kernels per row and grain yield per hectare compared to the parental lines. The higher median values and wider distribution observed in hybrids for these traits reflect the manifestation of heterosis and enhanced genetic complementation.

Conversely, parental lines tended to exhibit higher values for flowering duration and shelling percentage. The most pronounced difference was observed for grain yield per hectare, where hybrids substantially outperformed the parental lines, confirming the effectiveness of hybrid breeding in exploiting heterosis for yield enhancement. Similar trends were also evident for major yield-contributing traits such as cob length, cob girth and number of kernels per row, further emphasizing their importance in determining hybrid performance. The comparative boxplot analysis clearly demonstrates the superiority of hybrids over their parental lines for yield and related attributes and validates the usefulness of the testcross breeding approach in maize improvement.

Discussion

The highly significant differences observed among genotypes for all twelve quantitative traits indicate the existence of substantial genetic variability in the experimental material, which is a prerequisite for effective selection and genetic improvement. Similar observations of significant genetic variation among maize genotypes have been reported by Magar *et al.* (2021) ^[10], Antony *et al.* (2024) ^[2] and Suresh *et al.* (2021) ^[17]. The presence of considerable variability among hybrids, parental lines and checks suggests that the germplasm evaluated in the present study offers ample opportunities for identifying superior genotypes and developing high-yielding hybrids.

The magnitude of genotypic and phenotypic coefficients of variation provides valuable information regarding the extent of variability available for selection. The high GCV and PCV observed for grain yield per hectare, ear height, number of kernels per row, plant height and cob length indicate substantial genetic variability for these traits. The relatively narrow differences between GCV and PCV for most characters suggest limited environmental influence on their expression, thereby increasing the effectiveness of phenotypic selection. Similar findings were reported by Jilo *et al.* (2018) ^[8], Wedwessen and Zeleke (2020) ^[19] and Magar *et al.* (2021) ^[10], who observed high variability for grain yield and major yield components in maize.

Heritability estimates alone do not provide a complete picture of the inheritance of a trait; therefore, they should be interpreted together with genetic advance. In the present investigation, grain yield per hectare, ear height, number of kernels per row, plant height and cob length exhibited high heritability coupled with

high genetic advance as percent of mean. This combination suggests that additive gene effects play a major role in the inheritance of these traits and that substantial improvement can be achieved through direct selection. Similar conclusions were drawn by Wali, (2019) ^[18] and Wedwessen and Zeleke (2020) ^[19], who reported that traits exhibiting high heritability and high genetic advance are predominantly governed by additive genetic effects and respond effectively to selection.

The correlation analysis provided valuable insights into the relationships among yield and its component traits. Grain yield per hectare exhibited strong positive associations with cob length, number of kernels per row, cob girth, plant height, test weight and kernel rows per cob. These relationships suggest that improvement in these component traits is likely to result in a corresponding increase in grain yield. The exceptionally high positive association between cob length and number of kernels per row further indicates that longer cobs facilitate greater kernel development, thereby contributing directly to yield enhancement. Similar positive relationships among grain yield, cob traits and kernel traits have been reported by Pavan *et al.* (2011) ^[12], Devasree *et al.* (2020) ^[4], Magar *et al.* (2021) ^[10] and Antony *et al.* (2024) ^[2].

The significant negative correlations observed between flowering traits and grain yield indicate that early flowering genotypes tended to produce higher yields under the experimental conditions. Early flowering is often advantageous because it enables efficient utilization of available resources and helps plants escape terminal stress conditions. Therefore, selection for moderate earliness combined with superior yield-contributing traits could be beneficial in maize breeding programmes.

The comparative analysis between hybrids and parental lines clearly demonstrated the superiority of hybrids for grain yield and most yield-contributing traits. The enhanced performance of hybrids for plant height, ear height, cob length, cob girth, kernel rows per cob and number of kernels per row reflects the successful exploitation of heterosis and favorable gene interactions. The substantially higher grain yield observed in hybrids confirms the effectiveness of hybrid breeding in maize and highlights the importance of selecting parents with superior combining ability for developing productive hybrids. These findings are consistent with the fundamental principles of heterosis breeding and support the continued use of hybrid development as a major strategy for maize yield improvement.

Table 1: Analysis of variance for twelve quantitative traits in 100 maize (*Zea mays* L.) genotypes

Parameters	df	Traits											
		DTT	DTS	PH	EH	LA	CL	CG	KRN	NKPR	TW	SP	GYPHA
Replication	1	7.22	11.04*	139.72	787.38	684.5	0.5	0.11	1.62	34.72	0.5	1032.4	0.22
Genotype	99	11.48**	13.34**	1777.40**	541.85**	82.86**	17.65**	0.56**	3.2**	121.12**	63.61**	32.79**	20.79**
Error	99	1.99	2.74	163.07	69.53	69.76	1.73	0.1	0.95	10.77	25.71	15.32	0.38
Mean		62	63	144.87	59.96	53.12	14.82	3.92	13.46	30.65	27.15	78.58	8.14
CV (%)		2.29	2.63	8.81	13.9	10.27	8.87	8.28	7.25	10.71	18.68	4.98	7.55

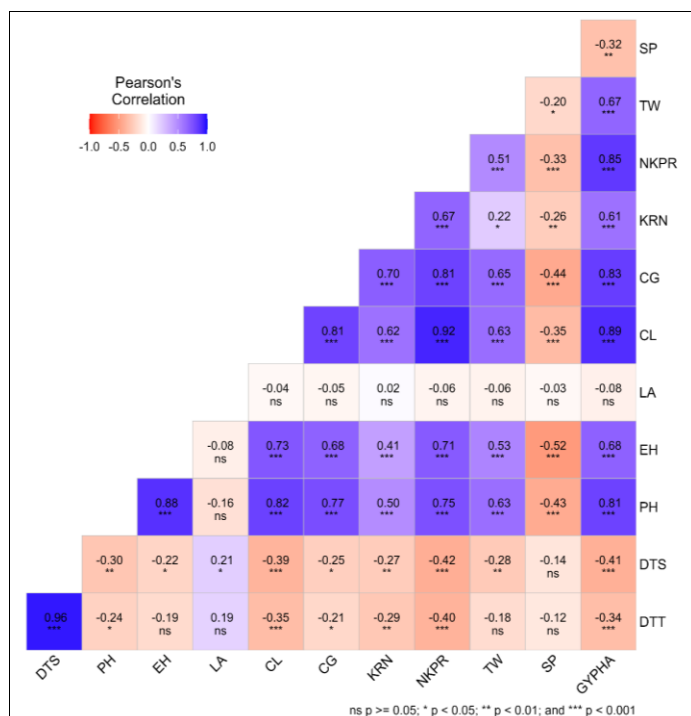
* – Significant at 5% and ** – Significant at 1% level of probability.

CV – Coefficient of variance, DTT – Days to 50% tasseling, DTS – Days to 50% silking, ASI – Anthesis-silking interval, LA – Leaf angle, PH – Plant height (cm), EH – Ear height (cm), CL – Cob length (cm), CG – Cob girth (cm), KRN – Kernel rows per cob, NKPR- Number of kernels per row, TW – Test weight (g), SP – Shelling percentage (%), GYPHA – Grain yield per hectare (t/ha).

Table 2: Genetic variability parameters of twelve quantitative traits among 100 maize (*Zea mays* L.) genotypes

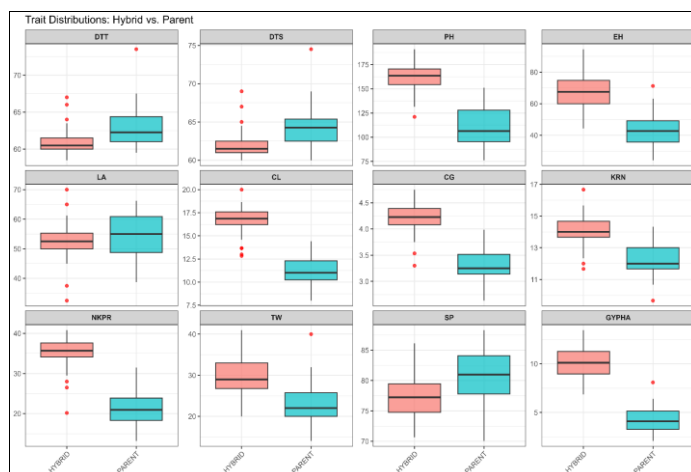
Trait	Range		Variance (%)		Coefficient of variance (%)		Heritability in broad sense (H^2_{bs}) (%)	Genetic advance (%) mean
	Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic		
DTT	58	73	4.74	6.74	3.53	4.21	70.35	6.1
DTS	60	74	5.3	8.04	3.65	4.5	65.9	6.11
PH	76.25	109.83	807.16	970.23	19.61	21.5	83.19	36.84
EH	24.25	94.5	236.16	305.69	25.63	29.16	77.25	46.4
LA	32.5	70	26.55	56.31	9.7	14.12	47.14	13.72
CL	8	20	7.96	9.69	19.04	21	82.17	35.56
CG	2.63	4.82	0.23	0.33	12.22	14.76	68.5	20.83
KRN	9.67	16.67	1.12	2.07	7.88	10.7	54.17	11.94
NKPR	13.17	40.83	55.18	65.95	24.23	26.49	83.67	45.66
TW	14	41	18.95	44.66	16.03	24.61	42.43	21.51
SP	70.04	88.31	8.73	24.06	3.76	6.24	36.3	4.66
GYPHA	2.07	13.46	10.21	10.58	39.23	39.95	76.42	62.90

DTT – Days to 50% tasseling, DTS – Days to 50% silking, ASI – Anthesis-silking interval, LA – Leaf angle, PH – Plant height (cm), EH – Ear height (cm), CL – Cob length (cm), CG – Cob girth (cm), KRN – Kernel rows per cob, NKPR- Number of kernels per row, TW – Test weight (g), SP – Shelling percentage (%), GYPHA – Grain yield per hectare (t/ha).



DTT – Days to 50% tasseling, DTS – Days to 50% silking, ASI – Anthesis-silking interval, LA – Leaf angle, PH – Plant height (cm), EH – Ear height (cm), CL – Cob length (cm), CG – Cob girth (cm), KRN – Kernel rows per cob, NKPR- Number of kernels per row, TW – Test weight (g), SP – Shelling percentage (%), GYPHA – Grain yield per hectare (t/ha).

Fig 1: Association among grain yield and its quantitative traits in 100 maize (*Zea mays* L.) genotypes



DTT – Days to 50% tasseling, DTS – Days to 50% silking, ASI – Anthesis-silking interval, LA – Leaf angle, PH – Plant height (cm), EH – Ear height (cm), CL – Cob length (cm), CG – Cob girth (cm), KRN – Kernel rows per cob, NKPR- Number of kernels per row, TW – Test weight (g), SP – Shelling percentage (%), GYPHA – Grain yield per hectare (t/ha)

Fig 2: Box-plots showing variation in yield and its component traits between test cross hybrids and parental lines

Conclusion

The present investigation revealed substantial genetic variability among the 100 maize genotypes comprising testcross hybrids, parental lines and checks for all twelve quantitative traits studied. High genotypic and phenotypic variability, coupled with high heritability and high genetic advance, were observed for grain yield per hectare, ear height, number of kernels per row, plant height and cob length, indicating the predominance of

additive gene action and the effectiveness of direct phenotypic selection for these traits. Correlation analysis identified cob length, number of kernels per row, cob girth, kernel rows per cob and test weight as major yield-contributing traits owing to their strong positive associations with grain yield. The comparative distribution analysis further demonstrated the superiority of hybrids over parental lines for grain yield and most yield-related attributes, highlighting the successful exploitation of heterosis in the testcross population. Therefore, selection based on cob length, cob girth, number of kernels per row, kernel rows per cob and test weight, along with grain yield, would be highly effective for developing superior maize hybrids. The identified variability and trait associations provide valuable information for future maize breeding programmes aimed at enhancing productivity and developing high-yielding hybrids adapted to diverse growing environments.

Acknowledgement

The authors acknowledge the support of Maize Research Centre, Rajendranagar, PJTAU for providing all the logistic support in conduct of the experiment, and IIMR- Winter Nursery Centre and CIMMYT for providing the genetic material under study.

References

1. Department of Agriculture and Farmers Welfare. Annual Report 2023–24. India Crop Coverage Report. New Delhi: Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare, Government of India; 2024. <https://www.agricoop.nic.in>
2. Antony BJ, Kachapur RM, Naidu GK, Talekar SC, Zerka M, Harlapur SI. Genetic variability and character association among maize (*Zea mays* L.) inbred lines. Bangladesh Journal of Botany. 2024;53(1):57-65.
3. Burton GW, Devane EM. Estimating heritability in tall fescue from replicated clonal material. Agronomy Journal. 1953;45:478-481.
4. Devasree S, Ganesan KN, Ravikesavan R, Senthil N, Paranidharan V. Relationship between yield and its component traits for enhancing grain yield in single cross hybrids of maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2020;11:796-802.
5. Dudley JW, Moll RH. Interpretation and use of estimates of heritability and genetic variance in plant breeding. Crop Science. 1969;9:257-267.
6. Food and Agriculture Organization. FAOSTAT: Crops and Livestock Products. Rome: FAO; 2023. <https://www.fao.org/faostat/en/#data/QCL>
7. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agronomy Journal. 1956;48:268-272.
8. Jilo T, Tulu L, Birhan T, Beksisa L. Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia. Journal of Plant Breeding and Crop Science. 2018;10:281-289.
9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47:314-318.
10. Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhyaya J, Shrestha J. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon. 2021;7:e07939.
11. Nwangburuka CC, Denton OA, Kehinde OB, Ojo DK, Popoola AR. Genetic variability and heritability in

- cultivated okra (*Abelmoschus esculentus* (L.) Moench). Spanish Journal of Agricultural Research. 2012;10:123-129.
12. Pavan R, Lohithaswa HC, Wali MC, Prakash G, Shekara BG. Correlation and path coefficient analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2011;2:253-257.
 13. Popat R, Patel R, Parmer D. Variability: genetic variability analysis for plant breeding research. 2020. <https://CRAN.R-project.org/package=variability>
 14. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlations in corn and their implications in selection. Agronomy Journal. 1951;43:282-287.
 15. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. New Delhi: Kalyani Publishers; 1985. p. 318.
 16. Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agricultural Journal. 1973;60:1139.
 17. Suresh D, Kachapur RM, Talekar SC, Gurumurthy R. Genetic variability and trait association studies in maize (*Zea mays* L.). Journal of Farm Sciences. 2021;34:122-125.
 18. Wali MC. Genetic variability and divergence studies in maize (*Zea mays* L.). EC Agriculture. 2019;5:2014-2015.
 19. Wedwessen T, Zeleke H. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. International Journal of Novel Research in Life Sciences. 2020;7:10-16.