



Unlocking Genetic Variability for Yield Enhancement in Popcorn (*Zea mays* var. *everta*)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

The present investigation assessed genetic variability and estimated key genetic parameters for yield, yield-attributing, and popping quality traits in popcorn (*Zea mays* var. *everta*) genotypes. Forty-four popcorn genotypes, comprising 42 hybrids and two checks, were evaluated during the maize Rabi season from November 2025 to April 2026 at the Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India. The experiment was laid out in a randomised complete block design with three replications. Data were collected for 13 traits, namely days to 50% anthesis, days to 50% silking, days to maturity, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight, grain yield per plant, popping expansion volume, and popping percentage. Analysis of variance revealed significant genotypic differences for all traits, indicating exploitable variability within the evaluated material.

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The phenotypic coefficient of variation exceeded the genotypic coefficient of variation for all traits, suggesting environmental influence on trait expression. Popping expansion volume showed the highest phenotypic and genotypic coefficients of variation, with values of 21.96% and 21.55%, respectively, whereas days to 50% silking showed the lowest variability. Broad-sense heritability ranged from 32.17% for days to 50% anthesis to 96.32% for popping expansion volume. Genetic advance as per cent of mean ranged from 1.96% to 43.57%. High heritability coupled with high genetic advance for popping expansion volume and ear girth indicates that these traits may respond effectively to selection in popcorn improvement programmes.

Keywords: Popcorn; popping expansion volume; variability; heritability; genotypic coefficient of variation; phenotypic coefficient of variation.

1. Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops globally because of its high productivity, wide adaptability, and diverse applications in food, feed, and industrial sectors. It plays a crucial role in global agri-food systems and is essential for ensuring food and nutritional security in the face of increasing demand for agricultural products (Erenstein et al., 2022). According to the Unified Portal for Agricultural Statistics (UPAg, 2025-2026), maize is cultivated in India over an area of 14.41 million hectares, producing 55.09 million tonnes with an average productivity of 3824 kg/ha. Recent work on maize under water-stress conditions has also demonstrated that environmental constraints can markedly influence plant growth and productivity, reinforcing the need to distinguish genetic variability from environmental effects during trait evaluation (Nassif et al., 2025).

Popcorn (*Zea mays* var. *everta*) is a speciality type of maize cultivated exclusively for human consumption and is distinguished by its unique popping ability. The growing popularity of ready-to-eat snacks, coupled with increasing consumer preference for healthier food products, has substantially expanded the global popcorn market. However, despite its commercial importance, genetic improvement in popcorn remains constrained by a relatively narrow genetic base and limited utilisation of diverse germplasm resources (Gopinath et al., 2024). Recent popcorn studies have further shown that morphological and genetic characterisation of local and breeding germplasm can reveal useful diversity for conservation and breeding (Lezzi et al., 2025).

The development of high-yielding popcorn hybrids with superior popping quality requires the identification and exploitation of genetic variability present within breeding materials. Genetic variability serves as the foundation of crop improvement, providing opportunities for the selection of desirable genotypes and the development of superior cultivars. The effectiveness of selection largely depends on the magnitude of heritable variation available for economically important traits. Assessment of genetic variability through quantitative genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance provides valuable information on the nature and extent of variation present in a population. While GCV and PCV indicate the degree of genetic and environmental influence on trait expression, heritability estimates the proportion of phenotypic variation attributable to genetic factors. Genetic advance, when considered together with heritability, helps predict the effectiveness of selection and the expected genetic gain in subsequent generations (Saritha et al., 2024). Combining-ability studies in popcorn have identified parental lines and hybrid combinations differing in grain yield and popping volume, indicating that targeted evaluation of breeding materials is necessary for hybrid development (Divya et al., 2024; Oloruntoba et al., 2025). Selection-based improvement studies have also reported gains for yield and popping expansion in popcorn populations, supporting the use of quantitative genetic parameters to guide breeding decisions (Zermeno-Campos et al., 2024).

Although recent studies have described genetic diversity, combining ability, and selection response in popcorn germplasm, limited information is available on the magnitude of heritable variation for yield-attributing and popping quality traits in the popcorn hybrids evaluated under the present experimental conditions.

In popcorn, grain yield and popping quality are complex traits influenced by several morphological and agronomic characters. Therefore, understanding the magnitude of variability and inheritance of these traits is essential for identifying promising genotypes and formulating efficient breeding strategies. The objective of the present investigation was to assess genetic variability, heritability, and genetic advance for yield and yield-related traits in popcorn hybrids.

2. Materials and Methods

2.1 Experimental Site and Design

The experimental site is located at 16°20' N latitude and 80°26' E longitude, at an altitude of 31.5 metres above mean sea level. The experimental material comprised 42 hybrids and two checks (VL Amber and Jawahar). Each genotype was sown in four rows of 4 m length, maintaining a spacing of 60 cm between rows and 20 cm between plants, resulting in a plot area of 9.6 m². Recommended agronomic practices were followed throughout the growing season to ensure optimum crop growth and development.

2.2 Collection of Data

Data were collected for the following traits: days to 50% anthesis, days to 50% silking, days to maturity, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows, number of kernels per row, grain yield (g/plant), hundred-kernel weight (g), popping expansion volume (ml/g), and popping percentage (%). Five inner plants were randomly selected and tagged from each plot to record observations for all quantitative traits, while days to 50% anthesis, days to 50% silking, and days to maturity were recorded on a plot basis. For each entry in each replication, the mean value of the five selected plants was calculated for each trait and used for statistical analysis.

2.3 Statistical Analysis

Analysis was carried out in the R programme using the variability package (R Core Team, 2025).

2.3.1 Analysis of Variance

Analysis of variance was performed to partition the total variation into variation due to treatments and replications, following the procedure outlined by Panse and Sukhatme (1967), for all the characters.

2.3.2 Phenotypic and Genotypic Coefficient of Variation

The genotypic and phenotypic coefficients of variation were computed according to Falconer (1996) and expressed as percentages.

$$GCV = \frac{(\sigma G)}{(\bar{x})} \times 100$$

$$PCV = \frac{(\sigma P)}{(\bar{x})} \times 100$$

2.3.3 Heritability in Broad Sense

Heritability in broad sense was computed using the formula described by Allard (1999) and expressed as a percentage.

$$\text{Heritability} = \frac{(\sigma G)}{(\sigma P)} \times 100$$

2.3.4 Genetic Advance as per cent of Mean (GAM)

Genetic advance as per cent of mean was computed using the formula described by Allard (1999) and expressed as a percentage.

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2_{(bs)}$$

K: Selection differential at 5% selection intensity (2.06); h^2_{bs} : heritability in broad sense; σ_p : Phenotypic standard deviation.

$$GAM = \frac{\text{Genetic Advance}}{\text{Grand mean}} \times 100$$

3. Results and Discussion

3.1 Analysis of variance

The mean sum of squares due to genotypes showed significant differences for all characters (Table 1), indicating the presence of substantial genetic variability among the genotypes. Similar results were reported by Kharel et al. (2017) and Reddy et al. (2024).

3.2 Phenotypic and Genotypic Coefficients of Variation

For all traits, PCV values were higher than the corresponding GCV values, indicating the influence of environmental factors on trait expression. However, the relatively narrow differences between PCV and GCV for some traits suggest a greater role of genetic factors in their inheritance (Table 2). Popping expansion volume was estimated to have high PCV and GCV values (21.96 and 21.55, respectively). Moderate PCV and GCV values were recorded for ear girth (15.33 and 14.03, respectively) and popping percentage (14.05 and 11.60, respectively). Similarly, low PCV and GCV values were estimated for ear height (9.96 and 7.26, respectively), ear length (9.05 and 7.20, respectively), plant height (8.21 and 5.63, respectively), days to maturity (4.83 and 4.42, respectively), days to 50% anthesis (2.96 and 1.68, respectively), and days to 50% silking (2.65 and 1.81, respectively). The remaining traits showed moderate PCV and low GCV, namely kernel rows per ear (14.15 and 9.74, respectively), hundred-kernel weight (11.25 and 9.22, respectively), and kernels per row (10.91 and 8.92, respectively). Grain yield per plant (20.91 and 15.90, respectively) recorded high PCV and moderate GCV, as reported earlier by Khan and Mahmud (2021). Similar findings were reported for days to 50% anthesis by Aman et al. (2020); days to 50% silking by Reddy et al. (2024); days to maturity and plant height by Veeravishnu et al. (2023); ear height by Magar et al. (2021); ear length and ear girth by Kumar et al. (2024); popping expansion volume, popping percentage, and number of kernels per row by Banjara et al. (2025); and number of kernel rows per ear and hundred-kernel weight by Jagadeesh et al. (2022).

3.3 Heritability

Heritability is a measure of the proportion of total phenotypic variation that is attributable to genetic factors and reflects the extent to which a trait is transmitted from parents to offspring (Lush, 1940). Low (0-30%), moderate (30-60%), and high (greater than 60%) heritability estimates were grouped according to the classification system recommended by Johnson et al. (1955). In the present investigation, the heritability estimates (Figure 1 and Table 2) were high for popping expansion volume (96.32%), ear girth (83.77%), days to maturity (83.65%), popping percentage (68.08%), hundred-kernel weight (67.26%), kernels per row (66.84%), and ear length (63.19%). High heritability offers better opportunities for selecting plant material with desirable characteristics, as trait expression is predominantly controlled by genetic factors. Moderate estimates of heritability were recorded for grain yield per plant (57.84%), ear height (53.23%), number of kernel rows per ear (47.37%), plant height (46.96%), days to 50% silking (46.56%), and days to 50% anthesis (32.17%). In the present study, broad-sense heritability estimates were computed, which include both additive and non-additive gene effects. High broad-sense heritability indicates that a large proportion of the observed variation is genetic in origin, although it does not distinguish between additive and non-additive genetic effects. Similar results have been reported for days to 50% anthesis and days to 50% silking by Gopinath et al. (2024); plant height by Damtie et al. (2021); ear height by Pradhan et al. (2022); popping expansion volume, popping percentage, and ear length by Banjara et al. (2025); days to maturity by Veeravishnu et al. (2023); ear girth and hundred-kernel weight by Khan and Mahmud (2021); kernel rows per ear by Jagadeesh et al. (2022); and grain yield by Jilo et al. (2018).

3.4 Genetic Advance

Heritability alone does not indicate the extent of genetic improvement that may be achieved through the selection of individual genotypes. Therefore, estimates of genetic advance in conjunction with heritability are more informative. Traits with high heritability do not necessarily exhibit a correspondingly high genetic advance. Genetic advance as a percentage of the mean was grouped as low (less than 10%), moderate (10-20%), and high (greater than 20%), according to the classification system recommended by Johnson et al. (1955). High genetic advance (Figure 1) was recorded for popping expansion volume (43.57%), grain yield (24.91%), and ear girth (26.46%). Similar findings were reported by Tesfaye et al. (2021) for grain yield and by Reddy et al. (2022) for ear girth. Expected genetic advance as per cent of mean indicates the mode of gene action in the

expression of a trait, which helps in choosing an appropriate breeding method. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and greater effectiveness of selection. In the present study, this pattern was observed for popping expansion volume and ear girth, suggesting that these traits can be improved through selection and progeny-selection approaches. However, when non-additive gene action controls a trait, it may result in high heritability but poor genetic advance. Days to 50% silking, days to 50% anthesis, and plant height exhibited moderate heritability with low genetic advance, while kernel rows per ear and ear height showed moderate heritability and genetic advance (Table 2). Days to maturity, ear length, kernels per row, hundred-kernel weight, and popping percentage exhibited high heritability coupled with low to moderate genetic advance. Grain yield exhibited moderate heritability coupled with high genetic advance, suggesting the involvement of additive gene effects along with environmental influence and indicating good prospects for improvement through selection. These results suggest the involvement of both additive and non-additive gene effects for most traits, whereas grain yield may respond effectively to selection.

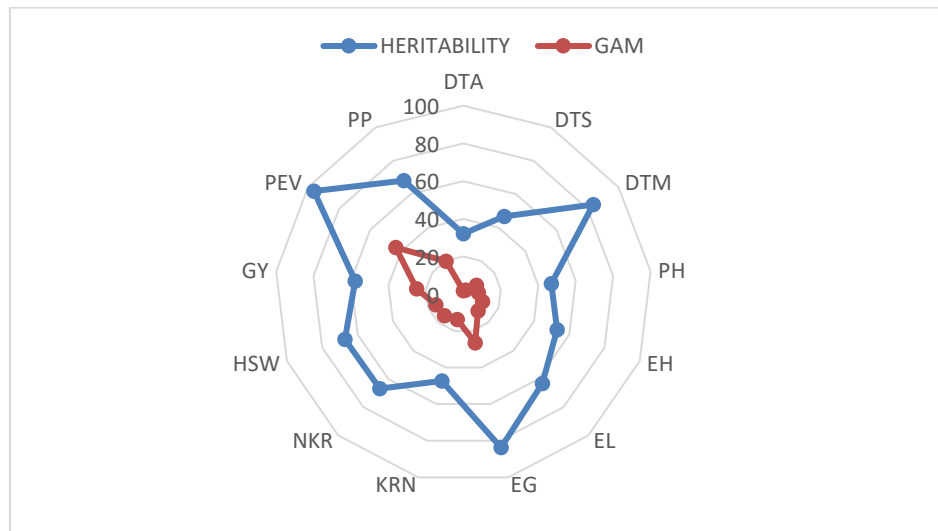


Fig. 1. Spider plot depicting the heritability and GAM for different traits in popcorn
 DTA: Days to 50% anthesis; DTS: Days to 50% silking; DTM: Days to maturity; PH: Plant height (cm); EH: Ear height (cm); EL: Ear length (cm); EG: Ear girth (cm); KRN: kernel rows per ear (no.); NKR: kernels per row (no.); HSW: 100-kernel weight (g); GY: Grain yield per plant (g); PEV: Popping expansion volume (ml/g) and PP: Popping percentage (%); GAM: Expected genetic advance as per cent of mean.

Table 1. Analysis of variance for 13 traits in popcorn hybrids.

S. No	Character	Replication (df: 2)	Treatment (df: 43)	Error (df: 86)
1	Days to 50% anthesis	0.23	3.16**	1.43
2	Days to 50% silking	1.52	3.36**	1.03
3	Days to maturity	0.04	124.95**	4.96
4	Plant height (cm)	100.57	443.52**	126.35
5	Ear height (cm)	4.14	208.49**	41.14
6	Ear length (cm)	0.72	7.28**	1.28
7	Ear girth (cm)	0.26	9.75**	0.61
8	Kernel rows per ear (no.)	0.94	8.88**	2.20
9	Kernels per row (no.)	12.15	49.80**	6.55
10	100-kernel weight (g)	0.07	8.38**	1.18
11	Grain yield per plant (g)	121.59	414.51**	76.05
12	Popping expansion volume(ml/g)	0.02	46.39**	0.53
13	Popping percentage	5.92	339.46**	44.27

***: 0.1% level of significance; df: Degrees of freedom.

Table 2. Estimation of variability parameters for 13 traits in popcorn hybrids

S. No	Character	PCV	GCV	H2(bs)	GA	GAM
1	DTA	2.96	1.68	32.17	0.94	1.96
2	DTS	2.65	1.81	46.56	1.29	2.54
3	DTM	4.83	4.42	83.65	9.48	8.33
4	PH	8.21	5.63	46.96	14.35	7.95
5	EH	9.96	7.26	53.23	11.06	10.92
6	EL	9.05	7.20	63.19	2.37	11.78
7	EG	15.33	14.03	83.77	3.37	26.46
8	KRN	14.15	9.74	47.37	2.04	13.81
9	NKR	10.91	8.92	66.84	6.19	15.02
10	HKW	11.25	9.22	67.26	2.65	15.58
11	GY	20.91	15.90	57.84	16.38	24.91
12	PEV	21.96	21.55	96.32	7.15	43.57
13	PP	14.05	11.60	68.08	16.82	19.71

DTA: Days to 50% anthesis; DTS: Days to 50% silking; DTM: Days to maturity; PH: Plant height (cm); EH: Ear height (cm); EL: Ear length (cm); EG: Ear girth(cm); KRN: kernel rows per ear (no.); NKR: kernels per row (no.); HKW:100-kernel weight (g); GY: Grain yield per plant (g); PEV: Popping expansion volume (ml/g) and PP: Popping percentage (%).

4. Conclusion

The study demonstrated substantial genetic variability among the 44 popcorn genotypes assessed for yield, yield-related attributes, and popping quality traits. Analysis of variance revealed significant differences among the genotypes for all 13 traits, indicating adequate variability for effective selection. For all traits, the phenotypic coefficient of variation exceeded the genotypic coefficient of variation, suggesting that environmental factors influenced trait expression to varying extents. Popping expansion volume exhibited the highest phenotypic and genotypic variability, while days to 50% anthesis and days to 50% silking showed comparatively low variability. High broad-sense heritability was recorded for popping expansion volume, ear girth, days to maturity, popping percentage, 100-kernel weight, kernels per row, and ear length. Among these traits, popping expansion volume and ear girth also showed high genetic advance as per cent of mean, indicating better prospects for improvement through selection. Grain yield per plant showed moderate heritability with high genetic advance, suggesting that selection may also be useful for yield improvement, although environmental influence should be considered.

5. Limitations

The study was conducted at one location during a single cropping season; therefore, genotype performance across environments could not be assessed. The use of broad-sense heritability estimates limits interpretation of the precise contribution of additive, dominance, and epistatic gene effects. The study also did not include molecular marker analysis or multi-environment validation. Further testing across locations and seasons would strengthen the identification of stable, superior popcorn genotypes.

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Declaration of AI Use

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contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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