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Genetic variability, heritability, and genetic advance for yield and yield-yield related traits in maize (*Zea mays* L.)

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Abstract

Maize (*Zea mays* L.) is one of the most important cereal crops worldwide, serving as a staple food, animal feed, and raw material for industries. Improving maize yield is essential to meet rising global food demand, and knowledge of genetic variability, heritability, and genetic advance of yield-contributing traits is crucial for effective breeding. In this study, 40 maize inbred lines along with two commercial check varieties were evaluated in a randomized block design with two replications during the *Kharif* season of 2024 at R. K. Nagar Farm, Kolhapur, under the All India Coordinated Research Project (AICRP) on Maize. Analysis of variance revealed significant differences among genotypes for all 13 traits studied, indicating ample genetic variability. Grain yield per plant, cob weight exhibited high genotypic and phenotypic coefficients of variation. High heritability coupled with high genetic advance as percent of mean was observed for grain yield per plant (h^2 = 95.5%, GAM = 60.37%), cob weight (h^2 = 96.1%, GAM = 54.42%), and number of kernel rows per cob (h^2 = 89.4%, GAM = 28.12%), suggesting predominance of additive gene action. These traits are therefore promising for effective selection and genetic improvement. The results provide valuable insights for maize breeders in developing high-yielding varieties.

Keywords: Genetic variability, heritability, genetic advance, maize, yield traits

Introduction

Maize (*Zea mays* L.) is a major cereal crop of global significance, ranking third after wheat and rice in terms of both cultivation area and total production (FAO, 2021) [10]. It is widely grown across diverse agro-ecological regions due to its adaptability and high yield potential. In addition to its role as a staple food, maize is extensively used as animal feed and as a raw material in numerous industrial applications, including starch production, ethanol, and biodegradable plastics (Shiferaw *et al.*, 2011) [25]. Given the increasing global population and growing demand for food and industrial products, enhancing maize productivity through genetic improvement is an essential priority for breeding programs worldwide.

The foundation of any successful crop improvement program lies in the availability and effective utilization of genetic variability within the breeding material. The extent of this variability determines the potential for selecting superior genotypes. Quantitative genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2), and genetic advance (GA) offer important insights into the genetic architecture of traits and the likelihood of achieving genetic gain through selection (Burton, 1952; Johnson *et al.*, 1955) [7, 15]. High heritability coupled with high genetic advance is generally indicative of additive gene effects and suggests that selection can be effective for improving those traits (Falconer & Mackay, 1996) [9].

Numerous studies have reported significant variability in maize for traits related to yield, including cob length, kernel row number, thousand-kernel weight, and grain yield per plant (Ali *et al.*, 2022; Mishra *et al.*, 2023; Kumar *et al.*, 2025) [3, 21, 16]. However, the degree of genetic variability and its heritable components can vary depending on the germplasm used and the environmental conditions under which the genotypes are evaluated (Bello *et al.*, 2012; Gowda *et al.*, 2020) [5, 12].

Therefore, continuous assessment of variability and heritability across different growing environments is essential for the identification of promising genotypes and the formulation of effective breeding strategies.

In light of these considerations, the present study was undertaken with the following objectives:

1. To assess the extent of genetic variability for yield and related traits in maize.
2. To estimate heritability and genetic advance to facilitate effective selection and improvement of key agronomic traits.

Materials and Methods

The experimental material comprised 40 maize inbred lines and two check varieties (DKC-9144 and PKC-02), sourced from the AICRP on Maize, R. K. Nagar Farm, Kolhapur. The experiment was conducted during *Kharif* 2024 in a randomized block design (RBD) with two replications. The details of all the genotypes and check varieties used in the study are presented in Table1.

Traits studied: Days to 50% tasseling, days to 50% silking, plant height, cob height, cob length, cob diameter, number of kernel rows per cob, number of kernels per row, cob weight, 100-kernel weight, protein content, starch content, and grain yield per plant.

Statistical analysis

- Analysis of variance (ANOVA) was carried out as per Panse and Sukhatme (1985) [23].
- Genotypic and phenotypic variances were estimated following Lush (1940) [18].
- GCV and PCV were computed using Burton and Devane (1953) [8].
- Broad-sense heritability was estimated using the method of Hanson *et al.* (1956) [13].
- Genetic advance and GAM were calculated as suggested by Johnson *et al.* (1955) [15].

Results and Discussion

The analysis of variance for 13 traits, as shown in Table 2, revealed that the mean sum of squares due to genotypic differences was highly significant for all traits studied. This indicates a substantial level of variability among the 40 inbred lines and 2 check varieties. The mean values of 40 inbreds and 2 checks for 13 characters studied are presented in Table 3.

A) GCV and PCV

The estimates of genotypic coefficient of variation were lower than phenotypic coefficient of variation for all the characters under this study. Highest phenotypic coefficient of variation was exhibited by grain yield per plant (30.67) followed by cob weight (27.48) and medium PCV was observed for Number of kernel rows per cob (15.27), 100 kernel weight (13.01), Cob diameter (11.91), Cob length (11.18), Protein (11.14) and Number of kernels per row (11.07). The lowest phenotypic coefficient of variation was observed for Cob height (8.13), Plant height (7.83), Days to 50 percent tasseling (7.83), Days to 50 percent silking (7.30) and Starch (3.79). Genotypic coefficient of variation (GCV) reflects the inherent genetic variability among traits. The highest GCV was recorded for grain yield per plant (29.98) followed by cob weight (26.94) and medium GCV was observed for Number of kernel rows per cob (14.43), 100 kernel weight (12.06), Cob diameter (11.23), Protein (10.55), Cob length (10.35). The lowest genotypic coefficient of variation was observed for Number of kernels per row (9.73), Days to 50 percent tasseling (7.75), Days to 50 percent silking (7.15), Cob height (6.66), Plant height (6.38) and Starch (3.60), suggesting relatively lower genetic variability for these traits.

In this study, genotypic coefficient of variation (GCV) values were found to be lower than the corresponding phenotypic coefficient of variation (PCV) values, suggesting that environmental factors significantly influenced the expression of these traits. As is typical for quantitative traits, environmental effects were considerable. However, traits such as grain yield per plant and cob weight, which exhibited high GCV and PCV values, appear promising for selection. Additionally, traits like number of kernel rows per cob, 100-kernel weight, cob diameter, protein content, and cob length, which showed moderate GCV and PCV values, may also serve as reliable indicators of genetic potential due to their consistent phenotypic expression. Similar patterns were observed by Magar *et al.* (2021) [20] and Mishra *et al.* (2023) [21], who reported high estimates of both genotypic and phenotypic coefficients of variation (GCV and PCV) for grain yield per plant. Likewise, Kumar *et al.* (2025) [16] also reported high GCV and PCV values for grain yield per plant and cob weight, indicating substantial genetic variability. In support of this, Bhadru *et al.* (2020) [6] observed moderate levels of GCV and PCV for cob length, while Rafiq *et al.* (2010) [24] reported moderate variability for 100-kernel weight and cob diameter. In contrast, Belay (2018) [4] found that traits such as days to 50% anthesis, days to 50% silking, and plant height exhibited low GCV and PCV values, suggesting limited genetic variation and greater environmental influence on these traits.

B) Heritability (h^2 b.s)

The heritability (b.s.) obtained in present investigation was of high magnitude for all the characters. Broad-sense heritability estimates were high (>60%) for all traits, ranging from 66.4% (plant height) to 98.1% (days to 50% tasseling). Highest estimate of heritability was recorded for Days to 50 percent tasseling (98.10%) followed by Days to 50 percent silking (96.10%), Cob weight (96.10%), Grain yield per plant (95.50%), Starch (90.10%), Protein (89.70%), Number of kernel rows per cob (89.40%), Cob diameter (88.90%), 100 kernel weight (85.90%), Cob length (85.60%), Number of kernels per row (77.20%), Cob height (67.00%), Plant height (66.40%). The findings of the current study are supported by the results of Ali *et al.* (2022) [3], who observed similar heritability values for cob length, number of kernels per row, and plant height. Likewise, Noor *et al.* (2018) [22] reported comparable broad-sense heritability estimates for days to 50% tasseling and silking. In another study, Mahmood *et al.* (2004) [19] recorded the highest heritability for grain yield per plant and plant height, along with a substantial genetic advance. These results suggest that these traits are predominantly controlled by additive genetic factors, highlighting the potential for rapid genetic gains through selection. Comparable findings were reported by Wannows *et al.* (2010) [28], who observed highest heritability in traits such as number of kernels per row, number of rows per cob, as well as cob length and width. Similarly, Bhadru *et al.* (2020) [6] also found high heritability in ear height, plant height, number of kernels per row, and grain yield per plant. Overall, the traits evaluated in the present study demonstrated high broad-sense heritability, indicating a strong genetic basis with minimal environmental influence. This suggests that these traits are promising targets for genetic enhancement through selection. These outcomes are further supported by Ghosh *et al*. (2014) [11], who emphasized that traits with high heritability are mainly governed by genetic factors and can be effectively utilized in breeding programs.

C) Genetic advance (GA)

Estimates of genetic advance were ranged from 0.95 to 63.39 Highest estimate of genetic advance was recorded for cob weight (63.39) followed by grain yield per plant (58.39), plant height (17.97), Days to 50 percent tasseling (7.55), Cob height (7.55), Days to 50 percent silking (7.37), 100 kernel weight (5.22), Number of kernels per row (4.98), Starch (4.41), Number of kernel rows per cob (3.73), Cob length (3.20),protein (1.67) and cob diameter (0.95).The results of the current investigation regarding genetic advance are consistent with previous studies that emphasize the considerable potential for genetic improvement across various traits in maize. Cob weight exhibited the highest genetic advance, aligning with the findings of Ali Q *et al*. (2015) [2], who reported that this trait showed high genetic advance along with heritability, implying a strong influence of additive genetic factors. Grain yield per plant showed a high genetic advance, highlighting its potential for improvement through direct selection, while traits such as days to 50 percent tasseling, days to 50 percent silking, ear length, number of kernel rows per cob, number of kernels per row, and 100-grain weight exhibited low genetic advance. These findings are consistent with the observations reported by Mahmood *et al*. (2004) [19]. The low genetic advance recorded for days to 50 percent tasseling and days to 50 percent silking is consistent with the findings of Bello *et al*. (2012) [5]. Comparable results were also reported by Lad *et al*. (2018) for days to 50 percent tasseling, 50 percent silking, 100-kernel weight, and protein content. As noted by Ghosh *et al*. (2014) [11], assessing genetic advance is useful for understanding the nature of gene action governing the expression of polygenic traits. High genetic advance typically suggests the involvement of additive gene action, whereas low genetic advance points toward non-additive gene action.

D) Genetic advancement as percent of mean (GAM)

Highest estimates of genetic advance as percent of mean were observed for grain yield per plant (60.37) followed by cob weight (54.42), number of kernel rows per cob (28.12), 100 kernel weight (23.01), cob diameter (21.81), protein (20.59), cob length (19.73), number of kernels per row (17.61), days to 50 percent tasseling (15.82), days to 50 percent silking (14.44), cob height (11.23), plant height (10.71) and starch (7.04). Mishra *et al*. (2023) [21] reported similar trends, with high genetic advance as a percentage of the mean observed for traits like grain yield per plant and protein content. Moderate genetic advance was noted for cob diameter, number of kernel rows per cob, number of kernels per row, 100-kernel weight, days to 50 percent tasseling, days to 50 percent silking, and plant height. These findings are consistent with those of Sravanti *et al*. (2017) [27], who observed that ear height and grain yield per plant demonstrated high heritability along with substantial genetic advance, indicating the influence of additive gene action. Such traits are promising targets for direct selection to enhance yield effectively. These results align with those of Singh *et al*. (2020) [26], who found high genetic advance as percent of mean for traits such as ear length, ear height, and grain yield. Jilo *et al*., (2018) [14] and Ahmed *et al*., (2020) [1] reported high genetic advance for ear length and thousand kernel weight. In the present study, high heritability combined with high genetic advance was recorded for grain yield per plant, cob weight, number of kernel rows per cob, and 100-kernel weight, indicating that these traits are primarily controlled by additive gene action and can be effectively improved through selection.

Table 3.1: List of maize genotypes employed in the present investigation

Sr. No.	Inbreds/Genotypes	Sr. No.	Inbreds/Genotypes
1.	AH23R-005-0063	22.	AH23R-005-0035
2.	AH23R-005-0012	23.	AH23R-005-0005
3.	AH23R-005-0024	24.	AH23R-005-0071
4.	AH23R-005-0041	25.	AH23R-005-0058
5.	AH23R-005-0009	26.	AH23R-005-0049
6.	AH23R-005-0021	27.	AH23R-005-0036
7.	AH23R-005-0007	28.	AH23R-005-0066
8.	AH23R-005-0073	29.	AH23R-005-0032
9.	AH23R-005-0040	30.	AH23R-005-0064
10.	AH23R-005-0018	31.	AH23R-005-0046
11.	AH23R-005-0045	32.	AH23R-005-0054
12.	AH23R-005-0067	33.	AH23R-005-0059
13.	AH23R-005-0016	34.	AH23R-005-0039
14.	AH23R-005-0002	35.	AH23R-005-0074
15.	AH23R-005-0025	36.	AH23R-005-0056
16.	AH23R-005-0031	37.	AH23R-005-0019
17.	AH23R-005-0068	38.	AH23R-005-0055
18.	AH23R-005-0065	39.	AH23R-005-0001
19.	AH23R-005-0057	40.	AH23R-005-0026
20.	AH23R-005-0060	41.	DKC-9144
21.	AH23R-005-0072	42.	PKC-02

Table 2: Analysis of variance for different characters in Maize (*Zea mays* L.)

Sr. No.	Character	Mean sum of square		
		Replication df = 1	Treatment df = 41	Error df=41
1	Days to 50 percent tasseling	0.43	27.90^{**}	0.53
2	Days to 50 percent silking	3.44	27.69^{**}	1.07
3	Plant height (cm)	457.33	345.30^{**}	116.11
4	Cob height (cm)	65.19	59.74^{**}	19.70
5	Cob length (cm)	0.57	6.58^{**}	0.95
6	Cob diameter (cm)	0.04	0.54^{**}	0.06
7	Number of kernel rows per cob	2.33	8.20^{**}	0.87
8	Number of kernels per row	5.76	19.61^{**}	4.47
9	Cob weight (g)	11.45	2049.14^{**}	79.32
10	100 kernel weight (g)	0.05	17.44^{**}	2.46
11	Protein (%)	0.49	1.63^{**}	0.17
12	Starch (%)	1.94	11.30^{**}	1.11
13	Grain yield per plant (g)	0.98	1760.31^{**}	78.52

*,** significant at 5% and 1% respectively

Table 3: Mean performance of 42 genotypes (40 inbreds and 2 checks) for 13 characters in maize.

Sr. No.	Genotypes/Inbreds	Days to 50 percent tasseling	Days to 50 percent silking	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob diameter (cm)	Number of kernel rows per cob	Number of kernels per row	Cob weight (g)	100 kernel weight (g)	Grain yield per plant (g)	Protein (%)	Starch (%)
1	AH23R-005-0063	47	50	195.00	78.00	18.85	5.00	15.00	31	129.21	21.05	109.00	7.45	65.85
2	AH23R-005-0012	44	47	158.50	63.50	15.05	3.88	12.00	28	91.63	19.60	72.88	8.90	60.17
3	AH23R-005-0024	44	47	183.00	73.50	17.00	4.38	13.00	29	152.67	30.46	135.93	7.73	63.43
4	AH23R-005-0041	44	46	177.50	71.00	19.25	5.20	16.00	33	114.40	20.37	94.25	7.30	64.47
5	AH23R-005-0009	45	47	143.50	57.50	17.00	4.53	15.00	30	122.34	20.05	101.82	7.45	64.51
6	AH23R-005-0021	47	51	155.50	62.00	16.25	4.39	13.00	29	121.76	22.13	94.55	8.10	63.06
7	AH23R-005-0007	50	54	178.50	71.00	16.40	4.43	14.00	30	140.15	23.65	120.69	7.47	65.08
8	AH23R-005-0073	48	51	160.00	64.00	19.75	5.34	18.00	35	195.03	25.50	173.77	6.30	67.75
9	AH23R-005-0040	44	46	162.50	65.00	16.75	4.53	14.00	31	102.65	19.83	80.87	8.25	62.33
10	AH23R-005-0018	43	45	161.50	64.50	15.25	4.12	13.00	27	105.56	25.79	86.65	8.65	61.30
11	AH23R-005-0045	46	48	153.00	61.50	19.15	5.45	18.00	35	201.73	29.12	173.59	8.05	63.34
12	AH23R-005-0067	42	46	167.50	67.00	14.15	3.82	11.00	28	116.06	26.56	94.98	8.55	62.23
13	AH23R-005-0016	44	47	172.00	69.00	15.90	4.30	13.00	30	116.88	24.17	98.88	5.90	66.96
14	AH23R-005-0002	43	50	169.50	67.50	17.30	4.67	15.00	31	120.78	21.05	100.00	7.53	64.25
15	AH23R-005-0025	46	50	171.50	68.50	13.65	3.69	12.00	23	74.19	19.60	54.50	9.04	60.60
16	AH23R-005-0031	47	51	172.50	69.00	15.40	4.16	13.00	29	132.88	26.49	112.90	7.39	64.81
17	AH23R-005-0068	48	52	163.00	65.50	14.95	4.04	12.00	26	88.31	20.85	66.47	8.70	61.51
18	AH23R-005-0065	45	48	177.50	71.00	18.70	5.05	14.00	33	154.39	23.68	136.90	6.50	64.72
19	AH23R-005-0057	52	55	174.00	70.00	14.90	4.03	11.00	28	126.88	25.60	107.93	8.75	63.63
20	AH23R-005-0060	45	49	160.00	64.00	15.70	4.24	14.00	28	91.65	19.88	83.09	8.89	59.89
21	AH23R-005-0072	47	51	158.00	63.00	14.05	3.79	10.00	22	137.87	29.19	115.85	7.00	64.02
22	AH23R-005-0035	51	54	161.50	64.50	14.55	3.93	12.00	26	100.03	21.85	79.75	8.25	63.86
23	AH23R-005-0005	44	48	155.00	62.00	16.75	4.53	13.00	29	68.77	19.84	69.95	7.82	60.57
24	AH23R-005-0071	52	56	160.00	64.00	14.75	3.99	11.00	26	75.33	23.34	78.75	9.02	60.90
25	AH23R-005-0058	51	54	197.50	79.00	15.90	4.30	13.00	27	111.91	23.02	90.60	7.83	63.44
26	AH23R-005-0049	52	56	150.00	60.00	13.85	3.74	10.00	24	77.58	20.70	58.30	9.90	59.16
27	AH23R-005-0036	50	53	165.50	66.50	15.45	4.17	13.00	28	124.42	21.60	107.50	7.35	65.40
28	AH23R-005-0066	51	54	165.00	66.00	14.80	4.00	12.00	21	73.57	20.73	57.15	9.68	57.95
29	AH23R-005-0032	50	52	170.00	68.00	16.65	4.50	14.00	28	130.20	25.41	111.80	7.24	64.48
30	AH23R-005-0064	49	52	169.50	68.00	14.95	4.04	12.00	26	98.25	21.33	77.75	8.61	62.60
31	AH23R-005-0046	46	49	151.50	60.50	16.60	4.48	13.00	32	93.53	18.10	73.74	8.91	60.69
32	AH23R-005-0054	50	53	166.00	66.50	17.35	4.69	15.00	29	86.13	19.57	65.97	7.92	62.95
33	AH23R-005-0059	46	48	150.50	60.00	18.95	5.12	16.00	30	83.29	18.88	59.90	8.90	61.07
34	AH23R-005-0039	52	56	170.50	68.00	20.05	5.42	16.00	28	114.10	22.06	92.95	8.67	61.20
35	AH23R-005-0074	56	58	182.00	73.00	15.45	4.19	12.00	29	133.37	24.89	113.20	7.37	63.12
36	AH23R-005-0056	56	58	152.50	61.00	13.62	3.29	9.00	24	92.27	22.61	71.05	9.65	57.93
37	AH23R-005-0019	52	55	159.50	64.00	14.50	3.92	12.00	28	118.67	23.04	98.20	8.75	62.41
38	AH23R-005-0055	51	54	156.00	62.50	13.50	3.65	11.00	26	90.72	20.91	70.30	8.03	59.05
39	AH23R-005-0001	48	52	182.50	73.00	15.00	3.86	12.00	29	92.47	20.27	68.75	8.93	59.56
40	AH23R-005-0026	56	56	180.50	72.00	16.50	4.46	14.00	31	149.20	21.34	105.55	7.17	63.28
41	DKC-9144	46	48	198.50	79.00	18.75	4.76	15.00	31	159.53	25.03	141.90	8.00	65.54
42	PKC-02	53	57	186.00	79.50	17.60	5.00	16.00	31	181.76	24.35	153.85	8.75	65.89
	Minimum	42.00	45.00	143.50	57.50	13.50	3.29	9.00	21.00	68.77	18.10	54.50	5.90	57.93
	Maximum	56.00	58.00	198.50	79.50	20.05	5.45	18.00	35.00	201.73	30.46	173.77	9.90	67.75
	Mean	47.74	51.01	167.71	67.21	16.21	4.36	13.26	28.29	116.48	22.70	96.72	8.11	62.73
	C.V. (%)	1.52	2.03	6.43	6.60	6.00	5.62	7.03	7.47	7.65	6.92	9.16	5.06	1.68
	S.E.±	0.51	0.73	7.62	3.14	0.69	0.17	0.66	1.49	6.30	1.11	6.27	0.29	0.75
	C.D. (5%)	1.46	2.09	21.76	8.96	1.96	0.49	1.88	4.27	17.99	3.17	17.90	0.83	2.13

Table 4: Estimates genetic variability parameters for 13 traits evaluated across 42 maize genotypes, including 40 inbred lines and 2 check varieties.

Sr. No.	Character	Mean	Range	GCV	PCV	Heritability% (b.s)	Genetic advance	G.A. as percent of mean
1	Days to 50 percent tasseling	47.74	42.00-56.00	7.75	7.83	98.10	7.55	15.82
2	Days to 50 percent silking	51.01	45.00-58.00	7.15	7.30	96.10	7.37	14.44
3	Plant height (cm)	167.71	143.50-198.50	6.38	7.83	66.40	17.97	10.71
4	Cob height (cm)	67.21	57.50-79.50	6.66	8.13	67.00	7.55	11.23
5	Cob length (cm)	16.21	13.50-20.05	10.35	11.18	85.60	3.20	19.73
6	Cob diameter (cm)	4.36	3.29-5.45	11.23	11.91	88.90	0.95	21.81
7	Number of kernel rows per cob	13.26	9.00-18.00	14.44	15.27	89.40	3.73	28.12
8	Number of kernels per row	28.29	21.00-35.00	9.73	11.07	77.20	4.98	17.61
9	Cob weight (g)	116.48	68.77-201.73	26.94	27.48	96.10	63.39	54.42
10	100 kernel weight (g)	22.70	18.10-30.46	12.06	13.01	85.90	5.22	23.01
11	Protein (%)	8.11	5.90-9.90	10.55	11.14	89.70	1.67	20.59
12	Starch (%)	62.73	57.93-67.75	3.60	3.79	90.10	4.41	7.04
13	Grain yield per plant (g)	96.72	54.50-173.77	29.98	30.67	95.50	58.39	60.37

Scoring for GCV, PCV, GA and GAM: Low <10%, Medium 10-20%, High >20%.
Scoring for Heritability (h^2 b.s): Low <30%, Medium 30-60%, High >60%.

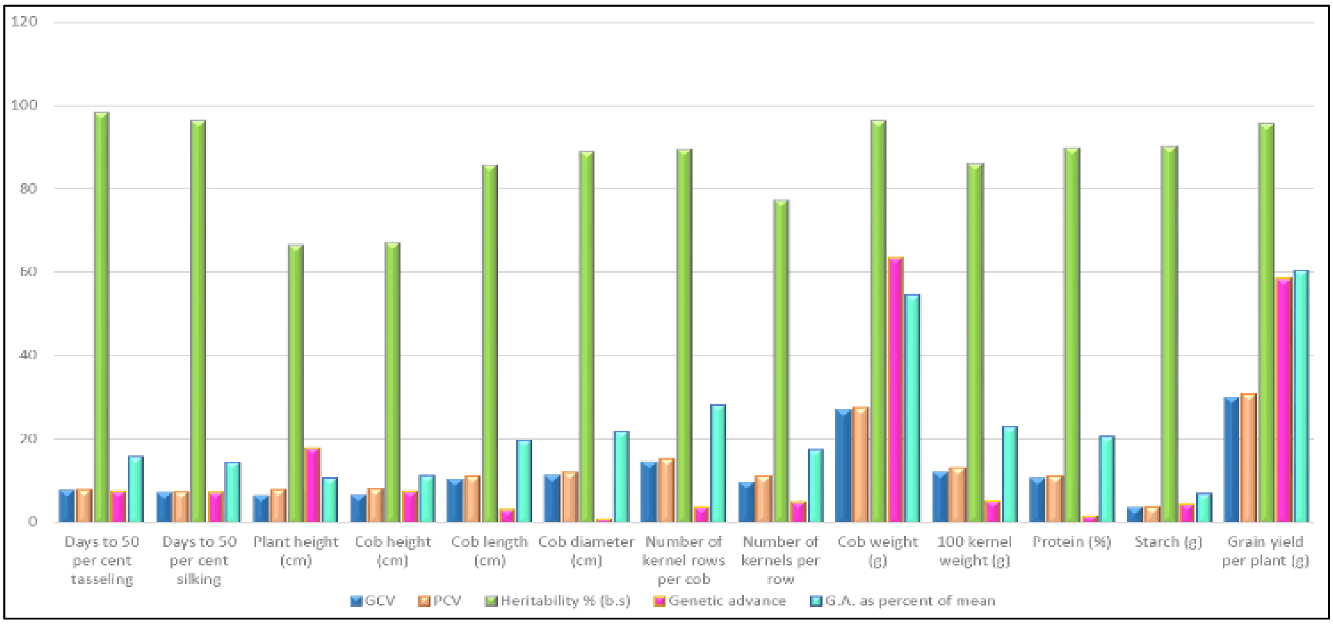

Fig 1: Genetic variability parameters for 13 traits evaluated across 42 maize genotypes.

Conclusion

The present investigation revealed significant genetic variability among 42 maize genotypes for yield and yield-related traits. Grain yield per plant, cob weight, number of kernel rows per cob, and 100-kernel weight exhibited high genotypic and phenotypic coefficients of variation, high heritability, and high genetic advance as a percent of mean, suggesting the predominance of additive gene action. These traits can be effectively improved through simple selection, making them promising targets for genetic enhancement in maize breeding programs. Overall, the findings provide valuable information for maize improvement programs and can guide breeders in developing high-yielding, stable maize varieties suited to diverse environment.

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