



RESEARCH ARTICLE

Appraisal of genetic variability, heritability and genetic advance for quantitative traits in maize (*Zea mays* L.)

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Abstract

Maize is a staple food crop globally, contributing significantly to food security. However, low productivity due to limited genetic understanding and inadequate exploitation of variability in genotypes remains a major challenge. This study aimed to assess genetic variability, heritability and genetic advance for kernel yield and related traits to identify potential genotypes for future breeding programs. The experiment was conducted using a randomized complete block design with three replications, involving 238 diverse maize genotypes. Data on fourteen yield and yield-contributing traits were subjected to statistical analyses. Significant variation among genotypes was observed for all traits, indicating genetic diversity. The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for most traits, highlighting environmental influence. High GCV and PCV were recorded for kernels per row, cob weight and kernel yield per plant indicating substantial variability. Broad-sense heritability was highest for cobs per plant followed by kernel yield per plant, ear height and cob weight suggesting strong genetic control. Traits such as plant height, ear height and kernel yield per plant exhibited high heritability and genetic advance, indicating the predominance of additive gene action and suitability for selection. Genotypes IGI-19-26, IL-12-11, IL-14-39, NAI-105-5, IL-17-61, IL-14-80 and IGI-19-47 demonstrated superior yield performance, making them promising candidates for maize improvement programs. These findings provide critical insights for developing high-yielding maize varieties through targeted breeding strategies.

Keywords

genetic variability; heritability; genetic advance; maize; kernel yield

Introduction

Maize (*Zea mays* L.) is the world's most extensively grown crop and an important cereal crop next to rice and wheat. Due to its high yield potential and versatility, maize is often referred to as the 'Queen of Cereals'. Maize can play an important role in crop diversification as it is a dual-purpose crop that produces kernels and fodder for human consumption and livestock feed respectively (1) and it is also increasingly exploited for bioethanol production to support sustainable energy demands. The crop requires less water than other comparable cereals and being a 'C4' as well as a 'day-neutral plant', it gives a higher yield per hectare in a shorter period. Maize (C4 plants) use three-fold less water, allowing them to grow in conditions of drought, high temperature and carbon dioxide limitation, making it a vital crop for climate resilience strategies (2).

The production of food crops is greatly influenced by maize, which is essential to the world's food security. Presently, more than 170 nations collectively produce approximately 1147.7 million MT of maize on an area of 193.7 million ha, with an average productivity of 5.75 t/ha (3). Currently, maize is the most important food crop in Sub-Saharan Africa and Latin America and a major crop in Asia. Among the maize-growing countries, India ranks 4th in area and 7th in production, representing around 4 per cent of the world maize area and 2 per cent of total production. In India, the maize area has reached 9.2 million hectares during 2018-19 (4). However, India's maize productivity is significantly lower than global standards-nearly half the world average. There is a substantial yield gap compared to countries like the US and China, indicating a need for improved hybridization to boost yields. Enhancing maize productivity in India is crucial not only for food security but also for increasing farmers' income and ensuring sustainable agricultural practices. The development of climate-resilient, high-yielding hybrids is imperative to bridge this yield gap.

The biological world is marked by diversity, with no two living beings being the same. Variability refers to differences in traits among organisms, while genetic variability specifically involves variations in alleles or DNA/RNA sequences within a species' gene pool, leading to phenotypic differences (5). Genetic variability is crucial for crop plant evolution and improvement, as it provides the foundation for selecting and enhancing desirable traits (6). Without genetic diversity, crop improvement would be impossible. Since the start of systematic plant breeding, natural variability and divergence have been key to advancing crop performance and adapting to changing environments. In recent years, advanced breeding approaches such as genomic selection, marker-assisted breeding and precision phenotyping have been leveraged to enhance maize genetic improvement. Knowledge of genetic

variability parameters such as genotypic coefficient of variation, heritability and genetic advance is necessary for the plant breeder to start a judicious breeding program. Furthermore, heritability measures the relative amount of the heritable portion of variation, while the genetic advance helps to measure the amount of progress that could be expected with the selection of a character. Traits with high heritability and genetic advance are more reliable for direct selection in breeding programs, especially under varying environmental conditions. High heritable estimates together with high genetic advance are more valid for selection than heritability estimates alone (7). Therefore, the present study was conducted with the objective of estimating genetic variability, heritability and genetic advance for yield and its attributes among maize genotypes for future breeding programs.

Materials and Methods

Climate of the site

The experiment was conducted at the Main Maize Research Station (MMRS), Anand Agricultural University, Godhra (Fig. 1), from November 2020 to March 2021. The site is located at 22° 45' N latitude and 77° 40' E longitude, at an altitude of 119 meters above mean sea level. The experimental soil is sandy loam, consisting of 80% sand and 20% clay, with low fertility and limited water-holding capacity. Soil depth is approximately 2.5 feet, with nitrogen availability ranging from 0.043% to 0.046%, medium phosphorus levels and high potassium content. The region's climate is semi-arid and tropical, with cold winters (minimum temperature 6.0°C) and hot summers (maximum temperature 44.0°C). The annual rainfall averages between 650-750 mm, spread over 32 rainy days. Meteorological observations during the maize growing season were recorded at the Meteorological Observatory of MMRS, Anand Agricultural University, Godhra.



Fig. 1. Field view of the experimental site.

Selection of the genotypes

The experimental materials for the study were obtained from the Winter Nursery Centre, Hyderabad and the Main Maize Research Station (MMRS) at Anand Agricultural University (AAU), Anand. The genotypes utilized in the experiment are detailed in genotype table (Table 1).

Experimental design and cultural practices

The 238 maize genotypes were evaluated using a Randomized Complete Block Design with three replications at MMRS, Godhra during the rabi season of 2020-21. To minimize damage and border effects, the experiment was surrounded by a border row. Standard agronomic practices and plant protection measures were implemented to ensure optimal crop growth and health.

Data collection and observations

Observations were made on fourteen quantitative traits for each row, with measurements taken from five randomly selected competitive plants per replication. The mean values were calculated for statistical analysis, except for days to 50% tasselling (FT), days to 50% silking (FS) and days to maturity (DM), which were recorded on a per-row basis. Plant height (PH) and ear height (EH) were measured after reproductive maturity. Cob dimensions, including Cobs per Plant (CPP), Kernel Rows per Cob (KRPC), Kernels per Row (KPR), Cob Length (CL), Cob Girth (CG), Cob Weight

(CW), 1000 Kernel Weight (1000K) and Shelling Percentage (SH), along with Kernel Yield per Plant (KYPP), were recorded at physiological maturity.

Statistical analysis

The mean data were primarily subjected to Analysis of Variance. The analysis of the variance technique suggested by (8) was followed to test the significance of differences between the genotypes for all the characters under study. The mean squares due to genotypes and error were used for the calculation of variance components by manipulation of expected mean squares. Genotypic, phenotypic and environmental variance were calculated as per the formula suggested by (7). The genotypic and phenotypic coefficient of variation was computed using the formula given by (9). The heritability in broad sense and expected genetic advance (at 5 % selection intensity using the constant 'K' as 2.06) was calculated for each character by adopting the procedure suggested by (10).

Statistical software

All the statistical analyses were carried out on the R Studio, R version 4.1.2 (11) software. The R package "variability" (12) was used to estimate variability, heritability and genetic advance. The "tidyverse" package (13) was applied to visualize the bar chart. Additionally, "ggplot2" package v3.3.3 (14) was utilized for data visualization.

Table 1. List of maize genotypes used in the study

Group	Genotypes	Source
Genotypes	IT-INA-011-2, LTP 1-1, NAI-105-5, PFSR-S3-5, VL-78	Main Maize Research Station, Godhra
H Series	H-07R-04-3, H07R-4-2, H07R-4-3, H07R-9-3, H07-49-3	Main Maize Research Station, Godhra
HKI Series	H-07R-04-3, H07R-4-2, H07R-4-3, H07R-9-3, H07-49-3, HKI-163, HKI 3-4-8-5 ER, HKI-193-1	Main Maize Research Station, Godhra
LM Series	LM13-2, LM-3, LM-5	Main Maize Research Station, Godhra
CM Series	CM-500-1, CM-111, CM-135, CM-140, CM-212-2, CM500, CM-500-2	Main Maize Research Station, Godhra
CML Series	CML-269, CML-296, CML-298, CML-307, CML-482	Main Maize Research Station, Godhra
GYL Series	GYL-1, GYL-10, GYL-11, GYL-2, GYL-4, GYL-5, GYL-6, GYL-7, GYL-8, GYL-9	Main Maize Research Station, Godhra
IGI Series	IGI-19-01, IGI-19-02, IGI-19-03, IGI-19-04, IGI-19-6, IGI-19-05, IGI-19-06, IGI-19-07, IGI-19-08, IGI-19-09, IGI-19-10, IGI-19-11, IGI-19-12, IGI-19-13, IGI-19-14, IGI-19-15, IGI-19-17, IGI-19-18, IGI-19-19, IGI-19-20, IGI-19-21, IGI-19-22, IGI-19-23, IGI-19-24, IGI-19-25, IGI-19-26, IGI-19-27, IGI-19-28, IGI-19-29, IGI-19-30, IGI-19-31, IGI-19-32, IGI-19-33, IGI-19-34, IGI-19-35, IGI-19-36, IGI-19-37, IGI-19-38, IGI-19-39, IGI-19-40, IGI-19-41, IGI-19-42, IGI-19-43, IGI-19-44, IGI-19-45, IGI-19-46, IGI-19-47, IGI-19-48, IGI-19-49, IGI-19-50, IGI-19-51, IGI-19-52, IGI-19-53, IGI-19-54	Winter Nursery Centre, Hyderabad-2019
	IL-12-06, IL-12-101, IL-12-109, IL-12-11, IL-12-12, IL-12-123, IL-12-129, IL-12-135, IL-12-16, IL-12-17, IL-12-19, IL-12-23, IL-12-26, IL-12-29, IL-12-38, IL-12-40, IL-12-51, IL-12-52, IL-12-58, IL-12-86, IL-12-95, IL-12-97	Winter Nursery Centre, Hyderabad-2012
	IL-14-01, IL-14-03, IL-14-10, IL-14-11, IL-14-15, IL-14-23, IL-14-24, IL-14-26, IL-14-34, IL-14-35, IL-14-38, IL-14-39, IL-14-40, IL-14-47, IL-14-48, IL-14-51, IL-14-52, IL-14-53, IL-14-56, IL-14-57, IL-14-59, IL-14-61, IL-14-62, IL-14-63, IL-14-64, IL-14-67, IL-14-68, IL-14-75, IL-14-77, IL-14-78, IL-14-80, IL-14-81, IL-14-85, IL-14-86	Winter Nursery Centre, Hyderabad-2014
IL Series	IL-15-01, IL-15-02, IL-15-03, IL-15-13, IL-15-19, IL-15-20, IL-15-21, IL-15-23, IL-15-24, IL-15-25, IL-15-26, IL-15-27, IL-15-28, IL-15-29, IL-15-30, IL-15-31, IL-15-34, IL-15-35, IL-15-38, IL-15-39, IL-15-41	Winter Nursery Centre, Hyderabad-2015
	IL-17-01, IL-17-02, IL-17-03, IL-17-04, IL-17-05, IL-17-06, IL-17-09, IL-17-10, IL-17-12, IL-17-13, IL-17-14, IL-17-15, IL-17-17, IL-17-19, IL-17-20, IL-17-21, IL-17-22, IL-17-24, IL-17-25, IL-17-26, IL-17-27, IL-17-28, IL-17-29, IL-17-30, IL-17-31, IL-17-32, IL-17-33, IL-17-34, IL-17-37, IL-17-38, IL-17-39, IL-17-41, IL-17-43, IL-17-44, IL-17-45, IL-17-46, IL-17-47, IL-17-48, IL-17-49, IL-17-50, IL-17-51, IL-17-52, IL-17-53, IL-17-54, IL-17-55, IL-17-56, IL-17-57, IL-17-58, IL-17-59, IL-17-60, IL-17-61, IL-17-62, IL-17-63, IL-17-64, IL-17-67, IL-17-68, IL-17-69, IL-17-70, IL-17-71, IL-17-72, IL-17-73, IL-17-76, IL-17-77, IL-17-78, IL-17-79, IL-17-80, IL-17-81, IL-17-82	Winter Nursery Centre, Hyderabad-2017

Results

Analysis of Variance

The analysis of variance revealed a highly significant ($P < 0.01$) mean sum of squares due to genotypes evaluated for the thirteen quantitative traits viz., days to 50% tasseling, days to 50% silking, plant height, ear height, cobs per plant, kernel rows per cob, kernels per row, cob length, cob girth, cob weight, 1000 kernel weight, kernel yield per plant and significant means sum of square due to genotypes for days to maturity ($P < 0.05$), indicated the presence of considerable genetic variability in the experimental material (Table 2). These results are in close agreement with (15-17) for all characters under study.

Mean performance

Mean is a relatively simple measure used in plant breeding to assess phenotypic variability and it serves as the basis for screening desirable genotypes. Mean performance, range and coefficient of variation of genotypes studied are given in (Table 3). Days to 50% tasseling ranged from 62.33 days to 84.67 days with a general mean of 75.89 days. Days to 50% Silking ranged from 64.67 days to 87 days with a general mean of 78 days. Silking and tasseling were early in IGI-19-45 and late in IL-14-26. The mean values for days to maturity ranged from 91.67 days to 114.33 days. Early maturity was observed in IGI-19-45 (91.67 days), while late maturity was recorded in IL-14-26 (114.33 days). The result indicated that the genotypes viz., IGI-19-45, GYL-2, IL-15-35, IGI-19-18, CM-135, GYL-1, IGI-19-02, IL-17-56, IL-14-75 and IL-14-77 were early in silking and maturity. Hence, these genotypes could be utilized in the future breeding programmes which may offer a vast scope for the development of early maturing traits in maize without yield penalty. Plant height showed vast range (150.95cm) with general mean of 135.4cm. The general mean for cob weight was 55.71g with a range from 21.2g to 118.4g. The mean value for 1000 kernel weight ranged from 133.3g to 330g with a general mean of 218.3g. Shelling % in maize genotypes ranged from 46.05% to 85.77% with a general mean value of 70.39%. Kernel yield per plant ranged from 39.33g to 176.67g with a general mean value of 67.06g. The comparison of mean values of genotypes revealed that the genotype IL-17-61 (167.67g) had the highest kernel yield per plant followed by IGI-19-46 (159.13g) and IGI-19-26 (157.45g). However, the genotypes IL-12-40 (39.33g) and CM-140 (39.33g) had the lowest kernel yield per plant.

Promising genotypes based on *per se* performance for kernel yield per plant also recorded considerable top performance for other yield contributing traits (Table 4). The genotypes IGI-19-26 and IL-12-11 registered high mean values for nine yield and yield contributing trait followed by IL-14-39 expressed high *per se* performance for seven traits. Similarly, NAI-105-5 showed high mean values for six traits. Further, IL-17-61, IL-14-80 and IGI-19-47 registered high *per se* performance for four yield traits (Table 4). The genotypes viz., IGI-19-26, IL-12-11, IL-14-39, NAI-105-5, IL-17-61, IL-14-80 and IGI-19-47 could be utilized as a potential source for the future breeding programme for improving yield and yield attributes.

Phenotypic and genotypic coefficient of variability

The estimation of Genotypic Coefficient of Variation (GCV%) and Phenotypic Coefficient of Variation (PCV%) computed for 14 yield and yield attributing traits in 238 genotypes of maize are summarized in (Table 3 and Fig. 2). GCV% and PCV% values were categorized as low when less than 10%, moderate, 10-20% and high, greater than 20% as indicated by (18). The result indicated that the difference between GCV% and PCV% was low for all the characters under investigation, suggesting that these traits studied have low environmental influence (Table 3). Traits like kernel yield per plant (41.45%, 43.81%) and cob weight (36.26%, 39.40%) exhibited high GCV and PCV, indicating strong genetic variability. These traits can be effectively improved through direct phenotypic selection. Similarly, cobs per plant (28.90%, 29.38%) and kernels per row (21.95%, 25.33%) also showed high variability, suggesting ample scope for genetic improvement. This was in conformity with the findings of (16, 19-21). Moderate estimates of GCV% and high estimates of PCV% were observed for ear height (19.74%, 21.17%). The findings are in close harmony with the results of (22-23). The traits such as plant height (15.94%, 17.66%) and 1000 kernel weight (13.99%, 18.67%) showed moderate estimates of GCV% and PCV% indicating the moderate variability present in the materials under present study. These results are in accordance with the results obtained by (20-21) Low estimates of GCV% and moderate estimates of PCV% were observed for kernel rows per cob (8.58%, 11.58%), cob girth (6.3%, 15.18%), cob length (8.64%, 15.97%) and shelling per cent (5.52%, 13.11%), indicating more influence of the environment on the variability of these characters and hence simple selection may not be rewarding. These findings agreed with

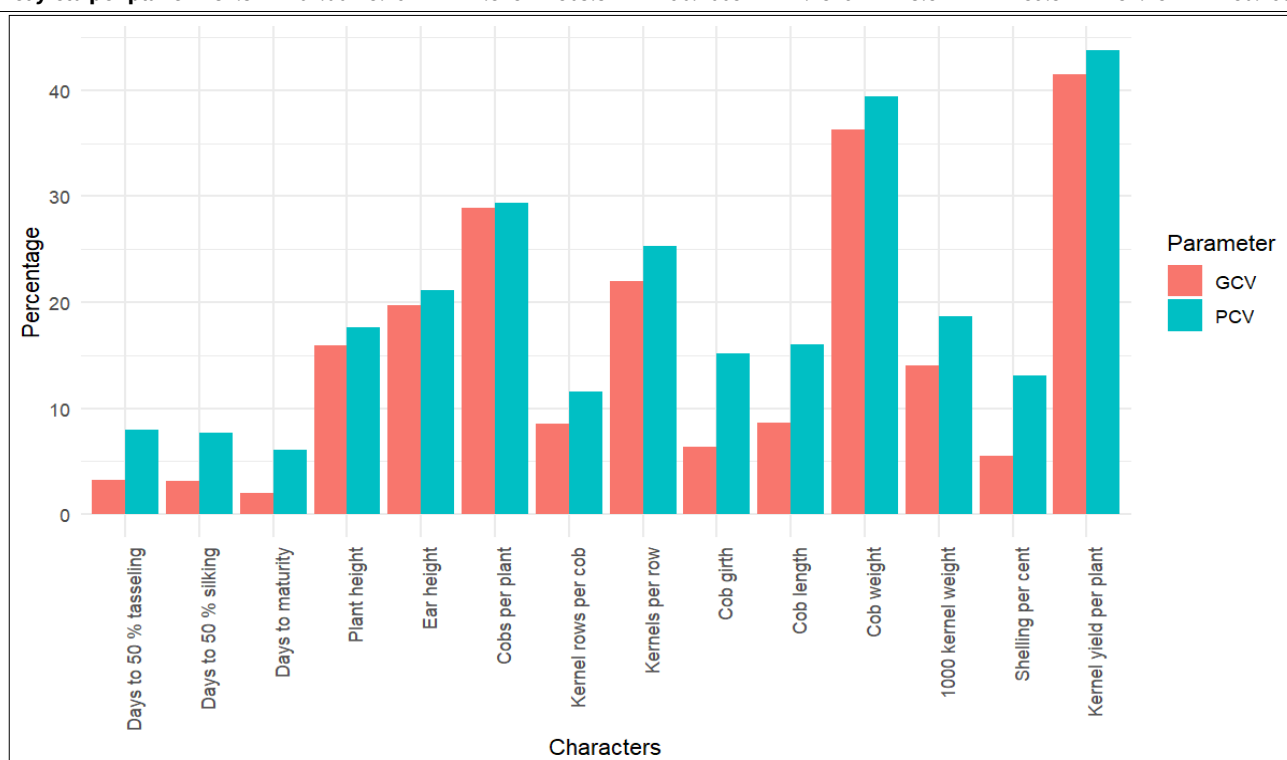
Table 2. Analysis of variance (ANOVA) showing the mean sum of squares for fourteen traits in maize genotypes

Source of Variation	df	Mean sum square of traits													
		FT	FS	DM	PH	EH	CPP	KRPC	KPR	CL	CG	CW	1000K	SH	KYPP
Replications	2	32.581	27.732	62.728	196.768	43.953	0.0035	1.754	10.946	9.1058	5.7955	204.284	531.647	61.773	134.393
Genotypes	237	48.08**	47.93**	49.58*	1867.81**	718.77**	0.45**	4.64**	81.57**	8.188**	3.67**	1288.62**	3528.16**	115.36**	2409.01**
Error	474	30.142	30.323	36.251	131.599	34.295	0.005	0.996	8.122	3.653	2.236	71.627	727.547	70.015	90.466
CD (5%)		8.81	8.83	9.66	18.41	9.4	0.11	1.6	4.57	2.4	3.07	13.61	43.28	13.42	15.26
CV%		7.23	7.06	5.72	7.6	7.65	5.33	7.77	12.64	13.78	13.43	15.44	12.35	11.89	14.18
P-value		P<0.01	P<0.01	P<0.05	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01	P<0.01

Notes: ** Significant at $P < 0.01$ level, df = Degrees of freedom, CD = Critical Difference, CV = Coefficient of variation, FT = Days to 50% tasseling, FS = Days to 50% silking, DM = Days to maturity, PH = Plant height, EH = Ear height, CPP = Cobs per plant, KRPC = Kernel rows per cob, KPR = Kernels per row, CL = Cob length, CG = Cob girth, CW = Cob weight, 1000K = 1000 kernel weight, SH = Shelling percentage, KYPP = Kernel yield per plant.

Table 3. Estimates of variability, heritability and genetic advance for fourteen traits in maize genotypes

Characters	Range	Mean $\pm$ SE _m	σ^2_g	σ^2_p	σ^2_e	GCV(%)	PCV(%)	h ² b(%)	GA	GAM
Days to 50% tasseling	22.34	75.89 $\pm$ 3.17	5.9807	36.1231	30.1424	3.2224	7.9195	16.56	2.0499	2.7011
Days to 50% silking	22.33	78 $\pm$ 3.179	5.8702	36.1934	30.3232	3.1062	7.7128	16.22	2.01	2.5769
Days to maturity	22.66	105.22 $\pm$ 3.476	4.4432	40.6947	36.2515	2.0034	6.0629	10.92	1.4348	1.3637
Plant height	135.4	150.95 $\pm$ 6.623	578.737	710.337	131.599	15.9366	17.6558	81.47	44.7318	29.6327
Ear height	78.99	76.51 $\pm$ 3.381	228.159	262.454	34.2952	19.7415	21.1732	86.93	29.012	37.9174
Cobs per plant	1.53	1.33 $\pm$ 0.041	0.1483	0.1533	0.005	28.9005	29.3837	96.74	0.7803	58.5594
Kernel rows per cob	5.67	12.84 $\pm$ 0.576	1.2136	2.2102	0.9966	8.578	11.5761	54.91	1.6816	13.0939
Kernels per row	25.66	22.55 $\pm$ 1.646	24.481	32.6037	8.1227	21.9462	25.3267	75.09	8.8321	39.175
Cob length	10.38	10.85 $\pm$ 0.863	0.4781	2.7144	2.2363	6.3713	15.1813	17.61	0.5978	5.5084
Cob girth	12.54	14.23 $\pm$ 1.104	1.5115	5.1649	3.6534	8.6403	15.9718	29.26	1.3701	9.6289
Cob weight	99.4	55.68 $\pm$ 4.897	397.517	469.454	71.9371	36.2602	39.4048	84.68	37.7943	68.7351
1000 kernel weight	196.67	218.32 $\pm$ 15.573	933.537	1661.08	727.547	13.9948	18.6679	56.2	47.1849	21.6124
Shelling per cent	39.72	70.39 $\pm$ 4.831	15.1138	85.1291	70.0153	5.523	13.1078	17.75	3.3744	4.7939
Kernel yield per plant	137.34	67.06 $\pm$ 5.491	772.848	863.314	90.4668	41.4549	43.8141	89.52	54.1847	80.799

**Fig. 2.** Graphical representation of Genotypic coefficient of variation (GCV%) and Phenotypic coefficient of Variation (PCV%) for fourteen traits in maize.

(16, 22, 24-25). Low estimates of GCV% and PCV% were observed for days to 50% tasseling (3.22%, 7.92%), days to 50% silking (3.11%, 7.71%) and days to maturity (2.00%, 6.06%), which showed the low range of variation for these traits in the genotypes, thus offering little scope for further improvement of these characters through simple selection. Similar kind of results were earlier reported by (17, 19, 21-22, 26).

Heritability and Genetic advance as percent of mean

The heritability, genetic advance and genetic advance expressed as percentage of mean for all the traits are presented in (Table 3 and Fig. 3). In broad sense, heritability (h^2b) is an estimate of the total contribution of the genetic variance to the total phenotypic variance of a trait. High values of heritability help breeders to select superior genotypes based on phenotypic expression of quantitative traits (7). Heritability is classified as low (<30%), medium

(30%-60%) and high (>60%). The result indicated that heritability ranges from 16.22% (days to 50% silking) to 96.74% (cobs per plant). High estimates of heritability were obtained for characters viz., plant height (81.47%), ear height (86.93%), cobs per plant (96.74%), kernels per row (75.09%), cob weight (84.68%) and kernel yield per plant (89.52%). Moderate estimates of heritability were obtained for 1000 kernel weight (56.2%) and kernel rows per cob (54.91%), which indicated that selection based on phenotypic performance would be rewarding on partitioning of environmental variances. Low estimates of heritability were recorded for days to 50% tasseling (16.56%), days to 50% silking (16.22%), days to maturity (10.92%), cob length (17.61%), cob girth (29.26%) and shelling per cent (17.75%). This is an indicative of the fact that character is rather more influenced by environment and may not respond much to selection.

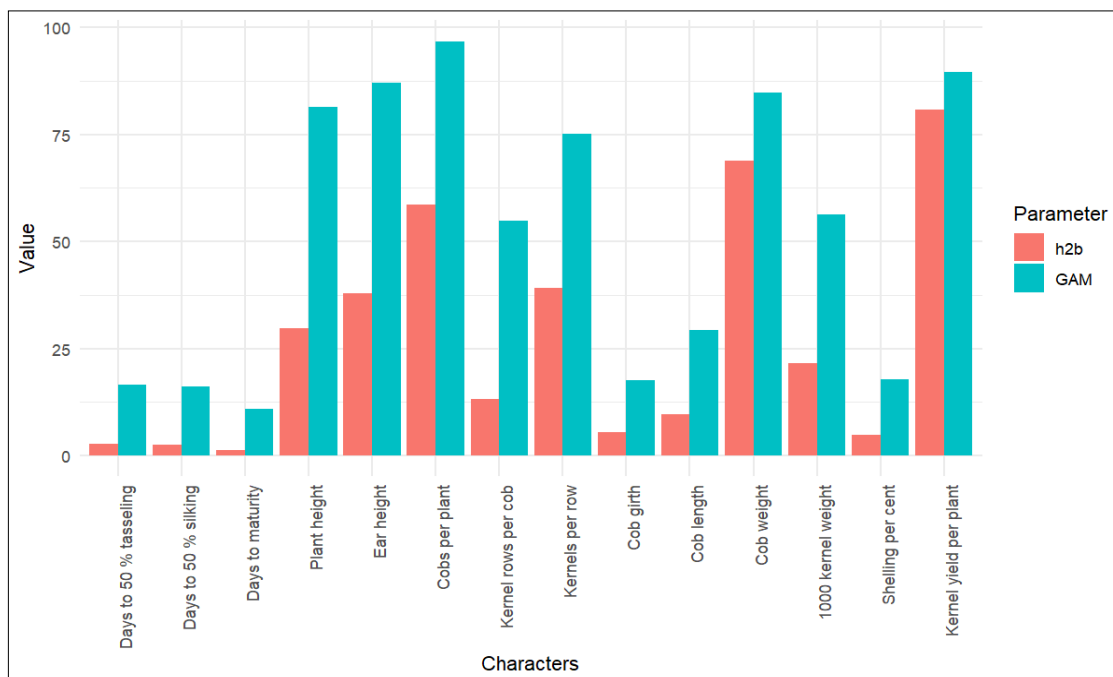


Fig. 3. Graphical representation of Heritability in broad sense (h^2_b) and Genetic advance as percent of mean for fourteen traits in maize.

Table 4. List of top ten genotypes identified for kernel yield and one or more other yield contributing traits based on *per se* performance

Sr. No.	Promising genotypes for kernel yield per plant based on <i>per se</i> performance	Top in performance for other yield contributing traits
1	IL-17-61	Cobs per plant, kernel row per cob, cob length and cob weight
2	IGI-19-46	Plant height, cobs per plant and kernel row per cob
3	IGI-19-26	Days to 50% tasseling, days to 50% silking, days to maturity, cobs per plant, kernel per row, cob length, cob weight, 1000 kernel weight and shelling per cent
4	NAI-105-5	Days to 50% tasseling, days to 50% silking, cobs per plant, kernel per row, cob length and cob weight
5	IL-14-39	Plant height, ear height, cobs per plant, kernel row per cob, kernel per row, cob weight and shelling per cent
6	IL-17-44	Cobs per plant
7	IL-12-11	Days to 50% silking, Days to maturity, Plant height, ear height, cobs per plant, kernel per row, cob girth, cob length and cob weight
8	IL-14-80	Cobs per plant, cob girth, cob length and 1000 kernel weight
9	IGI-19-36	1000 kernel weight
10	IGI-19-47	Kernel row per cob, cob girth, cob weight and shelling per cent

Genetic advance is the improvement of the mean of selected families over the base population. It can be classified as low (<10%), medium (10%-20%) and high (>20%). The results indicated that the characters viz., plant height (29.63), ear height (37.92), cobs per plant (58.56), kernels per row (39.18), cob weight (68.74), 1000 kernel weight (21.61) and kernel yield per plant (80.80) exhibited high genetic advance as per cent of mean. Moderate estimates of genetic advance as per cent of mean was exhibited by kernel rows per cob (13.09). The characters viz., days to 50 % tasseling (2.70), days to 50 % silking (2.58), days to maturity (1.36), cob length (9.63), cob girth (5.51) and shelling per cent (4.79) exhibited low genetic advance as per cent of mean.

Knowledge of heritability accompanied with genetic advance is most useful in predicting the scope for genetic improvement through selection. In the present investigation, high heritability (h^2_b) coupled with high genetic advance expressed as per cent of mean (GAM) was observed for plant height, ear height, cobs per plant, kernels per row, cob weight and kernel yield per plant. Therefore, phenotypic selection would be more effective for the

improvement of these traits. These results corroborates the findings of (21) for plant height, ear height, kernels per row and kernel yield per plant; (17) for ear height, ear height and kernel yield per plant. Moderate heritability coupled with high genetic advance expressed as per cent of mean was observed for 1000 kernel weight. Moderate heritability coupled with moderate genetic advance was registered for kernel rows per cob. The best possibility of improvement of these traits is through progeny selection or any modified selection procedures aiming to exploit the additive gene effects. The results are akin with the findings of (27) for 1000 kernel weight; (15, 28-29) for kernel rows per cob. Low heritability coupled with low genetic advance expressed as per cent of mean was observed for days to 50 % tasseling, days to 50 % silking, days to maturity, cob girth, cob length and shelling per cent that indicates high influence of environment and consequently its selection may not be effective, thus limited scope for improvement of these traits by selection. The results obtained were in confirmatory with (30) for cob girth; (20) for shelling per cent; (31) for cob length, cob girth; (15, 32) for cob length; (23) for days to 50 % tasseling and days to 50 % silking.

Discussion

The selection of elite parental lines is the key to the success of any hybrid development program. The selection of superior lines will be possible only when adequate variability exists in the gene pool (33). Hence, an attempt was made in the present study to estimate the genetic variability among the available genotypes along with heritability (broad sense) and genetic advance (expressed as per % of mean) to exploit these traits in breeding programmes for the development of potential hybrids. In the present study the fourteen traits revealed varied levels of variability, heritability and genetic advance. The traits kernel yield per plant, cob weight, cobs per plant and kernels per row having high genetic variability and a high level of total phenotypic variability suggest strong genetic influence, making them suitable for improvement through direct selection. However, environmental factors also contribute to the overall variation. In contrast, traits with low genetic and low total phenotypic variability, such as days to 50% tasseling, days to 50% silking and days to maturity, indicate stability with minimal influence from both genetic and environmental factors. The lack of variability might suggest that these traits are either highly conserved or have reached a selection plateau, thus offering little scope for further genetic improvement. Moderate to low variability for plant height and 1000 kernel weight indicates the need for improvement of base population. Selection might be less effective due to the low genetic variability. Breeders may need to focus on improving environmental conditions or management practices to reduce the environmental variance. The traits kernel yield per plant and cob weight showed high genetic variability with little environmental masking. This is an ideal situation for breeders, as selection will be highly effective, leading to rapid genetic gains.

The genotypic coefficient of variation does not reflect the amount of heritable variation, but it measures the amount of variation present in a particular character. Thus, the knowledge of heritability of a character enables the plant breeders in predicting genetic advance for any quantitative characters and course of selection procedure to be followed under a given situation. High heritability estimates coupled with high genetic advance as percent of mean for plant height, ear height, cobs per plant, kernels per row, cob weight and kernel yield per plant, confirming the predominance of additive gene action, making it an ideal target for selection in maize breeding. High heritability values indicate that the characters under study are less influenced by environment in their expression. Therefore, the plant breeders may perform their selection safely based on phenotypic expression of these characters in the individual plant by adopting simple selection methods. Genetic advance as percentage of mean (GAM) which coincide with high heritability is very useful than heritability alone in predicting the resultant effect during selection of best individual genotype, which was revealed in present study. In contrast the lower values of heritability coupled with genetic advance as percent of mean for days to 50 % tasseling, days to 50 % silking, days to maturity, cob girth, cob length and shelling per cent exhibits the high influence of environment and consequently its selection may not be

effective, thus limited scope for improvement of these traits by selection. Moderate heritability coupled with high genetic advance expressed as per cent of mean for 1000 kernel weight, which indicates the role of both additive and non-additive gene actions governing the inheritance of these traits and best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects.

The traits kernel yield per plant, cob weight, cobs per plant, kernels per row, plant height and ear height exhibited high genetic variability, high heritability and high genetic advance, indicating strong additive gene action and making them ideal for direct selection in breeding programs. 1000 kernel weight showed moderate heritability with high genetic advance, suggesting a mix of additive and non-additive effects, which necessitates progeny selection or modified breeding strategies. In contrast, days to 50% tasseling, days to 50% silking, days to maturity, cob girth, cob length and shelling percentage had low heritability and genetic advance, indicating a high environmental influence and limited scope for genetic improvement through selection alone. For future breeding strategies, direct selection should be prioritized for high-feasibility traits, recurrent selection and marker-assisted approaches for moderately heritable traits and environmental optimization or hybrid breeding for low-feasibility traits to enhance genetic gains effectively. Breeder should adopt appropriate breeding methods based on the estimates of variability, heritability and genetic advance for trait of interest to utilize in breeding program.

Conclusion

This study provided insights into genetic variability, heritability (broad sense) and genetic advance (as a percentage of the mean) in different maize genotypes. Traits such as plant height, ear height, cobs per plant, kernels per row, cob weight and kernel yield per plant, which exhibited high heritability with high genetic advance, should be prioritized for selection to achieve higher genetic gains. The presence of sufficient genetic variability among the experimental materials supports the selection of superior genotypes, including IL-17-73, IL-12-11, IGI-19-26, IL-17-55, IL-15-19, IL-12-17, IGI-19-53, IGI-19-17, GYL-4, IGI-19-03, IGI-19-09, IL-14-34, LTP 1-1, IGI-19-02, IL-17-63, IL-17-79, IL-14-39, IGI-19-29, IL-14-61 and IL-15-30, which demonstrated superior performance for yield-related traits and early maturity. Additionally, highly diverse genotypes can be further selected based on synchronous flowering and genetic divergence studies, enhancing breeding strategies for maize improvement.

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Authors' contributions

PMS carried out the entire research, writing-original draft preparation, data analysis and visualization. MBP conceptualized and supervised the study and reviewed and edited the manuscript. THB, KMA, JMV participated in research methodology, manuscript preparation and editing. DJP carried out the statistical analysis and visualization. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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