Genetic Variability, Heritability and Genetic Advance Assessment for Grain Yield and its Accrediting Traits in Maize (*Zea mays* L.)

Abstract: Understanding the variability, heritability, and genetic advance in maize is crucial for efficient plant breeding and genetic improvement programmes. The present investigation was conducted to evaluate the various parameters related to ~~the~~ assessment of genetic variability and nature of associations among traits affecting grain yield in 80 ~~genotypes~~inbred lines of maize (*Zea mays* L.) at the Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, Gwalior, M.P., India during the Rabi season of 2019-20~~ and *Kharif* 2020~~. The analysis of variance revealed that highly significant differences exist among the inbred lines, their hybrids and checks for all the characters. Under irrigated and partial irrigated conditions, traits *viz*., days to 50 percent tasselling and silking, anthesis silking interval (ASI), plant height and membrane stability index exhibited high GCV and PCV. The characters with the highest heritability coupled with higher genetic advance were found for the traits *namely*: days to 50% silking and 50% tasselling, anthesis silking interval, plant height, numbers of kernel rows per cob, numbers of kernel per rows, seed yield per plant (g), numbers of cobs per plant, days to maturity, cob girth (cm), turgid weight (g), saturation water deficit and membrane stability index for both under irrigated and partial irrigated conditions. High heritability with higher genetic advance as percent of mean indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield in maize.

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Key words: Maize, GCV (Genotypic Coefficient of variance), PCV (Phenotypic Coefficient of variance), GAM (Genetic advance as percent of mean)

INTRODUCTION

Maize belongs to the Panicoideae sub-family of the Poaceae family and the Maydeae tribe [1]. It is believed to have originated in Central America and Mexico, evolving from teosinte (*Zea mexicana*) approximately 7000 years ago in central Mexico from wild grass, and Native Americans played a significant role in its transformation into a more desirable food source [2]. It is a cheap source of easily digestible high-quality protein (22-28%), total amino acids (21-25%), lipids (1.53-2.63%), fat (1.0-1.5%), fibre (3.5-4.5%), ash (4-5%) and carbohydrates (59-65%) on a dry weight basis and provides 334-344 k/cal energy [3]. It contains certain antioxidants, such as zeaxanthin and lutein. These compounds have been associated with eye health and may help protect against age-related macular degeneration [3, 4]. Thus, maize stands as a pivotal crop due to its remarkable production figures and its nutritional profile, contributing significantly to global food security [5,6].

As a C_4 plant, maize exhibits greater physiological efficiency and higher daily productivity [6]. It exhibited broad adaptability to various environmental conditions, being cultivated across latitudes 58° N to 40° S, ranging from sea level to altitudes exceeding 3000 m, and in areas with annual rainfall ranging from 250 mm to 5000 mm [7]. Maize, known as the "queen of cereals," holds the top position in global cereal productivity, with 5.82 t/ha, followed by rice with 4.66 t/ha and wheat with 3.55 t/ha. Maize boasts the highest global production among crops, with wheat and rice following suit [6]. This crop is cultivated in more than 170 countries globally [8]. The leading maize-producing countries worldwide are the United States, China, and Brazil, collectively accounting to produce around 563 million metric tons per year out of a total of 717 million metric tons [2]. The United States, China, and Brazil together contribute approximately 62% to the global maize production. Maize cultivation spans across 193.7 million hectares worldwide, resulting in a total production of 1147.7 million metric tons and an average productivity of 5.75 tons per hectare. In India, maize is grown across an area of 9.9 million hectares, yielding a production of 31.51 million metric tons and a productivity of 3.07 tons per hectare [8]. Among the Indian states, Madhya Pradesh and Karnataka have the largest maize cultivation areas, each accounting for 15%, tracked by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%), and others [8].

The diverse characteristics found within maize contribute to its extensive range of morphological, physiological, and agronomic traits, making it a valuable crop for plant breeders seeking to enhance its qualities [1]. Variability, heritability, and genetic advance are crucial concepts that aid breeders in comprehending the genetic diversity present in populations and assist in identifying and selecting the most promising individuals for further advancements [9-13]. Breeders utilize these parameters to identify individuals with desirable traits and make informed decisions regarding parental selection, hybridization, and advancement of breeding populations [14-16]. Moreover, understanding the genetic architecture of traits helps optimize selection strategies and accelerate genetic gain in maize breeding [17].

~~During the last few decades, considerable efforts have been devoted to improving yield performance of maize under drought stress conditions through breeding and to understanding the mechanisms involved in drought tolerance [18]. In that context, CIMMYT developed some tropical maize drought tolerant populations while maintaining their yield potential under favourable conditions [19]. Developing such populations requires adoption of proper techniques of identifying and selecting tolerant genotypes to soil water stressed. This also requires identifying traits most suitable for selecting drought tolerant maize. Several investigators emphasized the role of maize genotypes in drought tolerance. Tolerant genotypes of maize were characterized by having shorter anthesis-silking interval (ASI) [20], more ears plant-1 [21-22] and greater numbers of kernels/ears [22-23]. The presence of genotypic differences in drought tolerance would help plant breeders in initiating successful breeding programmes to improve such a complicated character. Breeding for tolerance to drought is difficult because the genetic mechanism that controls the expression of such tolerance in crop plants is poorly understood and because of the polygenic nature of such a complicated character [24]. Selection for increased drought tolerance was associated with a significant reduction in the anthesis-silking interval (ASI) and barrenness, and an increase in ears plant~~$^{-1}$~~, stay green and harvest index [25-26].~~

Variability refers to the range and distribution of phenotypic traits within a population. Assessing the extent and nature of variability in maize populations provides valuable insights into the genetic potential and adaptability of the crop to different environments [~~27~~18]. Heritability estimates the proportion of phenotypic variation that can be attributed to genetic factors. High heritability indicates that a trait is pre-dominantly influenced by genetic factors, making it more amenable to selection in breeding programmes. Heritability estimates are crucial in determining the potential success of selecting for desired traits in maize populations [~~28~~19]. Genetic advance quantifies the expected gain from selection in a breeding programme. It represents the increase in mean performance of a population resulting from the selection of superior individuals as parents for the next generation. Understanding the genetic advance facilitates the design of effective selection strategies to improve maize populations for desired traits [~~29].~~20] .

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Genetic diversity among individuals or populations can be determined using different morphological [~~30-33~~21-24], biochemical [~~34-35~~25-26], and molecular approaches [~~36-51~~27-42]. It is now possible to quantify and evaluate the magnitude of diversity present among germplasm line (s) by employing diverse biometrical methods for use in ~~a~~ breeding programme. The aim of this study was to investigate the genetic variation within maize genotypes and identify genotype (s) that exhibit strong performance under conditions of limited water availability. Along with assessing range of different morpho-physiological parameters that are related to drought tolerance, and determine which of these parameter (s) could be effectively employed as selection criteria within maize breeding programmes.

MATERIALS AND METHOD

Experimental material: The seeds of 12 maize inbred lines were acquired from Sam Higginbottom Agriculture Science and Technology University, Prayagraj, U.P., India (Table 1).

Crossing Program: This was initiated following half diallel analysis as per method suggested by Jinks and Hayman [43] and 66 F_1 hybrids were raised.

Experimental site: The evaluation of the 66 hybrids, along with two check varieties (drought-tolerant HKI1105 and drought-susceptible HKI1128) and the parental lines, was conducted at the Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, Gwalior, M.P., India during the ~~*Rabi*2019-20 and *Kharif* 2020.~~ Rabi season of 2019-20.

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Experimental design: The experiment was laid out in a randomized block design (RBD) with two replications. A total of 80 entries (66 hybrids, 2 checks, and 12 parents) were included in the investigation.

Field conditions: The experiment was conducted under both irrigated and partially irrigated conditions.

Planting arrangement: Each genotype was sown in two rows, each measuring 4 meters in length. The spacing between rows was kept 60 cm, and between plants within a row was 20 cm.

Observations recorded : The observations were recorded for five randomly selected plants from each entry in each replication for 18 different parameters including days to 50 % tasseling, days to 50 % silking, anthesis silking interval, plant height (cm), cob length (cm), numbers of kernel rows per cob, numbers of kernel per rows, 100- grain weight (g), seed yield per plant (g), numbers of cobs per plant, days to maturity, cob girth (cm), shelling %, canopy temperature (°C), turgid weight (g), relative water content, saturation water deficit and membrane stability index.

Statistical analysis

Microsoft excel 2010 was used to process the experimental data, SPSS 20 were ~~employed~~used to analyse ~~data~~it. Randomized complete block design (RCBD) with one-way ANOVA was used to analyze data. The treatment means were compared using the least significant difference (LSD) at 5% level of significance [~~53~~44]. The genetic components of variance viz., phenotypic and genotypic coefficients of variation percent were computed by the formulae given by Burton [~~54~~45]. Heritability percent in broad sense was estimated by the formula as ~~suggested~~given by Singh ~~et al./ [55~~and Choudhary [46]. The estimates of expected genetic advance from selection, Genetic advance was estimated mean by using the formula suggested by Johnson *et al*.[~~56~~47] .

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RESULT AND DISCUSSION

Analysis of variance for different quantitative traits

Analysis of variance was performed to test the difference amongst parents and hybrids for all the eighteen traits and the result are presented in Table 2. The results revealed that the MSS (Mean Sum of Squares) due to genotypes were highly significant for all the characters investigated. The MSS due to genotypes was further partitioned into parents, hybrids and parents vs. hybrids. The analysis of variance for experimental design in individual environment revealed significant differences among genotypes for all the characters in both the environments. Further partitioning of genotypic variance into parents, hybrids and parent's v/s hybrids reveled that for all the characters under study there were significant difference in all environments (Table 2).

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The analysis of variance for experimental design revealed the presence of significant amount of variability among parents in individual environment for most of the characters this suggested that the parental lines selected were quite variable for most of the characters under study. Further, the analysis of variance revealed that the variation due to moisture stress at two different times affect genotypes significantly for all the traits indicating the presence of sufficient variability in the experimental material. Presence of adequate amount of variability encourages for screening of the genotypes for moisture stress tolerance. A wide range of significant differences for various traits has also been reported earlier by Kumar et al. [~~57],~~48] and Ertiro et al. [~~58~~49], Jumaa and Madab [~~59~~50], Chaurasia et al. [~~60~~51] and Mallikarjuna et al. [~~61~~52].

Genetic variability, heritability, genetic advance and genetic advance as percent of mean

The objective of this ~~investigation~~study was to analyse several genetic parameters, including genotypic ~~and~~coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance as a percentage of the mean. The investigation involved 12 inbred lines, 66 hybrids, along with two reference checks, evaluating 18 different traits under both irrigated and partially irrigated conditions~~ in two different seasons.~~. The findings from this analysis may provide valuable insights for formulating effective breeding strategies aimed at enhancing maize traits. These genetic parameters provide information about the extent of variation present among genotypes and the potential improvements that can be achieved. Detailed results for these parameters across different traits are outlined in Table 3 and Fig 1.

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Genotypic (GCV) and phenotypic (PCV) coefficients of variation

Genotypic and phenotypic coefficients of variation were calculated to assess the degree of genetic and environmental variation, respectively. These coefficients provide valuable insights into the extent of variability present in the studied traits and help ~~to determine~~in determining the potential for genetic improvement. The GCV and PCV values for various traits are presented in Table 3.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were compared in this study. Overall, the PCV tended to be higher than the GCV, indicating the influence of environmental factors on all the investigated traits. Among the maize genotypes examined, moderate to high variability was ~~documented~~observed for most of the traits. Under irrigated and partial irrigated condition, traits ~~*viz.,*~~as days to 50 percent tasselling ~~and~~, days to 50 percent silking, anthesis silking interval (ASI), plant height and membrane stability index exhibited high GCV and PCV. Gopalakrishna *et al*. [~~62~~53] also reported similar results for days to 50% tasselling, days to 50% silking, anthesis-silking interval, and plant height, whereas Sinana et al. [~~63~~54] reported high PCV and GCV for plant height. These findings are like the outcomes of Bhusal et al.[~~64~~55] and Sharma et al. [~~65] as well.~~56]. ASI under irrigated as well as partial irrigated conditions showed higher genotypic and phenotypic coefficients of variations. Kharel et al. [~~66~~57] and Sharma et al.[~~65~~56] also reported higher variability for ASI.

A higher GCV suggests a greater contribution of genetic factors to the observed variation, indicating that these traits are influenced by the genetic makeup of the maize lines. On the other hand, a higher PCV indicates a greater influence of environmental factors, such as growing conditions, on the expression of the traits. The GCV and PCV values can be used as indicators to prioritize traits for selection in maize breeding programmes. Traits with high GCV values are more likely to respond positively to selection, as they are under strong genetic control. Conversely, traits with high PCV values may require more attention to environmental management and may have limited genetic potential for improvement [9-16].

In contrast, under irrigated ~~as well as~~and partially irrigated conditions, moderate variability was ~~evidenced~~observed for numbers of kernels per row, seed yield per plant (g), days to maturity and saturation water deficit. This implied equal importance of additive and non-additive gene action for the traits. Lal *et al*.[~~67~~58] also recorded moderate PCV and GCV for characters viz., numbers of kernel rows per row. Bhadru et al. [~~68~~59] found moderate PCV and GCV for seed yield per plant. Overall, moderate PCV and GCV in maize indicate that there is potential for improvement through genetic research and breeding, but it may require a more comprehensive approach than simply selecting the best individuals based on phenotype alone.

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Whereas cob length (cm), numbers of kernel rows per cob, 100- grain weight (g), cob girth (cm), shelling %, canopy temperature (°C), turgid weight (g) and relative water content exhibited low PCV and GCV under irrigated as well as partial irrigated conditions. Sharma et al.[~~69~~60] obtained similar findings. When GCV and PCV values are low for a particular trait, it suggests that there is limited genetic and phenotypic variation within the investigated population for that specific trait. This implies that the expression of the trait is relatively consistent among the genotypes, and there is less potential for improvement through selective breeding.

Heritability in broad sense and genetic advance as percent of mean

Heritability estimates provide breeders with valuable insights into the proportion of phenotypic variation that can be attributed to genetic factors. By accurately estimating heritability, breeders can assess the potential for genetic improvement in specific traits [9-12]. This knowledge enables them to focus their efforts on traits with higher heritability, increasing the likelihood of success in genetic enhancement [12-14]. Heritability, coupled with genetic advances, plays a significant role in accelerating the improvement of traits in breeding programmes [15-16]. The integration of genetic technologies and techniques allows breeders to harness the genetic potential of plants and enhance desirable traits more effectively. Here's how heritability, in conjunction with genetic advances, can drive progress in plant breeding.

In this investigation, high heritability coupled with higher genetic advance as a percentage of mean (GAM) were determined for days to 50% silking and tasselling, anthesis silking interval, plant height, numbers of kernel rows per cob, numbers of kernel per rows, seed yield per plant (g), numbers of cobs per plant, days to maturity, cob girth (cm), turgid weight (g), saturation water deficit and membrane stability index for both irrigated and partial irrigated conditions. High heritability estimates in these traits indicated their higher response to selection ~~[70~~[61]. Prakash et al [~~71~~62]. also reported high heritability combined with higher genetic advance as percent of mean for cob weight, tassel length, numbers of tassel branches, grain yield per plant, chlorophyll index, plant height, cob length and anthesis silking interval. All other traits under consideration expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield.

Under irrigated and partial irrigated conditions moderate heritability coupled with moderate GAM were found for 100-grain weight (g) for both irrigated and partial irrigated conditions. The findings of Rajesh et al. [~~72~~63] were consistent with the current study, as moderate heritability coupled with moderate genetic advance values were observed for kernels per row, 100-kernel weight, and plant height. The moderate heritability values imply that a significant proportion of the observed variation in these traits is due to genetic factors, and the moderate genetic advance values indicate that selection for these traits could lead to substantial improvements in maize yields.

However, cob length (cm), canopy temperature (°C), and shelling percentage exhibited moderate heritability with low GAM under irrigated as well as partial irrigated conditions (Table 3). Moderate heritability coupled with low genetic advance as a per cent of mean, indicates that the expression of the trait is under the control of non-additive type of gene action and its response to selection would be poor [9-12]. Heritability estimates are useful because they demonstrate the potential for genetic relationships and evolution through natural selection in succeeding generations. It measures how consistently a certain trait has been displayed throughout time and between generations. It is more important to consider heritability and genetic advancement than to only rely on heredity in order to predict the outcomes of selecting the best candidates. It was therefore essential to understand heredity and genetic growth while selecting indices for programme development [15].

CONCLUSION

In this investigation, under irrigated as well as partial irrigated conditions traits as days to 50 percent tasselling and silking, anthesis silking interval (ASI), plant height and membrane stability index exhibited high GCV and PCV. The traits with the highest heritability coupled with higher genetic advance were found for the traits viz., days to 50% silking, days to 50% tasselling, anthesis silking interval, plant height, numbers of kernel rows per cob, numbers of kernel per rows, seed yield per plant (g), numbers of cobs per plant, days to maturity, cob girth (cm), turgid weight (g), saturation water deficit and membrane stability index for both irrigated and partial irrigated ~~conditions~~condition. The high heritability was associated with ~~higher~~high genetic advance suggesting additive gene action and these traits can easily be fixed in the genotypes by selection in the early generations. Therefore, these traits can serve as suitable targets for genetic improvement through selective breeding. The identification and selection of high-yielding maize genotypes with desirable traits in the early generations can help in the development of better hybrids for commercial production. This finding has important implications for future research, as it suggests that genetic advances could lead to significant improvements in these traits. Overall, our study highlights the importance of considering both variability and heritability in genetic research, as these factors ~~could mhave~~can have a significant impact on the outcomes of such studies.

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Table 1 List of inbred lines with their parentage used in study

S.No.	**Lines**	**Parentage**	**Source**
1	IL-1	CM-13	SHUATS, Allahabad
2	IL-2	CML-193	SHUATS, Allahabad
3	IL-3	CML-439	SHUATS, Allahabad
4	IL-4	NBPGR-36417	SHUATS, Allahabad
5	IL-5	NBPGR-36417 X NBPGR-33000	SHUATS, Allahabad
6	IL-6	(103) NBPGR-36548 X (97) NBPGR-36407	SHUATS, Allahabad
7	IL-7	DMR-N 21 X NBPGR-32809	SHUATS, Allahabad
8	IL-8	LM- 13 X NBPGR-31899	SHUATS, Allahabad
9	IL-9	CML-224-1 X NBPGR-32809	SHUATS, Allahabad
10	IL-10	NBPGR-36550 X NBPGR-36407	SHUATS, Allahabad
11	IL-11	KL- 153237 X VL- 1016536	SHUATS, Allahabad
12	IL-12	CML- 161 X VL- 1056	SHUATS, Allahabad

Table 2 Pooled ANOVA for different quantitative traits over (two) environments studied in maize (Zea mays L.) under irrigated and partial irrigated conditions

Source of Variations	**Watering Condition**	**df**	**Days to 50 % tasseling**	**Days to 50 % silking**	**Anthesis silking interval**	**Plant height (cm)**	**Cob length (cm)**	**Numbers of kernel rows per cob**	**Numbers of kernel per rows**	**100-grain weight (g)**	**Seed Yield per plant (g)**
Environment	**I**	1	7262051.28**	77143.70**	7020.51**	185644.12**	0.2	802.24**	307.4**	4160.27**	275.83**
	PI		5713232.1**	6829312.82**	23538.8**	57152.35**	1.58	974.14**	29.51**	5006753.37**	300.90**
Blocks Within Environment	**I**	2	10339.1**	105.4**	4402.56**	472.5**	10.92**	329.62**	182.25**	988.91**	62.40**
	PI		10339.10**	13805.13**	4119.55**	472.49**	10.92**	345.41**	219.91**	988.91**	62.41**
Treatments	**I**	77	16432.45**	159.87**	323.36**	1289.42**	6.88**	694.14**	65.03**	3590.61**	1652.03**
	PI		17336.8**	16555.58**	266.12**	1111.46**	5.67**	818.30**	54.18**	5192886.78**	1148.2**
Parent	**I**	11	24445.45**	245.59**	258.33**	2744.3**	3.4**	833.60**	91.91**	4588.9**	801.30**
	PI		23662.88**	22817.42**	483.90**	1930.29**	3.02**	1872.53**	106.07**	5029.63**	884.47**
Hybrid	**I**	65	13365.43**	122.76**	304.55**	866.82**	6.5**	652.25**	40.64**	3444.5**	1550.33**
	PI		14862.49**	14035.78**	231.59**	705.42**	5.53**	563.98**	38.31**	6136227.05**	1009.92**
Parent vs. Hybrid	**I**	1	127645.69**	1629.13**	2261.6**	12754.91**	71.25**	1883.08**	1355.01**	2107.05**	17620.77**
	PI		108579.55**	111462.06**	115.4**	18497.25**	43.72**	5753.02**	514.27**	942198.10**	13037.54**
Treatments * Environment	**I**	77	13616.47**	122.08	238.05**	673.42**	0.79	45.63	3.99**	335.06**	22.61**
	PI		16224.24**	15690.15**	247.54**	604.64**	3.90**	543.01**	14.39**	3838.02**	169.47**
Parent * Environment	**I**	11	14044.7**	140.56**	297.72**	1215.13**	0.85	48.65	3.76	1281.56**	26.28**
	PI		12231.72**	11391.26**	230.90**	871.49**	4.17**	256.02**	16.31**	6141254.47**	404.31**
Hybrid * Environment	**I**	65	12004.87**	107.83**	229.67**	485.5**	0.78	43.12	4.05**	141.37**	21.08**
	PI		12231.72**	11391.26**	230.90**	871.49**	4.17**	256.02**	16.31**	6141254.47**	404.31**
Parent vs. Hybrid. * Environment	**I**	1	77740.38**	844.77**	128.73*	6929.11**	0.66	175.51	3.01	2513.70**	81.38**
	PI		74939.16**	69363.70**	54.21*	2857.81**	3.50*	1626.4	15.34**	906789.06**	11.75*
Error	**I**	154	48.19	0.59	14.9	1.68	0.59	41.08	2.07	40.87	1.18
	PI		48.19	34.35	11.76	1.68	0.59	40.87	0.88	40.87	1.19
Total	**I**	311	30765.27	318.82	197.26	1086.78	2.26	208.2	20.28	1011.93	416.49
	PI		26124.54	29322.76	231.08	675.55	2.79	306.14	19.32	2588.42	376.77

* and ** significant at 5% and 1% level of significance, respectively, I - irrigated condition,   PI - Partial irrigated condition

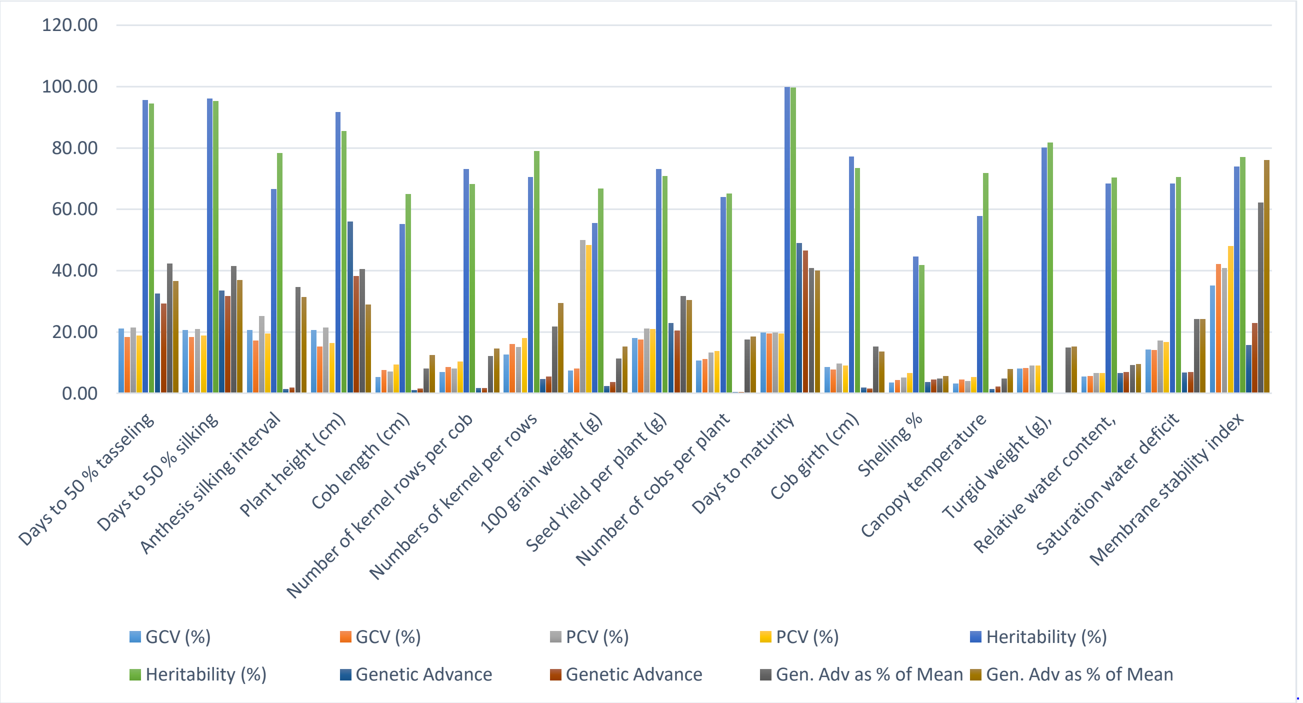
Source of Variations	**Watering Condition**	**df**	**Numbers of cobs per plant**	**Days to maturity**	**Cob girth (cm)**	**Shelling %**	**Canopy temp.** (°C)	**Turgid weight (g)**	**Relative water content**	**Saturation water deficit**	**Membrane stability index**
Environment	**I**	1	6.20*	17239601.28**	1453.85**	21.78	19.80**	29.54**	3.10*	3.20*	34318.24**
	PI		0.42	15490482.05**	3429.43**	84.4	49.28**	262.17**	5570.24**	5629.55**	556.51**
Blocks Within Environment	**I**	2	14.68**	10339.10**	988.91**	81.00**	32.57**	90.78**	16.05**	16.19**	12.22
	PI		16.32**	10339.10**	964.91**	40.51	32.57**	90.78**	2007.82**	2033.25**	0.32
Treatments	**I**	77	41.78**	2475.04**	719.98**	148.86**	7.57**	2180.38**	168.43**	168.49**	65578.13
	PI		31.12**	2903.45**	378.68**	124.13**	7.01**	2169.87**	16130.61**	16120.29**	1287.49**
Parent	**I**	11	39.17**	3396.97**	209.10**	74.66**	4.55**	2395.11**	272.68**	272.68**	53173.32**
	PI		37.63**	4187.88**	700.93**	108.75**	2.82*	2448.06**	27299.36**	27299.36**	858.27**
Hybrid	**I**	65	42.7**	2304.62**	756.17**	163.70**	7.76**	2001.40**	152.95**	153.01**	68576.49**
	PI		30.28**	2669.21**	272.50**	126.7**	7.75**	1989.64**	14474.15**	14462.08**	1354.80**
Parent vs. Hybrid	**I**	1	11.14*	3412.82**	3987.11**	0.46	28.94**	11451.92**	28.21**	28.08**	7137.67**
	PI		14.27**	4000.23**	3735.73**	126.32	3.88	10825.23**	944.51**	934.16**	1633.58**
Treatments * Environment	**I**	77	5.85**	2048.03**	67.71**	11.92**	0.21	27.56**	3.54**	3.53**	10529.90**
	PI		7.1**	2154.78**	266.31**	92.23**	4.6**	25.88**	576.91**	577.28**	98.37**
Parent * Environment	**I**	11	2.53*	984.09**	82.15**	23.25**	0.42	25.79**	5.03**	5.03**	11944.42**
	PI		5.48**	3208.33**	309.81**	107.38**	3.89**	30.75**	606.82**	606.82**	85.65**
Hybrid * Environment	**I**	65	6.5**	2224.80**	64.87**	9.58*	0.17	27.83**	3.31**	3.30**	10194.76**
	PI		7.47**	1950.42**	262.7**	90.6**	4.25**	24.01**	556.36**	556.59**	99.20**
Parent vs. Hybrid. * Environment	**I**	1	0.04	2261.6**	93.38	39.69*	0.8	29.76**	1.26	1.28	16754.37**
	PI		0.82	3849.01**	22.36	32.06	35.04**	94.64**	1583.66**	1597.13**	184.38**
Error	**I**	154	1.11	48.19	40.87	6.5	1.19	0.81	0.77	0.77	32.93
	PI		1.1	48.19	41.03	34.83	1.19	0.81	31.83	31.69	0.68
Total	**I**	311	12.46	56643.02	226.3	43.62	2.79	547.74	43.07	43.08	18970.2
	PI		10.12	51151.34	197.24	71.35	3.83	545.47	4183.17	4180.99	345.25

* and ** significant at 5% and 1% level of significance, respectively, **UI** - Under irrigated condition, **UPI** - Partial irrigated condition

Table 3 Coefficient of variation, heritability and genetic advance as percent of mean among the inbreeds, their hybrids and checks

Characteristics	**GCV (%)**		**PCV (%)**		**Heritability (%)**		**Gen. Adv as % of Mean**	
	I	**PI**	**I**	**PI**	**I**	**PI**	**I**	**PI**
Days to 50 % tasseling	20.99	18.22	21.47	18.74	95.50	94.50	42.27	36.48
Days to 50 % silking	20.51	18.32	20.93	18.76	96.00	95.30	41.38	36.84
Anthesis silking interval	20.57	17.19	25.20	19.42	66.60	78.30	34.59	31.33
Plant height (cm)	20.50	15.14	21.40	16.39	91.70	85.40	40.44	28.83
Cob length (cm)	5.24	7.48	7.06	9.28	55.10	64.90	8.02	12.42
Number of kernel rows per cob	6.88	8.53	8.05	10.33	73.00	68.20	12.11	14.50
Numbers of kernel per rows	12.60	16.03	15.00	18.03	70.50	79.00	21.79	29.35
100 grain weight (g)	7.33	7.95	49.85	48.33	55.40	66.70	11.25	15.25
Seed Yield per plant (g)	17.98	17.55	21.03	20.86	73.10	70.80	31.65	30.43
Number of cobs per plant	10.59	11.13	13.25	13.80	63.90	65.10	17.44	18.50
Days to maturity	19.82	19.41	19.84	19.44	99.80	99.70	40.79	39.92
Cob girth (cm)	8.44	7.70	9.60	8.98	77.20	73.40	15.27	13.58
Shelling %	3.41	4.20	5.11	6.50	44.60	41.70	4.69	5.58
Canopy temperature (°C)	3.06	4.50	4.02	5.31	57.80	71.80	4.79	7.86
Turgid weight (g),	8.07	8.20	9.03	9.07	80.00	81.70	14.88	15.27
Relative water content,	5.37	5.52	6.50	6.58	68.30	70.30	9.15	9.53
Saturation water deficit	14.23	14.02	17.21	16.71	68.40	70.40	24.23	24.23
Membrane stability index	35.10	42.05	40.83	47.91	73.90	77.00	62.15	76.02

I = Irrigated condition, **PI** = Partial irrigated condition



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Cob length (cm)
Number of kernel rows per cob
Numbers of kernel per rows
100 grain weight (g)
Seed Yield per plant (g)
Number of cobs per plant
Days to maturity
Cob girth (cm)
Shelling %
Canopy temperature
Turgid weight (g),
Relative water content,
Saturation water deficit
Membrane stability index
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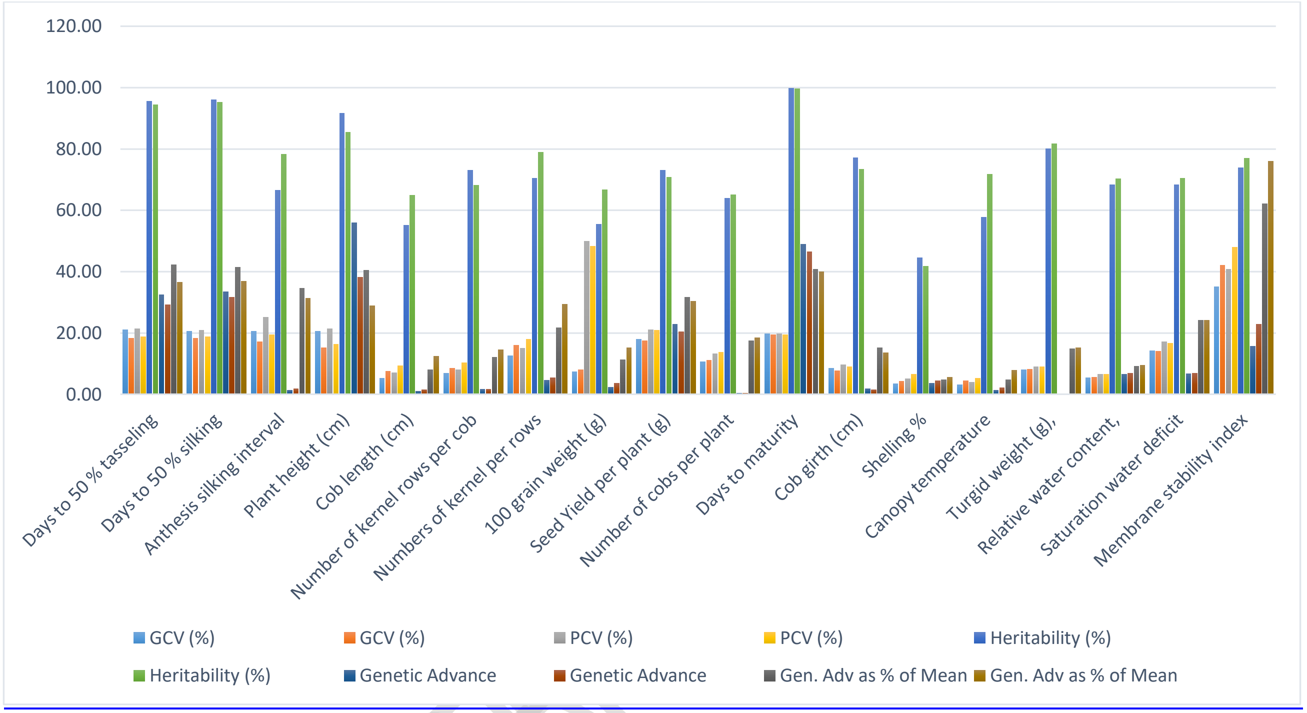

Fig 1 Graphical representation of coefficient of variation, heritability, and genetic advance as percent of mean among 80 genotypes in maize