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Studies on genetic variability, heritability and genetic advance in exotic maize (*Zea mays* L.) Inbreds for yield and yield component traits

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Abstract
The present investigation was carried out at the Wheat and Maize Research Station, VNMKV, Parbhani (M.S.) during *Rabi* 2022-23 to assess the genetic variability, heritability, and genetic advance among 47(38 fixed inbreds and 9 doubled haploids) with 3 checks including Phule Maharshi, Rajarshi and PAC 251. The trial was conducted in Randomized Block design with two replications and observations were recorded for 12 yield contributing traits in maize. Analysis of Variance (ANOVA) reported presence of significant variation in the genotypes for all the twelve traits. The values of phenotypic coefficient of variance is reported to be slightly higher than their corresponding genotypic coefficient of variation suggesting less effect of environment on expression of these traits. Based on the mean, the range of variation was more for characters *viz*., days to 50% to tassel, days to 50% to Silk, days to 75% dry husk, plant height, Cob placement height, cob length, cob girth, number of kernel rows, kernels/ row, grains /cob, 100 seed wt., grain yield / plant. Mean performances of grain yield and other morphological traits revealed that yielding potential of genotypes VL 18314, VL 19842 and KL 141702 were highest yielding potential and also as par the check, Rajarshi. High value of heritability together with high genetic advance were recorded for the traits *viz*., cob placement height, kernels per row, number of grains per cob, 100 grain weight and grain yield per plant.

Keywords: Maize, inbreds, variability, heritability, genetic advance

Introduction

Being a cross-pollinated species having protandry, which insures production of less than 5% grains by self-pollination, maize is among the most diversified crop species due to its wide morphological diversity and geographic adaptability. Physiological and morphological features in maize vary greatly, and the genetic sequences are highly polymorphic in its large genome (2.4 GB). For the creation of new inbred lines of maize, genetic diversity is a crucial component since it is critical for the realization of heterosis in hybrid combinations in maize breeding. There is a vast maize growing belt in India, including many states, where acreage of hybrid maize is almost 100%. A thorough genotypic and phenotypic assessment of inbred lines is pre-requisite for the successful development of hybrid maize varieties for commercial cultivation. The production of synthetic cultivars with specific genes for desirable characteristics including yield, tolerant to biotic and abiotic stresses, QPM, large amounts of micronutrients, and other quality attributes are also possible by using high quality inbred only. So, among maize breeders and cultivators, conserving genetic diversity and optimizing the management of genetic resources are crucial concerns. Success of hybrid maize breeding programme depends on thorough knowledge of the genetic diversity among commercially important maize inbred lines and planned utilization of promising inbreds according to their performance (Pushpavalli *et al*., 2001 and Stich *et al*., 2005) [12, 20]. The optimal breeding strategies, parental line selection, and broadening of the genetic base of maize germplasm in a breeding program can all be aided by knowledge of genetic diversity (Ajala *et al*. 2019) [1].

The amount and extent of genetic variability in a crop offers the foundation for efficient selection and a method for boosting yield and component traits through a strategic breeding programme. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are useful in determining the amount of variation present in genetic material,

which aids in the development of an effective breeding plan. Estimates of heritability are a good indicator for predicting character transmission from parents to offspring. Heritability coupled with genetic advance helps in understanding the mode of inheritance of quantitative traits**.**

Materials and Methods
The experimental material for present investigation included 47 exotic inbreds of maize (38 fixed inbreds and 9 doubled haploids) with 3 checks including Phule maharshi, Rajarshi and PAC 251. This trial was conducted at Wheat and Maize Research Unit, VNMKV, Parbhani during *rabi* 2022-23 with spacing of 60 cm × 20 cm and plot size 4.0 m × 0.60 m. The experiment was setup in in a Randomized block design having two replications. The crop was grown with all package and practice recommended for growing maize in this area. Observations were recorded from three random plants of each plot in each replication for twelve yield and it's contributing characters: days to 50% tasseling, days to 50% silking, days to 75% dry husk, plant height (cm), cob placement height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, kernels per row, number of grains per cob, 100 grain weight, grain yield per plant. Analysis of variance (ANOVA) was analyzed using mean values of the collected utilizing statistical analysis technique given by Panse and Sukhatme (1985) [11]. Burton's approach was used to determine genotypic and phenotypic variations. Allard's method was used for calculating broad sense heritability (h^2) and algorithm of Johnson *et al*. was used for calculating genetic

gain for each traits. All the statistical analysis was done using endostat software.

Result and Discussion
Genetic diversity is vital for any crop improvement program and plant breeding is all about controlling the diversity that is inherent in a population for the well-being of human kind. Maize is a highly cross-pollinated crop and majorly grown as hybrids followed by synthetics. Presence of significant genetic diversity in the inbreds is a prerequisite for developing of high value commercial hybrids for food, feed and industrial uses. The degree and magnitude of genetic makeup of the traits under study was disclosed by heritability and genetic advance study. Analysis of variance for forty seven inbreds and three checks are furnished in Table 1. The treatments *i.e.* mean sum of squares due to genotypes showed significant variance in all the twelve traits namely, days to 50% tasseling, days to 50% silking, days to 75% dry husk, plant height (cm), cob placement height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, kernels per row, number of grains per cob, 100 grain weight, grain yield per plant at 1% and 5% level of significance, indicating that they were genetically divergent. Similar results of significant mean sum of squares due to genotypes for all the traits studied were reported by (Rafiq *et al*., 2010; Reddy *et al*., 2013) [13, 15]. This suggests that there are plenty of scopes for selection of suitable inbreds to be used in crop improvement programs.

Table 1: ANOVA Table

Source	df	DT	DS	DH	PH	EH	CL	CG	nKR	K/R	G/C	100 SW	GY
Replication	1	30.86	0.09	0.53	4.37	8.24	1.16	1.43	4.07	2.71	112.73	15.66	211.46
Genotype	49	32.613**	29.925***	40.878***	391.67***	329.87***	5.593***	2.193***	4.201***	15.001***	5425.71***	35.318***	375.49***
Error	49	16.292	7.025	8.067	28.177	7.449	0.559	0.548	0.706	0.649	144.18	2.919	22.443

DT: Days to 50% Tasselling, DS: Days to 50% Silking, DH: Days to 75% Dry Husk, PH: Plant Height, CPH: Cob placement height, CL: Cob Length, CG: Cob girth, nKR: Number of kernel rows, K/R: kernels/ row, G/C: grains /cob, 100SW: 100 seed wt., GY: Grain yield / plant.

Mean Performance: The mean value for character yield/plant ranged from 51.57 g to 106.72 g with general mean of 81.82 gm. Genotype VL 18314 (106.72 g) followed by VL 19842 (105.72 g), KL 141702 (104.44 g) and Rajarshi

(check)(102.51 g) was reported the maximum grain yield/plant. The checks PAC 751 and Phule Maharshi showed 88.30 g and 81.45 g yield/plant.

Table 2: The mean performances of grain yield and its related traits

Genotype	DT	DS	DH	PH	EH	CL	CG	nKR	K/R	G/C	100 SW	GY
VL18323	77.39	79.40	108.23	167.51	74.88	13.37	15.01	12.86	18.69	250.87	36.88	87.12
VL107657	74.25	76.23	104.64	158.54	66.92	14.90	12.96	13.87	21.83	306.05	30.15	68.51
KL155738	82.62	78.72	109.44	155.81	63.18	13.17	15.38	11.76	16.58	199.09	42.13	59.60
VL1016532	80.40	76.80	107.52	173.87	72.54	15.28	14.18	13.57	22.23	295.62	35.09	100.68
VL18314	81.77	79.20	110.88	172.94	85.80	15.05	15.10	13.27	25.94	341.06	33.17	106.72
VL21975	78.54	75.84	108.23	159.32	64.64	14.70	12.97	13.87	21.11	310.28	25.81	71.71
VL21948	75.38	75.08	103.01	179.52	85.56	16.15	13.47	13.07	24.95	319.41	30.29	91.97
VL21971	77.52	78.54	103.01	154.38	71.36	15.18	13.57	13.56	26.18	364.32	21.91	72.93
VL181609	80.73	78.00	104.16	165.17	72.54	14.07	13.27	12.76	20.99	256.80	29.17	61.31
VL181619	82.62	78.44	106.95	159.94	69.81	18.05	15.11	14.08	28.81	403.61	32.16	95.01
VL21952	77.39	75.84	108.23	178.49	81.77	21.94	12.52	13.27	26.78	364.62	26.24	52.17
VL21959	77.39	75.84	106.56	140.54	50.89	16.32	13.97	13.66	26.08	359.27	25.70	74.66
VL181509	73.26	75.24	110.16	161.27	65.47	17.13	13.56	12.44	24.57	304.51	32.56	78.01
VL181675	79.20	83.64	116.28	189.95	87.42	16.32	11.76	10.00	24.57	237.12	31.01	72.97
VL21964	82.62	80.93	117.30	185.09	98.29	13.37	13.77	14.28	25.14	352.42	26.29	78.79
VL21968	80.58	77.76	106.79	159.32	67.72	13.07	13.46	13.46	22.87	301.83	26.23	68.54
VL181580	76.23	80.58	111.56	200.40	100.22	15.42	11.59	11.07	24.86	270.17	27.63	72.22

	DT	DS	DH	PH	CPH	CL	CG	nKR	K/R	G/C	100SW	GY
VL21980	80.58	80.19	108.48	147.07	57.62	14.37	11.12	11.02	26.62	283.01	25.81	79.56
VL21982	79.70	77.03	109.89	154.57	68.35	15.18	11.78	12.57	23.50	296.60	28.15	72.76
VL21987	79.70	78.21	104.90	148.90	53.18	14.87	14.49	13.14	19.10	256.63	30.95	70.17
VL185877	81.60	76.26	107.73	158.40	64.35	14.28	14.38	13.66	23.56	305.27	28.66	81.19
VL184659	78.54	79.40	106.56	153.28	66.53	13.87	13.87	14.28	28.28	414.12	20.20	86.19
VL184725	71.28	73.26	101.76	178.30	80.20	11.56	13.47	12.57	17.13	214.21	31.11	53.16
VL184560	78.21	78.00	107.52	157.41	63.36	14.70	13.66	13.87	21.48	279.17	32.19	93.05
VL184076	76.23	75.84	111.56	181.35	88.73	13.76	14.48	16.04	24.35	394.52	29.70	87.82
VL184141	81.60	76.26	109.44	133.06	44.66	14.28	14.07	15.32	24.92	374.44	27.74	86.19
VL183975	77.63	73.92	107.91	146.06	53.43	14.48	12.38	12.24	24.77	297.22	28.97	51.58
VL184330	85.91	84.15	115.83	156.26	55.87	15.05	14.79	12.76	24.28	321.30	38.30	97.89
VL1010982	68.31	66.30	93.00	180.10	88.90	16.93	13.87	11.88	24.35	292.25	33.76	89.45
VL1010930	70.35	67.10	105.06	150.66	67.34	14.69	13.16	10.69	22.24	233.05	37.54	78.03
VL1010960	73.44	74.46	103.95	175.23	79.95	14.26	13.46	13.27	22.66	303.71	29.08	84.66
KL141702	66.33	68.31	99.99	162.54	76.23	14.97	14.38	14.48	25.25	347.52	30.20	104.45
VL1011000	74.37	74.10	103.68	168.68	73.71	14.77	14.69	12.28	22.08	269.51	31.15	82.21
VL162291	81.77	78.98	110.18	195.98	104.94	12.97	12.87	13.25	23.34	308.30	25.70	77.32
VL19842	76.50	73.92	104.64	173.65	77.18	14.45	15.18	17.18	22.23	374.79	27.74	105.73
VL19562	76.23	74.66	104.90	154.44	62.77	18.32	13.67	12.86	28.34	352.07	31.15	97.70
VL18212	73.37	69.75	104.33	175.68	85.80	15.73	14.79	14.48	26.30	385.21	27.03	94.86
VL18201	75.48	77.52	102.06	167.90	71.62	14.85	13.36	12.47	24.00	302.40	30.25	80.80
VL183822	77.39	77.03	109.89	168.30	73.13	14.37	13.67	14.18	25.34	336.58	26.93	93.77
VL18223	78.21	78.98	113.57	165.42	68.90	16.08	15.20	14.89	26.04	391.68	24.75	97.42
VL183808	79.56	81.60	112.56	161.82	77.03	15.91	13.77	15.44	25.04	403.07	22.91	86.73
VL18211	73.49	74.46	99.23	171.67	75.26	13.46	15.42	13.46	21.55	293.09	28.84	67.32
VL1016977	73.26	75.24	103.68	171.47	77.42	12.86	13.17	13.27	20.69	261.02	28.46	76.30
VL183003	76.50	75.08	103.01	184.28	94.47	13.27	14.28	15.30	26.72	260.73	30.09	73.77
ZL2178	70.29	71.18	105.53	157.58	62.11	13.27	14.18	15.94	24.10	294.57	22.61	78.69
ZL2119	74.37	70.68	108.54	182.56	87.17	15.73	14.28	16.15	19.87	371.04	28.94	84.66
ZL2123	73.37	70.88	107.54	157.54	73.66	13.66	15.01	14.70	25.74	319.67	32.44	92.57
PAC 751	79.70	74.66	104.90	155.42	63.76	16.08	15.25	13.66	25.39	359.90	27.13	88.31
Rajarshi	81.77	80.40	105.84	152.15	65.86	15.28	13.66	11.68	27.89	372.93	28.61	102.51
Phule Maharshi	79.20	81.18	114.57	159.19	67.12	15.88	12.08	14.59	23.96	328.97	24.74	81.45
Mean	77.24	76.30	107.10	165.38	72.99	14.95	13.79	13.49	23.87	316.71	29.29	81.82
C.V.	5.23	3.47	2.65	3.21	3.74	5.00	5.37	6.23	3.38	3.79	5.83	5.79
F ratio	2.00	4.26	5.07	13.90	44.28	10.00	4.00	5.95	23.10	37.63	12.10	16.73
S.E.	2.85	1.87	2.01	3.75	1.93	0.53	0.52	0.59	0.57	8.49	1.21	3.35
C.D. 5%	8.11	5.33	5.71	10.67	5.48	1.50	1.49	1.69	1.62	24.13	3.43	9.52
Min	66.33	66.30	93.00	133.06	44.66	11.56	11.12	10.00	16.58	199.09	20.20	51.58
Max	85.91	84.15	117.30	200.40	104.94	21.94	15.42	17.18	28.81	414.12	42.13	106.72

DT: Days to 50% Tasselling, DS: Days to 50% Silking, DH: Days to 75% Dry Husk, PH: Plant Height, CPH: Cob placement height, CL: Cob Length, CG: Cob girth, nKR: Number of kernel rows, K/R: kernels/ row, G/C: grains /cob, 100SW: 100 seed wt., GY: Grain yield / plant.

Table 3: Genetic variability parameters for grain yield/plant and its attributing traits.

Characters	Range		Mean	Variances			Coefficients of Variation (%)		Heritability in broad sense (%)	Genetic Advance	Genetic Advance in (%) mean
	Min	Max		Genotypic	Phenotypic	Environmental	Genotypic	Phenotypic			
DT	66.33	85.91	77.241	8.16	24.45	16.29	3.698	6.402	33.40	3.400	4.401
DS	66.30	84.15	76.300	11.45	18.47	7.02	4.435	5.633	62.00	5.488	7.192
DH	93.00	117.30	107.102	16.40	24.47	8.06	3.782	4.619	67.00	6.831	6.379
PH	133.06	200.40	165.378	181.75	209.92	28.17	8.152	8.761	86.60	25.841	15.626
EH	44.66	104.94	72.991	161.21	168.66	7.44	17.395	17.792	95.60	25.572	35.034
CL	11.56	21.94	14.953	2.51	3.07	0.55	10.610	11.730	81.80	2.956	19.771
CG	11.12	15.42	13.790	0.82	1.37	0.54	6.576	8.488	60.00	1.447	10.497
nKr	10.00	17.18	13.489	1.74	2.45	0.70	9.799	11.613	71.20	2.298	17.034
K/R	16.58	28.81	23.866	7.17	7.82	0.64	11.225	11.721	91.70	5.284	22.143
G/C	199.09	414.12	316.711	2640.76	2784.95	144.18	16.226	16.663	94.80	103.083	32.548
100sw	20.20	42.13	29.285	16.19	19.11	2.91	13.744	14.931	84.700	7.632	26.061
GY	51.58	106.72	81.824	176.52	198.97	22.44	16.238	17.239	88.70	25.780	31.507

DT: Days to 50% Tasselling, DS: Days to 50% Silking, DH: Days to 75% Dry Husk, PH: Plant Height, CPH: Cob placement height, CL: Cob Length, CG: Cob girth, nKR: Number of kernel rows, K/R: kernels/ row, G/C: grains /cob, 100SW: 100 seed wt., GY: Grain yield / plant.

Genetic variability parameters for various characters

In population improvement, for improvement of a character, determination of extent of genetic variability is very important. Presence of wide range of variability in the experimental material will increase the chance of selecting desired genotype. The results are presented in table 3 and figure 1. A wide range of variability was observed for most of the yield and yield contributing traits in the genotypes under study. Based on the mean, the range of variation was more for characters *viz.*, days to 50% to tassel, days to 50% to Silk, days to 75% dry husk, plant height, Cob placement height, cob length, cob girth, number of kernel rows, kernels/ row, grains /cob, 100 seed wt., grain yield / plant. Wide-ranging variability for different yield contributing traits in maize was reported by several workers including Rafique *et al.* (2010) [13] for cob placement height, cob diameter, ear length, 100 grain weight and grain yield. Kharel *et al* (2017) [9] for ear height, number of kernels per row, 100 kernel weight, plant height. Wedwessen and Zeleke (2020) [21] for number of ears per plant, grain yield per hectare, 100 kernel weight and ear height.

GCV and PCV

For all the yield-contributing traits in the current experiment, genotypic coefficients of variation were less than phenotypic coefficients of variation, although there was only a small difference among the values of GCV and PCV. A relative resilience to environmental changes is shown by the small distinction between PCV and GCV. Low (10%), moderate (10- 20%), and high (>20%) genotypic and phenotypic coefficients of variation, according to Shivasubramanian and Menon (1973) [18]. Cob placement height, cob length, number of kernels per row, number of grains per cob, 100 seed weight and grain yield per plant all showed moderate estimates of genotypic and phenotypic coefficient of variation in the current study. These findings concur with those of other researchers, including those from Kharel *et al.* (2017) [9] for kernels/row and cob placement height, and moderate for days to 50% silking, 100 seed weight and ear length, Rahman *et al.* (2015) [14] for grain yield/plant, and Kapoor and Batra (2015) [8] for plant height and number of grains/cob.

Lower phenotypic and genotypic coefficients of variance were found for plant height, cob girth, days to 50% tasseling, days to 50% silking, days to 75% dry husk, and days to 50% silking. These findings concur with those for the number of kernel rows /ear, days to 50% silking, and ear diameter published by researchers Kandel *et al.* (2018) [7] and days to 75% dry husk according to Oruganti *et al.* (2023) [10].

For all the characteristics under examination, the phenotypic coefficient of variation was larger than the corresponding genotypic coefficient of variation, which is consistent with findings by Ghimire and Timsina (2015) [2], Rahman *et al.* (2015) [14], and Sravanti *et al.* (2017) [19]. The graphical representations of the genetic parameters are interpreted in figure 1.

Heritability and genetic advance

In addition to understanding genetic diversity, understanding heritability and genetic advance can assist breeders in choosing the best breeding strategy to swiftly accomplish their breeding goals by measuring the proportional degree to which a character will inherit to the next generation. The high degree of heritability estimates indicated that the traits were under genotypic control and selection might be relatively simple, with improvement practicable through selective breeding for these traits. The combination of heritability and genetic advance estimates provides a valid selection program criteria and insight into the gene action involved in the development of diverse polygenic traits. Robinson *et al.* (1949) [16] classified heritability estimates into three categories: high (above 60%), moderate (between 30 and 60%), and low (below 30%). genetic advance as percent of mean are divided into three categories: high (20% and above), moderate (11-20%), and low (below 10%) by Johnson *et al.* (1955) [5].

In present study, High value of heritability were recorded for all the characters *viz.*, days to 50% silking, days to 75% dry husk, plant height (cm), cob placement height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, kernels per row, number of grains per cob, 100 grain weight and grain yield per plant except days to 50% tasseling. High value of heritability indicates that greater portion of phenotypic variance has been attributed to genotypic variance in compare to lower portion of environmental variance. Hence it can be concluded that on the basis of phenotypic performance reliable selection can be made. Similar results were reported by Sravanti *et al.* (2017) [19] for grain yield/plant and cob height. Jilo *et al* (2018) [4] for cob length, plant height and 100 seed weight. Kharel *et al.* (2017) [9] for days to 59% silking, numbers of kernel/row and cob length.

High value of genetic advance were recorded for characters *viz.*, cob placement height (35.03), kernels per row (22.14), number of grains per cob (32.54), 100 grain weight (26.06) and grain yield per plant (31.50). While moderate for plant height (15.62), cob length (19.77), cob girth (10.49), number of kernel rows (17.03).

The estimates of heritability combined with expected genetic advance are more useful than heritability estimates alone for estimating yield under phenotypic selection. High heritability coupled with high expected genetic advance suggests that the additive gene action predominates and ensures better gain on selection of these traits. High heritability along with high expected genetic advance were exhibited for the characters *viz.* cob placement height, kernels per row,

number of grains per cob, 100 grain weight and grain yield per plant. Similar results were reported by Sandeep *et al.* (2015) [17] for cob placement height, number of kernels per row, grain yield per plant, 100 seed weight, Kabdal *et al.* (2003) [6] for grain yield, plant height, ear height and ear length. For grain yield per plant and number of kernels per row (Hepziba *et al.* 2013) [3].
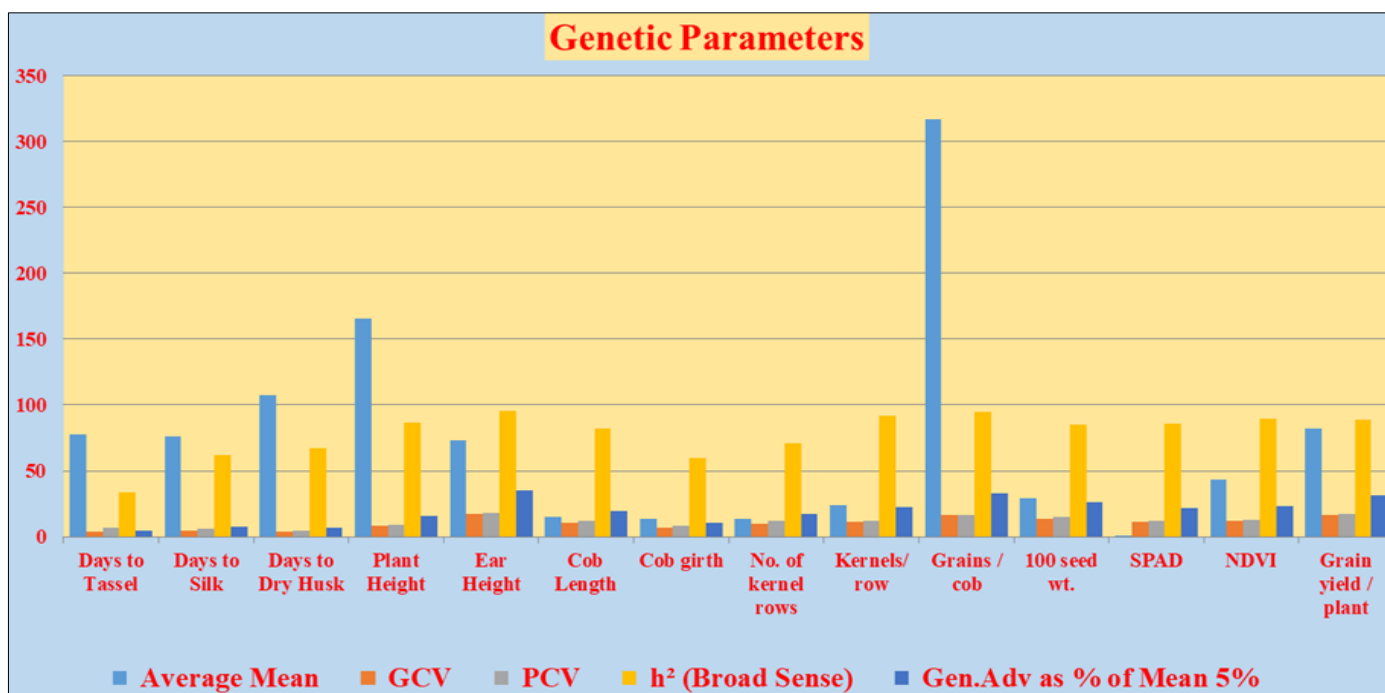
Fig 1: Graphical representation of genetic parameters for grain yield and contributing traits

Conclusion
The current study revealed considerable amount of genetic variability as reported by analysis of variance for all the 14 traits under study. The variability among the genotypes was also validated by statistical analysis of data collected from genotypes. The phenotypic coefficient of variation was larger than the corresponding genotypic coefficient of variation, suggesting least environmental effect. The traits *viz*., days to 50% to tassel, days to 50% to Silk, days to 75% dry husk, plant height, Cob placement height, cob length, cob girth, number of kernel rows, kernels/ row, grains /cob, 100 seed wt. and grain yield / plant reported higher range of variation, based on the mean performance. High heritability along with high expected genetic advance were exhibited for the characters *viz*. cob placement height, kernels per row, number of grains per cob, 100 grain weight and grain yield per plant. The experiment indicated higher variability among the genotypes, which provide an opportunity for selection of inbreds for hybrid development. It will also be helpful for increasing maize production and productivity by hybrid development programs.

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