

## GENETIC VARIABILITY AND CHARACTER ASSOCIATION AMONG MAIZE (*ZEA MAYS L.*) INBRED LINES

BJ ANTONY, RM KACHAPUR\*, GK NAIDU, SC TALEKAR, M ZERKA<sup>1</sup>  
AND SI HARLAPUR

*University of Agricultural Sciences, Dharwad, Kumbapur-M-Narendra,  
Karnataka 580005, India*

*Keywords:* Genetic variability, Heritability, GAM, GCV, PCV, Correlation, Maize

### Abstract

Genetic analysis of variability, heritability and character association was studied among 25 maize inbred lines for eleven traits. The ANOVA indicated significant variation among the inbred lines chosen for the study for all the traits. Wide range of variability was observed for all the traits among them grain yield varied from 16.03 to 62.52 q/ha with an average mean value of 45.75 q/ha. Phenotypic variance was higher as compared to genotypic variance and highest phenotypic variance was observed for plant height followed by grain yield. However, the difference between phenotypic and genotypic variance was very narrow for majority of the traits. Similarly, phenotypic coefficient of variation (PCV) was marginally higher than the genotypic coefficient of variation (GCV) and highest GCV and PCV was recorded for grain yield (37.03, 38.12) followed by ear height (24.12, 26.48) indicating that these characters are under genetic control and have high potential for selection. High amount of broad-sense heritability coupled with high genetic advance as a percent of mean (GAM) was observed for grain yield (0.94 and 74.12) followed by number of kernels per row (0.90 and 32.88) indicating that phenotypic based selection for these traits would be successful. Hundred grain weight had the highest genotypic correlation (0.834) with grain yield followed by number of kernels per row (0.623).

### Introduction

Among the coarse grain cereals Maize (*Zea mays L.*) is an important crop of immense genetic potential for yield because of commercially exploitable heterosis. Maize drives the economy of many countries as it is an industry-oriented crop required for extraction of starch, glucose, maltose syrup, ethanol and as a poultry feed around the world. Therefore, it is being grown in 165 countries around the world with the production of 1147.6 million tons and productivity of 5.92 t/ha during 2019-2020. The demand for maize in developing countries is estimated to double by the year 2050 (Rosegrant *et al.* 2009). In India, maize is the third most important crop among cereals after rice and wheat occupying an area of 9.26 m. ha with average productivity of 3.0 t/ha during 2019-20. Even though, the area under maize crop has increased over the decades the productivity must increase to satisfy the growing demand to meet the requirements of poultry / animal feed, human food, and industrial processing. One way of enhancing production is by bringing in more area under maize cultivation which is not possible in the present situation in that case exploiting the genetic potential of the crop through conventional / molecular breeding, good agronomic management practices, developing climate resilient hybrids with resistance to biotic and abiotic stress would be the best approach to increase the productivity of maize for per unit area, so that it can result in increased production.

To do that plant breeding comes to rescue wherein, the knowledge of genetics and plant breeding methodologies assist in selecting genetically potential lines for different traits and using

\*Author for correspondence: <kachapurr@uasd.in>. <sup>1</sup>CIMMYT, C/o ICRISAT, Patancheru, Hyderabad, India.

them to generate heterotic hybrids to achieve higher grain yield. The main objective of maize breeding programs worldwide is to improve grain yield and it is a continuous process of creating variability, selecting superior lines from a pool, and utilizing them to achieve this goal. An assessment of variability and heritability is necessary to make an effective artificial selection and to understand variation in the material (Begum *et al.* 2016).

The selection process is most effective when there is ample variability in the base material. Hence, it is more important to assess variability in the base material for artificial selection before exercising selection. It is possible to assess variability by using genetic parameters such as range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Sesay *et al.* 2016). Despite the presence of variability, the efficiency of selection is influenced by heritability and selection intensity (Dudly and Moll 1969). The estimates of broad sense heritability and genetic advance as a percent of mean (GAM) provides a reliable information about the heritable portion of the trait. High broad sense heritability along with high GAM also indicates the presence of additive gene action and hence selection could be effective (Nwangburuka *et al.* 2012).

Besides variability it is also necessary to know the association of various characters to the trait of economic interest *i.e.*, grain yield. Since, grain yield is a complex trait it is affected by several yield-related characters, selection based on yield attributes is more effective (Grafius 1956). So, a detailed description of the associations between grain yield and other yield contributing characters is more valuable, which can be obtained by a correlation study. Additionally, dividing the correlation into direct and indirect effects by path analysis allows a better understanding of the influence of each yield attributing trait on yield, which in turn helps to design the selection strategy (Azam *et al.* 2014). Hence, the present study was undertaken to assess variability and association of various quantitative traits in maize using twenty-five maize inbred lines as a base material.

### Materials and Methods

The material for the present study comprised of 25 maize inbred lines, where 23 lines were selected based on their resistance reaction to turicum leaf blight from the screening nursery. These lines were evaluated along with two genetically diverse checks CM-111 (flint) and CM-202 (dent). All these 25 lines were evaluated in randomized complete block design (RCBD) with three replications during *rabi*, 2020-21 at All India Co-ordinated Maize Improvement Project, MARS, Dharwad. Each entry was raised in two rows of four-meter length with a spacing of 60 x 20 cm and following all the recommended package of practice.

The observations were recorded from each inbred lines for eleven quantitative traits *viz.*, days to 50 per cent tasseling (DTT), days to 50 per cent silking (DTS), days to 75 per cent dry husk (DTM), plant height (PH) (cm), ear height (EH) (cm), number of kernel rows per cob (NKRC), number of kernels per row (NKR), cob girth (CG) (cm), cob length (CL) (cm), hundred grain weight (HGW) (g) and grain yield (GY) (q/ha). The mean values of the data from these genotypes was subjected to analysis of variance (ANOVA) using variability package (Popat *et al.* 2020) in R-studio Rx643.6.2 and ANOVA was tested for significance. Genotypic and phenotypic variances were determined according to Singh and Chaudhary (1985) using MS-Excel programme.

The genotypic coefficient of variation and phenotypic coefficient of variation were computed according to Burton and De vane (1953) using the following formula.

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{y}} \times 100$$

$$\text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where,  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance and  $\bar{x}$  = sample mean. The GCV and PCV were classified according to Sivasubramanian and Menon (1973) as low (less than 10 %), moderate (10-20%) and high (more than 20%).

Heritability Broad Sense ( $h^2_{bs}$ ) was computed for each character as the ratio of genotypic variance to the total variance as suggested by Hanson *et al.* (1956).

$$\text{Heritability broad sense } (h^2_{bs}) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,  $\sigma_g^2$  = genotypic variance and  $\sigma_p^2$  = phenotypic variance. It was categorized by Robinson *et al.* (1951) as low (less than 30%), moderate (30–60%) and high (more than 60%). Genetic advance and genetic advance as percent of mean were estimated according to Johnson *et al.* (1955) using the following formula,

$$\text{GA} = i \times h^2_{bs} \times \sigma_p,$$

Where,  $i = 2.06$  (selection intensity at 5%)

$\sigma_p$  = Phenotypic standard deviation

$h^2_{bs}$  = Heritability in broad sense

$$\text{Genetic advance as per cent of mean (GAM)} = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

The GAM is grouped as low (less than 10%), moderate (10-20%) and high (more than 20%) respectively, according to Johnson *et al.* (1955).

Karl Pearson's simple correlation coefficients for all the eleven characters both at genotypic and phenotypic level and path analysis using grain yield as a dependent character at genotypic level was worked out using variability package (Popat *et al.* 2020) and the heatmap of the correlation was made using function corrplot in R-studio Rx643.6.2. This heat map representation helps in visualizing data using colour variations. The colour intensity of the box indicates how strongly they are associated, while the colour indicates whether they are associated positively or negatively.

## Results and Discussion

The analysis of variance for grain yield and yield contributing characters among the test inbred lines is presented in Table 1. The mean sum of squares due to genotypes was found to be significant for all the eleven quantitative traits, indicating significant variation existed among the inbred lines chosen for the study. Hence from this, one can understand that the genotypes which were used in the study can be used for further breeding programme. However, the variation due to number of kernel rows/ cob and cob length was low as compared to other characters. The variability among the inbred lines was measured using range, mean, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) with regard to all the 11

characters, along with that broad sense heritability and genetic advance over mean was calculated and displayed in Table 2.

**Table 1. Analysis of variance for eleven quantitative traits in maize (*Zea mays* L.).**

Traits	df	DTT	DTS	DTM	PH	EH	NKRC	NKR	CG	CL	HGW	GY
Replications	2	4.96	0.85	0.57	59.92	74.89	0.13	1.38	0.03	0.74	2.09	9.26
Genotypes	24	111.87**	93.56**	21.63**	1090.53**	535.23**	4.84**	59.51**	0.51**	10.41**	54.78**	878.25**
Error	48	3.62	1.08	0.74	95.22	34.3	0.43	2.08	0.01	0.43	1.54	17.05
CV (%)	-	2.64	1.42	0.82	7.35	9.65	4.17	6.24	3.41	4.86	4.08	13.91
CD @5%	-	3.12	1.71	1.41	15.85	8.49	0.94	2.54	0.21	1.09	2.04	10.59

\* - Significant at 5 % and \*\* - Significant at 1 % level of probability.

DTT - Days to 50 per cent tasseling, DTS -Days to 50 per cent silking, DTM - Days to 75 per cent dry husk, PH - Plant height (cm), EH - Ear height (cm), NKRC-Number of kernel rows per cob, NKR - Number of kernels per row, CG - Cob girth, CL - Cob length (cm), HGW – Hundred grain weight (g), GY - Grain yield (q/ha).

**Table 2. Genetic parameters with respect to yield and yield contributing traits in maize (*Zea mays* L.) inbred lines.**

Parameters	Traits										
	DTT	DTS	DTM	PH	EH	NKRC	NKR	CG	CL	HGW	GY
Mean	72.16	73.25	105.05	129.69	53.580	13.98	26.03	3.87	13.70	30.69	45.75
Minimum	57.00	60.00	101.00	86.40	24.40	11.20	17.50	2.83	9.70	22.00	16.03
Maximum	81.50	82.00	111.00	165.20	73.60	16.00	32.55	4.56	16.50	36.50	62.52
$\sigma_g^2$	36.08	30.83	6.96	331.61	166.98	1.47	19.14	0.17	3.33	17.75	287.07
$\sigma_p^2$	39.70	31.91	7.70	426.83	201.28	1.90	21.23	0.19	3.76	19.29	304.12
GCV	8.32	7.58	2.51	14.04	24.12	8.68	16.81	10.53	13.31	13.73	37.03
PCV	8.73	7.71	2.64	15.93	26.48	9.87	17.70	11.12	14.16	14.31	38.12
$H_{bs}^2$	0.91	0.97	0.90	0.78	0.83	0.77	0.90	0.90	0.88	0.92	0.94
GAM	16.35	15.35	4.92	25.49	45.25	15.72	32.88	20.56	25.77	27.13	74.12

$\sigma_g^2$  - Genotypic variance,  $\sigma_p^2$  - Phenotypic variance, GCV - Genotypic coefficient of variation (%), PCV- Phenotypic coefficient of variation (%),  $H_{bs}^2$  - Broad sense heritability, GAM – Genetic advance over mean (%).

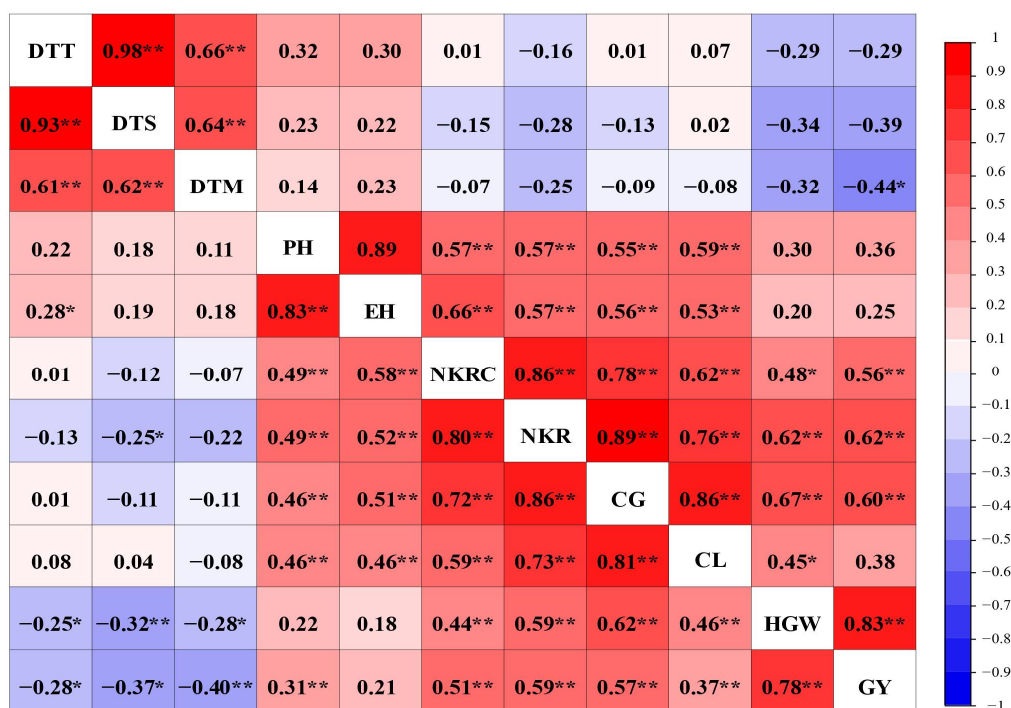
DTT - Days to 50 per cent tasseling, DTS -Days to 50 per cent silking, DTM - Days to 75 per cent dry husk, PH - Plant height (cm), EH - Ear height (cm), NKRC Number of kernel rows per cob, NKR - Number of kernels per row, CG - Cob girth (cm), CL - Cob length (cm), HGW – Hundred grain weight (g), GY - Grain yield (q/ha).

There was a wide range of variability exhibited for all the traits, among them grain yield varied from 16.03 to 62.52 q/ha with a mean value of 45.75 q/ha (Table 2). Similarly, there was a wide range of variability observed for flowering and maturity traits, plant height, number of kernels/rows, cob length and hundred seed weight. This amount of variability is a pre-requisite in any breeding programme to create further variation.

Overall, the phenotypic variance ( $\sigma_p^2$ ) was higher than genotypic variance ( $\sigma_g^2$ ) for plant height (426.83 and 331.61), grain yield (304.12 and 287.07) and ear height (201.28 and 166.98) indicating the influence of environmental factors in expression of these traits. However, the difference was very marginal for number of kernel rows per cob, number of kernels/ row, cob length, cob girth and days to maturity indicating that environmental factors influencing the expression of these traits was very low/nil, thereby whatever selections were made based on the genotypic performance for these traits will easily be expressed in the next generation. In general,

PCV was marginally higher than GCV for majority of the traits but the difference was of very low magnitude except for ear height and cob length indicating the environmental factors influenced the expression of these two traits (Table 2).

Highest GCV and PCV was recorded for grain yield (37.03, 38.12) followed by ear height (24.12, 26.48) indicating that these characters are under genetic control and have high potential for selection. Whereas moderate GCV and PCV were observed for number of kernels per row (16.81, 17.70), plant height (14.04, 15.93), hundred grain weight (13.73, 14.31), cob length (13.31, 14.16) and cob girth (10.53, 11.12). Low GCV and PCV was recorded for number of kernel rows per cob (8.68, 9.87), days to 50 per cent tasseling (8.32, 8.73), day to 50 per cent silking (7.58, 7.71) and days to 75 per cent dry husk (2.51, 2.64). For all the traits, the difference between GCV and PCV was very low, indicating environmental influence in the experiment is low. Moderate to high GCV and PCV for grain yield, hundred grain weight and cob characters excluding number of kernel rows per cob suggested that there is ample of opportunity for selection in the present experimental material. Earlier high GCV and PCV for grain yield and moderate GCV and PCV for cob characters were observed by Jilo *et al.* (2018) and Magar *et al.* (2021), where they suggested moderate to high GCV and PCV provides opportunity to practice selection in the genotypes for the trait improvement.



\*- Significant at 5 % and \*\* - Significant at 1 % level of probability.

DTT - Days to 50 per cent tasseling, DTS -Days to 50 per cent silking, DTM - Days to 75 per cent dry husk, PH - Plant height (cm), EH - Ear height (cm), NKRC-Number of kernel rows per cob, NKR - Number of kernels per row, CG - Cob girth, CL - Cob length (cm), HGW – Hundred grain weight (g), GY - Grain yield (q/ha).

Fig 1. Heat map indicating correlation among yield and yield contributing charaters in maize (*Zea mays* L.) (above diagonal genotypic correlation, below diaagnoal phenotypic correlation).

Even though the trait has high variability in terms of GCV and PCV, the effectiveness of the selection could be evaluated only based on the heritable portion of the character. Which could be identified based on heritability and genetic advances as a percent of mean (Rao and Rao 2015). In general, high broad-sense heritability coupled with high GAM for the trait, is considered to have a positive response to the phenotypic selection (Wali *et al.* 2019). All the eleven traits exhibited high broad-sense heritability. Whereas, days to 50 per cent silking had a maximum value of 0.97 followed by grain yield (0.94). The high amount of broad-sense heritability for all the quantitative traits indicated the least influence of the environment on these characters.

GAM was high for grain yield, ear height, number of kernels per row, plant height, hundred grain weight, cob length and cob girth. Wedwessen and Zeleke (2020) also observed high heritability with high GAM for grain yield, hundred grain weight, number of kernels per row and cob length supporting the findings of the present study. Furthermore, number of kernel rows per cob, days to 50 per cent tasseling and days to 50 per cent silking had moderate GAM and days to 75 per cent dry husk had low GAM in the present study, even though all these traits had high heritability. It also indicates that high heritability is always not associated with high GAM. Since, heritability does not always lead to high genetic gain. Thus, it is recommended to consider heritability and GAM together to predict the response of selection (Ogunniyan and Olakojo 2014). Grain yield, hundred grain weight, number of kernels per row, cob length and cob girth exhibited high broad-sense heritability along with high GAM, as a result, phenotypic performance-based selection for these traits would be more successful.

The information about the direction and magnitude of association of various quantitative traits help in indirect selection for grain yield in the breeding programme, as the direct selection of a complex trait like grain yield is ineffective due to the influence of many genes and the environment (Grafius 1956). The traits which show a strong association with grain yield and had high heritability could be used for indirect selection to improve grain yield. The heat map representation of correlation coefficient among the eleven quantitative traits, both at genotypic and phenotypic level displayed in Fig. 1, where the intensity of blue and red colour depicts the magnitude of negative and positive correlation among the traits, respectively.

Association of days to 50 per cent tasseling was positive and significant at both genotypic and phenotypic levels with days to 50 per cent silking (0.98, 0.93), days to 75 per cent dry husk (0.66, 0.61). Likewise, days to 50 per cent silking also had significantly high positive association with days to 75 per cent dry husk (0.64, 0.62) at both genotypic and phenotypic levels (Fig. 1). Suresh *et al.* (2021) also noticed a positive association among the flowering and maturity traits in maize. Days to 75 per cent dry husk recorded significantly negative genotypic (-0.44) and phenotypic (-0.40) correlation with grain yield. While, days to 50 per cent silking (-0.37) and days to 50 per cent tasseling (-0.28) showed a significant negative correlation at the phenotypic level. This indicates early maturity gives the advantage to improve yield.

Among the yield contributing traits hundred grain weight recorded highly significant and positive correlation (0.83, 0.78) with grain yield both at genotypic and phenotypic level followed by the number of kernels per row (0.62, 0.59), cob girth (0.60, 0.57) and the number of kernel rows per cob (0.56, 0.51) indicating that by exercising selection for these strongly associated traits, grain yield can be enhanced directly. Pavan *et al.* (2011) reported a similar kind of association in their study. However, cob length (0.37), plant height (0.31) exhibited a significant positive correlation with grain yield only at the phenotypic level.

A significant inter-trait association was found between yield attributes in this study. The cob length was significantly associated in a positive direction both at genotypic and phenotypic levels with cob girth (0.86, 0.81), number of kernels per row (0.76, 0.73) and number of kernel rows per

cob (0.62, 0.59). There is also a significant and positive association between cob girth, number of kernels per row and number of kernel rows per cob both at genotypic and phenotypic levels. Similar results were also noticed by Devasree *et al.* (2020). Thus, the cob characters and hundred grain weight are considered as important yield contributing traits. Hence, all of them are strongly associated with each other, improving all these traits simultaneously or improving a few traits without compensating others could help in improving the grain yield of maize crop.

Although the correlation coefficient indicates the association between the traits, it does not indicate their direct and indirect effects. By partitioning the correlation coefficient using path analysis, it is possible to calculate the direct and indirect effects (Wali *et al.* 2012). Due to its importance, grain yield was considered a dependent trait and a genotypic correlation coefficient was partitioned. Five of the ten quantitative characters at the genotypic level exhibited positive direct effect on grain yield (Table 3). The trait hundred grain weight (0.5733) had a maximum positive direct effect, followed by plant height (0.4672), number of kernel rows per cob (0.3552), cob girth (0.3292) and days to 50 per cent silking (0.0371). The characters, cob length (-0.3382), ear height (-0.3245), days to 75 per cent dry husk (-0.2598), number of kernels per row (-0.2209) and days to 50 per cent tasseling (-0.0528) on other hand had a negative direct effect on yield. Similarly, direct positive effect of hundred grain weight, number of kernel rows per cob and cob girth on grain yield was reported by Patil *et al.* (2016).

**Table 3. Direct (diagonal) and indirect effects of different quantitative traits on grain yield (q/ha) in maize (*Zea mays* L.) at genotypic level.**

Characters	DTT	DTS	DTM	PH	EH	NKRC	NKR	CG	CL	HGW	Genotypic correlation of grain yield
DTT	<b>-0.0528</b>	0.0364	-0.1718	0.1473	-0.099	-0.0009	0.0348	0.0011	-0.0226	-0.1653	<b>-0.29</b>
DTS	-0.0517	<b>0.0371</b>	-0.1667	0.107	-0.0717	-0.055	0.0613	-0.0417	-0.0080	-0.1972	<b>-0.39</b>
DTM	-0.0349	0.0238	<b>-0.2598</b>	0.0677	-0.0735	-0.0259	0.0548	-0.0304	0.0265	-0.1851	<b>-0.44*</b>
PH	-0.0167	0.0085	-0.0377	<b>0.4672</b>	-0.2891	0.203	-0.1263	0.1821	-0.2003	0.1701	<b>0.36</b>
EH	-0.0161	0.0082	-0.0588	0.4163	<b>-0.3245</b>	0.2337	-0.1261	0.184	-0.1802	0.1167	<b>0.25</b>
NKRC	0.0001	-0.0057	0.019	0.2671	-0.2135	<b>0.3552</b>	-0.1893	0.2567	-0.2099	0.2769	<b>0.56**</b>
NKR	0.0083	-0.0103	0.0645	0.267	-0.1852	0.3044	<b>-0.2209</b>	0.2952	-0.2561	0.3556	<b>0.62**</b>
CG	-0.0002	-0.0047	0.024	0.2585	-0.1814	0.277	-0.1981	<b>0.3292</b>	-0.2909	0.3829	<b>0.60**</b>
CL	-0.0035	0.0009	0.0204	0.2767	-0.1729	0.2205	-0.1673	0.2832	<b>-0.3382</b>	0.2584	<b>0.38</b>
HGW	0.0152	-0.0128	0.0839	0.1386	-0.0661	0.1715	-0.1371	0.2198	-0.1524	<b>0.5733</b>	<b>0.83**</b>

Residual effect = 0.192.

\* - Significant at 5 % and \*\* - Significant at 1 % level of probability.

DTT - Days to 50 per cent tasseling, DTS -Days to 50 per cent silking, DTM - Days to 75 per cent dry husk, PH - Plant height (cm), EH - Ear height (cm), NKRC Number of kernel rows per cob, NKR - Number of kernels per row, CG - Cob girth (cm), CL - Cob length (cm), HGW – Hundred grain weight (g).

These results suggest 100-grain weight, number of kernel rows per cob, cob girth and plant height were the important traits that affected the grain yield directly. The residual effect of the study was found to be lower (0.192). Thus, this study suggests that hundred grain weight, number of kernel rows per cob, cob girth and plant height traits are directly contributing to grain yield in maize. Therefore, the indirect selection of these traits would be appropriate to improve the yield.

As a conclusive remark of the present study, it was noticed from the results that, sufficient variability was present among the inbred lines for yield and yield attributes. High broad-sense heritability with high genetic advance over mean for grain yield, hundred grain weight, number of kernels per row, cob length and cob girth indicate selection of these traits based on the phenotype would be effective. Furthermore, hundred grain weight, cob girth and the number of kernel rows per cob are positively associated with grain yield and also had a positive direct effect. Therefore, the selection of these traits would directly improve yield in maize.

### Acknowledgments

The authors acknowledge the support of AICRP-Maize, University of Agricultural Sciences, Dharwad for providing all the logistic support in conduct of the experiment and CIMMYT for having used their genetic material. Additionally, they would like to thank the Indian Council of Agricultural Research (ICAR) for granting ICAR-Junior research fellowship to the first author for his M. Sc degree programme.

### References

- Azam MG, Sarker U and Banik BR 2014. Genetic variability of yield and its contributing characters on CIMMYT maize inbreds under drought stress. *Bangladesh J. Agril. Res.* **39**: 419-426.
- Begum S, Ahmed A, Omy SH, Rohman MM and Amiruzzaman M 2016. Genetic variability, character association and path analysis in maize (*Zea mays* L.). *Bangladesh J. Agr. Res.* **41**: 173-182.
- Burton GW and Devane EM 1953. Estimating heritability in tall fescue from replicated clonal-material. *Agron. J.* **45**: 478-481.
- Devasree S, Ganesan KN, Ravikesavan R, Senthil N and Paranidharan V 2020. Relationship between yield and its component traits for enhancing grain yield in single cross hybrids of maize (*Zea mays* L.). *Electron. J. Plant Breed.* **11**: 796-802.
- Dudly JW and Moll RH 1969. Interpretation and use of estimates of heritability and genetic variance in plant breeding. *Crop Sci.* **9**: 257-267.
- Grafius JE 1956. Components of yield in oats: A geometrical interpretation. *J. Agron.* **48**: 419-423.
- Hanson CH, Robinson HF and Comstock RE 1956. Biometrical studies of yield in segregating populations of Korean lespedera. *Agron. J.* **48**: 268-272.
- Jilo T, Tulu L, Birhan T and Beksisa L 2018. Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia. *J. Plant Breed. Crop Sci.* **10**: 281-289.
- Johnson HW, Robinson HF and Comstock RE 1955. Estimates of genetic and environmental variability in soybeans. *J. Agron.* **47**: 314-318.
- Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhyaya J and Shrestha J 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon* **7**: 07939.
- Nwangburuka CC, Denton OA, Kehinde OB, Ojo DK, Popoola AR 2012. Genetic variability and heritability in cultivated okra (*Abelmoschus esculentus* (L.) Moench). *Spanish. J. Agric. Res.* **10**: 123-129.
- Ogunniyan DJ and Olakojo SA 2014. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Niger. J. Genet.* **28**: 24-28.
- Pavan R, Lohithaswa HC, Wali MC, Prakash G and Shekara BG 2011. Correlation and path coefficient analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.). *Electron. J. Plant Breed.* **2**: 253-257.
- Patil SM, Kumar K, Jakhar DS, Rai A, Borle UM and Singh P 2016. Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.). *Int. J. Agric. Environ. Biotechnol.* **9**: 1103-1108.



- Popat R, Patel R and Parmer D 2020. Variability: genetic variability analysis for plant breeding research <https://CRAN.R-project.org/package=variability>.
- Robinson HF, Comstock RE and Harvey PH 1951. Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.* **43**: 282-287.
- Rao P and Rao VT 2015. Genetic analysis for yield and its components in pigeonpea (*Cajanus cajan* (L.) Mill Sp). *Int. J. Appl. Biol. Pharmaceut. Technol.* **6**: 189-190.
- Rosegrant MR, Ringler C, Sulser TB, Ewing M, Palazzo A, Zhu T, Nelson GC, Koo J, Robertson R, Msangi S and Batka M 2009. Agriculture and food security under global change: Prospects for 2025/2050. International Food Policy Research Institute, Washington, DC, pp. 145-178.
- Sesay S, Ojo D, Ariyo OJ and Meseka S 2016. Genetic variability, heritability and genetic advance studies in topcross and three-way cross maize (*Zea mays* L) hybrid. *Maydica* **61**: 1-7.
- Suresh D, Kachapur RM, Talekar SC and Gurumurthy R 2021. Genetic variability and trait association studies in maize (*Zea mays* L.). *J. Farm Sci.* **34**: 122-125.
- Singh RK and Chaudhary BD 1985. Biometrical Methods in Quantitative Genetic Analysis. Kalayani Publishers, New Delhi, India, pp. 318.
- Sivasubramanian S and Menon M 1973. Heterosis and inbreeding depression in rice. *Madras Agric. J.* **60**: 1139.
- Wali MC 2019. Genetic variability and divergence studies in maize (*Zea mays* L.). *EC Agric.* **5**: 2014-15.
- Wali MC, Kachapur RM, Kulkarni VR and Hallikeri SS 2012. Association studies on yield related traits in maize (*Zea mays* L.). *Maize J.* **1**: 131-133.
- Wedwessen T and Zeleke H 2020. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *Int. J. Novel Res. Life Sci.* **7**: 10-16.

*(Manuscript received on 22 November 2022; revised on 10 March, 2024)*