Assessment of Genetic Variability, Heritability, and Genetic Advance in Maize (*Zea mays* L.) Segregating Generations

Naveen Keshamalla [a*], Rajendra Prasad K. [a], Sunil Neelam [b] and Mallaiah B. [c]

[a] *Department of Genetics and Plant Breeding, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad-500 030, India.*
[b] *Winter Nursery Centre, ICAR-Indian Institute of Maize Research, Rajendranagar, Hyderabad, India.*
[c] *Maize Research Centre (MRC), ARI, Rajendranagar, Hyderabad, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

The recent experiment aimed to investigate genetic traits for eleven characteristics, namely, Days to 50% tasselling, Days to 50% silking, Plant height (cm), Tassel length (cm), Ear length (cm), Ear diameter (cm), Ear height (cm), Number of kernel rows per cob, Number of kernels per row, Cob weight (g), and Grain yield (g) during the Kharif and Rabi seasons of 2023-24. The Alpha Lattice Design was employed with two replications. Genotypes were sown in single row, each 2 meters

_____

long in each replication. The analysis of variance revealed significant variations among all traits, with phenotypic coefficients of variation (PCV) generally exceeding genotypic coefficients of variation (GCV). Grain yield (K; 53.45, 51.7: R;101.56, 101.2) and Cob weight (K;38.9, 36.92: R;91.14, 90.81) exhibited the highest phenotypic and genotypic coefficients of variation (PCV and GCV) across both seasons, signifying significant genetic variability in the studied material. r Grain yield showed the highest heritability (99.4) with cob weight (99.2) coming in second. The high heritability indicates a strong likelihood that these traits will be successfully passed on to offspring, making selection more effective. Traits such as Grain yield (g), Cob weight (g), Ear diameter(cm), Ear height(cm), and Tassel length(cm). Demonstrated high heritability and genetic advancement in both seasons, making them promising candidates for enhancement through selection based on additive genetic factors.
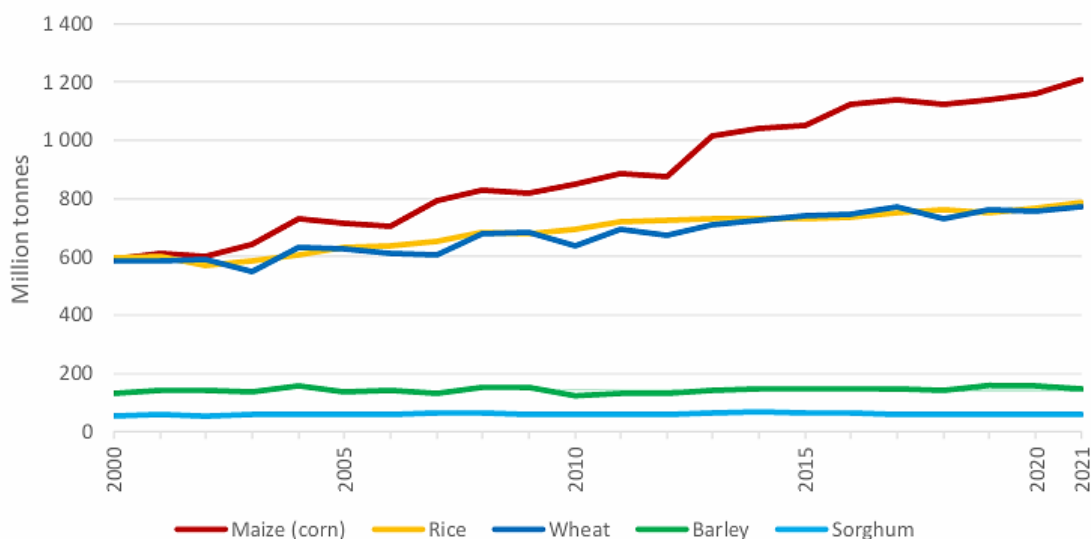
1. INTRODUCTION

Maize (*Zea mays* L.) is the world's most important crop and is extensively grown as a cereal grain that originated in Central America. It is one of the most flexible developing crops, offering more versatility. Maize is renowned as the "Queen of Cereals" due to its tremendous genetic yield potential. Maize is the only food cereal crop that can be cultivated in various seasons, environments, and applications [1]. It is the second most widely grown crop in the world after wheat, FAOStat, Maize is an industry-oriented crop used to extract starch, glucose, maltose syrup, ethanol, and poultry feed, contributing to the global economy in many nations [2]. For billions of people, maize is a vital crop that is used for food, feed, and industrial raw materials. Currently, nearly 1137.3 million MT of maize is being produced together by over 170 countries from 197.4 million ha with an average productivity of 5.8 t/ha [3] (According to 3rdAdvance Estimates of Production of Food grains for 2023-24, all India aize production estimated was 35.67 million tonnes. It is grown on around 1.58 lakh hectares in Telangana, accounting for 2.09% of the total cultivated area, with an estimated yield of 28.80 lakh metric tons in the state [4].

In maize breeding projects, the goal perpetually is to improve economically essential characteristics while retaining a reasonable level of heterogeneity. To promote Genetic diversity in germplasm, it is necessary to understand the level of existing genetic variability in the genotypes. Estimating genetic diversity in available germplasm is an important part of any crop development strategy. hence it is necessary to assess the genotypic and phenotypic coefficients of variation, broad sense heritability, and genetic advance as a percent of the mean. Zhang et al. [5] highlighted the necessity of assessing genetic heterogeneity among maize cultivars produced in a given location before beginning a breeding effort. Genetic variability is essential for the consistent improvement of complex traits, which can be measured using phenotypic and genotypic coefficients of variation. With this consideration.

"The success of any crop improvement program is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection", Bello OB et al. [6]. "Variability is the presence of variations between genotypes as a result of variances in their genetic composition or the environment in which they are cultivated". Wedwessene et al, [7]. The present investigation aimed to find out the genetic variability, heritability, and genetic advance as percent of mean, to find out the association of different morphological and yield traits, and also to analyze the nature and magnitude of the association of the studied c using 54 different maize segregating lines in the kharif season and 49 f_{2-3} lines in the rabi season. Majhi, P.K. et al. [8] defined heritability as the extent of genotype's contribution to phenotypic variation for a trait in a population, which is often represented as the ratio of genetic variance to the total variance. According to Johnson et al. [9], heritability estimates in cultivated plants can be placed in the categories; low (0-30%), moderate (30-60%), and high (> 60%). Genetic advance for each character was estimated by using the formula of Johnson et al. [9] and genetic advance as percent of mean (GAM) was categorized according to him as low (0-10%), moderate (10-20%) and high (> 20%).

Fig. 1. Scenario of a crop improvement program
Source: FAO. 2022. FAOSTAT: Production: Crops and livestock products. In: FAO. Rome. Cited December 2022.
https://www.fao.org/faostat/en/#data/QCL(3)

2. MATERIALS AND METHODS

The experiments including selfing was carried out in *Kharif* 2023, and further segregating generation in *Rabi,* 2023-24 were carried out at Winter Nursery Centre, Rajendranagar, Hyderabad. Winter Nursey Centre, Hyderabad is located at the Southern Telangana agro-climatic zone of Telangana state. Geographically it lies at 17.19 °N latitude, 78.24 °E longitude with an altitude of 542.6 meters above Mean Sea Level (MSL). The rainfall of the Research Station ranged from 606 to 853 mm (long-term range).

The experimental material consists of 54 maize segregating lines in the first season (Kharif 2023) and 49 f_{2-3} lines and these were sown in two replications with Alpha Lattice Design. Each genotype was planted in a single row, 2 meters in length in each replication, with a spacing of 60 cm between rows and 20 cm within rows. The crop was cultivated with the recommended agricultural practices. Observations were recorded for eleven quantitative traits *viz.,* Days to 50 percent tasselling, Days to 50 percent silking, Plant height (cm), tassel length (cm), ear length (cm), ear diameter (cm), ear height (cm), Number of kernel rows per cob, Number of kernels per row, cob weight (g) and grain yield (g).

Johnson et al. [9] developed a method to determine heritability in the broad sense (h2 bs) and genetic progress. Burton's techniques [10]

were used to calculate the genotypic and phenotypic coefficients of variation. The PCV and GCV estimations were classified as low (0-10%), moderate (10-20%), and high (>20%) using Sivasubramanian and Madhavamenon's criteria [11].

Statistical analysis: The analysis of variance (Table 1) was conducted for F2 and F3 generations. Two analyses of variance were conducted. The first was for all genotypes in selected families, and the second was for the chosen families to determine heritability and GCV and PCV. R 4.4.1-win was used to carry out the analysis.

Coefficient of variation: The genotypic and phenotypic coefficients of variation were calculated using the formulae given by Burton [10].

Phenotypic coefficient of variation (PCV %)
$$= \frac{\sqrt{V_p}}{\bar{X}} \times 100$$

Genotypic coefficient of variation (GCV %)
$$= \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

Where,

V_p = Phenotypic variance
V_g = Genotypic variance
$\bar{X}$ = Mean of the character

- Heritability in a broad sense was estimated as $H = \sigma g / 2\,\sigma p2 \times 100$.

3. RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance revealed significant differences among genotypes for all traits in both seasons viz., including Days to 50 percent tasselling, Days to 50 percent silking, Plant height (cm), Tassellength (cm), Earlength (cm), Eardiameter (cm), Earheight (cm), Number ofkernel rows per cob, Number of kernels per row, Cobweight (g), Grain yield (g). (Table 1), indicating genotypic variation among the evaluated genotypes. There is a chance to choose favorable genotypes with improved yield component qualities, which might perform well and lead to greater yield. These findings are congruent with those of other studies, including Ahmad, M.S.H. [12], Chandel et al. [13], Sinha and Thakur [14], Meena et al. [15].

Variability and Heritability: The variability of eleven quantitative traits in 54 maize segregating lines in the first season (Kharif 2023) and 49 f$_{2\text{-}3}$ lines in rabi (2023-24) were assessed using a phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as a percentage of the mean (Table 2).

In this study, the Phenotypic Coefficient of Variation (PCV) was higher than the Genotypic Coefficient of Variation (GCV) for almost all quantitative traits (Table 2) in both the Kharif and rabi seasons of 2023-24. Although the value of the phenotypic coefficient of variation (PCV) for all characters were always found to be higher than the genotypic coefficient variation (GCV) the differences were small in magnitude. This suggests the environment's lower influence on the characters' expression.

The highest values of phenotypic and genotypic coefficients of variation (PCV and GCV) were recorded for grain yield (K; 53.45, 51.7: R;101.56, 101.2) in both seasons followed by cob weight (K;38.9, 36.92: R;91.14, 90.81), indicating significant genetic variability in the material studied. High PCV and GCV values for grain yield and cob weight in maize were also reported by Magar, B.T et al. [16], Bartaula, S et al. [17]. The traits Ear height (K;34, 33.8; R 22.68, 22.59) and ear diameter (K; 32.4, 26.7; R 42.03: 41.83) show height PCV and GCV during both the seasons. The traits KRPE (K;26.5: R;

36.05), KPR (K;26.3: R; 52.5), Ear length (K; 22.65: R; 38.46) and Tassel length (K; 20.17, 22.42) showed the highest PCV for both seasons.

"Moderate GCV and PCV values were observed for the traits of Tassel length (K;19.96), Ear length (K; 15.74), KRPE (K; 13.05), and KPR (K; 12.75) showed moderate GCV values during Kharif season 2023-24 and Plant height (R; 13.9) showed moderate PCV during Rabi season. These results are consistent with the experimental findings" of Barathi et al. [18] Kandel et al. [19]

"Low GCV and PCV were observed for the traits of days to 50% anthesis (K; 6.67, 6.15: R; 6.50, 5.53) and days to 50% silking (K; 7.34,6.89: R; 6.87, 6.04) in both seasons. The minimal difference between genotypic and phenotypic coefficients of variation suggests that environmental factors had little effect on the expression of these traits. These findings are consistent with the experimental results" of Barathi et al. [18] and Ellandula et al. [20].

A large number of traits had considerably high heritability estimates, indicating that additive gene action predominated. The highest heritability was found in Grain yield (R; 99.4), followed by Cob weight (99.2), Ear height (R; 99.2) during rabi season and during Kharif season highest heritability was found in Ear height (K; 98.7) followed by Plant height (K; 98.2). However, improving such traits may not be beneficial as broad sense heritability is based on total genetic variance, including additive, dominant, and epistatic variances. Heritability values with high genetic progress are more trustworthy for determining selection criteria. Higher heritability suggests additive gene activity, which allows selection to be successful in early generations. Akbar et al. [21], Rafiq et al. [22], and Rafique et al. [23] have similarly found substantial heritability for many yield-controlling characteristics in maize.

Moderate heritability was found in Ear length (K; 48.3) during the Kharif season which aligns with findings reported by Khan, S.et al. [24], least heritability was observed in KPR (K; 23.4) followed by KRPE (K; 25.8) indicating a considerable effect of environmental influences. These data show the occurrence of non-additive gene activities. These findings are consistent with the experimental results of Magar, B.T. et al. [16].

Table 1. Analysis of Variance for Yield and Yield-Contributing Traits in Maize

| S. No. | Character/trait | Mean sum of squares | | | | | | | | | |
| | | Replication | | Genotypes | | Blocks | | Error | | CV% | |
		Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24	Kharif 2023	Rabi 2023-24
1	Days to 50 percent silking	137.81	25.51	52.09**	46.83**	4.12	6.39	4.241	6.003	2.6	3.3
2	Days to 50 percent anthesis	78.3	36.73	58.05**	45.20**	0.881	5.92	3.96	7.37	2.6	3.4
3	Plant height (cm)	4.32	38.65	2519.38**	846.96**	35.39	6.38	20.41	35.07	2.9	4.1
4	Tassel length (cm)	0.106	1.17	84.74**	102.67**	0.461	0.314	0.80	0.46	2.8	2.1
5	Ear length (cm)	9.61	0.29	11.63**	24.56**	6.39	0.193	3.81	0.302	15.8	6
6	Ear diameter (cm)	12.62	0.24	8.86**	20.94**	2.52	0.1643	1.62	0.08	18	3.8
7	Ear height (cm)	7.01	0.33	1391.87**	389.62**	20.37*	2.39	7.61	1.31	3.5	1.9
8	Kernel rows Per Ear	46.01	119.179	132.10**	27.439**	5.42	8.03	85.3	2.99	20	15.8
9	Kernel Per Row	89.87	6.221	188.02**	107.376**	36.8	4.097	124.77	1.87	19.89	9.7
10	Cob weight (g)	2.72	29.23	520.12**	2777.7*	4.17	13.94	29.98	9.57	12.9	7.6
11	Grain yield (g)	0.81	22.30	443.91**	2105.65**	4.56	7.44	15.49	5.89	13.9	7.6

*** Significant at 1% level   *Significant at 5% level*

Table 2. Genetic Variability Parameters for Yield and Yield-Contributing Traits in Maize

| S. No. | Character | Mean | | Range | | | | Coefficient of Variation | | | | Heritability (broad sense) h²(bs) (%) | | GAM | |
| | | | | Minimum | | Maximum | | PCV (%) | | GCV (%) | | | | | |
		K	R	K	R	K	R	K	R	K	R	K	R	K	R
1	DS	75.61	74.7	64	62	87	86	7.34	6.87	6.89	6.04	88.1	77	13.3	10.9
2	DA	79.46	78.7	66	65	99	88	6.67	6.50	6.15	5.53	84	72	11.6	9.7
3	PH	157.9	145.06	55.8	96.86	217.3	216.32	22.56	14.4	22.37	13.9	98.2	92.83	45.69	27.62
4	TL	32.44	32.02	22.8	12.24	68.2	65.52	20.17	22.42	19.96	22.32	98.19	99.14	40.76	45.78
5	EL	12.36	9.16	6.3	2.85	18.5	18.21	22.65	38.46	15.74	38.01	48.3	97	22.54	77.3
6	ED	7.7	7.712	2.90	3.14	13.4	14.65	32.4	42.03	26.7	41.83	67.6	99.1	45.2	85.7
7	EH	77.76	61.65	17.15	31.98	17.7	94.72	34	22.68	33.8	22.59	98.7	99.2	69.2	46.37
8	KRPE	38.59	10.93	15.3	4.52	65.1	24.01	26.5	36.05	13.05	31.56	25.8	76.6	14.14	56.94
9	KPR	46.9	14.08	16.7	3.30	78.17	33.02	26.3	52.5	12.75	51.52	23.4	96	12.73	104
10	CW	42.50	40.96	16.11	5.06	81.45	148.56	38.9	91.14	36.92	90.81	89.9	99.2	72.1	186.39
11	GY	28.31	31.99	5.10	3.01	65..85	125.22	53.45	101.56	51.7	101.2	93.6	99.4	103.17	208.1

PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation
DA: Days to 50 per cent Anthesis, DS: Days to 50 per cent Silking, PH: Plant height, TL: Tassel Length, EH: Ear Height, EL: Ear Length, ED: Ear Diameter, KRPE: Kernel Rows Per Ear, KPR: Kernels Per Row, CW: Cob Weight, GY: Grain Yield.
K: Kharif 2023, R: Rabi 2023-2024

Genetic advance as a percentage of the mean indicated that additive genetic factors predominantly influence these traits. Utilizing heritability estimates alongside genetic advances enhances the reliability and utility of selection procedures. According to Johnson et al. [9], the observed GAM values were classified as low (less than 10%), moderate (10–20%), and high (greater than 20%). In the present study, genetic advance was calculated and expressed as a percentage of the mean for all traits (Table 2). High genetic advances were observed for total grain yield (K; 103.17: R; 208.1), followed by cob weight (K; 72.1: R; 186.39) in both seasons. Beulah, G et al. [25], and Bharathi, et al. [18] reported high genetic advance values for total grain yield. Moderate GAM values were observed in days to 50% silking and days to 50% anthesis in both seasons. Similar values were obtained by Wedwessen et al. [7]. DA and DS showed high heritability but low GAM. This could be due to environmental factors, indicating that selection for these traits might not be beneficial. Similar findings were reported by Tesfaye, D. et al. *[26]* and Beulah, G. et al. [25]

High heritability combined with high genetic advance was observed for Grain yield, Cob weight, Ear diameter, Ear height, and Tassel length. These findings suggest that these traits are promising targets for improvement through selection, likely driven by additive genetic factors. Beulah, G. et al. [25], Lal, K. et al. [27], and Wedwessen, T. et al. [7] all discovered significant heritability and high genetic progress for the previously mentioned characteristics in maize.

4. CONCLUSION

The analysis of variance revealed significant variation between the inbred lines, with phenotypic coefficients of variation (PCV) greater than genotypic coefficients of variation (GCV) for all traits. This suggests that direct selection will be effective in improving these traits. The highest PCV and GCV traits were total grain yield and cob weight during both seasons, indicating significant variability among the genotypes and indicating that phenotypic selection will be beneficial for improving these traits due to their high heritability and high genetic advance. Heritability is the proportion of phenotypic variance that can be attributable to genetic variation. In the current study, heritability was high (more than 60%) for many characteristics. A high heritability means that environmental influences are minimal on traits. As a result, any of the characters can be selected. High heritability combined with high genetic advance for ear height, total grain yield, cob weight, ear diameter, and tassel length illustrates that these traits are governed by additive gene action, making them heritable and fixable, implying that phenotypic selection for these traits would be advantageous.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Available:https://iimr.icar.gov.in/
2. Al-Amin M, Azad MAK, Shovon SR, Haque MF. Genetic variability and character association in maize (*Zea mays* L.) inbred lines. Turkish Journal of Agriculture-Food Science and Technology. 2019;7(8):1125-1131.
3. FAO. FAOSTAT: Production: Crops and livestock products. In: FAO. Rome. Cited December 2022; 2022.
   Available:https://www.fao.org/faostat/en/#data/QCL
4. Available:https://www.pjtsau.edu.in/files/AgriMkt/2023/February/Maize-February-2023.pdf
5. Zhang X, Zhang H, Li L, Lan H, Ren Z, Liu D, Wu L, Liu H, Jaqueth J, Li B, Pan G. Characterizing the population structure and genetic diversity of maize breeding germplasm in Southwest China using genome-wide SNP markers. BMC genomics. 2016;17:1-16.
6. Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmaliq SY, Mahamood J. Heritability

and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). International Journal of Plant Research. 2012;2(5):138-145.

7. Wedwessen T, Zeleke H. Genetic variability, heritability, and genetic advance estimates in maize (*Zea mays* L.) inbred lines. International Journal of Novel Research in Life Sciences. 2020;7(2):10-16.

8. Majhi PK, Mogali SC, Abhisheka L. Genetic variability, heritability, genetic advance and correlation studies for seed yield and yield components in early segregating lines (F3) of green gram [*Vigna radiata* (L.) Wilczek]. International Journal of Chemical Studies. 2020;8(4):1283-1288.

9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans.

10. Burton GW. Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress. Pennsylvania State College, USA; 23 August 1952;277-283.

11. Sivasubramanian P, Menon PM. Inheritance of short stature in rice. Madras Agricultural Journal. 1973;60:1129-1133.

12. Ahmad MSH. Studies on genetic variability, heritability, and genetic advance in segregating generations of faba bean (*Vicia faba* L.). Middle East Journal of Agriculture Research. 2016;5(1):82-89.

13. Chandel U, Kumar D, Guleria SK. Combining ability effects and heterotic grouping in newly developed early maturing yellow maize (*Zea mays* L.) inbreds under sub-tropical conditions. Electronic Journal of Plant Breeding. 2019 Sep 30;10(3):1049-59.

14. Sinha SK, Thakur D. Estimation of combining ability in maize (*Zea mays* L.) using Line x tester analysis International Journal of tropical Agriculture. 2017;35(4):1035-1046.

15. Meena MK, Singh R, Meena HP. Genetic variability, heritability and genetic advance studies in newly developed maize genotypes (*Zea mays* L.). The Bioscan. 2016;11(3):1787-91.

16. Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhayaya J, Shrestha J. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon. 2021;7(9).

17. Bartaula S, Panthi U, Timilsena K, Acharya SS, Shrestha J. Variability, heritability, and genetic advance of maize (*Zea mays* L.) genotypes. Research in Agriculture Livestock and Fisheries. 2019;6(2):163-169.

18. Bharathi P, Ravikesavan R, Yuvaraja A, Boopathi NM, Iyanar K. Genetic variability and correlation in maize inbred lines under irrigated and moisture stress condition. Electronic Journal of Plant Breeding. 2021;12(3):928-33.

19. Kandel BP, Sharma BK, Sharma S, Shrestha J. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) genotypes in Nepal. Agricultura. 2018;107(3-4):29-35.

20. Ellandula A, kumar Singh S, Narayan A, Karla U, Sagar US. Exploring genetic variability and association in QPM maize (*Zea mays*) inbred lines. Electronic Journal of Plant Breeding. 2023 Oct 3;14(3):1222-9.

21. Akbar M, Shakoor MS, Hussain A, Sarwar. Evaluation of maize 3-way crosses through genetic variability, broad sense heritability, characters association and path analysis. Journal of Agricultural Research (Pakistan). M, J. Agric. Res. 2008;46(1):39e45.

22. Rafiq CM, Rafique M, Hussain A, Altaf M. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). Journal of Agricultural Research (03681157), 48(1). Agric. Res. 2010;48(1):35e38.

23. Rafique M, Hussain A, Mahmood T, Alvi AW, Alvi B. Heritability and interrelationships among grain yield and yield components in maize (*Zea mays* L). Int. J. Agric. Biol. 2004;6(6):1113e1114.

24. Khan S, Mahmud F. Genetic variability and character association of yield components in maize (*Zea mays* L.). American Journal of Plant Sciences. 2021;12(11):1691-1704.

25. Beulah G, Marker S, Rajasekhar D. Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). Journal of Pharmacognosy and phytochemistry. 2018;7(1):2813-2816.

26. Tesfaye D, Abakemal D, Habte E. Genetic variability, heritability and genetic advance estimation of highland adapted maize (*Zea mays* L.) genotypes in Ethiopia. Journal of Current Opinion in Crop Science. 2021;2(2):184-191.

27. Lal K, Kumar S, Singh SK, Singh M, Singh HC, Singh Y. Heritability and genetic advance estimates for certain quantitative traits in maize (*Zea mays* L.). Journal of Pharmacognosy and Phytochemistry. 2020;9(3): 571-573.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/121634