Original Research Article

EVALUATION OF GENETIC VARIABILITY IN MAIZE (*Zea mays* L.) BASED ON YIELD AND ITS ATTRIBUTED TRAITS

ABSTRACT

Maize is commonly referred to as the queen of cereals because of its major share in the food for people in the world. It provides food, feed, and edible oil with low cholesterol levels for humans as well as for livestock consumption. It is a short-duration crop being cultivated in both spring and summer seasons to meet the desirable yield and to boost the economy. The aim of this study was to assess genetic variation in 20 genotypes of maize and the nature of associations between traits that affect grain yield. The analysis of variance demonstrated that for each trait, each genotype significantly differed from the other genotype. To determine the extent of genetic and environmental variation, respectively, the genetic (GCV) and phenotypic (PCV) coefficient of variation were calculated. The PCV generally had a higher tendency than the GCV, indicating that environmental factors affected all of the investigated traits. Heritability, coupled with genetic advances, plays a vital role in improving certain traits in breeding programs. The association between various traits can be found using correlation coefficient analysis. Grain yield (GY) exhibited a significant positive genotypic and phenotypic association with number of grains per row, total grain per cob, number of rows per cob, and 100-grain weight. The yield of maize could therefore be increased by directly selecting for these traits.
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Keywords: Maize Breeding, Genetics, Heritability, Maize yield, Genetic advance

1. INTRODUCTION

Maize is a cereal crop which is a member of the Poaceae family. Its origin is South Mexico with a chromosome number 2n=20. Every part of this crop is useful to animals, humans, and industries. There, it is called as “Queen of Cereals” (Mounika et al., 2018). Domestication of maize started eight thousand years ago from its wild form and spread all over the world. Maize has a strong, thick, erect column with internodes and nodes. Leaves are arranged in an alternative manner. Maize is native to South Mexico and America (Sleeper and Poehlman, 2006). Maize is a high-yielding and short-duration crop that can be cultivated both in the spring and kharif seasons in Pakistan (Maqbool et al., 2019).

Globally maize stands third in the most cultivated food crops (Ahmad et al., 2020). This cereal crop is extensively grown in the whole world with a production of roughly seven hundred million metric tons (Ranum et al., 2014). In Pakistan, maize ranked third after wheat and rice crops. Primarily, 65% of maize is produced for livestock and poultry feed and 35% for human dietary purposes. It is also used in the production of various industrial products (Reddy and Jabeen, 2016).

Maize is a great source of macronutrients, micronutrients and phytochemicals that are beneficial for health. Both genetic engineering and plant breeding focus on raising the yield of maize grains in order to fulfill consumer needs for animal feed, food, and commercial applications. (Wu et al., 2019).

In comparison to developed countries, maize production in Pakistan is less. Early maturing and more yielding maize hybrids and synthetic cultivars are essentially required to be identified and developed by the maize breeders (Hussain et al., 2016). Producing genetically diverse maize inbred for grain yield and a hybrid program based on morphological traits are the most important steps toward varietal development (Khan et al., 2019). To identify the superior genotypes, crop breeders mostly execute the selection of desired characters.

It is the diversity of the parental inbred lines used in the cross combination, that eventually determines the degree of heterosis, which ultimately determines the extent of the increase in maize productivity. However, the degree of heterosis varies depending on the genetic distance between parents, the method of reproduction, the characteristics of the traits being studied, and the environment in which the parental lines thrive (Tian et al., 2017).

The range of variability is quantified using parameters like genotypic (GCV) and phenotypic (PCV) coefficient of varience, which also provide information on the overall degree of variation in altered traits. As a result, an investigative valuation of the yield components is required to have a complete understanding. The degree of quantitative trait inheritance is revealed by heritability (Sumathie et al., 2010). Breeders can choose a superior genotype from a diverse genetic component by using the tool of heritability. GCV and PCV values are categorized as low if they fall below 10%, moderate if they fall between 10% and 20%, and high if they exceed 20% (Deshmukh et al., 2010). Heritability levels below 40% are considered low, levels between forty percent and fifty-nine percent are considered medium, levels between sixty and nearly eighty percent are considered moderately high, and levels above 80% are considered extremely high. (Singh, 2001).

The selection of superior genotypes of a crop depends upon the availability of genetic resources. More chances of selection of a superior genotype are available when a large level of genetic variation is available. A disadvantage is that with the selection of superior genotypes, the remaining material is often lost which may contain useful genes for different desirable traits (Karp, 1995). Selection of superior genotypes from diversified germplasm leads to the development of a narrow genetic base germplasm. Developed hybrids had a better yield and related traits as compared to diversified materials. This process caused genetic erosion and decreased genetic diversity (Keneni et al., 2012).

With regard to parental selection in the hybridization program, genetic divergence is a useful tool. The study also selects genetically different parents, desirable combinations in segregating generations. Breeders can choose the best parents for their breeding program with available data on the type and degree of genetic variation. Given this, the experiment was carried out with the aim of investigating the genetic variability and diversity of seed lines alone based on yield and its attributed traits. (Freeman, 2019).

The ANOVA test to test the significance, genotypic and phenotypic correlation, and study of heritability, and genetic advance are mostly used for evaluating the genetic diversity of superior lines in breeding programs of crop improvement. Correlation analysis provides the information about association of different traits with yield. Yield is a complex quantitative control. Correlation analysis helps to focus on desirable traits. The phenotype that is observed in the field is the combination of environmental and genetic factors. Quantitative traits are badly affected by the environment so the effect of the environment cannot be neglected during the selection of superior genotypes. The best method to select the superior genotypes is to grow the maize germplasm in the open field environment.

The aims of this study are the assessment of the performance of different maize genotypes from the available germplasm for evaluating genetic diversity based on yield and its attributed characters and to analyze the association among under-studied morphological traits. Those selected high-yielding genotypes could be useful in further breeding programs.

2. MATERIAL AND METHODS

This experiment was performed in the research area of the PBG department of the University of Agriculture Faisalabad. RCB design was used to evaluate 20 genotypes of maize with three replications. All optimum agronomic practices will be applied at the field level. The fertilizer dose will be applied as per agronomic recommendations from sowing to harvesting. The blocks were 5 meters long and 4 meters wide. The block area was 20 m2. Three replications were applied to minimize the environmental error.

Table 1. Name and source of 20 maize genotypes evaluated under the stud

Sr. No.	Genotypes	Source
1	CH 31206 (6072)	PBG Department, UAF
2	CH 13950 (6065)	PBG Department, UAF
3	CH13969 (6066)	PBG Department, UAF
4	CH 13958 (6052)	PBG Department, UAF
5	CH 131268 (6075)	PBG Department, UAF
6	CH 131268 (6075)	PBG Department, UAF
7	CH 131272 (6079)	PBG Department, UAF
8	CH 13935 (6085)	PBG Department, UAF
9	CH 131266 (6084)	PBG Department, UAF
10	CH 131243 (6076)	PBG Department, UAF
11	CH 131265 (6077)	PBG Department, UAF
12	CH 13890 (6090)	PBG Department, UAF
13	CH 13971 (6069)	PBG Department, UAF
14	PBG-2022	PBG Department, UAF
15	PBG-6187	PBG Department, UAF
16	PBG-6186	PBG Department, UAF
17	PBG-6185	PBG Department, UAF
18	PBG-6184	PBG Department, UAF
19	PBG-6182	PBG Department, UAF
20	PBG-6182	PBG Department, UAF

The data was recorded for five indiscriminately chosen plants and the average was calculated from each entry in each replication for 11 different parameters including days for 50 (%) silking (D50% S), 100-grain weight (100-GW), days for 50 (%) tasselling (D50% T), cob length (CL), number of days to pollination (NDP), the number of grains per row (NGPR), cob height (CH), total grains per cob (TGPC), cob diameter (CD), number of rows per cob (NRPC), grain yield per plant (GYPP) and plant height (PH). To check the significance among genotypes, statistical analysis was carried out with the help of analysis of variance also known as ANOVA test. (Steel et al., 1997). Association among different traits was measured according to Kown and Torrie (1964).

3. RESULTS AND DISCUSSION

3.1 ANOVA Test for Different Quantitative Traits

The selection of the best superior lines in maize germplasm depends upon the availability of genetic variation in maize germplasm. Since maize is a cross-pollinated crop therefore, maize shows a higher level of variation as compared to other crops at the phenotypic and genotypic levels. The findings of the analysis of variance were used to ascertain whether there were any variations in genotypes for eleven understudied traits (Table 2). The results showed that the genotype-related MSS (Mean Sum of Squares) of all the investigated characters was significant. According to the results of an ANOVA test, genotypes significantly differed from one another for every trait. The majority of the characters had a lot of variation, which suggested that all of the characters under study had quite variable lines. A wide range of significant differences for different traits like these has also been stated earlier (Kumar et al. 2011; Jumaa and Madab 2018; Chaurasia et al. 2020; Mallikarjuna et al. 2020).

Table 1. Mean Sum Square of Morphological traits

SOV	DF	D50% S	D50% T	NDP	PH	NGPR	TGPC	NRPC	CD	CH	CL	100GW	GYPP
Replication	2	4.01	12.8	4.01	16.11	1.017	1493.3	3.12	0.00098	0.37	0.029	0.029	7.63
Genotypes	19	55.32**	68.01**	55.59**	206.7**	152.5**	16.75**	10.47**	1.63**	32.51**	138.6**	138.3**	7441**
Error	38	0.64	0.308	0.91	5.23	2.66	2979.1	3.04	0.204	0.1667	0.121	0.121	23.32

SOV=Source of variation, DF= Degree of freedom
**Significance at the *P* < 0.01 of the Probability

3.2 Coefficients of Variation (GCV and PCV), Heritability (HA), Genetic Advance (GA), and Genetic Advance as Percent of Mean (GAPM)

The goal of this study was to examine a number of genetic factors, such as heritability, the GCV, PCV, and genetic advance as a percentage of the mean (GAPM). The investigation involved 20 inbred lines, with three replications, evaluating 11 different traits. The findings from this analysis provide valuable insights for formulating effective breeding strategies aimed at enhancing maize traits. These genetic parameters provide information that how much variation is present among genotypes and how potential improvements can be achieved. Detailed results for these parameters across various traits are outlined in Table 3 and Fig. 1

Table 2. Coefficient of variation (GCV and PCV), heritability, and genetic advance as percent of the mean (GAPM)

Characteristics	GCV (%)	PCV (%)	Heritability (%)	GAPM
Days to 50 (%) silking	5.98	6.09	0.965	12.11
Days to 50 (%) tasseling	7.46	7.52	0.986	15.27
Number of days to pollination	5.85	6.004	0.952	11.78
Plant height (cm)	12.52	12.61	0.985	25.62
Number of grains per row	24.43	25.07	0.949	49.03
Total grains per cob	32.61	35.59	0.84	61.59
Number of rows per cob	12.00	17.91	0.448	16.57
Cob diameter (cm)	17.83	18.16	0.963	36.07
Cob height (cm)	25.11	25.24	0.999	51.67
Cob length (cm)	20.07	20.23	0.984	41.04
100 grains weight (g)	24.29	24.33	0.997	49.99
Grain yield per plant (g)	43.79	43.99	0.990	89.79

3.2.1 Genotypic (GCV) and Phenotypic (PCV) Coefficients of Variation

To determine the extent of genetic and environmental variation, respectively, GCV and PCV evaluations were conducted. The potential for genetic improvement is determined by these coefficients, which offer useful insights into the amount of variation present in the studied traits. The values of genotypic CV and phenotypic CV for 11 different traits are presented in Table 3 and were compared in this study. With the exception of the NRPC, the PCV values for all of the characters under study were slightly higher than the GCV values, indicating a significant contribution of the environment to the expression of these traits. Therefore, a response to direct selection may be successful in enhancing these traits. Most of the traits showed moderate to high variability among the maize genotypes analyzed. Characters such as D50% S (5.98%, 6.08%), D50% T (7.46%, 7.51%), and NDP (5.85%, 6.003%) reported low (less than 10%) phenotypic and genotypic coefficients of variation. Moderate (10–20%)

PCV and GCV were present for traits like PH (12.52%, 12.61%), NRPC (12.003%, 17.91%), and CD (17.83%, 18.16%). These outcomes matched those of Singh et al. (2003) and Choudhary and Choudhary (2002), among others. High (more than 20%) phenotypic and genotypic coefficients of variation were present for all remaining morphological traits such as TGPC (32.61%, 35.59%), CH (25.11%, 25.24%), PH (12.52%, 12.61%), and GYPP. For GYPP, high estimates of phenotypic (43.79%) and genotypic (43.99%) coefficient of variation were discovered. These findings agreed with those made public by Bhusal et al. (2017) and Sharma et al. (2018). A higher GCV suggests a greater contribution of genetic factors to the observed variation, demonstrating that these traits are influenced by the genetic makeup of the maize lines. However, a higher PCV indicates that environmental factors, such as growing conditions, have a greater impact on the expression of the traits. These values can be used as indicators to prioritize traits for selection in maize breeding programs. 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.

3.2.2 Heritability (HA) and Genetic Advance as Percent of Mean (GAPM)

Heritability assessments provide breeders with valuable insights into the share 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. This knowledge enables them to focus their efforts on traits with higher heritability, increasing the likelihood of success in genetic enhancement. Heritability, coupled with genetic advances, plays a vital role in improving certain traits in breeding programs. The integration of genetic technologies and techniques allows breeders to harness the genetic potential of plants and enhance desirable traits more effectively. In traits like D50% S, 100-GW, D50% T, CD, NDP, NGPR, CH, TGPC, CD, GYPP, and PH, high heritability estimates were found. If heritability values were combined with high genetic advance, selection criteria could be correlated in a way that is more useful and accurate. Genetic advance as a percent of the mean (GAPM) is categorized as such below 10 % is considered as low, between 10 to 20 percent is considered as moderate, and more than 20 % is categorized as high. Among the characters under study, traits namely D50% S (12.11%), D50% T (15.27%), and NDP (11.77%) showed moderate GAPM. The findings of Mallikarjuna et al. (2020) were consistent with the present study, as moderate GA values were observed for D50% T and D50% S. All other traits showed high estimates of GAPM. Prakash et al. (2017) also reported high GA as a percent of the mean for GYPP, 100-GW, CL, CH, and NGPR. The character GYPP (89.79%) recorded a high magnitude of GAPM followed by TGPC (61.59%), CH (51.67%), 100-GW (49.99%), and NGPR (49.03%). For the present study, GYPP, CH, 100-GW, CL, and NGPR, high heritability along with high GAPM were observed. (Table 3). These characteristics can therefore be enhanced through selection because they are primarily governed by additive gene action. Mohammad Akbar et al. (2006); Ali et al. (2010); and Ram Reddy et al. (2012) all reported similar findings.

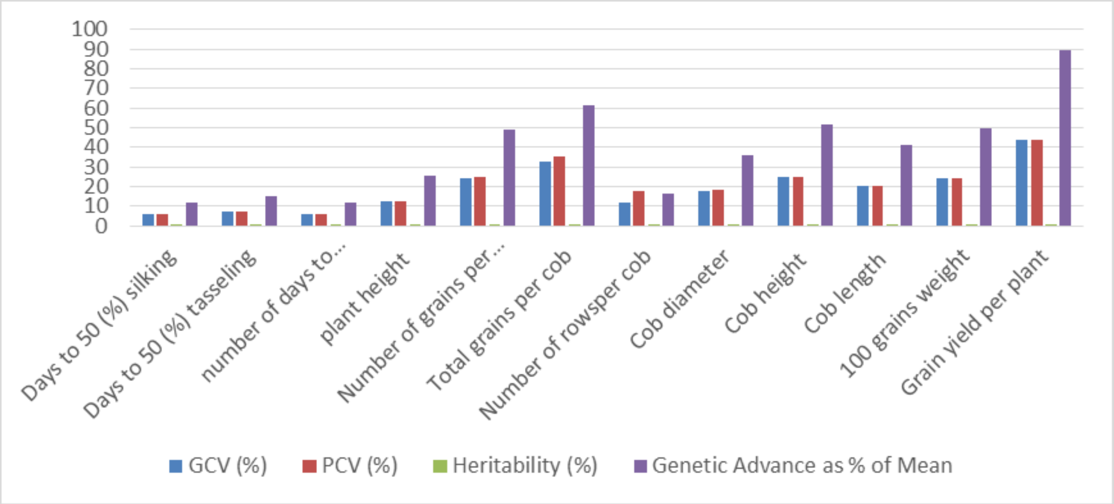

Fig. 1. Graphical representation of coefficient of variation, heritability, and genetic advance as percent of mean among 20 genotypes in maize

3.3 Correlation coefficient Analysis

The association between various traits can be found using correlation coefficient analysis. The correlation coefficient may be positive or negative. Positive correlation describes the direct association between two traits and negative correlation coefficient describes the indirect association between two traits. On the basis of genetics, there are two types of correlation. One is genotypic correlation (GC) and the other is phenotypic correlation (PC). PC is the combination of genotypic and environmental correlation. A correlation study helps to determine the antagonism and synergism of traits. Phenotypic and genotypic correlation coefficients are shown in Tables 4 and 5 respectively.

D50% S exhibited significant positive phenotypic and genotypic association with D50% T, 100-GW, and NDP and exhibited significant negative phenotypic and genotypic association with PH. D50% T exhibited significant positive phenotypic (PC) and genotypic (GC) correlation with D50% S, CD, GYPP, NDP, and 100-GW and revealed significant negative phenotypic and genotypic association with PH. NDP exhibited significant positive GC and PC with D50% S and D50% T while showing a significant negative phenotypic association with PH. Plant height exhibited significant positive genotypic and phenotypic association with NRPC and exhibited significant negative phenotypic association with 100-GW. NGPR revealed a significant positive genotypic association with CL, TGPC, and GYPP. TGPC exhibited a significant positive phenotypic association with CL, NGPR, PH, NRPC, and GYPP. NRPC showed significant positive phenotypic and genotypic association with TGPC, PH, and GYPP while exhibiting significant and negative genotypic association with CH. CD exhibited a non-significant correlation among all studied traits at the genotypic level. CH exhibited a meaningful positive association with NGPR, NDP, and PH and exhibited a significant negative genotypic association with NRPC. CL exhibited a noteworthy positive genotypic association with NGPR and phenotypic association with TGPC and CD. 100-GW exhibited a meaningful positive genotypic association with GRPP and phenotypic association with GYPP, D50% S, CD, D50% T, and NDP. GYPP exhibited significant positive genotypic and phenotypic association with TGPC and NRPC. GYPP exhibited a significant positive genotypic association with NGPR, TGPC, NRPC, and 100-GW while showed a phenotypic association with D50% T, NGPR, TGPC, NRPC, and 100-GW. The results of these observations are consistent with Bankole et al. (2019); Raghu et al. (2011); Bhusal et al. (2017); Sadek et al., (2006); (Ravi et al., (2012).

Table 4. Genotypic correlation among studied traits

	D50% S	D50% T	NDP	PH	NGPR	TGPC	NRPC	CD	CH	CL	100-GW	GYPP
DT50% S	1 **											
DT50% T	0.7549 **	1 **										
NDP	1.0024 **	0.7648 **	1 **									
PH	-0.3831	-0.3956	-0.3723	1 **								
NGPR	-0.0778	-0.0715	-0.0714	0.221	1 **							
TGPC	-0.1478	-0.0832	-0.1436	0.3778	0.931 **	1 **						
NRPC	-0.2445	-0.0769	-0.2441	0.5484*	0.3877	0.6953 **	1 **					
CD	0.1739	0.3435	0.1623	-0.0938	0.0219	0.1657	0.3385	1 **				
CH	0.8979 **	0.9727 **	0.984 **	0.703**	0.6051 **	0.2287	-0.5864 **	-0.0892	1 **			
CL	-0.0768	0.0312	-0.0641	0.217	0.4823 *	0.4181	0.1076	0.4123	0.286	1 **		
100-GW	0.4317	0.4204	0.4251	1 **	1 **	0.0938	0.1357	0.296	0.3859	-0.113	1 **	
GYPP	0.2418	0.2777	0.2434	0.221	0.931 **	0.6261 **	0.4889 *	0.2393	0.3957	0.075	0.6811 **	1 **

*Significance at the *P* < 0.05 of the Probability

**Significance at the *P* < 0.01 of the Probability

Table 5. Phenotypic correlation among studied traits

	D50% S	D50% T	NDP	PH	NGPR	TGPC	NRPC	CD	CH	CL	100-GW	GYPP
DT50% S	1 **	0.7376 **	0.993 **	-0.380 **	-0.0679	-0.11	-0.1249	0.1753	0.2075	-0.0709	0.4231 **	0.2348
DT50% T		1 **	0.7413 **	-0.390**	-0.0635	-0.0602	-0.0259	0.337 **	0.1912	0.0315	0.4176 **	0.2752 *
NDP			1 **	-0.365 **	-0.0608	-0.1001	-0.1154	0.1613	0.1923	-0.0597	0.4139 **	0.2329
PH				1 **	0.205	0.3405 **	0.3708 **	-0.0964	0.1014	0.2098	-0.3235 *	0.0077
NGPR					1 **	0.8674 **	0.2489	0.0239	0.1141	0.4675 **	0.0548	0.5409 **
TGPC						1 **	0.6928 **	0.1633	0.0387	0.3899 **	0.0844	0.5812 **
NRPC							1 **	0.2474	-0.0827	0.0902	0.0838	0.3398 **
CD								1 **	-0.0246	0.4091 **	0.2885 *	0.2394
CH									1 **	0.0469	0.0775	0.079
CL										1 **	-0.1112	0.0735
100-GW											1 **	0.6779 **
GYPP												1 **

*Significance at the P < 0.05 of the Probability

**Significance at the P < 0.01 of the Probabilit

4. CONCLUSION

The selection efficiency for particular traits in crops can be improved by using estimates of genetic parameters, which are crucial for plant 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 emphasizes how crucial it is to take into account both variability and heritability in genetic research because these elements can have a big impact on the results of such investigations.

REFERENCES

1. Ahmad, I., B. Ahmad, K. Boote and G. Hoogenboom. Adaptation strategies for maize production under climate change for semi-arid environments. European Journal of Agronomy. 2020;115:126040.

2. Ali, A. W., Hasan, K.A. and Samir, A. Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (*Zea mays* L.). Agriculture and Biology Journal of North America. 2010;1(4):630-637.

3. Badu-Apraku B, Akinwale RO, Ajala SO, Menkir A, Fakorede MAB, Oyekunle M. Relationships among traits of tropical early maize cultivars in contrasting environments. Agronomy Journal 2011;103(3):717–729.

4. Bankole, F., A. Menkir, G. Olaoye, O. Olakojo, G. Melaku. Association studies between grain yield and agronomic traits of a MARS maize (*Zea mays* L.) population under drought and non-stress conditions. Acta agriculturae Slovenica 2019;114:75-84.

5. Bhusal T, GM Lal, S Marker and GJ Synrem. Genetic variability and traits association in maize (*Zea mays* L.) genotypes. Annals of Plants and Soil Research, 2017;19(1): 59-65

6. Chaurasia, N. K., Nirala, R. B. P., Singh, B., & Mandal, S. S. Trait association and path coefficient analysis in maize (*Zea mays* L.) for grain yield and its attributes. Journal of Pharmacognosy and Phytochemistry, 2020;9(6), 527-531.

7. Choudhary AK and LB Chaudhary LB. Genetic studies in some crosses of maize (*Zea mays* L.). Journal of Research Birsa Agricultural University. 2002;5 (1/2): 10-16

8. Deshmukh SNN, Basu MS, Reddy PS. Genetic variability, character association and path coefficients of quantitative traits in Virginia Bunch varieties of Groundnut. Indian Journal of Agricultural Sciences.1986;56:816–821.

9. Dewey, D. R. and K. H. Lu. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 1959;51: 515-518.

10. Freeman, T. A. Genetic Variability and Divergence Studies in Maize (*Zea mays* L.). EC Agriculture. 2019;5:284-290.

11. Hussain, H., B. Rehman and K. Fazal. Phenotypic and genotypic association between maturity and yield traits in maize hybrids (*Zea mays* L.). African Journal of Food, Agriculture, Nutrition and Development. 2016;4:157-160.

12. Jumaa, R. F., & Madab, D. S. Estimation of genetic diversity by using cluster, D2 and principle component analysis of maize inbred lines (*Zea mays* L.). Tikrit Journal for Agricultural Sciences, 2018;18(4).

13. Karp, A. Somaclonal variation as a tool for crop improvement. Euphytica. 1995;85: 295-302.

14. Keneni, G., E. Bekele, M. Imtiaz, and K. Dagne. Genetic variability of Modern Crop Cultivars: Causes, Mechanism and Remedies. International Journal of Plant Research 2012;2(3): 69-70.

15. Khan, M.U., S.M.A. Shah, H. Rahman, A. Iqbal and E. Aslam. Evaluation of maize hybrids for yield and maturity traits. Sarhad Journal of Agriculture. 2019;35:7-12.

16. Kumar, S. T., D. M. Reddy, K. H. Reddy and P. Sudhakar. Targeting of traits through assessment of interrelationship and path analysis between yield and yield components for grain yield improvement in single cross hybrids of maize (*Zea mays* L.) International Journal of Applied Biology and Pharmaceutical Technology. 2011;2: 123-129.

17. Kwon, S.H. and J.H. Torrie. Heritability and interrelationship of two soybeans (*Glycine max* L.) populations. Crop Science. 1964;4: 196-198.

18. Mallikarjuna, S., Roja, V., Kumar, I. S., & Srinivas, T. Genetic diversity studies in newly developed maize inbreds. Journal of Pharmacognosy and Phytochemistry. 2020;9(5). 517-522.

19. Maqbool, M.A., M. Aslam, A. Beshir, M.S. Khan and M.T. Saeed. Studying selection criteria and genetic variability for improvement of indigenous maize in Pakistan. Pakistan Journal of Agricultural Sciences. 2019;6(4):819-827.

20. Mounika, K., M.L. Ahamed and U.S. Nafeez. 2018. Principal component and cluster analysis in inbred lines of maize (*Zea mays* L.). International journal of current microbiology and applied sciences. 2018;7:3221-3229.

21. Muhammad Akbar., Shabbir, M., Amer Hussain. and Muhammad Sarwar. Evaluation of maize three-way crosses through genetic variability, broad sense heritability, character association and path analysis. Journal of Agriculture Research. 2006;46 (1): 39-45.

22. Owusu GA, Ribeiro PF, Abe A. Genetic analysis of grain yield and agronomic traits of quality protein maize inbred lines and their single-cross hybrids under drought stress and well-watered conditions. Ecological Genetics and Genomics. 2021;22:100–105.

23. Prakash, R., Ravikesavan, R., Vinodhana, N. K., & Senthil, A. (2019). Genetic variability, character association and path analysis for yield and yield component traits in maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2019;10(2), 518-524.

24. Raghu, B., J. Suresh, S. S. Kumar and P. Saidaiah. Character association and path analysis in maize (*Zea mays* L.). Madras Agricultural Journal. 2011;98: 7-9.

25. Ram Reddy, V., Seshagiri Rao, A. and Sudarshan, M.R. Heritability and character association among grain yield and its components in maize (*Zea mays* L.). Journal of Research. ANGRAU. 2012;40(2): 45-49.

26. Ranum, P., J.P. Peña-Rosas and M.N. Garcia-Casal. Global maize production, utilization, and consumption. Annals of the New York Academy of Sciences. 2014;1312:105-112.

27. Ravi, V.M., Chikkalingaiah. and Shailaja, H. Correlation study for protein content, grain yield and yield contributing traits in quality protein maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2012;3(1):649-651.

28. Reddy, V. R. and F. Jabeen. Narrow sense heritability, correlation and path analysis in maize (*Zea mays* L.) SABRAO Journal of Breeding and Genetics 2016;48: 120-126.

29. Sadek, S.E., Ahmed, M.A. and El- ghaney, H.M. Correlation and path coefficient analysis in five parent inbred lines and their six white maize (*Zea mays* L.). Journal of Applied Sciences Research. 2006;2 (3): 159-167.

30. Sharma BK, S Sharma, BP Kandel and J Shrestha. Varietal evaluation of promising maize genotypes. Azarian Journal of Agriculture, 5(4): 120-124. Mallikarjuna, N. M., Chandrashekhar, H., Shashibhaskar, M. S., & Prahalada, G. D. (2011). Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays* L.). Current Biotica. 2018;5(2), 157-163.

31. Signor, C. E. L., Dousse, S., Lorgeou, J., Denis, J. B., Bonhomme, R., Carolo, P., & Charcosset, A. Interpretation of genotype× environment interactions for early maize hybrids over 12 years. Crop Science. 2001;41(3), 663-669.

32. Singh BD. Plant breeding: principles and methods. Kalyani Publishers, New Delhi, India. 200.

33. Singh P, S Das, Y Kumar, Y Dutt and O Sangwan,. Variability studies for grain yield and its component traits in maize (*Zea mays* L.). Annals of Agri-Bio Research. 2003;8: 2-31.

34. Sleeper, D. A. and J. M. Pohlman. Breeding corn (maize). In. Breeding field crops (5th ed.). Blackwell publishing professional. Ames. U.S.A. 2006.

35. Steel, R.G.D., J.H. Torrie and D.A. Dicky.. Principles and procedures of Statistics. A Biometrical Approach 3rd Ed. McGraw Hill Book Co. Inc. New York. 1997;400-428.

36. Sumathi P, Madineni S, Veerabad Hiran P. Genetic variability for different biomaterial traits in pearl millet genotypes [*Pennisetum glaucum* (L) R.Br.]. Electronic Journal of Plant Breeding. 2010;1(14):437–440).

37. Tian HY, Channa SA, Hu SW. Relationships between genetic distance, combining ability and heterosis in rapeseed (*Brassica napus* L.). Euphytica. 2017;213.

38. Wu, J., S.J. Lawit, B. Weers, J. Sun, N. Mongar, J. Van Hemert, R. Melo, X. Meng, M.Rupe and J. Clapp. Overexpression of zmm28 increases maize grain yield in the field. Proceedings of the National Academy of Sciences. 2019;116:23850-23858