

## **Study of Genetic Variability and Diversity in Maize (*Zea mays* L.) Inbred Lines**

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### **Authors' contributions**

*This work was carried out in collaboration among the authors. Authors DB and BM designed the study, evaluated and performed the statistical analysis and wrote the first draft of the manuscript. Author VS collected the material and managed the literature. Authors DS, MVNK and MLR managed the analysis. All authors read and approved the final manuscript.*

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### **ABSTRACT**

The present investigation was aimed to generate adequate knowledge and understanding of the genetic parameters and genetic diversity among the eighteen maize inbred lines which are important for assessing breeding strategies and predicting hybrid performance. A wide range of variability was noticed among the inbred lines under study. Traits like plant height, ear height, grain yield per cob, cob length and number of kernels per row recorded medium to high range of PCV and GCV estimates, heritability and genetic advance as percent of mean. Hence, these traits are important for selection of genotypes to improve maize yield. The cluster II recorded maximum intra cluster distance (60.49) followed by cluster I (43.81). The clusters III, IV, V and IV are solitary clusters. The highest inter cluster distance of 386.89 was observed between the clusters IV and V, followed by cluster I and IV (326.90), clusters I and VI (309.98), cluster II and V (297.76), cluster III

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and V (239.32) and Cluster I and III (252.68). To develop high heterotic hybrids in maize select of inbreds as lines from cluster I and testers from Cluster III, IV and VI and also from cluster II and clusters III and V will be rewarding.

*Keywords: Maize; genetic variability; genetic diversity and inbred lines.*

## 1. INTRODUCTION

Maize is the very important crop with multiple uses for human and poultry industry and grown in different ecological systems. Development of adapted varieties/hybrids for targeted environmental conditions with diverse ecogeographic and environmental conditions is a challenge and a continual activity. Also, the vagaries of climate change/ variability needs to be addressed with appropriate breeding methods to add new germplasm for the benefit of target environments [1] and to develop more climate resilient maize systems [2]. Plant breeding mainly considers assessment and utilization of genetic variability, selection of desirable types and testing of selected superior genotypes. The efficacy of selection depends on the direction and magnitude of association between yield and its components. Further, this is highly dependent on estimates of genetic parameters, as they allow identifying the nature of gene action involved in the control of quantitative traits. The major goal of maize breeder is to increase the maize yield attributes to meet the future demands of maize by developing inbreds suitable for this purpose [3]. Grain yield is the most economically important trait in maize breeding programs and many breeders use relevant traits, including days to 50 per cent anthesis and silking, plant height, ear height and cob traits generate desirable plant architecture and for indirect selection of high-yielding maize varieties [4].

High yielding hybrids in maize required diverse parental lines and genetic diversity present in the breeding material forms valuable resource to plan a hybrid breeding program. Knowledge on inbred lines diversity and the relationship among elite breeding materials has a significant impact on maize improvement. This information is also useful in planning crosses for hybrid and line development, in assigning lines to heterotic groups.  $D^2$  analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic level and in

assessing relative contribution of different components to the total divergence both intra and inter-cluster level [5]. Most of the authors emphasized the importance of genetic parameters for yield and yield attributing traits in maize by studying inbred lines [6],[7],[8],[9],[10] including biofortified inbred lines [11]. Previous studies have reported that analysis of genetic diversity for a given germplasm helps the breeder to select parental combinations to realize high heterosis in maize [12,13]. Hence, the present investigation was carried out to study the nature and magnitude of genetic variability and diversity among the inbred lines for selection of traits for improvement of maize yield and assortment of diverse parents to get heterotic hybrids.

## 2. MATERIALS AND METHODS

A total of eighteen inbred lines were collected from CIMMYT during the field day at ICRISAT, Patancheru, Hyderabad during rabi, 2018 (Table 1). These inbred lines were evaluated in randomized block design with two rows of 3m length in two replications during kharif, 2019 at Maize Research Centre, Rajendranagar, Hyderabad (Altitude of 542.6 m and around 79°23'E longitude and 17°19'N latitude). All recommended package of practices were followed to raise the healthy crop. Data recorded on nine yield and yield attributing traits viz., days to 50% pollen shed and silking, plant height (cm), ear height (cm), cob length (cm), number of kernels per cob, number of rows per kernel and grain yield per cob (g). Days to 50% pollen shed and silking recorded on plot basis and remaining traits recorded on randomly selected 10 plants and made average. The mean data of yield and yield attributing traits used for statistical analysis as per standard procedures for analysis variance [14], heritability in broad sense [15], genetic advance and genetic advance as per cent of the mean [16], phenotypic and genotypic coefficient of variation [17] and  $D^2$  analysis by Tocher's method [18] by using WINDOW STAT 9.2 version as formulas detailed below

**Chart 1. View on different coefficient of variation**

i	Phenotypic coefficient of variation (PCV)	$PCV = \frac{\sqrt{\sigma^2_p}}{x} \times 100$	Where: $\sigma^2_p$ = phenotypic variance; X = mean of the trait
ii	Genotypic coefficient of variation (GCV)	$GCV = \frac{\sqrt{\sigma^2_g}}{x} \times 100$	Where: $\sigma^2_g$ = genotypic variance; X = mean of the trait
iii	Broad sense heritability	$h^2_B = \frac{\sigma^2_g}{\sigma^2_p}$	Where: $\sigma^2_g$ = genotypic variance; $\sigma^2_p$ = phenotypic variance
iv	Expected genetic advance	$GA = K \times \sqrt{\sigma^2_p} \times h^2_B$	Where: K = constant that represents the selection intensity (when k is 5% the value is 2.06); $\sqrt{\sigma^2_p}$ = standard deviation of phenotypic variance; $h^2_B$ = heritability in a broad sense

**Table 1. List of inbred lines used in study**

S.No	Code	Pedigree
1	GP 170	Selection from CIMMYT lines
2	BML 10	X2Y Pool Suwan 1 (T)-B98k-1-2-1-1-2-3-A#-2-A#-1-A#b-A#b-A#b
3	MGC 6	(CML451-B*7/([CML511/CL-RCY016]-B-18-1-1-1-BBB)-B-11-BB
4	MGC 8	(CML451-B*7/(CML395/MBRC5BcF114-1-2-3-B-4-2-B)DH-3018-B*4)-B-8-BB
5	MGC 12	((CML161Xcml451)-B-18-1-BBB/CML161-B)-B-13-BB(NonQ)-BBB(MBRC5BcF108-2-3-1-B-5-2-B/CML444)DH-3017-B*4)-B-7-2-B
6	MGC 15	(AMDROUT1(DT-Tester)c1F2-36-B*5/(POP502C5#18/GEMN-0145)-B-21-2-1-B)-B-1-BB
7	MGC 16	(AMDROUT2c2-17-B*4/(POP502C5#4/GEMN-0159)-B-19-3-1-1-B)-B-3-2-B
8	MGC 19	(L451-B*4//CML451-BBB/LaPostaSeqC7-F18-3-2-2-3-B*7//CML451-B*4//CML451-BBB/DRB-F2-60-1-1-1-BBB-3-B)-1-1-3-BB
9	MGC 56	(CML451-B*4//CML451-BBB/ZEWBc1F2216-2-2-B-2-B*4-1-B-BB//CML451-B*4//CML451-BBB/CML444-1-BB)-1-8-B-2-BB
10	MGC 80	(VL105541/LaPostaSeqC7-F18-3-2-2-3-B*7)-B-11-BB-#-BB
11	MGC 81	(CML286/CML505//CM286)-6-B-4-B*4
12	MGC 83	(CML472/CML468//CM444)-15-B-1-B*4
13	MGC 98	(CLQG2508-B*8/Composite11(InSel)-2-BB-1-B-3-BB)-B-10-1-B
14	MGC 106	((P73TLC3#-111-2-4-##-BB)x(RCW01)]-1-150-B*4/(CML474/S92145-2EV-7-3-B*5)-F2-58-1-B*12)-B-2-BB
15	MGC 109	((G9BC0RL34-1P-5P-2-IP-3P-B/G9BC1TSR8P-1P-1P-5P-3P-1P-1P)-3-1-1-1-B*8/((CML161x CML451)-B-18-1-BBB/CML161-B)-B-13-BB(NonQ)-BBB)-B-3-BB
16	MGC 113	(CML451-B*7/G9AC6RL6-1-1P-1P-1P-2P-1P-2P-B*12)-B-2-1-B
17	MGC 116	((CML161Xcml451)-b-18-1-BBB/CML161-B)-B-13-BB(NonQ)-BBB/TZM1713)-B-5-2-B
18	MGC 234	(VL111354/CML472)-7-B-1-BB-1-BB

**3. RESULTS AND DISCUSSION**

The present study was carried out to study the genetic variability and diversity among the eighteen inbred lines of maize. The analysis of variance was significant for all the characters,

indicating the presence of adequate genetic differences among the inbred lines (Table 2). Selection of genetically diverse inbred lines for development of hybrids and required sufficient genetic variability and high heritability in the base population. The inbred lines evaluated in the

present study registered wide variability for all the traits assessed (Table 3). Inbred line MGC 106 recorded shortest plant height (135.5cm) and MGC 15 recorded tallest (210.0 cm) with a mean of 171.0 cm indicating high range of genetic variability. Lower cob placement is very important in maize and inbred line MGC 109 was observed with lowest ear height (50.0 cm) and MGC 56 recorded the highest ear height (85.5 cm) with a mean of 68.4 cm. Wide range of variability observed for days to 50 % silking with a mean of 58.8 days and the inbred line MGC 8 registered early (56 days) and MGC 56 late (65 days). Days to 50% pollen shed recorded was 53 days in the inbred line MGC 15, while 62.5 days was noticed in the by inbred line MGC 80 with a mean of 58.4 days. The range of genetic variability for the trait number of rows per cob varied from 10.0 (MGC 81) to 16.0 (MGC 113) with a mean of 13.8. The range of variation for number of kernels per row was 14.0 (MGC 81) to 27.5 (MGC 106) with a mean of 23.9. The inbred line MGC 81 and MGC 6 recorded 9.7 cm and 17.3 cm cob lengths respectively with a mean of 13.6 cm. Similarly, for the trait cob girth inbred line MGC 16 showed low cob girth (10.5 cm) and MGC 234 recorded higher cob girth (14.0 cm) with a mean of 12.1 cm. Wide range of variability noticed for the trait yield per cob with range of 53.5 g (MGC 19) to 91.0 g (BML 10) with a mean of 74.2 g.

Phenotypic Coefficient of Variation (PCV) slightly higher than Genotypic Coefficient of Variation (GCV) for all the traits, indicating the less influence of environment in expression of the traits (Table 3). Therefore, selection on the basis of phenotype alone can be effective for the selection of genotypes and improvement of these traits. Medium range of GCV and PCV were observed for ear height (15.20, 15.75), number of kernels per row (14.60, 15.74), cob length (14.00, 15.74), grain yield per cob (13.12, 14.12) and plant height (12.14, 12.81). Traits cob girth (7.39, 9.38), number of rows per cob (7.01, 10.07), days to 50% pollen shed (4.32, 4.52) and sillking (4.08, 4.42) recorded lower estimates of GCV and PCV. High to medium range of coefficient of variation provides great scope for the selection of desirable genotypes.

Coefficient of variations provides the information on the genetic variability present in various quantitative characters, but it is not possible to determine the amount of variation that was heritable. Coefficient of variation together with heritability estimates would give the best picture

of the amount of advance to be expected from selection [19]. Thus the heritable portion of the variation could be more useful with the help of heritability estimates. All the characters under present investigation showed high heritability except for number of rows per cob. Heritability in broad sense was the highest for the trait ear height (93.16%) followed by days to pollen shed (91.33%), plant height (89.71%), grain yield per cob (86.32%) and number of kernels per row (85.97%). Selection of the genotypes based on these characters could be useful as these traits successfully transferred to offspring and selection for such trait is easy and quick. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation. Heritability estimates coupled with genetic advance would be more reliable and useful in formulating selection procedure. Genetic advance was estimated and transferred into genetic advance as percent of mean for all the traits (Table 2). The trait ear height (30.22) registered the highest genetic advance as per cent of mean followed by number of kernels per row, cob length, grain yield per cob and plant height. Lowest genetic advance as percent of mean was observed for days to 50% silking and pollen shed. High heritability along with high genetic advance as percent of mean recorded for the traits like plant and ear height and grain yield per cob, suggesting that these characters can be considered as favourable attributes for improvement through selection and this may due to additive gene action. These results are in conformation with earlier workers [9,10,11,20,21,22] for medium to low range of genetic parameters in maize for the most of the yield traits.

For development of high yielding single cross hybrids assessing the genetic divergence among the inbred lines available with them is very important. The eighteen inbred lines were grouped in to six clusters (Table 4 & Fig. 1), out of which cluster I was the largest, having eight genotypes followed by cluster II with six genotypes indicating the genetic similarity among the genotypes present in these clusters. Remaining four clusters III, IV, V and VI are the solitary clusters having only one inbred line indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes present study. The clustering pattern revealed that the inbred lines showed considerable genetic diversity among themselves by occupying six different clusters.

**Table 2. Analysis of variance of yield and yield attributing traits of inbred lines of maize**

Characters/ Source of variation		D.F	Plant height (cm)	Ear height (cm)	Days to 50% pollen shed	Days to 50% silking	Number of rows/ cob	number of kernels /row	Cob length (cm)	Cob girth (cm)	Grain yield/ cob
Mean sum	Replication	1	18.778	14.694	1.000	0.250	1.000	4.694	0.047	1.821	26.694
of squares	Treatment	17	910.882	223.812	12.529	13.309	2.882	26.368	8.208	2.080	204.126
	Error	17	49.425	7.930	1.000	0.603	1.000	1.989	0.960	0.486	14.989

**Table 3. Estimates of genetic parameters in inbred lines of maize**

Characters	Mean	Range	GCV	PCV	Heritability (%)	Genetic Advance	Genetic Advance value % means
Plant height (cm)	171.0	135.5-210.0	12.14	12.81	89.71	40.49	23.68
Ear height (cm)	68.4	50.0-85.5	15.20	15.75	93.16	20.66	30.22
Days to 50% pollen shed	58.8	56.0-65.0	4.08	4.42	85.22	4.57	7.76
Days to 50% silking	58.4	53.0-62.5	4.32	4.52	91.33	4.96	8.49
Number of rows/ cob	13.8	10.0-16.00	7.01	10.07	48.49	1.39	10.06
number of kernels /row	23.9	14.0-27.5	14.60	15.74	85.97	6.67	27.88
Cob length (cm)	13.6	9.7-17.3	14.00	15.74	79.05	3.87	25.63
Cob girth (cm)	12.1	10.5-14.0	7.39	9.38	62.12	1.45	12.00
Grain yield/ cob	74.2	53.5-91	13.12	14.12	86.32	18.61	25.09

The intra cluster distances were lower than the inter cluster distances (Table 5 & Fig. 2). Thus the inbred lines included within a cluster had less diversity among them. The cluster II recorded maximum intra cluster distance (60.49) followed by cluster I (43.81). The intra cluster distance from clusters III to VI was 0.00, revealed that these are solitary clusters with single inbred lines in them indicating the uniqueness of those genotypes compared to other inbred lines included in the study. The highest inter cluster distance 386.89 was observed between cluster IV and V followed by clusters I and IV (326.90), I and VI (309.98), II and V (297.76), III and V (239.32) and cluster I and III (252.68), suggesting more variability in genetic makeup of the inbred lines included in the clusters and make the crosses in line x tester passion between lines of cluster I and Cluster III, IV and VI to realize high yielding single cross hybrids in maize. Similarly, selection of the inbred lines from clusters II, III and V having statistical

distance could be used in crossing programme for obtaining a wide spectrum of variation among the sergeants. The lowest inter cluster distance was observed between cluster III and IV (38.50) and III and IV (82.20) indicating genetic closeness of the inbred lines included in these clusters. Earlier workers [23,24,25,26,27] reported similar findings for different clustering patterns and selection of parents in hybridization programme for yield improvement in maize. The greatest range of mean values among the clusters was observed for different characters (Table 6). A wide range of variations for most of the characters among single as well as multi genotypic clusters was observed. Cluster V recorded highest the mean values for days to 50% silking and pollen shed number of kernels per row, cob length and girth. Ear height and grain yield per cob registered the highest mean values in the cluster VI. Cluster I was observed with the highest mean value for number of rows per cob.

**Table 4. Distribution of inbred lines into clusters based on Mahalanobis D<sup>2</sup> statistic**

Cluster group	Genotypes	No of genotypes
Cluster I	MGC-113, MGC-234, MGC-116, MGC -12, MGC-19, MGC-106, MGC-8, GP 170	8
Cluster II	BML 10, MGC-98, MGC-109, MGC-16, MGC-6, MGC-83	6
Cluster III	MGC-81	1
Cluster IV	MGC-15	1
Cluster V	MGC-80	1
Cluster VI	MGC-56	1

**Table 5. Average inter- cluster (above diagonal) and Intra-cluster (diagonal) D<sup>2</sup> values among inbred lines**

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	43.81	181.32	252.68	326.90	110.07	308.98
Cluster II		60.49	103.66	113.31	297.76	229.90
Cluster III			0.00	38.50	239.32	82.20
Cluster IV				0.00	386.89	173.14
Cluster V					0.00	174.25
Cluster VI						0.00

**Table 6. Cluster means for yield and yield attributing traits in different clusters of inbred lines**

	Plant height (cm)	Ear height (cm)	Days to 50% pollen shed	Days to 50% silking	Number of rows/cob	number of kernels /row	Cob length (cm)	Cob girth (cm)	Grain yield/cob
Cluster I	169.06	65.56	57.50	59.50	14.38	24.94	14.63	12.39	80.75
Cluster II	159.25	61.92	59.75	57.08	14.00	21.58	12.07	11.76	83.17
Cluster III	195.00	85.00	59.00	56.00	11.00	14.00	9.70	11.25	72.00
Cluster IV	210.00	80.00	56.00	53.00	12.00	24.00	11.50	11.25	69.50
Cluster V	170.00	84.50	60.50	62.50	13.00	26.00	16.00	14.00	69.00
Cluster VI	195.00	85.50	65.00	61.50	14.00	24.00	15.45	11.15	90.50

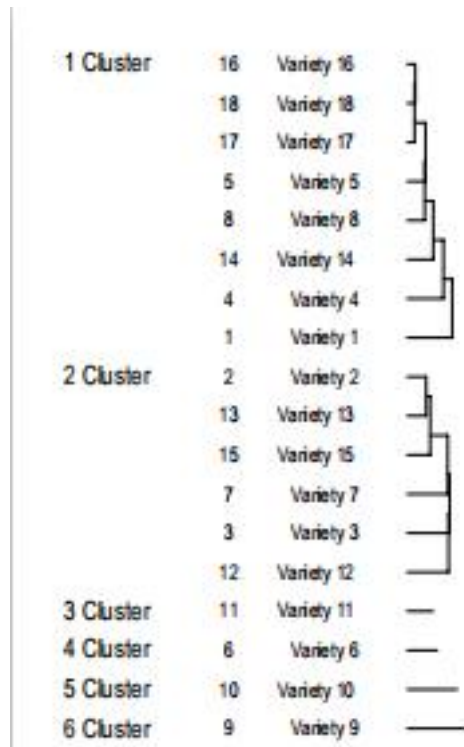


Fig. 1. Clustering pattern by Tocher’s method

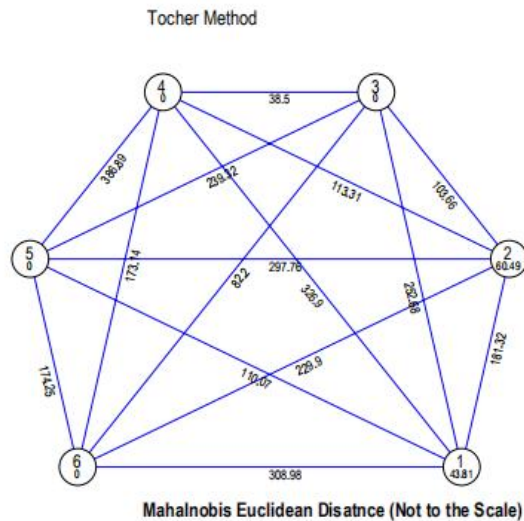


Fig. 2. Mahalanobis Euclidean distances by Tocher’s method

**4. CONCLUSION**

From the above investigation it can be concluded that plant height, ear height, grain yield per cob, cob length and number of kernels per row are the important traits for selection of genotypes for

improvement of yield in maize as they recorded medium to high range of PCV and GCV estimates, heritability and genetic advance as per cent of mean. Selection of inbred lines from cluster I as lines and lines from Cluster III, IV and VI as tester would yield large number of

segregants and can be exploit for the identification of genotypes with the desirable traits in maize.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

## REFERENCES

1. Cairns JE, Sonder K, Zaidi PH, Verhulst PN, Mahuku G, Babu R, Nair SK, Das B, Govaerts B, Vinayan MT, Rashid Z, Noor JJ, Devi P, Vicente F. san, and Prasanna BM. Maize production in a changing climate: Impacts, adaptation, and mitigation strategies. *Advances in Agronomy*. 2012;114:1-65.
2. Cairns, J E, Jose Crossa, P. H. Zaidi, Pichet Grudloyma, Ciro Sanchez, Jose Luis Araus, Suriaphat Thaitad, Dan Makumbi, Cosmos Magorokosho, Marianne Bänziger, Abebe Menkir, Sarah Hearne, and Gary N. Atlin. Identification of drought, heat, and combined drought and heat tolerant donors in maize. *Crop Science*. 2013;53:1335–1346.
3. Fisher MT, Abate, Lunduka RW, Asnake W, Alemayehu Y, Madulu RB. Drought tolerant maize for farmer adaptation to drought in sub-Saharan Africa: Determinants of adoption in Eastern and Southern Africa. *Clim. Change*. 2015;133(2):283-299.
4. Tadesse Ertiro B, Olsen M, Das B, Gowda M, Labuschagne M. Genetic dissection of grain yield and agronomic traits in maize under optimum and low-nitrogen stressed environments. *International Journal of Molecular Sciences*. 2020;21(2):543.
5. Murty BR, Arunachalam V. The nature of genetic divergence in relation to breeding systems in crop plants. *Indian J. Genet. Plant Breed*. 1966;26:188–198.
6. Nzuve F, Githiri S, Mukunya DM, Gethi J. Genetic variability and correlation studies of grain yield and related agronomic traits in maize. *Journal of Agricultural Science*. 2014;6(9):166-176.
7. Maruthi RT, Jhansi Rani K. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *Journal of Applied and Natural Science*. 2015;7(1):149–154.
8. Dawood SM, Al-Obaidy, Jasim M, Al-Juboory, Ahmad H. Al-Juboory. Estimating of genetic parameters and construction of selection indices for exotic and endogenous maize genotypes. *Journal Tikrit Univ. For Agri. Sci*. 2015;15(1):8-17.
9. Kharel R, Ghimire SK, Ojha BR, Koirala KB. Estimation of genetic parameters, correlation and path coefficient analysis of different genotypes of maize (*Zea mays* L.). *International Journal of Agriculture Innovations and Research*. 2017;6(1):191-195.
10. Niharika Shukla, Mishra DK. Study of genetic parameters and association analysis among maize (*Zea maize* L.) germplasms. *Ecscan*. 2016;9(Special Issue):183-189.
11. Priyanka Jaiswal, Banshidhar, Sonam Rani Agrahari, Rajesh Singh. Estimation of genetic parameters for yield related traits and grain zinc concentration in biofortified inbred lines of maize (*Zea mays* L.). *The Pharma Innovation Journal*. 2019;8(3):87-91.
12. Rohman MM, Banik BR, Biswas A, Rahman MS. Genetic diversity of maize (*Zea mays* L.) inbreds under salinity stress. *Bangladesh J. Agril. Res*. 2015;40(4):529-536.
13. Ali Abdikadir Hassan, Mohamed Abdikadir, Mehedi Hasan, Md. Abul Kalam Azad, Md. Hasanuzzaman. Genetic variability and diversity studies in maize (*Zea mays* L.) inbred lines. *IOSR Journal of Agriculture and Veterinary Science*. 2018;11(11):69-76.
14. Panse VG, Sukhatme PV. *Statistical methods agricultural workers*. ICAR, New Delhi. 1985;235-246.
15. Hanson CH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population of Korean lespedesa. *Agron. J*. 1956;48:268-272.
16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agro. J*. 1955;47: 314-318.
17. Burton GW. Quantitative inheritance in grasses. *Proc. 6th Int. Grasslands Cong. J*. 1952;1:227-283.



18. Rao CR. Advanced statistics methods in Biometric Research, Ed. John Wiley and Sons Inc. New York. 1952;390.
19. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
20. Pandey Y, Vyas RP, Kumar J, Singh L, Singh HC, Yadav PC, Vishwanath. Heritability, correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in maize (*Zea mays* L.). Int. J. Pure App. Bio Sci. 2017;5(2):595-603.
21. Belay N. Genetic variability, heritability, correlation and path coefficient analysis for grain yield and yield component in maize (*Zea mays* L.) hybrids. Advances in Crop Science and Technology. 2018;6(399):1-9.
22. Nlima Ahmed, Abul Kashem Chowdhury, Saleh Uddin Md, Mainul Islam Rashad Md. Genetic variability, correlation and path analysis of exotic and local hybrid maize (*Zea mays* L.) genotypes. Asian Journal of Medical and Biological Research. 2020;6(1):8-15.
23. Varaprasad BV, Shivani D. Genotype clustering of maize (*Zea mays* L.) germplasm using Mahalanobis  $D^2$  statistic. Journal of Global Biosciences. 2017;6(2): 4776-4783.
24. Neha Rani RB, Nirala P, Sweta Kumari, Birender Singh, Hemlata Kumari. Genetic diversity under heat stress condition in maize (*Zea mays* L.) inbred lines. Int. J. Curr. Microbiol. App. Sci. 2018(Special Issue-7):4539-4547.
25. Adu GB, Awuku FJ, Amegbor IK, Haruna A, Manigben KA, Aboyadana PA. Genetic characterization and population structure of maize populations using SSR markers. Annals of Agricultural Sciences. 2019;64: 47-54.
26. Alimatu Sadia Osuman, Bafffour Badu-Apraku, Beatrice E. Ififie, Pangirayi Tongoona, Ebenezer Obeng-Bio, Ana Luísa Garcia-Oliveira. Genetic diversity, population structure and inter-trait relationships of combined heat and drought tolerant early-maturing maize inbred lines from West and Central Africa. Agronomy. 2020;10(1324):1-19.
27. Nusrat Ul Islam, Ali G, Dar ZA, Maqbool S, Kumar B, Bhat A. Genetic divergence in maize (*Zea mays* L.) inbred lines. International Journal of Chemical Studies. 2020;8(1):425-428.

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