Genetic Diversity and Yield Determinants in Maize (Zea Mays L.)

Liban Said Ali[1], P.N. Verma[2], Usman Sayeed[3]

[1]M.Sc. (Agriculture), Department of Agriculture, Integral Institute of Agricultural Science & Technology, Integral University, Lucknow-226026 (INDIA)

[2,3]Assistant Professor Department of Agriculture, Integral Institute of Agricultural Science & Technology, Integral University, Lucknow-226026 (INDIA)

**Corresponding author: pnverma@iul.ac.in

Abstract

Genetic analysis of variability, heritability and character association was studies among 18 maize F_1 hybrids for eleven traits. The analysis of variance revealed that genotypic mean squares were significant for all traits, indicating that all the F_1 hybrids under study had a higher level of genetic diversity. In terms of genotypic and phenotypic coefficient variation, the most significant coefficient was found in plant height (10.129 and 11.907), 100 seeds weight (9.393 and 14.008), seed yield per cob (9.366 and 11.931), grain yield per plant (8.654 and 12.054), respectively. The Grain yield per plant has shown highly significant positive correlations with seed yield per cob (0.908), 100-seed weight (0.879), number of grains per row (0.722), cob length (0.701), cob diameter (0.715), number of rows per cob (0.526), plant height (0.431), and indicate a close genetic association between traits favouring larger seed size and increased seed yield per cob with augmented grain yield per plant might all be employed as selection criteria to increase the maize grain yield.

Keywords: Genetic variability, diversity, heritability, genetic advance.

Introduction

Maize, scientifically known as *Zea mays* L., is a cereal crop from the Poaceae (Gramineae) family and Maydeae tribe, boasting a diploid chromosome number of 2n=2x=20. Renowned for its adaptability and resilience to varying Agro-climatic conditions, maize holds a pivotal commercial position among grain crops. Often hailed as the "**Queen of cereals**" within the Gramineae family, maize stands out due to its exceptional productivity potential.The crop has gained global prominence, extending its cultivation from the equatorial regions to temperate zones, thriving in diverse environments.Global maize production, exceeding 1147.7 million metric tons annually, involves over 170 countries, with an average productivity of 5.75 tons per hectare. The United States, China, Brazil, and Argentina are significant producers, collectively contributing to over two-thirds of the world's production. In Asia, India and Indonesia play substantial roles.Maize grains are valued for their versatile applications, serving as a staple food, animal feed, and an essential raw material for various industrial products. The demand for maize in developing countries is estimated to double by the year 2050 (Rosegrant *et al.* 2009).

Key maize-growing states in India include Andhra Pradesh, Karnataka, Rajasthan, Maharashtra, Bihar, Uttar Pradesh, Madhya Pradesh, and Himachal Pradesh. Uttar Pradesh, particularly the upper Gangetic Plain, emerges as a prominent maize producer, with significant production centres in Bulandshahar, Jaunpur, and Ghaziabad districts. Maize cultivation in India predominantly occurs as a rain-fed Kharif crop, sown before the monsoon and harvested afterwards. Uttar Pradesh, however, also cultivates maize during the Rabi season before the onset of winter.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). Effective breeding programs rely on assessing genetic diversity and variability within maize populations, ensuring the development of superior cultivars. Parameters like phenotypic and genotypic coefficients of variation aid in evaluating the extent of variation within maize varieties, laying the foundation for successful varietal/hybrid development initiatives. 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 present research was carried out during *kharif* season 2023at Instructional Farm Unit-4, Integral Institute of Agricultural Science and Technology, Integral University, Lucknow (UP), India. The experimental material comprised 18 diverse maize F_1hybrids sourced from various regions of Uttar Pradesh, India. The experiment was conducted in a randomized complete block design with three replications. Each plot consisted of a single row of plants sown using the line sowing method at a depth of 3-5 cm, with a row-to-row spacing of 60 cm and a plant-to-plant spacing of 30 cm. A total of 54 plots were utilized for the study.Five randomly selected plants from each of the was selected for recording the observations on various traits.

Results and Discussion

In agricultural research, ANOVA serves as a fundamental statistical tool for understanding the variability within and between different components of a study. The ANOVA results indicate significant variations among genotypes for most of the studied traits. This suggests that genetic factors play a crucial role in determining the performance of maize hybrids across different traits. Further analysis can help in identifying superior genotypes for enhanced agricultural productivity and quality (table-1).

The current study revealed distinct levels of genotypic coefficient of variance (GCV) across various traits. Traits exhibiting high GCV include plant height (10.129%), 100 seeds weight (9.393%), seed yield per cob (9.366%), grain yield per plant (8.654%), plant height (10.129%) and cob diameter (5.618%). These traits showcase significant genetic variation within the population, indicating the potential for diverse phenotypic expressions among individuals. Moderate GCV were observed in traits such as cob length (4.182%), days to 50% tasseling (3.875%), number of grains per row (3.305%), days to 50% silking (2.902%), and number of rows per cob (2.808% While these traits display variability, they are of a moderate degree compared to those with high GCV. Conversely, days to maturity (1.84) emerge as a trait with low genotypic coefficient of variance (GCV), suggesting minimal genetic variation in the population regarding the time required for maturity (table-3). 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.The present study offers insight into the phenotypic coefficient of variance (PCV) across various traits, akin to the earlier analysis based on the genotypic coefficient of variance (GCV). Traits demonstrating high PCV include grain yield per plant (12.054%), plant height (11.907%), 100 seeds weight (14.008%), and seed yield per cob (11.931%). These traits exhibit substantial phenotypic variation within the population, indicating diverse phenotypic expressions among individuals. Traits with moderate PCV encompass cob diameter (8.351%), number of rows per cob (5.152%), days to 50% tasseling (4.116%), cob length (5.611%), and number of grains per row (4.966), days to 50% silking (3.183) (table-3).Genotypic and phenotypic variances were determined according to Singh and Chaudhary (1985) using MS-Excel programme.

Traits exhibiting high heritability, including days to 50% tasseling (88.638%), days to 50% silking (83.117%), plant height (72.37%), days to maturity (66.246%), seed yield per cob (61.624%), cob length (55.54%) and grain yield per plant (51.549%) suggest that a significant portion of their phenotypic variance stems from genetic differences among individuals rather than environmental influences.Thus, these traits hold promise for substantial enhancement through selective breeding endeavours. the genetic advance percentage estimates the anticipated improvement in a trait through selection. Traits with higher genetic advance percentage mean, such as plant height (17.751%), seed yield per cob (15.145%), and grain yield per plant (12.8%), signify more significant potential for enhancement through selective breeding. Conversely, traits with lower genetic advance percentage mean, like days to 50% tasselling (7.516%), days to 50% silking (5.451%), and a number of rows per cob (3.153%), may necessitate more nuanced breeding approaches or may exhibit inherent limitations in their improvement potential (table-3).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). 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. Thus, it is recommended to consider heritability and GAM together to predict the response of selection (Ogunniyan and Olakojo 2014).

Table-1. Analysis of Variance (ANOVA)

	Df	DT	DS	CL	CD	NR/C	NG/R	DM	PH	HSW	SY/C	GY/P
Replication	2	0.2468	0.2198	0.3332	0.1539	0.0305	2.6352	3.7055	470.55	12.5895	58.109	200.522
Genotypes	17	16.3924**	10.7815**	1.6924**	1.6834**	0.5579**	2.9339**	8.9865**	1314.56**	17.3834**	140.241**	302.491**
Errors	34	0.6717	0.6837	0.3564	0.4835	0.246	0.8667	1.3047	148.41	5.0365	24.107	72.158

**** = Significant at 1 % and * = Significant at 5 % level of significance**

Table-2. Treatment Means and Overall Means

Genotypes	GY/P	DT	DS	CL	CD	NRC	NGR	DM	PH	HSW	SY/C
UM-10	98.377	56.700	61.200	15.733	10.587	11.740	23.000	87.190	207.067	20.427	65.583
UM-20	90.035	59.987	63.717	15.373	10.663	11.923	25.650	87.507	174.187	19.823	60.673
UM-30	98.295	60.683	64.413	16.503	11.793	11.370	26.550	87.087	224.527	22.270	66.180
UM-40	114.150	59.280	63.010	15.390	10.680	11.620	26.607	88.820	169.833	25.423	76.750
UM-50	109.670	59.020	62.750	16.937	12.227	11.840	26.140	88.383	203.163	24.317	73.763
UM-60	113.805	60.493	64.223	16.380	11.670	11.810	26.600	88.660	218.457	23.820	76.520
UM-70	108.960	59.090	62.820	17.173	12.463	11.710	25.277	86.030	200.583	22.707	70.923
RASI-4212	104.480	61.817	65.547	15.797	11.087	11.733	24.810	85.593	176.283	18.867	59.870
MANGALAM	108.615	62.420	66.150	16.143	11.433	11.633	25.270	85.870	201.887	23.480	61.903
KAVERI-2021	103.565	63.687	67.417	17.173	12.463	11.567	24.330	89.980	212.500	23.947	67.410
TRIMURTI-826	81.797	56.533	61.100	14.620	11.323	10.663	23.650	85.363	168.457	17.960	54.530
VIRAT	84.850	56.500	61.933	16.167	9.563	11.293	24.320	84.717	167.847	16.653	56.563
VARDAN-1108	93.107	56.600	61.533	15.610	11.320	10.740	25.220	84.297	218.187	19.100	62.070
KANCHAN-101	108.963	56.567	61.200	16.403	11.030	10.990	25.277	86.030	163.493	22.253	72.640
SRI-5455	104.483	56.567	61.100	15.027	11.080	11.210	24.810	85.593	196.823	21.147	69.653
PIO-3401	108.617	56.567	61.533	15.373	11.220	11.180	25.270	85.870	212.117	21.827	72.410
PBM-101	103.565	60.770	64.500	16.403	11.693	12.370	24.330	89.980	213.407	23.597	69.693
DHM117	86.985	59.990	63.720	15.027	10.317	11.293	24.980	88.153	174.797	21.130	58.640
Overall Mean	**101.240**	**59.071**	**63.215**	**15.957**	**11.256**	**11.483**	**25.116**	**86.951**	**194.645**	**21.597**	**66.432**

Table-3. Heritability, Genotypic Coefficient of Variation % & Phenotypic Coefficient of Variation % (GCV & PCV)

Response Variable	Range	Grand mean	SEm	SED	Heritability	GCV	PCV	Gen-Advance	Gen-Adv % Means
GY/P	127.80-76.41	101.23	4.9043	14.095	51.549	8.654	12.054	12.959	12.8
DT	64.78-56.40	59.07	0.4732	1.36	88.638	3.875	4.116	4.44	7.516
DS	68.51-61.00	63.21	0.4774	1.372	83.117	2.902	3.183	3.446	5.451
CL	17.42-14.17	15.95	0.3447	0.991	55.54	4.182	5.611	1.024	6.42
CD	12.71-9.12	11.25	0.4015	1.154	45.268	5.618	8.351	0.877	7.787
NR/C	12.95-10.34	11.48	0.2864	0.823	29.71	2.808	5.152	0.362	3.153
NG/R	27.56-21.32	25.11	0.5375	1.545	44.29	3.305	4.966	1.138	4.531
DM	91.13-83.23	86.95	0.6595	1.895	66.246	1.84	2.261	2.683	3.086
PH	232.64-153.12	194.64	7.0335	20.214	72.37	10.129	11.907	34.551	17.751
HSW	28.29-16.21	21.59	1.2957	3.724	44.969	9.393	14.008	2.802	12.976
SY/C	85.85-50.94	66.43	2.8347	8.147	61.624	9.366	11.931	10.061	15.145

Days to 50% Tasseling (DT), Days to 50 % silking (DS), Plant height (PH), Days to maturity (DM), Cob length (CL), Cob diameter (CD)

No. of Grain rows per cob (NG/R), No. of Grains per row (NR/C), Hundred grain weight (HSW), Seed yield per cob (SY/C), Grain yield per plant (GY/P)

Table-4. Correlation Matrix (Above diagonal Genotypic and below diagonal Phenotypic)

	GY/P	DT	DS	CL	CD	NRC	NGR	DM	PH	HSW	SY/C
GY/P	**1.000**	0.35^{NS}	0.305^{NS}	0.701**	0.715**	0.526*	0.722**	0.375^{NS}	0.431*	0.879**	0.908**
DT	0.840 **	**1.000**	0.986**	0.497*	0.507*	0.790**	0.297^{NS}	0.655**	0.266^{NS}	0.620**	0.051^{NS}
DS	0.197 ^{NS}	0.983 **	**1.000**	0.500*	0.444*	0.715**	0.213^{NS}	0.590**	0.275^{NS}	0.543**	-0.021^{NS}
CL	0.142 ^{NS}	0.390 **	0.398 **	**1.000**	0.671**	0.607**	0.210^{NS}	0.437*	0.470*	0.731**	0.541**
CD	0.230 ^{NS}	0.365 **	0.331 *	0.569 **	**1.000**	0.416*	0.213^{NS}	0.429*	0.753**	0.800**	0.546**
NR/C	0.286 ^{NS}	0.426 **	0.377 **	0.338 *	0.082 ^{NS}	**1.000**	0.297^{NS}	0.878**	0.338^{NS}	0.868**	0.434*
NG/R	0.329 *	0.224 ^{NS}	0.181 ^{NS}	0.241 ^{NS}	0.260 ^{NS}	0.038 ^{NS}	**1.000**	0.199^{NS}	0.145^{NS}	0.901**	0.724**
DM	0.285 ^{NS}	0.492 **	0.422 **	0.235 ^{NS}	0.234 ^{NS}	0.505 **	0.207 ^{NS}	**1.000**	0.235^{NS}	0.983**	0.524**
PH	0.278 ^{NS}	0.214 ^{NS}	0.216 ^{NS}	0.365 **	0.461 **	0.156 ^{NS}	0.162 ^{NS}	0.242 ^{NS}	**1.000**	0.582**	0.435**
HSW	0.232 ^{NS}	0.314 *	0.230 ^{NS}	0.226 ^{NS}	0.378 **	0.201 ^{NS}	0.202 ^{NS}	0.415 **	0.175 ^{NS}	**1.000**	0.853**
SY/C	0.727 **	0.016 ^{NS}	-0.048 ^{NS}	0.267 ^{NS}	0.329 *	0.263 ^{NS}	0.346 *	0.379 **	0.270 *	0.770 **	**1.000**

**** = Significant at 1 % and * = Significant at 5 % level of significance**

Table-5. Estimate of direct (diagonal) and indirect effects (off diagonal) at genotypic level

	DT	DS	CL	CD	NR/C	NG/R	DM	PH	HSW	SY/C
DT	**0.228**	0.051	-0.039	-0.012	0.056	-0.004	-0.128	0.004	0.027	0.015
DS	0.224	**0.051**	-0.040	-0.011	0.050	-0.003	-0.110	0.004	0.020	-0.042
CL	0.089	0.020	**-0.101**	-0.018	0.045	-0.004	-0.061	0.006	0.019	0.235
CD	0.083	0.017	-0.057	**-0.032**	0.011	-0.004	-0.061	0.008	0.032	0.289
NR/C	0.097	0.019	-0.034	-0.003	**0.131**	-0.001	-0.131	0.003	0.017	0.231
NG/R	0.051	0.009	-0.024	-0.008	0.005	**-0.017**	-0.054	0.003	0.017	0.303
DM	0.112	0.022	-0.024	-0.007	0.066	-0.004	**-0.260**	0.004	0.035	0.333
PH	0.049	0.011	-0.037	-0.015	0.021	-0.003	-0.063	**0.018**	0.015	0.237
HSW	0.072	0.012	-0.023	-0.012	0.026	-0.003	-0.108	0.003	**0.085**	0.675
SY/C	0.004	-0.002	-0.027	-0.010	0.035	-0.006	-0.099	0.005	0.065	**0.877**

Residual value: 0.211

The genetic correlation experiment revealed valuable insights into the genetic relationships between grain yield per plant and various phenotypic traits. Grain yield per plant has shown highly significant positive correlations with seed yield per cob (0.908**), 100-seed weight (0.879**), number of grains per row (0.722**), cob length (0.701**), cob diameter (0.715**), number of rows per cob (0.526*), plant height (0.431*), and indicate a close genetic association between traits favouring larger seed size and increased seed yield per cob with augmented grain yield per plant (table-4).Pavan *et al.* (2011) reported a similar kind of association in their study. Similar results were also noticed by Devasree *et al.* (2020).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). 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 direct and indirect effects of eleven characters on grain yield per plant estimated by path coefficient analysis using simple correlations are given in Table-5. The highest positive direct effect on grain yield per plant was exerted by seed yield per cob (0.877), days to 50% tasseling (0.228), 100 seeds weight (0.085), number of rows per cob (0.131), days to 50% silking (0.051) and plant height (0.018). 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).The characters that contributed a negative direct effect on grain yield per plant were days to maturity (-0.260), cob length (-0.101), cob diameter (-0.032), and number of grains per row (-0.017).The highest positive indirect effect on grain yield was exerted by 100 seed weight (0.675) via seed yields per cob, days to maturity (0.333) via seed yields per cob, number of grains per row (0.303) via seed yields per cob, cob diameter (0.289) via seed yields per cob, plant height (0.237) via seed yields per cob, cob length (0.235) via seed yields per cob, number of rows per cob (0.231) via seed yields per cob.

The analysis of various traits contributing to genetic divergence in maize reveals that the most significant contributors are days to 50% tasseling (47.71%), 100 seeds weight

(18.95%), and plant height (13.07%), indicating their crucial role in differentiating genotypes and adaptation to different environments.Grain yield per plant (3.92%), days to 50% silking (3.27%), number of grains per row (3.27%), days to maturity (7.19%), and seed yield per cob (2.61%) also contribute to divergence, though to a lesser extent, highlighting their influence on yield and crop performance. Notably, cob length, diameter, and number of rows per cob show no contribution (0%), suggesting uniformity among these traits across genotypes (table-6).Understanding these contributions helps select traits for breeding programs to enhance yield, adaptation, and overall genetic improvement in maize.Cluster-1, the largest group with ten genotypes, indicates a high degree of genetic similarity among its members, suggesting a significant portion of shared genetic makeup is likely due to common ancestry or similar selective pressures(Madhav *et al*., 2016). Cluster-2, comprising six genotypes, is closely related but distinct enough to form a separate group from Cluster-1, potentially indicating different evolutionary paths or adaptations. Clusters-3 and 4 each contain only a single genotype, with genotype 18 and genotype 3 representing unique genetic makeups that do not align closely with other clusters (table-7). Regarding other traits, Cluster 3 showed the highest means for days to 50% tasseling, days to 50% silking, cob length, number of grains per row, days to maturity, and plant height. Cluster 1 had the highest means for cob diameter and 100-seed weight, as well as the number of rows per cob and seed yield per cob.The clustering patterns suggest diverse genetic backgrounds and trait associations among the genotypes. These insights can guide selection of parents and design of cross combinations to maximize variability and yield improvement in maize breeding programs (table-8).The average intra- and inter-cluster distances between different clusters are presented in table-9. The intra-cluster D^2 values ranged from 37.7244 (Cluster I) to 0 (Clusters II, III, IV), indicating varying compactness within the clusters. Regarding inter-cluster distances, the average D^2 values suggested varying dissimilarity among clusters. The most diverse pairs were III and IV (528.4817), followed by I and IV (316.9605), I and III (176.3658), II and III (373.1148), II and IV (84.8648), and I and II (37.7244).

Grain yield/plant	3.92 %
Days to 50% tasseling	47.71 %
Days to 50% silking	3.26 %
Cob length	0
Cob diameter	0
No. of rows/cobs	0
No. of grains/rows	3.26 %
Days to maturity	7.18 %
Plant height	13.07 %
100 seeds weight	18.95 %
Seed yield/cob	2.61 %

Table-6. Contribution of various traits to divergence

Table-7.Number of genotypes in different cluster

Clusters	No. of genotypes	Genotypes
CLUSTER= 1	10	9 10 12 13 11 14 8 16 15 17
CLUSTER= 2	6	4 7 6 1 2 5
CLUSTER= 3	1	18
CLUSTER= 4	1	3

Table-8. Cluster mean

CLUSTER	GY/P	DT	DS	CL	CD	NR/C	NG/R	DM	PH	HSW	SY/C
1	60.36	64.09	16.11	11.40	11.73	25.62	87.61	195.71	22.54	67.49	103.86
2	56.59	61.28	15.46	11.09	11.09	24.54	85.72	194.36	20.45	66.15	99.22
3	63.69	67.42	17.17	12.46	11.57	24.33	89.98	212.50	23.95	67.41	103.57
4	56.50	61.93	16.17	9.56	11.29	24.32	84.72	167.85	16.65	56.56	84.85

Table-9. Inter and intra cluster distance

Cluster	I	II	III	IV
I	37.7244	176.3658	79.9711	316.9605
II		35.3815	373.1148	84.8648
III			0	528.4817
IV				0

This study investigated the genetic variability within a set of F_1 maize hybrids, revealing substantial diversity for key agronomic traits. The significant genotypic variation observed for all traits underscores the potential for selection and improvement within this material. High heritability estimates for days to 50% silking and tasseling suggest these traits are primarily under genetic control, making them amenable to selection. Furthermore, the strong positive correlations observed between grain yield per plant and yield components such as seed yield per cob, 100-seed weight, and cob characteristics highlight the importance of these traits in determining yield potential. Path coefficient analysis confirmed the direct and positive influence of these yield components on grain yield, indicating their utility as selection criteria in breeding programs.

Acknowledgement

The author acknowledge the support of Integral University, Lucknow for providing all the logistic support in conduct of the experiment and UPCAR for having used their genetic material.

References

Azam MG, Sarker U and Banik BR. “Genetic variability of yield and its contributing characters on CIMMYT maize inbreds under drought stress”. Bangladesh J. Agril. Res. 39: 419-426, 2014.

Begum S, Ahmed A, Omy SH, Rohman MM and Amiruzzaman M. “Genetic variability, character association and path analysis in maize (*Zea mays* L.)”. Bangladesh J. Agr. Res. 41: 173-182, 2016

Devasree S, Ganesan KN, Ravikesavan R, Senthil N and Paranidharan V. “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, 2020.

Grafius JE. Components of yield in oats: “A geometrical interpretation. J. Agron”. 48: 419-423, 1956.

Jilo T, Tulu L, Birhan T and Beksisa L. “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, 2018.

Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhayaya J and Shrestha J. “Genetic variability and trait association in maize (*Zea mays* L.)” varieties for growth and yield traits. Heliyon 7: 07939, 2021.

Nwangburuka CC, Denton OA, Kehinde OB, Ojo DK, Popoola AR. “Genetic variability and heritability in cultivated okra (*Abelmoschus esculentus* (L.) Moench)”. Spanish. J. Agric. Res. 10:123-129, 2012.

Ogunniyan DJ and Olakojo SA. “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, 2014.

Patil SM, Kumar K, Jakhar DS, Rai A, Borle UM and Singh P. “Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.)”. Int. J. Agric. Environ. Biotechnol. 9: 1103 1108, 2016.

Pavan R, Lohithaswa HC, Wali MC, Prakash G and Shekara BG. “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, 2011.

Rao P and Rao VT. “Genetic analysis for yield and its components in pigeonpea (*Cajanus cajan* (L.) Mill Sp)”. Int. J. Appl. Biol. Pharmaceut. Technol. 6: 189-190, 2015.

Rosegrant MR, Ringler C, Sulser TB, Ewing M, Palazzo A, Zhu T, Nelson GC, Koo J, Robertson R, Msangi S and Batka M. “Agriculture and food security under global change: Prospects for 2025/2050”. International Food Policy Research Institute, Washington, DC, pp. 145-178, 2009.

Singh RK and Chaudhary BD. “Biometrical Methods in Quantitative Genetic Analysis”. Kalayani Publishers, New Delhi, India, pp. 318, 1985.

Wali MC, Kachapur RM, Kulkarni VR and Hallikeri SS. “Association studies on yield related traits in maize (*Zea mays* L.)”. Maize J. 1: 131-133, 2012.

Wali MC. “Genetic variability and divergence studies in maize (*Zea mays* L.)”. EC Agric. 5: 2014-15,2019