www.ThePharmaJournal.com

The Pharma Innovation



ISSN (E): 2277-7695 ISSN (P): 2349-8242 NAAS Rating: 5.23 TPI 2023; 12(5): 295-299 © 2023 TPI

www.thepharmajournal.com Received: 07-03-2023 Accepted: 16-04-2023

S Veera Vishnu

M.Sc. Research Scholar, Department of Genetics and Plant Breeding, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Odisha, India

I Sudhir Kumar

Senior Scientist, Department of Genetics and Plant Breeding, Agricultural Research Station, Peddapuram, Andhra Pradesh, India

SR Harish Chandar

M.Sc. Research Scholar, Department of Genetics and Plant Breeding, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Odisha, India

Pushpalatha G

Professor & Head, Department of Biotechnology, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Odisha, India

K Krishnam Raju

Associate Professor and Head, Department of Genetics and Plant Breeding, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Odisha, India

Corresponding Author: S Veera Vishnu

M.Sc. Research Scholar, Department of Genetics and Plant Breeding, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Odisha, India

Genetic variability and association studies for grain yield and its component traits in maize (Zea mays L.) in breds

S Veera Vishnu, I Sudhir Kumar, SR Harish Chandar, Pushpalatha G and K Krishnam Raju

Abstract

Therefore, the experiment was conducted during *Rabi*, 2022 at College Farm, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha, India to estimate the genetic variability in 52 inbred lines tested in randomized block design with three replications. The data was recorded for days to 50% tasseling, days to 50% silking, anthesis-silking interval, days to maturity, plant height, ear height, number of ears per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per row, shelling percentage, 100 kernel weight, protein content, oil content and grain yield per plant. Analysis of variance indicated the existence of significant differences among the genotypes for all the traits studied. High GCV and PCV values were observed for anthesis-silking interval. High heritability coupled with high genetic advance as percent of mean was observed for anthesis-silking interval, number of kernel rows per ear, number of kernels per row, show per ear, number of kernels per row, 100 kernel weight, oil content and grain yield per plant suggesting the role of additive genes in governing the inheritance of these traits which could be improved through simple selection.

Keywords: Maize, variability, heritability, genetic advance as percent of mean, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV).

Introduction

Maize (*Zea mays* L.) is a member of the sub-family Panicoideae of the family Poaceae and tribe Maydeae. It is believed to be the native of Central America and Mexico and is evolved from teosinte (*Zea mexicana*). Maize, known as queen of cereals, globally occupies 1st rank in productivity among cereals with 5.82 t/ha followed by 4.66 t/ha of rice and 3.55 t/ha of wheat. Maize, being a C4 plant, is physiologically more efficient with higher per day productivity. It has wider adaptation over different environmental conditions and cultivated from latitude 58° N to 40° S, from mean sea level to higher than 3000 m altitude and in areas receiving 250 mm to 5000 mm yearly rainfall (Walne and Reddy, 2022)^[17].

As per FAOSTAT (2020)^[4] the worldwide maize is grown in 193.7 million hectares with a total production of 1147.7 million metric tons and average productivity of 5.75 t/ha. Worldwide maize is grown in over 170 countries. The United States, China and Brazil accounted for about 62% of global maize production (2020). In India it is grown in an area of 9.9 m ha with a production of 31.51mt and a productivity of 3.07 t/ha (FAOSTAT, 2020)^[4]. In India Madhya Pradesh and Karnataka states (15% each) have the major maize area followed by Maharashtra (10%), Rajasthan (9%), Uttar Pradesh (8%) and others. Karnataka has the highest maize productivity because of some highly productive districts like Krishna, West Godavari etc.

The rapidly increasing demand of maize is driven by increase in demand for direct human consumption as a staple food crop and for livestock feed (Ghimire *et al.*, 2018)^[5]. Maize starch can be hydrolyzed and enzymatically treated to produce syrups, particularly high fructose corn syrup sweetener that upon fermentation and distillation produces grain alcohol (Kay *et al.*, 2010)^[10]. In Odisha around seven major cluster districts contributed 74% of the total production, of which Nabarangpur district alone contributed 30% share in total production. Adoption of high yielding varieties in 89% of total land area contributed 93.3% of the total production. Almost 92% of the total maize is produced in *Kharif* season alone (APICOL 2020)^[16].

Maize directed evolution through breeding started when humans realized the potential of the species for food, feed, fodder, and fuel (Hallauer *et al.*, 2010) ^[7]. Morphologically maize exhibits greater diversity of phenotypes than any other grain crop (Rajesh *et al.*, 2013) ^[13] and is extensively grown in temperate, subtropical and tropical regions of the world. The existence of variability is essential for resistance to biotic and abiotic factors and also for wider adaptability in different agro-climatic zones. Hence the present study was under taken to evaluate the best performing inbred lines that can either be used as parents or evaluate further for synthetic and composites.

Materials and Methods

The experiment was conducted to estimate the genetic variability in 52 inbred lines that are tested in randomized block design with three replications at CUTM Farm, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha during *Rabi*, 2022. The farm is located between 18°.48' to 19°.39' North latitude and 83°.48' to 84°.08' East Longitude. The climatic condition of Gajapathi district varies between 16° to 40°C and receives a rainfall of 1403.30 mm. The sand loam texture soil with pH of 6.5 units and soil consist good organic carbon and nitrogen.

Fifty-two genotypes of maize were sown in Randomized Block design (RBD) with three replications. Each genotype was sown in three rows of three-meter length each with a spacing of 60cm between the rows and 25cm within the row. Recommended agronomical package of practices and need based plant protection measures were followed to raise a healthy crop.

Data Collection

Observations were recorded on five randomly selected plants in each treatment and in each replication. The plants were selected from the middle of the row excluding the border plants were subjected to record the observations for fourteen quantitative traits *viz.*, days to 50% tasseling, days to 50% silking, anthesis-silking interval (ASI), days to maturity, plant height (cm), ear height (cm), number of ears per plant, ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, shelling percentage (%), 100 kernel weight (g) and grain yield per plant (g) followed by two qualitative traits *viz.*, protein content (%) is estimated through the Lowry's method and oil content (%) is estimated through the Soxhlet apparatus method.

Statistical Analysis

The data from the 16 quantitative and quality traits were analyzed in 'R Studio (4.1.2)' using various packages. ANOVA, genetic parameters (Phenotypic and genotypic coefficient of variance, heritability, genetic advance per mean) analysis were done using the 'Variability' package with level of significance 5%.

Results and Discussion

Analysis of variance

The mean sum of square for grain yield per plant and their constituent characters in 52 diverse inbreed lines of maize are computed in (Table 1). The results showed that significant

differences and amount of variation present between the genotypes for most of the characters (p>0.05 and p>0.01) revealed that there was considerable genetic variability amongst the material under study. There is no significant variation for replication which shows that error due to environmental error was less. High significant amount of variability was recorded for plant height, ear height, shelling percentage and grain yield per plant in case of genotypes. The traits days to 50% tasseling, days to 50% silking, anthesissilking interval (ASI), days to maturity, number of ears per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100 kernel weight, protein content and oil content showed significant differences between genotypes. A wide range of significant differences for various traits has been observed earlier by Chaurasia et al. (2020) [3]; Mallikarjuna et al. (2020) ^[12] and Jumaa and Madab, (2018) [9]

 Table 1: Analysis of variance for sixteen morphological and maturity parameters in fifty two maize genotypes

ст	Characters	Mean sum of squares							
S.L No	Source of variation	Replication	genotype	Error					
INO	Degree of Freedom	2	51	102					
1	Days to 50% tasseling	46.952	11.212**	2.142					
2	Days to 50% silking	145.148	16.646**	1.994					
3	Anthesis-silking interval (ASI)	2.216	5.960**	0.013					
4	Days to maturity	260.446	58.884**	6.704					
5	Plant height (cm)	2584.750	359.031**	112.926					
6	Ear height (cm)	8042.709	266.807**	29.054					
7	Number of ears per plant	0.008	0.063**	0.003					
8	Ear length (cm)	12.757	13.540**	1.559					
9	Ear girth (cm)	3.624	0.749**	0.078					
10	Number of kernel rows per ear	12.577	11.822**	1.004					
11	Number of kernels per row	7.556	71.478**	8.438					
12	Shelling percentage %	3139.923	52.012**	13.570					
13	100 kernel weight (g)	43.180	32.279**	2.163					
14	Protein content (%)	19.629	2.141**	0.157					
15	Oil content (%)	0.664	0.967**	0.045					
16	Grain yield per plant (g)	12262.900	2271.32**	151.206					

Mean performance

Wide range of variation was observed for all the characters under study. Out of 52 genotypes, the better genotypes of each character by mean performance of genotypes (Table 2). Adequate number of fertile ears per plant and heavy kernels were important traits which should be considered in selection for high yield. Similar results were reported by Mallikarjuna et al. (2020)^[12] and Hussain et al. (2020)^[8]. Thus, some of the genotypes had higher mean values more than one character thus offering more scope for selecting superior genotypes in the respective study. According to the findings, changes in breeding practices, breeding time, and geoecological circumstances of the genotypes from which they were produced may account for the majority of genotype variances and variation in the traits that were investigated. There is considerable space to choose competent genotypes from the current study for further development in breeding programmes, according to the large diversity in yield and other attributes that genotypes demonstrated.

	C	6 5 0 .	· · · · · · · · · · · · · · · · · · ·	1.00 / 11	
Table 7. Mean	nertormances	of 57 maize	genotypes for	different vield	affrihuting fraite
Labic 2. Micall	performances	01 JZ maile	genotypes for	unificitint yiciu	autouting trans
	1		2 21	2	0

Sr. No.	Genotypes	DT	DS	ASI	DM	PH	ЕН	NEP	EL	EG	KRPE	KPR	SP	100KW	PC	OC	GYP
1	VL18444	64.00	71.60	7.67	116.00	190.60	94.60	1.20	18.00	4.80	14.00	40.00	73.18	25.50	8.40	4.30	142.80
2	VL18211	63.30	71.00	7.30	112.60	196.40	90.30	1.40	22.00	4.90	14.00	44.00	74.14	24.00	8.60	4.60	147.84
3	VL111341	62.30	70.00	7.60	103.60	186.60	89.60	1.20	16.00	4.00	16.00	32.50	68.12	28.00	7.80	4.10	143.36
4	VL107406	65.00	71.70	6.67	106.00	206.40	94.60	1.20	18.00	5.20	14.00	45.00	76.30	22.00	9.40	3.80	138.60
5	VL18327	63.70	67.30	3.67	101.60	180.20	92.60	1.40	21.00	4.80	16.00	41.00	71.73	26.00	8.60	5.60	170.56
6	VL18333	65.00	69.30	4.33	105.60	199.00	80.00	1.60	23.00	4.50	18.00	45.00	73.65	22.00	8.10	5.40	178.20
/	VL13692	62.00	60.30	5.55	114.00	204.00	88.00	1.20	19.00	4.40	16.00	41.00 24.50	76.84	27.00	7.40	4.80	1/7.12
0	VI 1017169	61.30	69.30	0.00	112.60	208.00	97.50	1.20	20.00	3.30 4 30	18.00	34.30 44.00	70.04	23.30	0.30	4.00	127.04
10	VL109452	61.50	69.30	7.60	102.00	211.00	95.60	1.20	22.00	5 20	15.00	36 50	76 10	28.00	9.50	5 20	151 20
10	VL109457	61.70	65.00	3.33	115.00	220.00	101.80	1.20	21.00	4.10	16.00	40.00	77.40	31.00	9.00	5.10	198.40
12	VL1016417	64.00	68.00	4.00	101.00	213.00	90.60	1.40	18.50	4.10	16.00	35.50	75.20	29.00	8.00	4.90	162.40
13	VL1016452	62.00	69.00	7.00	107.60	195.00	83.60	1.40	19.00	3.90	18.00	32.50	64.70	23.00	8.10	4.40	132.48
14	VL109499	63.30	67.00	3.67	117.50	203.60	108.60	1.60	22.50	4.00	16.00	44.50	67.38	27.00	8.70	4.70	198.72
15	VL109501	62.70	66.70	4.00	117.50	188.00	81.30	1.40	21.00	4.40	18.00	39.00	69.47	29.50	8.30	4.00	207.09
16	VL1016977	63.30	69.70	6.33	115.00	218.00	90.60	1.60	16.00	4.60	10.00	28.50	70.58	25.00	8.00	3.80	170.00
17	VL1017223	64.30	68.00	3.67	113.50	184.20	94.30	1.60	22.50	4.90	12.00	44.50	73.99	32.00	9.60	4.30	172.80
18	VL1010764	63.00	67.00	4.00	101.00	180.20	98.80	1.40	23.50	4.80	14.00	42.00	72.51	30.00	9.20	4.60	1/6.40
19	VL13855	64.70	68.70	4.00	102.50	190.00	/9.00	1.40	23.00	4.40	18.00	34.00	60.28 77.10	27.00	9.00	4.00	105.24
20	VL143905	65.00	69.00	0.00	105.50	206.60	83.30 105.00	1.00	20.00	4.30	12.00	38.00	74.86	28.00	9.40	4.80	128.70
21	VL143892	62.00	68 30	6 30	113.50	188.00	80,000	1.20	16.00	4.00	16.00	28.16	75.15	23.00	7.60	5.50	103.03
23	VL18523	64.70	68.70	4.00	112.50	192.50	97.50	1.40	22.50	4.90	16.00	42.00	68.35	25.00	8.20	5.90	168.00
24	KL154678	64.70	68.70	4.00	116.00	190.00	101.50	1.40	22.50	5.00	14.00	42.00	67.61	27.00	7.50	5.00	158.76
25	KL155993	65.30	69.70	4.33	110.60	196.00	92.60	1.40	24.00	5.10	14.00	41.00	66.56	28.50	7.10	4.60	163.59
26	KL155994	61.30	68.00	6.67	111.60	205.00	90.30	1.40	18.00	5.40	14.00	38.50	81.64	25.00	7.70	4.90	133.00
27	KL155988	60.70	65.00	4.33	114.00	230.00	101.30	1.60	24.00	5.80	14.00	43.00	67.98	31.50	8.60	4.70	189.63
28	KL155989	63.00	66.30	3.33	112.00	210.00	81.70	1.60	22.50	5.90	14.00	46.00	71.97	28.00	8.40	5.30	180.32
29	KL155991	64.00	68.00	4.00	111.50	210.00	73.30	1.40	21.00	5.80	14.00	45.00	74.14	25.00	9.50	4.80	157.50
30	KL156003	62.00	67.70	5.67	115.00	214.00	80.70	1.40	22.00	4.40	16.00	44.00	71.25	24.00	9.20	3.80	168.96
31	KL156009	61.60	68.00	6.33	114.60	211.00	79.60	1.20	21.00	4.30	14.00	45.50	62.18	22.00	9.80	4.40	141.68
32	KL154685 VI 154632	60.30	67.70	3.55	11/.60	210.00	/3.50	1.60	17.00	4.20	14.00	32.00	12.29	29.00	8.70	3.60	129.92
34	VL162206	65 30	69.30	4 00	114.00	196.00	71.30	1.20	21.00	4.10	18.00	43.00	66 35	26.00	7.80	4.90	201 24
35	KL154688	63.00	68.70	5.67	114.00	200.00	90.00	1.20	18.00	4.40	18.00	31.50	72.51	25.50	8.40	5.10	142.29
36	VL1110501	64.30	68.30	4.00	113.60	213.00	91.60	1.60	23.00	4.50	14.00	42.00	69.86	27.00	8.20	4.50	158.76
37	VL1110514	60.00	65.00	5.00	112.00	209.00	90.00	1.40	21.50	4.60	18.00	43.00	78.61	27.50	8.90	4.50	212.85
38	VL1110519	64.00	67.70	3.67	110.60	204.00	80.20	1.40	21.50	4.40	18.00	41.00	69.23	22.50	8.30	4.70	166.05
39	VL1110532	64.00	67.70	3.67	114.00	201.00	90.70	1.40	21.00	4.50	18.00	39.00	73.04	22.50	8.60	5.20	157.95
40	VL1110517	64.00	68.30	4.33	112.60	205.00	83.00	1.40	20.50	4.80	16.00	39.00	70.84	26.00	9.40	3.90	162.24
41.	VL1110458	64.00	68.30	4.33	111.50	206.00	84.30	1.40	21.00	4.00	12.00	41.00	71.79	25.50	9.00	3.50	125.46
42.	KL153241	60.30	64.00	3.67	114.60	214.00	68.60	1.60	17.50	5.50	18.00	29.50	69.45	21.00	10.10	4.60	109.62
43.	VL133/35	63.70	08.00 71.70	4.33	112.00	215.00	89.60	1.60	19.00	5.10	16.00	34.00	70.47	22.00	9.60	4.50	119.68
44.	KL155730	63 30	67.30	4.00	112.50	214.00	93.30	1.40	20.00	3.00 1 00	16.00	42.00	78.08	24.00	10.20	4.40	131.20
46	KL154714	58.00	62.00	4.00	112.00	216.00	97.20	1.40	21.00	3.90	18.00	40.00	76.00	25.00	10.20	5.20	180.00
47.	VL13656	60.70	64.30	3.67	114.00	215.00	111.00	1.60	21.50	4.10	18.00	42.00	70.76	26.00	7.10	5.00	196.56
48.	KL153072	62.00	65.30	3.33	104.60	199.00	107.00	1.20	21.00	4.00	14.00	40.50	73.70	34.50	7.40	4.80	193.20
49.	KL153092	62.70	66.00	3.33	114.50	198.00	96.40	1.40	22.00	4.80	14.00	42.00	71.90	31.00	8.40	5.00	182.28
50.	KL155978	58.30	62.00	3.67	113.00	188.00	95.30	1.40	21.00	4.70	14.00	41.00	76.80	24.00	8.80	4.10	137.76
51.	VL144234	60.60	64.30	3.67	114.60	199.00	89.00	1.60	21.00	4.40	18.00	41.50	70.38	26.00	7.40	5.60	191.88
52.	(CHEEK) VNR 4226	58.60	61.60	3.00	111.50	205.00	90.50	1.40	21.50	4.60	16.00	45.00	73.77	31.50	7.90	4.80	226.80
	G.M	62.71	67.47	4.73	111.80	203.00	89.73	1.39	20.57	4.64	15.48	39.46	72.11	26.50	8.60	4.68	162.74
	C.V.	2.33	2.09	2.40	2.31	5.23	6.00	4.29	6.06	6.04	6.47	7.36	5.10	5.54	4.61	4.55	7.55
	S.Em±	0.84	0.81	0.06	1.49	0.13	5.11 8 70	0.03	0.72	0.16	0.57	1.6/	2.12	0.84	0.22	0.12	10.09
	R Lowest	2.37 58.00	2.28 61.60	3.00	4.19 101.00	180.20	0.72 68.60	1.09	2.02 16.00	3 00	10.00	4.70	5.90	2.58	7 10	0.54	19.91
	R Highest	67 70	71 70	5.00	117.60	230.00	111.00	1.20	24.00	5.90	18.00	26.10	81.64	35.00	10.40	5.50	226.80
	it. inglicat	57.70	/ 1./0	1.07	117.00	250.00	111.00	1.00		5.70	10.00	10.00	01.04	55.00	10.40	5.70	220.00

DT: Days to 50% tasseling; DS: Days to 50% silking; ASI: Anthesis-silking interval; DM: Days to maturity; PH: Plant height; EH: Ear height; NEP: Number of ears per plant; EL: Ear length; EG: Ear girth; KRPE: Number of kernel rows per ear; KPR: Number of kernels per row; SP: Shelling percentage; 100KW: 100 kernel weight; PC: Protein content; OC: Oil content; GYP: Grain yield per plant

Parameters of genetic variability: The parameters of genetic variability *viz.*, mean, range, phenotypic and genotypic

coefficient of variation, broad sense heritability and genetic advance as percentage of mean have been depicted in Table 3.

Parameters	GCV (%)	PCV (%)	Heritability (%)	GA as % of Mean (5%)
Days to 50% tasseling	2.77	3.62	58.50	4.37
Days to 50% silking	3.27	3.88	71.00	5.68
Anthesis-silking interval (ASI)	29.73	29.82	99.30	61.04
Days to maturity	3.73	4.39	72.20	6.52
Plant height	4.46	6.87	42.10	5.96
Ear height	9.92	11.59	73.20	17.48
Number of ears per plant	10.12	10.99	84.70	19.19
Ear length	9.71	11.45	71.90	16.96
Ear girth	10.17	11.83	73.90	18.02
Number of kernel rows per ear	12.26	13.87	78.20	22.34
Number of kernels per row	11.61	13.75	71.30	20.21
Shelling percentage	4.96	7.12	48.60	7.12
100 kernel weight	11.95	13.17	82.30	22.33
Protein content	9.44	10.51	80.70	17.48
Oil content	11.84	12.68	87.10	22.77
Grain yield per plant	16.33	17.99	82.40	30.54

Table 3: Estimation of variability (GCV and PCV), Heritability and Genetic Advance of 52 genotypes of maize.

Phenotypic and Genotypic coefficient of variation

Phenotypic and genotypic coefficient of variation for yield and characters under study are given in Table 3. The phenotypic coefficient of variation was significantly higher in magnitude than as usual of genotypic coefficient of variation for all the traits under each analysis revealed that all character phenotypic variations were higher than the genotypic variances, which reflect the influence of environment on genotypes. То make inferences regarding these characteristics, PCV and GCV were divided into low (below 10%), medium (10%–20%), and high (beyond 20%) categories.

High estimates of PCV and GCV were observed for anthesis silking interval (29.82, 29.73), moderate PCV and low GCV values for ear height (11.59, 9.92) and ear length (11.45, 9.71), low PCV and low GCV values for days to 50% tasseling (3.62, 2.77), days to 50% silking (3.88, 3.27) plant height (6.87, 4.46) and days to maturity (4.39, 3.73) were reported by Grace et al. (2018) [6]. These findings are in good agreement with the observations of Hussain et al. (2020)^[8] reported moderate PCV and GCV for number of ears per plant (10.99, 10.12) and number of kernels per row (13.75, 11.61). Likewise Sing et al. (2019) ^[15] recorded moderate PCV and moderate GCV for characters namely; ear girth (11.83, 10.17) and number of kernel rows per ear (13.87, 12.26) while, shelling percentage (7.12, 4.96) chronicled low PCV and low GCV. Similar findings of Sharma et al. (2016) reported moderate PCV and GCV for oil content (12.68, 11.84). Likewise Mallikarjuna et al. (2020) [12] reported moderate PCV and low GCV for protein content (10.51, 9.44). Similarly Magar et al. (2021) [11] where in the 100 kernel weight (13.17, 11.95) reported moderate PCV and GCV. Likewise Bhadru et al. (2020) [1] reported moderate PCV and GCV for grain yield per plant (17.99, 16.33). Furthermore higher values of PCV than GCV for the traits studied suggested environmental influence on these traits.

Heritability and Genetic advance percent mean

Heritability estimates are useful because they demonstrate the potential for genetic relationships and evolution through natural selection in succeeding generations. It measures how consistently a certain trait has been displayed throughout time and between generations. It is more important to consider heritability and genetic advancement than to only rely on heredity in order to predict the outcomes of selecting the best candidates. It was therefore essential to understand heredity and genetic growth while selecting indices for programme development. Heritability was categorized as high (61% and above), medium (31-60%) and low (0-30%); as well as the genetic advance was classified as high (more than 20%), moderate (10-20%) and low (less than 10%) in order to draw conclusions about these parameters.

Heritability and Genetic advance percent mean were exhibited high in 100 kernel weight (82.30, 22.33), grain yield per plant (82.40, 30.54) and oil content (87.10, 22.77) followed by high heritability and moderate genetic advance percent mean for protein content (80.70, 17.48) followed by high heritability and low genetic advance percent mean for days to 50% silking (71.00, 5.68) and days to maturity (72.20, 6.52) and moderate heritability and low genetic advance percent mean for shelling percentage (48.60, 7.12) were reported by Sharma et al. (2016). These findings are in good agreement with the observations of Chaudhary et al. (2016) reported high heritability and genetic advance percent mean for number of kernel rows per ear (78.20, 22.34) and number of kernels per row (71.30, 20.21) followed by high heritability and moderate genetic advance percent mean for ear girth (73.90, 18.02). Similar findings of Hussain *et al.* (2020) ^[8] reported high heritability and moderate genetic advance percent mean for number of ears per plant (84.70, 19.19) and ear length (71.90, 16.96). Likewise Grace et al. (2018)^[6] were reported high heritability and moderate genetic advance percent mean for anthesis-silking interval (99.30, 61.04) followed by high heritability and moderate genetic advance percent mean for ear height (73.20, 17.48) and moderate heritability and low genetic advance percent mean for days to 50% tasseling (58.50, 4.37). Similarly Magar et al. (2021) ^[11] where in the plant height (42.10, 5.96) reported moderate heritability and low genetic advance percent mean.

Conclusion

In this study anthesis-silking interval exhibited genetic large genetic variability followed by number of ears per plant, ear girth, number of kernel rows per ear, number of kernels per row, 100 kernel weight, oil content and grain yield per plant exhibited moderate genetic variability. Anthesis-silking interval, number of kernel rows per ear, number of kernels per row, 100 kernel weight, oil content and grain yield per plant showed high heritability was associated with high genetic advance suggesting additive gene action and these traits can easily be fixed in the genotypes by selection in the early generations. Better genotypes can be selected based on mean values of days to 50% tasseling (KL154714), ear length (KL155993), number of kernel rows per ear (VL18333), number of kernels per row (KL155989) and grain yield per plant (VNR4226) can be utilized as selection criteria in this study based on heritability, genetic diversity and genetic progress.

References

- Bhadru D, Swarnalatha V, Mallaiah B, Sreelatha D, Kumar MN, Reddy ML. Study of genetic variability and diversity in maize (*Zea mays* L.) inbred lines. Current Journal of Applied Science and Technology. 2020;39(38):31-39.
- 2. Chaudhary A, Srivastava K, Agrawal V, Kumar S. Elucidation of Variability, Interrelationships and Path-coefficient in Maize (*Zea mays* L.). Nature Environment and Pollution Technology. 2016;15(2):653.
- Chaurasia NK, Nirala RBP, Singh B, Mandal SS. 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.
- 4. Faostat, 2020. Retrieved from http://www.fao.org/faostat/en/#data/QC
- 5. Ghimire YN, Timsina KP, Devkota D, Gautam S, Choudhary D, Poudel H, *et al.* Dynamics of maize consumption and its implication in maize technology demand in Nepal. CIMMYT, 2018.
- 6. Grace B, 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.
- Hallauer AR, Carena MJ, Miranda Filho JD. Quantitative genetics in maize breeding. Springer Science & Business Media, 2010, Vol-6.
- Hussain K, Sudan RS, Praveen S, Sharma M, Mahrukh. Genetic divergence studies among inbred lines in maize (*Zea mays* L.). Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu Main Campus, Chatha, Jammu, 2020. https://krishikosh.egranth.ac.in/displaybitstream?handle= 1/5810161249&fileid=863714fd-fc6e-4fdd-a53f-0d8cca8adbc8
- Jumaa RF, Madab DS. Estimation Genetic Diversity by Using Cluster, D2 and Principle Component Analysis of Maize Inbred Lines (*Zea mays* L). Journal Tikrit Univ. For Agri. Sci, 2018, 18(4).
- Kay P, Michelle S, Veronica CN. High fructose corn syrup: production, uses and public health concerns. Biotechnology and Molecular Biology Reviews. 2010;5(5):71-78.
- 11. 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):e07939.
- Mallikarjuna S, Roja V, Kumar IS, Srinivas T. Genetic diversity studies in newly developed maize inbreds. Agricultural college, Bapatla Acharya N.G. Ranga Agricultural University, Guntur, Andhra Pradesh, 2020.

https://krishikosh.egranth.ac.in/displaybitstream?handle= 1/5810143865&fileid=bd0bccb3-d07a-4335-b5e0a9543062eb7c

- Rajesh V, Sudheer Kumar S, Narsimha Reddy V, Siva Sankar A. Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). International Journal of Applied Biology and Pharmaceutical Technology. 2013;4(4):242-245.
- Sharma P, Punia MS, Kamboj MC, Singh N, Chand M. Evaluation of quality protein maize crosses through line x tester analysis for grain yield and quality traits. Agricultural Science Digest-A Research Journal. 2016;37(1):42-45.
- Singh R, Sinha SK, Dinesh T, Kiran T. Genetic Variability and Diversity Analysis for the Selection of Diverse Inbred Lines in Maize (*Zea mays* L.) crop. International Journal of Genetics. 2019;11(4):578-582.
- 16. Source: APICOL Website, MSME Department, Govt. of Odisha, 2020.
- 17. Walne CH, Reddy KR. Temperature Effects on the Shoot and Root Growth, Development, and Biomass Accumulation of Corn (*Zea mays* L.). Agriculture. 2022;12(4):443.