Original Research Article

Unraveling the Genetic Framework Underlying Yield Dynamics in Maize (*Zea mays* L.): A Genetic Variability Perspective

ABSTRACT

Aims: The improvement in crop yield depends upon the magnitude of genetic variability available in breeding material and the extent to which the yield component traits are heritable from generation to generation.

Study design: Randomized Block Design.

Place and Duration of Study: Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BU Campus, Jhansi (U.P.) between Kharif-2018 and June 2019.
Methodology: During the Kharif season of 2018, a thorough field investigation was conducted at the Horticulture Research Farm, Institute of Agricultural Sciences, BU Campus, Jhansi (U.P.) involving a total of 30 different maize inbred lines. The findings revealed a notable genetic diversity among the maize lines, as indicated by the considerable sum of squares attributed to genotypic variations across all observed characteristics. Notably, the variation in plant height was particularly prominent, followed by traits such as biological yield per plant, seed yield per cob, seed yield per plant, number of seeds per row and harvest index in maize. The significant values of PCV and GCV observed for characteristics like plant height, number of cobs per plant, and biological yield per plant suggest a substantial level of variability, thereby highlighting the potential for enhancing these traits through selective breeding. Furthermore, the combination of high heritability and significant genetic progress in traits such as plant height, harvest index, cob ear weight, rows per plant, seed yield per cob, biological yield per plant, days to 50 per cent germination, shelling per cent, days to 50 per cent silking suggests that these traits can be improved through direct selection.

Keywords: Variability, heritability, GCV, PCV, maize inbred lines, genetic advancement

1. INTRODUCTION

Zea mays L., commonly referred to as maize, holds significant global importance, particularly in developing nations (Lopes and Larkins, 1995). Maize, a C4 photosynthetic plant, earns the prestigious title of the "Queen of Cereals" due to its remarkable yield potential. In India, maize cultivation spans across various regions and contributes significantly to crop production. On a global scale, maize ranks as the third most abundant cereal grain, following wheat and rice. Its significance is equally as profound as that of wheat. Maize exhibits exceptional adaptability and thrives during the Kharif season.

Maize boasts multifaceted importance. It serves as a vital source of nourishment for both humans and animals. Moreover, maize finds application in the production of a diverse range of products, including starch, oil, protein, alcoholic beverages, sweeteners, and even biofuel. Every component of the maize plant, ranging from its grains to leaves and other parts, holds value and offers a wide array of uses in the food and industrial sectors. The utilization of maize grains extends beyond staple foods such as bread, popcorn, and porridge; they also contribute to the production of starch, alcohols, organic acids, paper products, textiles, and polymers. Maize assumes a paramount role in the industrial realm.

While maize does not surpass wheat and sorghum in terms of nutritional value, it surpasses rice. Its grains contain 10% protein, 4% oil, 70% carbohydrates, 2.3% crude fiber, 10.4% albuminoids, and 1.4% ash content (Singh and Bajpai, 1999).

The significance of genetic factors in determining plant characteristics should not be underestimated. This study aims to scrutinize the genetic variability, heritability, and genetic progress within maize germplasm to identify the most optimal genotypes for high-yield maize breeding endeavors.

2. MATERIAL AND METHODS

The investigation was conducted at the Horticulture Research Farm, Institute of Agricultural Sciences, BU Campus, Jhansi (U.P.) in the Kharif season of 2018-19. The analysis included 30 different maize inbred lines, which were systematically evaluated using a randomized complete block design (RCBD) with three separate replications. Each replication consisted of two rows, each spanning three meters and positioned 45 cm apart. These particular inbred lines, as specified in Table-1, were obtained from Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.).

The observations were recorded for 18 quantitative characters *viz.,* Days to 50% germination, days to 50% flowering, days to 50% silking, days to 50 % tasselling, plant height, leaf/plant, days to 50% maturity, biological yield/plant, cob ear weight, cob length, rows/cob, seeds per row, total seed/cob, 100 seed weight, seed yield per cob, shelling %, harvest index and seed yield per plant.

Five competing plants were chosen at random for each genotype to be observed for yield and its contributing features. In this investigation, standard procedures were used to evaluate the associated yield characteristics.

RESULT AND DISCUSSION

Analysis of variance revealed significant differences among 30 maize inbred lines for all 18 characters studied is presented in (Table 2).

The mean performance of the genotypes (Table 3) revealed a wide range of variability for all the traits. The variation was highest for biological yield per plant (177.33-342.67g) followed by, number of seed per cob (236.93-330.33), plant height (168.13-224.00), cob ear weight (62.71-109.41g), days to 50% maturity (77.67-83.00days), seed yield per plant (40.33-68.86) seed yield per cob (37.22-67.90g), days to 50% silking (50.00-53.67), days to 50% tasselling (43.00-46.67), 100 seeds weight (15.23g – 35.51 g), number of seed per row (20.87-29.93), cob length (19.47-27.20), harvest index (15.26-27.04), number of row per cob (10.73-13.67), number of leaves per plant (9.87-12.47), days to 50% germination (4.00-6.00) and number of cobs per plant (1.07-1.27).Similar findings were reported byBhiusal*et al.*, (2017) and Bisen *et al.*, (2018).

The phenotypic coefficient of variation exceeded the genotypic coefficient of variation across traits, indicating genetic predominance in attribute expression. This allowed effective selection based on phenotypic performance, with comparable findings by Nagaraju (2012) and Mohammad Quamrul et al. (2017).

The phenotypic coefficient of variation ranged from 2.08% for days to 50% maturity to 38.73% for 100 seed weight (g). The phenotypic coefficient of variation was highest for plant height (cm), followed by characters viz., seed yield per plant (24.34), indicating that these characters would respond to selection.Similar findings were reported by Bhiusal*et al.*, (2017) and Bisen *et al.*, (2018).

The genotypic coefficient of variation varied from 0.71% for days to 50% silking to 11.64% for biological yield per plant. The high genotypic coefficient of variation was noted for biological yield per plant (11.64). Days to 50% maturity (1.27%), days to 50% germination (1.47%) plant height (5.57%) leaf per plant (6.04%) cobs length (6.33%) showed lowest genotypic coefficient of variation, while it was moderate for rest of the characters such as 100 seed weight (9.62%), seed per cob (5.18%) harvesting index (2.63%).Similar findings were reported by Ali *et al.*, (2016) and Guo *et al.*, (2018).

Heritability estimates were observedvery high for number of leaves per plant (40.47%) days to 50% maturity (36.98%) However,it was recorded to be high for cob length (33.87%), plant height (26.69) biological yield(24.25%) cob ear weight (21.08) seed per cob (15.85%).High broad-sense heritability values signify minimal environmental influence on characters. Phenotypes truly mirror genotypes, underpinning dependable phenotypic-based selection. This is consistent with the observations of Nataraj et al. (2014), Ghimire and Timsina (2015).

Low estimates of Heritability were recorded for harvest index (1.36%) days to 50% silking (5.61%) 100 seed weight (6.18%) seed yield per plant (6.32%) number of seed per cob (8.20) number of seed per row (9.80). This suggests that the observed traits are notably influenced by the environment, potentially complicating selection efforts. Notably, shelling% (-1.19%) exhibited a moderate influence, implying effective selection based on phenotypic performance.

Genetic advance as a percentage of mean ranged between 0.01% for days to 50% germination to 31.90% for biological yield per plant. The highest estimate of genetic advance as percentage of mean was recorded for biological yield per plant (31.90%) followed byplant height (11.93%), number of seed per cob (8.44%), cob ear weight (7.25%) seed yield per cob (3.56) cob length (1.75%) seed yield per plant (1.68%), days to 50% tasselling (1.47%),days to 50% maturity (1.26%). 100 seed weight (0.94%) had lowest estimates were observed for leaf per plant (0.90%), number of seed per row (0.69%) showed moderate value of genetic advance as percentage of mean. Whereas, low estimates were observed for, number of row per cob (0.28%), days to 50% silking (0.18%), harvest index (0.13%), and days to 50% germination (0.01%). Similar findings were reported by Kumar *et al.*, (2015), and Prasad and Shivani (2017).

High heritability coupled with high genetic advances was observed for traits like biological yield per plant, plant height, cobs per plant, and cob ear weight. The prevalence of additive genes was suggested, indicating the potential for effective selection of high-yielding genotypes due to additive gene actions. Similar conclusions were reported by Bhiusal et al., (2017) and Bisen et al., (2018).

Traits such as total seed per cob, seed yield per plant, and silking% exhibited high heritability supplemented by moderate genetic advances as a percentage of mean. This pattern may be attributed to additive gene action influencing their expression. Phenotypic selection could effectively enhance these traits, as supported by findings by Ghimire and Timsina (2015) and Bisen et al., (2018).

In contrast, high heritability coupled with low genetic advances as a percentage of mean characterized traits like days to 50% maturity, biological yield per plant, 100 seed weight, seed yield per plant, cobs per plant, cob length (cm), days to 50% germination, and flowering days to maturity. This pattern pointed towards non-additive gene action influencing these traits' expression, as also indicated by Bhiusal et al., (2017) and Bisen et al., (2018).

Traits such as leaves per plant, cobs per plant, rows per cob, and cob length showed low estimates of heritability along with limited genetic advances as a percentage of mean. These traits were evidently highly influenced by environmental factors, making their selection ineffective.

CONCLUSION

The evaluation reveals notable genetic variation within the tested material, as indicated by the significant genotypic mean sum of squares for all attributes. This variation is particularly evident in characteristics like the height of the plants, followed by factors such as the biological yield per plant and the yield of seeds. When comparing the phenotypic coefficient of variation (PCV) to the genotypic coefficient of variation (GCV), the former consistently surpasses the latter for all observed traits.

Importantly, traits such as plant height, number of cobs per plant, and biological yield per plant exhibit high levels of both PCV and GCV, suggesting that they are excellent candidates for improvement through selection. Characteristics that combine high heritability with significant genetic progress, such as plant height, harvest index, weight of cob ears, number of rows per plant, metrics of seed yield, days to mid-germination, shelling percentage, and days to mid-silking, are well-suited for direct selection methods. These findings provide a roadmap for developing customized breeding strategies aimed at enhancing the quality of traits and overall performance of the crop.

Table:-1. List of genotypes of understud

S. No.	Name of Genotypes	S. No.	Name of genotypes
1	D-7	16	CIMMYT-171
2	D 1-2	17	Hybrid 8
3	K16/ 1384 A	18	Hybrid 5
4	K16/ 1384 B	19	D-1
5	Hybrid 6	20	JNPW WFW 5
6	IMR 413/ K 16	21	TSK 11-1
7	JN Pearl	22	Hybrid 5
8	CML-150	23	REH 2009-12 Hybrid Check
9	POP-65	24	TSK11-1
10	Hybrid 7	25	DHOLI-M7
11	D 2-2	26	D3-3 OSDW 5
12	D 3-1 YOFW 5	27	CIMMYT-9
13	JNY YOFW 5	28	TSK 11-1
14	REH 2003 Hybrid check 2	29	Azad Kamal OFWs
15	60-828K- CML-115	30	IMR 414/ K16

Table: 2. Analysis of variance for eighteen characters of maize genotypes

SN.	Character	MEAN SUM OF SQUARE		
		Replications [2]	Genotypes [29]	Error [58]
1	Days to 50% Germination	0.03	1.00	0.99
2	Days to 50% Tasseling	1.01	9.91**	4.54
3	Days to 50% Sillking	0.93	2.63	2.23
4	Plant height (cm)	368.81	721.91**	345.04
5	No. of leaves per plant	5.00**	2.09**	0.69
6	No. of Cobs Per Plant	0.04	0.02	0.02
7	Days to 50% Maturity	0.41	4.75**	1.72
8	Biological Yield Per Plant (g)	5536.85	6054.45*	3088.18
9	Cob Ear Weight (g)	193.82	396.59*	220.18
10	Cob length (cm)	3.52	10.54**	4.16
11	No. of Row Per Cob	0.04	1.23	0.83
12	No. of Seed Per Row	10.33	14.03	10.58
13	No. of Seed Per Cob	3094.25	2910.85	2295.94
14	100 Seed Weight (g)	17.45	61.62	51.46
15	Seed Yield Per Cob (g)	128.08	156.66	100.09
16	Seed Yield Per Plant (g)	327.83	187.24	155.72
17	Shelling % in Maize	6.24	58.19	60.33
18	Harvesting Index in Maize	115.88**	21.00	20.17

*, ** Significant at 5% and 1%, respectively

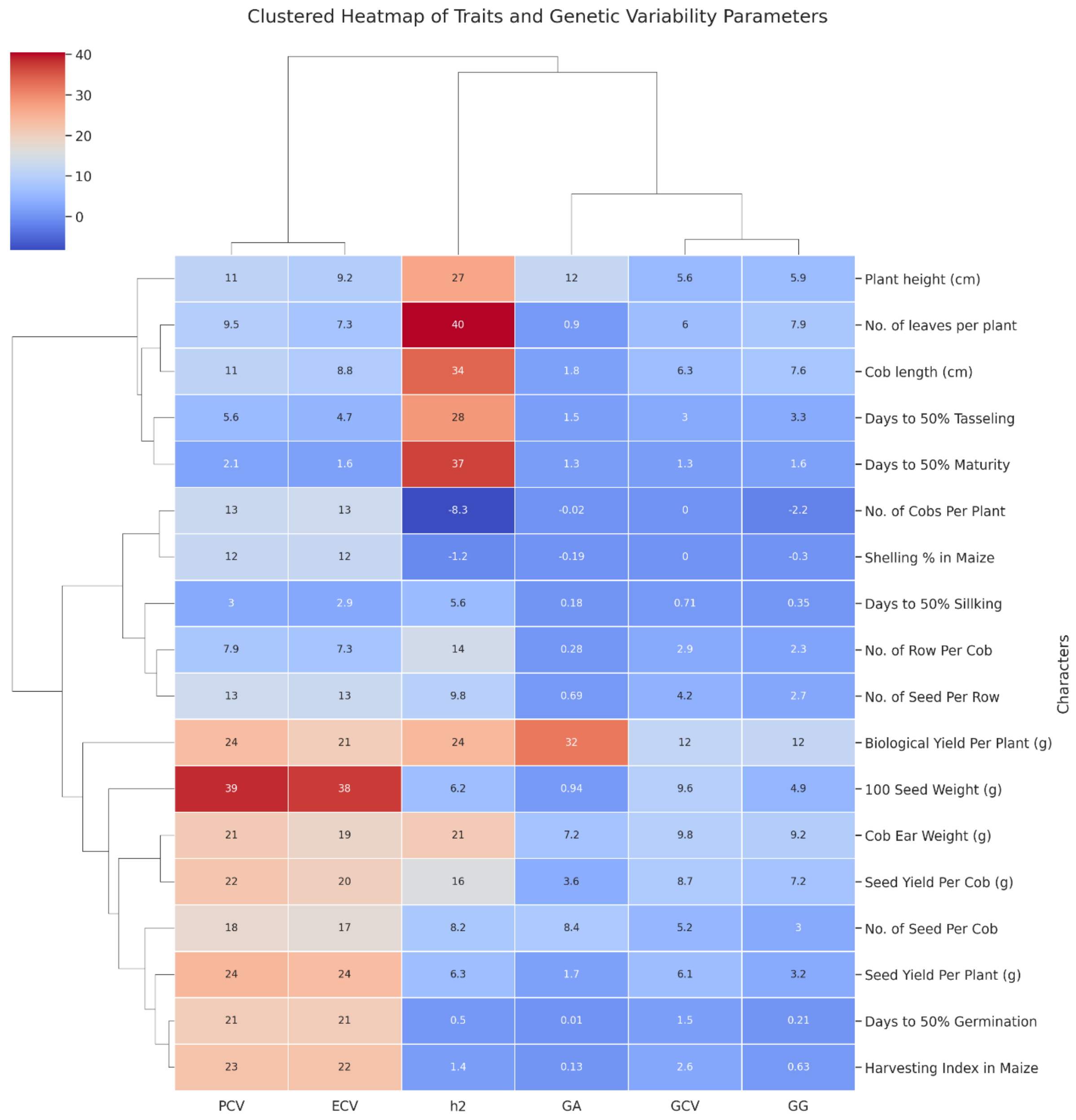
Table 3. Mean performance of maize genotypes for yield and attributing characters

SN	Genotype	Days to 50% Germination	Days to 50% Tasseling	Days to 50% Sillking	Plant height (cm)	No. of leaves per plant	No. of Cobs Per Plant	Days to 50% Maturity	Biological Yield Per Plant (g)	Cob Ear Weight (g)	Cob length (cm)	No. of Row Per Cob	No. of Seed Per Row	No. of Seed Per Cob	100 Seed Weight (g)	Seed Yield Per Cob (g)	Seed Yield Per Plant (g)	Shelling %	Harvesting Index
1	D-7	5.00	46.67	51.00	184.20	11.27	1.07	79.33	254.00	77.45	21.93	11.53	24.53	249.33	20.31	49.09	52.31	62.97	21.37
2	D 1-2	4.00	45.33	51.00	205.07	11.40	1.27	79.33	285.67	71.56	22.47	12.73	25.27	244.67	17.62	42.79	50.89	59.40	18.69
3	K16/1384 A	5.67	45.67	51.33	197.87	11.13	1.20	79.33	248.67	90.16	22.33	11.87	27.93	300.20	19.82	59.03	64.35	64.85	25.60
4	K16/ 1384 B	5.67	46.67	50.33	197.47	12.00	1.07	80.67	298.00	75.41	22.00	11.73	26.47	248.47	19.41	47.29	48.69	64.68	16.70
5	Hybrid 6	5.67	43.00	50.00	235.07	11.67	1.20	81.33	333.33	89.03	25.17	12.33	29.33	330.33	18.83	59.64	68.30	67.77	20.71
6	IMR413/K16	4.33	43.00	50.33	215.40	10.53	1.07	79.00	285.00	82.68	23.53	12.07	22.80	250.53	19.83	49.90	51.07	59.77	17.87
7	JN Pearl	5.00	43.00	51.00	186.20	10.40	1.13	79.00	203.33	80.87	21.47	12.67	27.33	313.27	17.49	48.76	55.05	61.55	27.04
8	CML-150	4.33	50.00	53.00	212.27	12.47	1.20	83.00	342.67	88.72	26.53	12.73	26.47	293.00	16.65	46.19	51.67	52.47	15.26
9	POP-65	4.67	49.33	51.00	212.80	11.53	1.13	81.00	299.33	80.33	24.80	11.93	27.00	265.33	17.49	49.05	52.84	61.05	17.59
10	Hybrid 7	5.00	43.67	50.67	190.13	10.27	1.00	79.67	236.33	69.31	20.93	13.00	23.40	255.33	16.97	43.25	43.25	62.86	18.28
11	D 2-2	4.33	43.00	51.33	224.00	11.07	1.13	79.00	303.00	86.59	23.27	12.53	27.13	302.13	20.02	60.67	62.72	70.66	20.70
12	D 3-1YOFW5	5.00	43.67	51.33	196.73	10.33	1.00	76.00	279.67	69.65	21.33	12.60	25.47	291.87	15.23	47.95	47.95	68.86	19.70
13	JNY YOFW 5	4.00	44.33	50.67	220.27	13.47	1.07	78.67	358.00	109.41	26.20	12.73	28.27	321.13	34.00	67.90	68.86	61.57	19.23
14	REH 2003 H. check 2	5.67	47.33	50.67	210.94	12.00	1.27	78.67	328.00	85.88	24.93	10.73	27.67	278.40	21.23	56.33	62.97	65.97	19.34
15	60-828K- CML 115	5.00	44.00	50.33	187.87	10.87	1.07	79.33	218.33	62.71	22.47	12.40	23.87	259.87	35.51	41.89	43.79	67.36	20.05
16	CIMMYT-171	5.00	44.33	53.67	168.13	10.27	1.00	79.33	177.33	51.23	19.47	13.27	20.87	229.80	16.08	37.22	40.33	71.05	21.55
17	Hybrid 8	4.33	46.00	52.33	193.27	11.20	1.07	79.33	234.07	65.51	20.80	11.87	22.40	239.47	18.39	40.54	45.63	62.14	19.40

18	Hybrid 5	4.00	44.33	51.00	177.80	10.53	1.00	79.00	269.67	67.79	21.33	13.67	23.27	267.80	16.43	46.81	46.81	70.75	17.76
19	D-1	4.00	44.00	51.00	172.13	10.07	1.07	77.67	184.00	63.92	21.20	13.13	23.53	279.20	16.54	43.04	45.00	67.53	24.43
20	JNPW WFW 5	4.33	46.33	50.67	201.60	10.67	1.07	78.33	255.67	77.71	21.13	12.8	23.60	244.27	19.87	49.13	51.49	63.07	20.02
21	TSK 11-1	4.67	45.33	53.67	206.47	12.20	1.07	79.67	255.00	91.66	23.20	13.33	26.47	323.33	16.49	55.38	60.98	61.19	24.80
22	Hybrid 5	4.67	43.33	51.00	198.33	11.20	1.07	77.33	221.67	69.97	23.87	12.07	26.07	253.60	17.57	43.87	48.96	62.72	21.90
23	REH 2009-12 H. Cheack	4.33	43.00	50.67	184.80	9.87	1.00	78.00	231.67	82.35	22.07	12.33	27.88	248.27	16.45	43.19	43.19	53.16	18.85
24	TSK11-1	4.33	43.67	50.67	209.47	12.13	1.13	78.67	323.67	90.58	27.20	12.93	28.33	339.40	17.79	61.92	64.61	68.36	20.65
25	DHOLI-M7	5.67	44.00	52.33	205.00	11.67	1.07	80.00	266.67	71.87	22.27	11.73	21.80	236.93	19.71	44.56	46.19	62.73	17.67
26	D3-3 OSDW 5	6.00	46.00	51.00	216.07	11.80	1.07	79.33	272.00	78.23	24.47	12.73	26.20	280.13	16.64	48.67	50.35	62.11	18.75
27	CIMMYT-9	4.67	45.67	50.67	199.00	11.20	1.07	80.00	280.00	87.09	24.07	11.80	27.20	298.60	19.45	56.27	57.81	63.65	21.27
28	TSK 11-1	4.67	44.00	51.67	216.73	11.87	1.07	80.00	296.33	76.46	23.40	13.27	25.33	268.20	19.07	50.34	54.36	65.62	18.28
29	Azad Kamal OFWS	5.00	43.67	52.33	211.67	12.40	1.13	79.33	295.67	89.39	24.93	12.73	26.80	317.60	15.89	55.80	59.34	62.52	20.11
30	IMR 414/ K16	5.00	46.00	51.33	198.53	11.73	1.13	79.33	266.33	73.75	22.13	12.93	25.13	264.93	16.89	48.55	49.25	65.41	18.45
	G.M.	4.80	44.94	51.27	201.18	11.31	1.10	79.29	270.10	78.58	23.03	12.47	25.59	276.51	19.12	49.83	52.97	63.79	20.07
	S.E.	0.57	1.23	0.86	10.72	0.48	0.08	0.76	32.08	8.57	1.18	0.53	1.88	27.66	4.14	5.78	7.20	4.48	2.59
	C.D. 5%	1.62	3.48	2.44	30.36	1.35	0.24	2.14	90.82	24.25	3.33	1.49	5.32	78.31	11.72	16.35	20.39	12.69	7.34
	C.D. 1%	2.16	4.63	3.25	40.41	1.80	0.32	2.85	120.88	32.28	4.43	1.98	7.08	104.23	15.60	21.76	27.14	16.90	9.77
	C.V.	20.70	4.74	2.91	9.23	7.33	13.27	1.65	20.57	18.88	8.85	7.31	12.71	17.33	37.51	20.08	23.56	12.18	22.38

Table 4. Genetic variability parameters

SN	Characters	GCV	PCV	ECV	h^2	GA	GG
1	Days to 50% Germination	1.47	20.75	20.70	0.50	0.01	0.21
2	Days to 50% Tasseling	2.98	5.60	4.74	28.28	1.47	3.26
3	Days to 50% Sillking	0.71	3.00	2.91	5.61	0.18	0.35
4	Plant height (cm)	5.57	10.78	9.23	26.69	11.93	5.93
5	No. of leaves per plant	6.04	9.50	7.33	40.47	0.90	7.92
6	No. of Cobs Per Plant	0.00	12.75	13.27	-8.33	-0.02	-2.19
7	Days to 50% Maturity	1.27	2.08	1.65	36.98	1.26	1.59
8	Biological Yield Per Plant (g)	11.64	23.64	20.57	24.25	31.90	11.81
9	Cob Ear Weight (g)	9.76	21.26	18.88	21.08	7.25	9.23
10	Cob length (cm)	6.33	10.88	8.85	33.87	1.75	7.59
11	No. of Row Per Cob	2.94	7.88	7.31	13.91	0.28	2.26
12	No. of Seed Per Row	4.19	13.38	12.71	9.80	0.69	2.70
13	No. of Seed Per Cob	5.18	18.09	17.33	8.20	8.44	3.05
14	100 Seed Weight (g)	9.62	38.73	37.51	6.18	0.94	4.93
15	Seed Yield Per Cob (g)	8.71	21.89	20.08	15.85	3.56	7.15
16	Seed Yield Per Plant (g)	6.12	24.34	23.56	6.32	1.68	3.17
17	Shelling % in Maize	0.00	12.10	12.18	-1.19	-0.19	-0.30
18	Harvesting Index in Maize	2.63	22.53	22.38	1.36	0.13	0.63



Characters	PCV	ECV	h2	GA	GCV	GG
Plant height (cm)	11	9.2	27	12	5.6	5.9
No. of leaves per plant	9.5	7.3	40	0.9	6	7.9
Cob length (cm)	11	8.8	34	1.8	6.3	7.6
Days to 50% Tasseling	5.6	4.7	28	1.5	3	3.3
Days to 50% Maturity	2.1	1.6	37	1.3	1.3	1.6
No. of Cobs Per Plant	13	13	-8.3	-0.02	0	-2.2
Shelling % in Maize	12	12	-1.2	-0.19	0	-0.3
Days to 50% Sillking	3	2.9	5.6	0.18	0.71	0.35
No. of Row Per Cob	7.9	7.3	14	0.28	2.9	2.3
No. of Seed Per Row	13	13	9.8	0.69	4.2	2.7
Biological Yield Per Plant (g)	24	21	24	32	12	12
100 Seed Weight (g)	39	38	6.2	0.94	9.6	4.9
Cob Ear Weight (g)	21	19	21	7.2	9.8	9.2
Seed Yield Per Cob (g)	22	20	16	3.6	8.7	7.2
No. of Seed Per Cob	18	17	8.2	8.4	5.2	3
Seed Yield Per Plant (g)	24	24	6.3	1.7	6.1	3.2
Days to 50% Germination	21	21	0.5	0.01	1.5	0.21
Harvesting Index in Maize	23	22	1.4	0.13	2.6	0.63

Fig 1: Clustered Heatmap of Traits and Gentetic Variability Parameters

REFERENCE

Ali, F., Ahsan, M., Ali, Q., and NailaKanwal (2017). Phenotypic stability of maize (*Zea mays*) grain yield and its attributing traits under drought stress. *Plant Science,* 8: 1-11.

Bhiusal T.N., Lal G.M., Marker S. and Synrem G. J. (2017). Genetic variability and traits association in Maize (*Zea mays* L.) genotypes. *Annals of Plant and SoilResearch,* 19**(1)**: 59-65.

Bisen N., Rahangdale C.P. and Sahu R.P. (2018). Genetic variability and Correlation studies of yield and yield component in maize hybrid (*Zea mays* L.) Under Kymore Plateau and Satpura Hill Region of Madhya Pradesh. *InternationalJournal of Agriculture, Environment and Biotechnology.* 11**(1)**: 71-77.

Ghimire B. and Timsina D. (2015). Analysis of Yield and Yield Attributing Traits of Maize Genotypes in Chitwan, Nepal. *World Journal of AgricultureResearch,* 3**(5)**: 153-162.

Guo X, Duan X, Wu Y, Cheng J, Zhang H, Li, B. (2018). Genetic Engineering of Maize (*Zeamays* L.) with Improved Grain Nutrients. *J. Agric. Food chem.,* 66**(7)**: 1670-1677.

Kumar B., Jambagi P. and Mruthunjaya C. Wali (2015). Heritability, correlation and path coefficient analysis in maize germplasm for starch and oil content. *J.Farm Sci.,* 29**(2)**: 257-260.

Lopes, M.A. and B.A. Larkins (1995). Genetic analysis of opaque-2 modifier gene activity in maize endosperm. *Theor. Appl. Genet.*, 19: 274-281.

Mohammad Quamrulislam Matin, Md. Shalim Uddin, Md. Motiar Rohman, Mohammad Amiruzzaman, Abul Kalam, Bhagya Rani Banik (2017). Genetic variability and path analysis studies in Hybrid Maize (*Zea mays* L.). *American Journalof Plant Sciences,* 8: 3101-3109.

Nagaraju, K. (2012). Studies on genetic variability for yield and yield attributing characters in maize (*Zea*mays L.). *Acharya N. G. Ranga Agricultural UniversityRajendranagar, Hyderabad.*

Nataraj, V., Shahi, J.P. and Agarwal, V. (2014). Correlation and Path Analysis in Certain Inbred Genotypes of Maize (*Zea mays* L.) at Varanasi. *InternationalJournal of Innovative Research & Development,* 3**(1)**: 14-17.

Prasad, Vara B.V.V. and Shivani, D. (2017). Correlation and Path analysis in maize (*Zea mays* L.). *Journal of Genetics, Genomics & Plant Breeding,* 1**(2)**: 1-7.

Singh, V.K. and Bajpai, R.P. (1999). Intercropping in maize (*Zea mays* L.) under rainfed condition. *Indian J. Agron.,* 36**(30)**: 398-399.