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Study of Genetic Divergence Using Metroglyph Analysis in Maize (*Zea mays* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

The present trial was carried out at the field experimentation center of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, during *kharif* 2022 to study genetic variability and metroglyph analysis in 21 maize genotypes, including one check variety MAKKA 3 for fifteen quantitative traits. Based on mean performance of 21 genotypes of maize, grain yield per plant was highest in case of VL 183957 (87.8g), VL 19465 (70.26g), VL 183927 (69.6g), VL 19270 (69.2g) genotypes. On the basis of Analysis of variance, significant difference was recorded for all the grain yield and its components indicating presence of large amount of variability in the genotypes. The magnitude of GCV and PCV recorded highest for Days to 50% tasseling and Anthesis-silking interval. High heritability recorded in biological yield per plant, Days to 50% silking, Days to 50% tasseling. High genetic advance was recorded in biological yield per plant, Days to 50% tasseling and cob weight. High genetic advance as percent mean was recorded in Days to 50% tasseling, Anthesis-Silking

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interval. In metroglyph analysis six complexes are formed, based on biological yield and plant height which were the most variable characters. The maximum index scored by genotype VL-19465 and MAKKA 3 (check) (34) both belongs to complex III and respectively has higher index value for cob weight, grain rows per cob, number of grains per row, 100 seed weight, harvest index, days to 50% tasseling, days to 50% silking, Anthesis-Silking interval, Days to 75% maturity and cob length. Therefore, these two genotypes present in these two complexes should be given priority during selection for maize yield improvement. These genotypes can be crossed to have maximum variability and good combination of characters.

Keywords: Maize (Zea mays L.); genetic variability; heritability; genetic advance; metro glyph analysis; index score.

1. INTRODUCTION

The most frequently grown crop in the world is maize (*Zea mays* L.; 2n=20), a domesticated cereal grain that originated in Central America. Known as "Miracle Crop" and "Queen of the Cereals" because of its highest genetic production potential, it is one of the most adaptable crops that can be produced in a variety of seasons and ecologies. There is no other crop that compares to maize in terms of adaptability to various settings. It is grown between latitudes 58°N and 40°S, at elevations higher than 3000 m, and in regions with annual rainfall ranging from 250 mm to 5000 mm rainfall per year [1] Maize plays a pivotal role in Indian economy. Besides being a potential source of food for humans, it is also used as feed for cattle, poultry and in the production of glucose, starch, syrup, alcohol, acetic acid, lactic acid, etc. in industries. Maize is a rich source of starch (71-72%), protein (9-10%), fiber (9-10%), oil (4-5%), sugar (2-3%) and minerals (1-2%) (Munsundire et al., 2019). Nutraceutical properties of phenolic and anthocyanin compounds in maize offer antioxidant activities that protect from various degenerative diseases (Shikha et al*.,* 2019). Currently, 1206.6 million MT of maize is being produced from an area of 203.5 million ha with an average productivity of 5.85 t/ha (OECD-FAO 2022). The global consumption pattern of maize is: livestock feed -61%, human food-17% and industrial use 22%. It has attained the position of industrial crop globally as 83% of its production in the world is used in feed, starch and biofuel industries [2,3]. Over the next decade, cereal production is expected to increase by 343 Mt (+ 12 %). Almost half of this production will come from maize, while wheat and rice account for about 20% each. (OECD-FAO, 2022).

Among the maize growing countries India stands 4th in area and 7th in production, representing around 4% of world maize area and 2% of total production. In India, during the 2021-2022 cropping seasons, 9.89 million ha of land was covered with maize with productivity of 3.19 tons/ha and production of 31.65 million tons is still far below the world average 5.85 tons/ha [4-6]. Whereas in Uttar Pradesh, it occupies an area of 0.69 million hectares with an average productivity of 2.12 tones/ha and production of 1.46 million tons. (Ministry of Agriculture and Farmers welfare 2021-2022)

2. MATERIALS AND METHODS

The seed material for the study consisted of 21 genotypes with two checks namely MAKKA 3. The study was carried out at the experimental farm of genetics and plant breeding department SHUATS prayagraj the crop was raised in RBD with three replications during Kharif July, 2022. The spacing adopted was 45cm between each entry rows and 60 cm among the plants. Necessary cultural practices were practised as required for a successful crop. Observations on days to fifty per cent flowering, days to fifty % silking, Anthesis silking interval, Days to 75% maturity, height of the plant, Ear height, cob length (cm), cob grith, cob weight (g), Number of grain rows per cob, Number grains per row, 100 grain weight, Biological yield per plant, harvest index(%), Grain yield per plant were recorded. Data were collected in all genotypes by averaging five plants selected randomly from all three replication for the characters except days to fifty per cent flowering which was documented on plot wise [7-9]. The coefficients of genotypic and phenotypic variations were estimated using ,the formulae suggested by Falconer (1981) and the assigning the level of variation was carried out as given by Sivasubramanian and Madhavamenon (1973). Broad sense heritability (h^2bs) was estimated according to the formula proposed by Allard (1960) and the genetic advance was categorized as per cent of mean, given by Johnson et al. [10]. Data from 21 genotypes for fifteen quantitative traits were used for Metroglyph analysis in the R program. The pattern of morphological variation among the 21 genotypes for thirteen quantitative characters was computed as given by Anderson [11]. Two characters with high variability were selected out of fifteen characters for plotting the graph. One of the characters is used on the X axis and the other one on the Y axis. The mean values of X for each genotype are plotted on the graph against the mean values of Y. The plotted glyphs are open since the genotypes are indigenous. Index scores were developed for all traits and divided into low, medium and high classes (Table 1). The remaining thirteen traits were represented as rays on glyphs with varied length depending upon the index score

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The mean sum of squares values for 15 quantitative traits was presented in the Table 1. The mean sum of squares due to the genotypes were significant for all the characters studied at both level of significance 1% and 5%, suggesting the existence of high genetic variability among the genotypes for all the traits. This indicates that there is ample scope for selection of genotypes from the present gene pool for yield and its component traits. The presence of large amount of variability might be due to diverse source of material as well as environmental influence affecting the phenotypes. Analysis of variance revealed that amount of variations present in the population. This analysis is the most important and first step of data analysis. The genotypes contain considerable amount of genetic variance and it will be used for further process and best genotypes will be identified used for many hybridizations programme by plant breeders. After identification of variance among the genotypes the data will be used for other statistical analysis.

3.2 Genotypic and Phenotypic Coefficient of Variation

In the present investigation, it is depicted from the Table 4 that in general, estimates of phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the influence of environment on the expression of these characters. However, good correspondence was observed genotypic coefficient of variation and phenotypic coefficient in all characters. In general, Variability is classified as low if coefficient of variation is less than 10 percent (10%), moderate (10 – 20%) and high (>20%) as proposed by Sivasubrahmanian and Menon [12].

Genotypic coefficient of variation was ranged from cob girth (7.80) to days to 50 % tasseling (32.26). High genotypic coefficient of variation was recorded for days to 50 % tasseling (32.26), anthesis – silking interval (29.33), days to 50 % silking (26.47), harvest index (24.19), and ear height (20.23). The traits seed weight (19.14), biological yield per plant (18.69), grain yield per plant (17.93), days to 75 % maturity (17.82), plant height (17.36), cob weight (16.94), grain rows per cob (14.42), cob length (14.12), and number of grains per row (12.05) expressed moderate genotypic coefficient of variation. The trait cob girth (7.80) expressed low genotypic coefficient of variation.

Phenotypic coefficient of variation ranged from 10.99 for cob girth to 33.45 for days to 50 % tasseling. High phenotypic coefficient of variation was observed for days to 50 % tasseling (33.45), anthesis – silking interval (30.63), days to 50 % silking (27.37), harvest index (27.27), grain yield per plant (21.36), ear height (21.23), and 100 seed weight (20.89). The traits days to 75 % maturity (19.60), plant height (19.33), biological yield per plant (19.13), cob weight (18.31), grain rows per cob (16.61), cob length (15.84), and number of grains per row (14.48) expressed moderate PCV whereas cob girth (10.99) expressed lowest PCV. From Table 3 it is evident that phenotypic coefficient of variation values are higher than genotypic coefficient of variation for all the traits under study indicating the influence of environment on studied characters.

The results are in conformity with the findings of Bello et al. [1], Kumar et al. (2015) and Rai et al. (2021).

3.3 Heritability

Lush [13] gave the concept of broad sense heritability, which is the ratio of genotypic

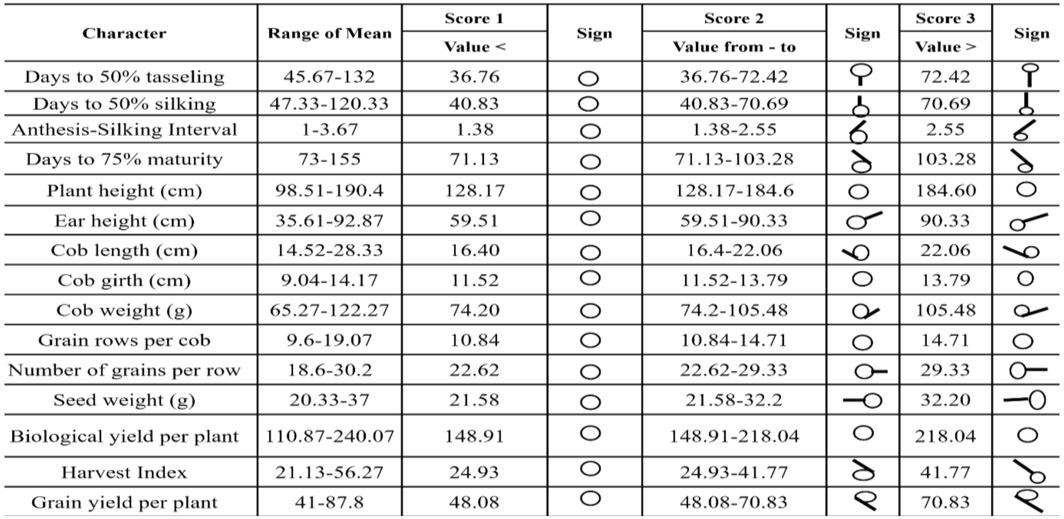
Table 1. Annova for 15 characters in maize genotypes

S. No.	**Source**	**Mean Sum of Squares (MSS)**		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**df=2**	**df=20**	**df=40**
1	Days to 50% tasseling	2.3970	953.73**	23.147
2	Days to 50% silking	2.0480	668.705**	15.131
3	Anthesis-Silking Interval	0.0630	1.03**	0.03
4	Days to 75% maturity	3.8250	775.183**	50.475
5	Plant height	393.8640	2388.671**	176.99
6	Ear height	15.5340	712.547**	23.309
7	Cob length	2.8510	24.02**	1.911
8	Cob girth	0.0450	3.887**	0.961
9	Cob weight	38.4850	733.913**	38.982
10	Grain rows per cob	0.7840	11.284**	1.11
11	Number of grains per row	1.2420	33.759**	4.355
12	Seed weight	9.4180	84.567**	5.057
13	Biological yield per plant	86.8650	3583.611**	56.086
14	Harvest Index	17.1890	212.899**	17.598
15	Grain yield per plant	131.0770	388.465**	47.691

Table 2. Mean performances of 21 maize genotypes for fifteen characters

S. No.	Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis-Silking Interval	Days to 75% maturity	Plant height	Ear height	Cob length	Cob girth	Cob weight	Grain rows per cob	Number of grains per row	100 Seed weight	Biological yield per plant	Harvest Index	Grain yield per plant
1	VL 19458	52.333	54.333	2	87.667	104.867	36.267	16.688	13.553	93.933	12	23.933	23.333	157.333	36.458	57.333
2	VL 19457	52.667	54	2	83.667	137.667	61	17.367	13.653	102.133	14	29.733	23.333	216.6	31.446	68.133
3	VL 183879	50.333	53	2	86.333	141.733	68.8	21.22	14.174	101.667	13.467	27.4	30.667	216.533	29.957	64.867
4	VL 19453	50	53	3	86.667	132.087	71.067	22.993	13.667	117.667	11.733	28	27.667	162.933	32.871	53.6
5	VL 183957	52.333	54.333	2	85.667	133.507	73.266	19.64	13.767	122.267	13.467	27.867	28.333	212.333	41.299	87.8
6	VL 183959	52.667	55	2	86.667	162.04	78	18.147	11	67.667	11.866	25.866	24.733	155	31.061	48.467
7	VL 19478	50.333	52.333	2	81	178.907	65.733	20.54	13.12	77.333	11.2	22.733	21	225.6	22.313	50.333
8	VL 183963	51.667	53	1	87.333	185.067	78.133	19.113	12.76	93.133	11.333	28.533	37	166.2	38.091	63.333
9	VL 183889	49	50.667	2	82.667	182.933	80.4	17.573	13.26	81.734	10.8	25.8	31.333	163.667	39.917	65.233
10	VL 19270	52.333	54.333	2	88.333	186.087	85.933	18.527	12.993	95.133	12.4	27	32.333	196.333	35.288	69.2
11	VL 19403	52.667	54.667	2	85.667	176.467	77.934	14.52	9.04	65.267	9.6	18.6	28.333	150.533	30.587	46.067
12	VL 19461	48	49.333	2	77	190.4	90.333	19.04	12.56	78.2	14	29.267	21.333	154.867	42.812	66.4
13	VL 183927	51	52.667	2	86	98.507	76.8	18.007	12.166	101.467	11.333	24.733	22.667	240.067	29.007	69.667
14	VL 19456	48.333	49	1	77	164.067	87.533	21.187	13.073	87	12.8	29.533	21.333	155.6	29.055	45.8
15	VL 19271	50.333	52	2	88.333	151.6	77.267	16.333	12.787	71.333	14.934	23.6	20.333	203.4	21.13	43.4
16	VL 19374	52.333	54.333	2	85.667	181.933	81.8	20.787	12.547	91.6	12	27.8	30	237.267	22.167	52.6
17	VL 183958	50.333	52.333	2	79.667	171.867	92.8	19.34	12.747	87.067	13.467	28.533	20.667	170.4	36.206	61.667
18	VL 183954	45.667	47.333	1.667	73	180.067	92.867	17.333	13.127	82.2	13.067	21.933	29.667	219.267	28.322	62
19	VL 19465	50.667	52.333	1	84	137.066	84.867	18.566	12.587	109.067	19.066	30.2	32.667	166.867	42.191	70.267
20	VL 19476	51.333	52.667	2	84	116.247	76.933	18.527	11.56	71.333	11.733	25.534	21.667	171.333	23.916	41
21	MAKKA 3 (CHECK)	132	120.333	3.667	155	170.98	35.613	28.333	11.586	89.467	14	18.934	36.333	110.867	56.268	61.4
Mean		54.59	55.76	1.97	87.21	156.39	74.92	19.23	12.65	89.84	12.77	25.98	26.89	183.48	33.35	59.46
CV		8.81	6.98	8.82	8.15	8.51	6.44	7.19	7.75	6.95	8.25	8.03	8.36	4.08	12.58	11.62
CD at 5%		7.94	6.42	0.29	11.72	21.95	7.97	2.28	1.62	10.3	1.74	3.44	3.71	12.36	6.92	11.4
CD at 1%		10.62	8.59	0.38	15.69	29.38	10.66	3.05	2.16	13.79	2.33	4.61	4.97	16.54	9.26	15.25
SEm		2.78	2.25	0.1	4.1	7.68	2.79	0.8	0.57	3.6	0.61	1.2	1.3	4.32	2.42	3.99
RANGE	Minimum	45.67	47.33	1	73	98.51	35.61	14.52	9.04	65.27	9.6	18.6	20.33	110.87	21.13	41
	Maximum	132	120.33	3.67	155	190.4	92.87	28.33	14.17	122.27	19.07	30.2	37	240.07	56.27	87.8

Table 3. Index score and signs used for metroglyph analysis of maize genotype



Character	Range of Mean	Score 1	Sign	Score 2	Sign	Score 3	Sign
		Value <		Value from - to		Value >	
Days to 50% tasseling	45.67-132	36.76	○	36.76-72.42	⫯	72.42	⫯
Days to 50% silking	47.33-120.33	40.83	○	40.83-70.69	⫰	70.69	⫰
Anthesis-Silking Interval	1-3.67	1.38	○	1.38-2.55	○╱	2.55	○╱
Days to 75% maturity	73-155	71.13	○	71.13-103.28	╲○	103.28	╲○
Plant height (cm)	98.51-190.4	128.17	○	128.17-184.6	○	184.60	○
Ear height (cm)	35.61-92.87	59.51	○	59.51-90.33	○╱	90.33	○╱
Cob length (cm)	14.52-28.33	16.40	○	16.4-22.06	╲○	22.06	╲○
Cob girth (cm)	9.04-14.17	11.52	○	11.52-13.79	○	13.79	○
Cob weight (g)	65.27-122.27	74.20	○	74.2-105.48	○╱	105.48	○╱
Grain rows per cob	9.6-19.07	10.84	○	10.84-14.71	○	14.71	○
Number of grains per row	18.6-30.2	22.62	○	22.62-29.33	○─	29.33	○─
Seed weight (g)	20.33-37	21.58	○	21.58-32.2	─○	32.20	─○
Biological yield per plant	110.87-240.07	148.91	○	148.91-218.04	○	218.04	○
Harvest Index	21.13-56.27	24.93	○	24.93-41.77	╲○	41.77	╲○
Grain yield per plant	41-87.8	48.08	○	48.08-70.83	○╲	70.83	○╲

Table 4. Genetic variability parameters in 21 maize genotype

Sl. No.	Characters	ECV	GCV	PCV	h2 (Broad Sense)	Genetic Advancement 5%	Gen.Adv as % of Mean 5%
1	Days to 50% tasseling	8.814	32.265	33.447	93.056	34.999	64.116
2	Days to 50% silking	6.976	26.47	27.373	93.506	29.402	52.727
3	Anthesis-Silking Interval	8.823	29.333	30.631	91.703	1.139	57.865
4	Days to 75% maturity	8.147	17.823	19.596	82.717	29.12	33.391
5	Plant height (cm)	8.507	17.362	19.334	80.64	50.228	32.118
6	Ear height (cm)	6.444	20.231	21.233	90.789	29.751	39.71
7	Cob length (cm)	7.189	14.119	15.844	79.413	4.984	25.919
8	Cob girth (cm)	7.747	7.805	10.997	50.375	1.444	11.411
9	Cob weight (g)	6.95	16.941	18.311	85.596	29.007	32.287
10	Grain rows per cob	8.248	14.416	16.608	75.338	3.293	25.775
11	Number of grains per row	8.033	12.051	14.483	69.238	5.366	20.658
12	Seed weight (g)	8.362	19.144	20.89	83.976	9.718	36.139
13	Biological yield per plant	4.082	18.689	19.13	95.447	69.012	37.613
14	Harvest Index	12.578	24.193	27.267	78.721	14.747	44.218
15	Grain yield per plant	11.615	17.926	21.36	70.43	18.425	30.99

Table. 5. Distribution of 21 maize genotypes based on metroglyph analysis

Complex	Name of complex	No. of lines	Name of lines	Range and average score
I	Higher plant height with moderate biological yield per plant	7	VL 183959, VL 183963, VL 183889, VL 19403, VL 19461, VL 19456, VL 183958	28.00-33.00 (30.28)
II	Moderate plant height with moderate biological yield per plant	4	VL 19457, VL 183879, VL 183957, VL 19271	24.00-32.00 (29.00)
III	Lower plant height with lower biological yield per plant	4	VL 19458, VL 19453, VL 19465, VL 19476	26.00-32.00 (29.00)
IV	Higher plant height with higher biological yield per plant	4	VL 19478, VL 19270, VL 19374, VL 183954	30.00-34.00 (31.25)
V	Higher plant height with lower biological yield per plant	1	MAKKA 3 (CHECK)	26.00
VII	Lower plant height with higher biological yield per plant	1	VL 183927	34.00

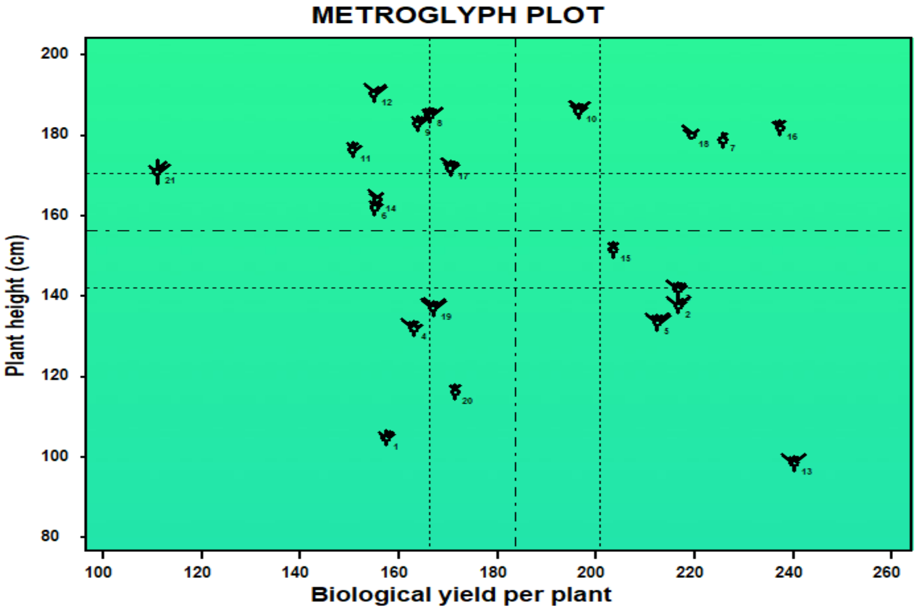


Fig. 1. Scattered diagram of metroglyph analysis of maize genotypes

variance (VG) to phenotypic variance (VP). It determines efficiency with which we can utilize the genotypic variability in breeding programme. Burton [14] suggested that genetic variation along with heritability will give better idea about expected efficiency of selection. Thus, a character possessing high GCV along with high heritability be valuable in a selection program. The range of heritability was considered low (<30 %), medium (30 – 60%) and high (>60%) as proposed by Johnson et al*.* [10]. The estimates of broad sense heritability in the broad sense for all studied traits ranged from cob girth (50.37) to biological yield per plant (95.45).

3.4 Metroglyph

Metroglyph analysis is a semi graphical method for assessing the pattern of morphological variation in substantial number of germplasm lines. The results obtained on metroglyph analysis in 21 genotypes of maize are discussed below. It was observed that maximum range of variability was in biological yield (110.87-240.07) followed by plant height (98.51-190.4), days to 50% tasseling (45.67-132), days to 50% silking (47.33-120.33), ear height (35.61-92.87), and cob weight (65.27-122.27). These traits thus were most variable for classificatory analysis in maize [15-18]. The range of variability for characters, their values for index score and signs with rays are represented in Table 3. The total index score varied from 24-34. The maximum index scored by genotype VL 19465 and MAKKA 3 CHECK (34.00) followed by VL 19453 (33.00), VL 183957, VL 19270, VL 19461 (32.00), VL 19457, VL 183879, VL 183963, and VL 183954 (31.00), whereas VL 19403 (24.00) scored minimum. Mean and index scores for maize genotypes represent 3 scores for the following characters, genotype VL 19457 for number of grains per row, VL 183879 for cob girth, VL 19453 for cob length, cob weight, VL 183957 for cob weight, grain yield per plant, VL 19478 for biological yield per plant, VL 183963 for plant height, 100 seed weight, VL 19270 for plant height, 100 seed weight, VL 19461 for plant height, ear height, harvest index, VL 183927 for biological yield per plant, VL 19456 for number of grains per row, VL 19271 for grain rows per cob, VL 19374 for biological yield per plant, VL 183954 for ear height, biological yield per plant, VL 19465 for cob weight, grain rows per cob, number of grains per row, 100 seed weight, harvest index , MAKKA 3 (CHECK) for days to 50% tasseling, days to 50% silking, anthesis-silking interval, days to 75% maturity, cob length, 100 seed weight, and harvest index [19-21].

A scattered diagram has been prepared by taking biological yield on X-axis and plant height on Y-axis and signs with ray pattern which were the most variable characters. In classificatory analysis based on biological yield per plant and plant height for all the 21 genotypes formed six complexes (Table 5 and Fig. 1).

Complex: This complex consists of seven genotypes. Complex consist of genotypes VL 183959, VL 183963, VL 183889, VL 19403, VL 19461, VL 19456, VL 183958 which possessed the higher plant height with moderate biological yield per plant with an index score range from 28.00 to 33.00 and an average score 30.28. Among these genotypes which recorded higher values for the component traits is represented, VL 183959 had moderate values for the characters, VL 183963 for plant, 100 seed weight, VL 19461 for plant height, ear height, harvest index, VL 19456 for number of grains per row, VL 183958 for ear height. Genotypes VL 183963, VL 19461 were having higher total index score than that of average index score of this complex (30.28). The remaining genotypes were low having grain yield per plant with low total index score [22-25].

Complex: This complex consists of four genotypes. Complex consist of genotypes VL 19457, VL 183879, VL 183957, VL 19271 which possessed the moderate plant heighr with moderate biological yield per plant with an index score range from 24.00 to 32.00 and an average score 29.00. Among these genotypes which recorded higher values for the component traits is represented, VL 19457 for number of grains per row, VL 1838789 for cob width, VL 183957 for cob weight, grain yield per plant, VL 19271 for grain rows per cob. Genotypes VL 19457, VL 183879, VL 183957 were having higher total index score than that of average index score of this complex (29.00). The remaining genotypes were having low grain yield per plant with low total index score.

Complex: This complex consists of four genotypes. Complex consist of genotypes VL 19458, VL 19453, VL 19465, and VL 19476 which possessed lower plant height with lower biological yield per plant with an index score range of 26.00 to 34.00 and an average score of 30.00. Among these genotypes which recorded higher values for the component traits is represented, VL 19458 had moderate values for the characters, VL 19453 for cob length, cob weight, VL 19465 for cob weight, grain rows per cob, number of grains per row, 100 seed weight, harvest index, VL 19476 had moderate values for the characters. Genotypes VL 19453, VL 19465 were having higher total index score than that of average index score of this complex (30.00). The remaining genotypes were having low grain yield per plant with low index score.

Complex: This complex consists of four genotypes. Complex consist of genotypes VL 19478, VL 19270, VL 19374, and VL 183954 which possessed higher plant height with higher biological yield per plant with an index score range 29.00 to 32.00 and an average score 30.25. Among these genotypes which recorded higher values for the component traits is represented, VL 19478 for biological yield per plant, VL 19270 for plant height, 100 seed weight, VL 19374 for biological yield per plant, VL 183954 for ear height, biological yield per plant. Genotypes VL 19270, VL 183954 were having higher total index score than that of average index score of this complex (30.25). The remaining genotypes were having low grain yield per plant with low index score.

Complex: This complex consists of one genotype MAKKA 3 (CHECK) which possessed higher plant height with lower biological yield per plant with an index score 34.00. This genotype recorded higher values for the component traits days to 50% tasseling, days to 50% silking, anthesis-silking interval, days to 75% maturity, cob length, 100 seed weight, and harvest index**.**

Complex: This complex consists of one genotype VL 183927 which possessed lower plant height with higher biological yield per plant with an index score 30.00. This genotype recorded higher values for the component traits biological yield per plant.

4. CONCLUSION

Analysis of variance revealed significant differences for all the 15 characters studied indicating the presence of sufficient variation in the materials and it provides an opportunity for further analysis and estimation of genetic parameters. Among 21 genotypes, genotype VL 183957 (87.8gm), VL 19465 (70.26gm), VL 183927 (69.6gm), VL 19270 (69.2gm) were found to be superior in seed yield than MAKKA 3 check (61.4gm). Days to 50% tasseling followed by Anthesis and silking interval and days to 50% silking traits has highest estimation of GCV and PCV. The estimation of heritability and genetic advance were highest in biological yield per plant whereas highest GAM observed in days to 50% tasseling. Six complexes were made based on biological yield per plant and plant height which were the most variable characters. The maximum index scored by VL 19465 (34) and MAKKA 3 (34) belongs to complex 3 and complex 5 respectively.

Therefore, these two genotypes present in these two complexes should be given priority during selection for yield improvement of maize.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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