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Evaluation of maize (*Zea mays* L.) genotypes to estimate the genetic parameters of variability for various polygenic traits

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Abstract

The experiment was conducted in a randomized block design with three replications during Kharif, 2021 at RMD College of Agriculture and Research Station, Ambikapur (Chhattisgarh). A total of seventy seven maize genotypes (18 parents and 56 F1's including 3 checks) were used to evaluate for genetic variability, heritability and genetic advance analysis in 16 polygenic traits. The result of analysis of variance revealed presence of significant variation among the genotypes. The phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV) for all the traits however, high GCV and PCV were recorded for the traits viz. grain yield plant⁻¹, biological yield plant⁻¹, no. of kernels row⁻¹, ear height, 100-seed weight, plant height, ear length, ear girth and harvest index which showed, direct selection will be rewarding for improving these traits. High heritability (%) together with high genetic advance as percentage of mean (GAM) was recorded for 100-seed weight, grain yield plant⁻¹, biological yield plant⁻¹, plant height, ear height, no. of kernels row⁻¹, ear girth, ear length and harvest index which indicated that these traits are governed by additive gene action hence and are heritable and fixable thus, phenotypic selection for these traits could be rewarding.

Keywords: genotypes, genetic variability, heritability, genetic advance and maize

Introduction

Maize (*Zea mays* L.) is a highly cross pollinated and world's leading cereal grain cultivated widely across the world and due to its potential to give high yield it is famously known by the name "Queen of Cereals" (Downswell *et al.*, 1996) [5]. In one of the most important cereals crops cultivated globally, it comes in third position after rice and wheat and contributed nearby 10% of the total food grain production. Maize is cultivated in an area of 201.98 m ha in the world which yielded 1162.35 mt (FAOSTAT, 2020) [6]. In India, it occupies an area of 9.87 m ha with the production of 30.16 mt (FAOSTAT, 2020) [6] and comes in sixth rank among the maize growing countries in the world. There are many other names for maize such as; Corn, Makka, Silk corn, Zea, Barajovar etc. (Kumar and Jhariya, 2013) [11]. The grain of maize is used as a staple food, as feed for poultry, fishes and livestock as well as in many industries it is used as a raw material and yields many industrial products like starch, sugar, cornflakes, oil, syrup or alcohol etc. (Lal, K. *et al.*, 2020) [12]. Because of the wide use in numerous ways demand of Corn is increasing day by day and to accomplish the requirement there is need of developing high yielding maize cultivars.

To conduct a successful crop improvement programme it is very crucial to know the magnitude of genetic variability present among the population studied and its nature in governing the inheritance of polygenic traits (Vashistha *et al.*, 2013) [21]. It gives an idea for adopting the appropriate breeding method for improvement of those genotypes. Genetic parameters such as variances, coefficients of variation, heritability and genetic advance offers an insight into the magnitude of genetic variability existing in a population as well as selection gains. To know whether the observed variability is heritable or not; heritability is an effective measure which indicates the proficiency of a genotype to transmit its character into the upcoming generations. However, heritability alone cannot give a clear indication of the genetic progress may arises from choosing the best plants. Therefore, it's better to combine it with genetic advance which confirms us about the magnitude of additive and non-additive genetic variances involved with the respective characters of concern. Hence, those trait are considered for selection which possess high estimates of both heritability and genetic advance.

Giving due consideration to the aforesaid phases, this experiment was conducted with the aim to analyse genetic variability and heritability along with genetic advance for yield and its attributing traits among the several maize genotypes under experiment.

Materials and Methods

The experimental material in this research involved 56 F1s, their 18 parents (14 lines and 4 testers) along with 3 checks and these materials were evaluated in a Randomized Block Design (RBD) during Kharif, 2021 where, all of them were replicated thrice. Each block is divided into no. of plots where each plot length was kept 4m with plants spacing of 60 X 20 cm. The research was conducted at the Research cum Instructional Farm, Genetics and Plant Breeding section, RMD College of Agriculture and Research Station, Ambikapur (Chhattisgarh) situated at a latitude of 20°8'N, longitude of 83°15'E and altitude of 592.62 m MSL (mean sea level). All the essential operations required to grow a healthy crop were done as recommended. The observations were taken on 5 randomly selected plants in each plot of all the genotypes for plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows cob⁻¹, number of kernels row⁻¹, grain yield plant⁻¹, shelling percentage, 100 seed weight (g), biological yield plant⁻¹ and harvest index (%), while for days to 50% tasseling, days to 50% silking, days to maturity, number of cobs plot⁻¹ and plant population (thousand ha⁻¹) data were taken on plot basis.

Statistical analysis

The average data of each genotype for several traits were used to calculate the various genetic parameters such as Analysis of variance (Panse and Sukhatme, 1961) [16], genotypic and phenotypic coefficient of variations (Burton, 1952) [4] and heritability (broad sense) as the ratio of genotypic to phenotypic variance. Following the method given by Sivasubramanian and Madhavamenon (1973) [18], the genotypic and phenotypic coefficient of variation are categorized as low (<10%), moderate (10-20%) and high (>20%). Nevertheless, heritability, expected genetic advance and genetic advance as per cent of mean were estimated and further categorized according to the method recommended by Johnson *et al.*, (1955) [9]. Heritability was partitioned into three classes viz., low (below 30%), moderate (30-60%) and high (above 60%) heritability even though, genetic advance as per cent of mean was categorized into three classes such as low (< 10%), moderate (10-20%) and high (> 20%). The analysis of data for several genetic parameters was accomplished with the help of INDOSTAT software.

Results and Discussion

Analysis of variance

The aim of this experiment was to estimate several genetic parameters for 16 quantitative traits by using 77 maize genotypes consisting 18 inbred lines (14 lines and 4 testers), 56 F1's and 3 commercial checks. From the result of analysis of variance it can be seen that all the genotypes under study showed significant differences for every single trait studied (Table 1) which is an indication of existence of considerable genetic variation in the experimental material. Significant differences for these traits were also reported by Thakur *et al.* (2016) [20], Bisen *et al.* (2018) [3], Bartaula *et al.* (2019) [1], Prakash *et al.* (2019) [17] and Lal *et al.* (2020) [12].

Genetic variability studies

The mean performance of all genotypes for 16 characters with their range, genotypic and phenotypic coefficient of variation (GCV & PCV) are presented in Table 2. For each trait, phenotypic coefficient of variation was found higher than genotypic coefficient of variation indicating that performance of all these characters are influenced by the environment. The highest value of genotypic and phenotypic coefficient of variation (GCV & PCV) was noted for grain yield/plant (40.24; 41.19) followed by biological yield/plant (37.63; 38.56), no. of kernels/row (27.40; 28.53), ear height (24.43; 25.30), 100-seed weight (23.04; 23.33) and plant height (21.38; 22.01) which showed that among the genotypes adequate amount of variability existed hence, direct selection will be effective for improving these traits. The maximum value of GCV and PCV for grain yield plant⁻¹ were earlier confirmed by Reddy *et al.*, (2012) [23] and Lal *et al.* (2020) [12], for number of kernels row⁻¹ by Bhadru *et al.* (2020) [2], and for plant height by Ghosh *et al.* (2014) [7] and Maruti and Jhansi (2015) [14]. The trait viz., ear length, ear girth and harvest index showed moderate value of genotypic and phenotypic coefficient of variation (GCV & PCV) which reveals that selection is possible to find the appropriate genotypes for these traits.

Heritability in broad sense (h²_b)

The assessment of heritability gives estimates that assists the plant breeder for opting suitable genotypes over a diverse genetic population. Broad sense heritability (h²_b) in this aspect helps in prediction of extent of transmissible portion of total variance of a character to the successive generation. It is an estimate of overall contribution of genetic variance towards the total phenotypic variance of a character and can be calculated from genotypic and phenotypic variance. Heritability, genetic advance and genetic advance as percentage of mean are presented in Table 3.

The high estimate of heritability (%) was found for all the traits under consideration where maximum heritability was recorded for 100-seed weight (97.60) followed by grain yield/plant (95.40), biological yield/plant (95.20), plant height (94.40), ear height (93.30), no. of kernels/row (92.20), shelling % (88.90), ear girth (88.20), days to 50% tasseling (83.70), days to 50% silking (78.20), ear length (77.80), days to maturity (76.60), plant population (75.20), no. of cobs/plot (73.60), harvest index (68.20) and no. of kernel rows/cob (61.30). The high value of heritability for several traits indicated less influence of environment on these traits thus, selection of these genotypes on the basis of phenotypic performance will be effective for further improvement of these characters. These results of heritability can be validated with the conclusions of Kharel *et al.* (2017) [10] for days to 50% tasseling, days to 50% silking, plant height and number of kernels row⁻¹, high heritability for grain yield, number of rows cob⁻¹, days to 50% silking and plant height were confirmed with the finding of Prakash *et al.* (2019) [17] and while, Supraja *et al.* (2019) [19] showed similarity with the result for days to tasseling, days to silking, plant height, ear length and number of kernel rows ear⁻¹.

Genetic advance as per cent of mean (GAM)

Genetic advance is an extent of genetic gain under selection and are more reliable because it involves phenotypic standard deviation, heritability and selection intensity. It aids in

understanding that which type of gene action intricated in expression of various quantitative traits. To simplify the comparison of progress in several traits of diverse genotypes, genetic advance was calculated in the form of percentage of mean.

Genetic advance as per cent of mean was noticed high for grain yield plant⁻¹ (80.97), biological yield plant⁻¹ (75.64), no. of kernels row⁻¹ (54.20), ear height (48.61), 100-seed weight (46.88), plant height (42.78), ear length (27.27), ear girth (26.21) and harvest index (%) (23.85) however, the trait viz., no. of kernel rows cob⁻¹ (13.12), no. of cobs plot⁻¹ (11.73) plant population (11.67), days to 50% tasseling 10.34) and shelling % (10.06) were recorded for moderate value of genetic advance as per cent of mean (Table 3).

Instead of only considering heritability (%), its value together with GAM is considered more reliable to estimate the effect of selection [Johnson *et al.* (1955)]^[9]. The high estimates of heritability along with high genetic advance as per cent of mean was noticed for the traits such as 100-seed weight ($h^2_b=97.60$, GAM = 46.88) followed by grain yield/plant ($h^2_b=95.40$, GAM = 80.97), biological yield/plant ($h^2_b=95.20$, GAM = 75.64), plant height ($h^2_b=94.40$, GAM = 42.78), ear height ($h^2_b=93.30$, GAM = 48.61), no. of kernels/row ($h^2_b=92.20$, GAM = 54.20), ear girth ($h^2_b=88.20$, GAM = 26.21), ear length ($h^2_b=77.80$, GAM = 27.27) and harvest index ($h^2_b=68.20$, GAM = 23.85) which revealed significant role of additive gene action in controlling these traits and therefore improvement in these traits could be possible through selection and hybridization. These results can validated with the findings of Mahajan *et al.* (2011)^[13], Kharel *et al.* (2017)^[10], Pandey *et al.* (2017)^[15], Bhadru *et al.* (2020)^[2], Lal *et al.*

(2020)^[12] and Wedwessen and Zeleke (2020)^[22] for the most of the yield attributing traits.

The trait viz. days to 50% silking ($h^2_b=78.20$, GAM = 9.01) and days to maturity ($h^2_b=76.60$, GAM = 5.65) showed high heritability (%) with low GAM revealed that these traits are govern by non-additive gene action and the reason for high value of heritability (%) might be due to favourable effect of environment hence, selection for such traits may not be effective. Similar results for days to maturity were obtained by Prakash *et al.* (2019)^[17] and for days to 50% silking by Ghosh *et al.* (2014)^[7], Jilo *et al.* (2018)^[8] and Bhadru *et al.* (2020)^[2].

Conclusion

The result of analysis of variance showed significant variation existed in the materials under experiment. The phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV) for all the traits. The highest value of GCV and PCV was recorded for grain yield plant⁻¹, biological yield plant⁻¹, no. of kernels row⁻¹, ear height, 100-seed weight and plant height revealed adequate amount of variability existed among all the genotypes hence, direct selection will be effective for improving these traits. High heritability (%) together with high genetic advance as percentage of mean (GAM) was recorded for 100-seed weight, grain yield plant⁻¹, biological yield plant⁻¹, plant height, ear height, no. of kernels row⁻¹, ear girth, ear length and harvest index indicating that these traits are governed by additive gene action hence, they are heritable and fixable thus, phenotypic selection for these traits will be rewarding.

Table 1: Analysis of variance for 16 characters in 77 genotypes of maize

S. No.	Characters	Mean sum of squares		
		Replications (df=2)	Treatments (df=76)	Error (df=152)
1.	Days to 50% tasseling	16.38	30.22**	1.85
2.	Days to 50% silking	10.18	28.28**	2.40
3.	Days to maturity	17.33	30.16**	2.78
4.	Plant height (cm)	2524.82	5029.97**	98.43
5.	Ear height (cm)	856.73	1385.59**	32.49
6.	Ear length (cm)	2.63	12.38**	1.08
7.	Ear girth (cm)	0.14	10.72**	0.46
8.	No. of kernel rows/cob	0.93	4.16**	0.72
9.	No. of kernels/row	40.74	166.42**	4.55
10.	Pulatio Plant population (Lakhs/ha)	0.01	0.029**	0.00
11.	No. of cobs/plot	6.08	63.01**	10.72
12.	Grain yield/plant (g)	25.53	7899.56**	252.24
13.	Shelling %	0.26	49.38**	1.98
14.	100-seed weight (g)	16.06	157.80**	8.92
15.	Biological yield/plant (g)	597.99	66061.13**	3524.22
16.	Harvest index (%)	1.31	32.48**	14.23

* Significant at 5% level; ** Significant at 1% level

Table 2: Mean, range, genotypic and phenotypic coefficient of variation for 16 characters in 77 genotypes of maize

S. No.	Characters	Mean	Range		GCV	PCV
			Min.	Max.		
	Days to 50% tasseling	56.06	47.67	63.33	5.49	6.00
1.	Days to 50% silking	59.38	52.00	66.67	4.95	5.59
2.	Days to maturity	96.45	88.67	101.67	3.13	3.58
3.	Plant height (cm)	189.64	91.47	242.13	21.38	22.01
4.	Ear height (cm)	86.93	38.13	116.40	24.43	25.30
5.	Ear length (cm)	12.93	6.93	17.13	15.01	17.02
6.	Ear girth (cm)	13.65	8.80	16.53	13.55	14.43
7.	No. of kernel rows/cob	13.15	10.00	15.20	8.14	10.39

8.	No. of kernels/row	26.81	10.40	35.67	27.40	28.53
9.	Plant population (thousand/ha)	0.76	0.43	0.90	6.53	7.53
10.	No. of cobs/plot	32.30	17.33	40.33	6.64	7.74
11.	Grain yield/plant (g)	123.86	26.53	204.47	40.24	41.19
12.	Shelling %	76.67	67.77	80.90	5.18	5.50
13.	100-seed weight (g)	32.38	15.20	43.53	23.04	23.33
14.	Biological yield/plant (g)	368.26	92.93	586.67	37.63	38.56
15.	Harvest index (%)	33.55	28.40	44.27	14.01	16.96

Table 3: Genetic parameters for 16 characters in 77 genotypes of maize

S. No.	Characters	h ² (Broad Sense)	Genetic Advance (GA)	Genetic advance as per cent of mean (%)
1.	Days to 50% tasseling	83.70	5.80	10.34
2.	Days to 50% silking	78.20	5.35	9.01
3.	Days to maturity	76.60	5.45	5.65
4.	Plant height (cm)	94.40	81.13	42.78
5.	Ear height (cm)	93.30	42.25	48.61
6.	Ear length (cm)	77.80	3.53	27.27
7.	Ear girth (cm)	88.20	3.58	26.21
8.	No. of kernel rows/cob	61.30	1.73	13.12
9.	No. of kernels/row	92.20	14.53	54.20
10.	Plant population (thousand/ha)	75.20	9.24	11.67
11.	No. of cobs/plot	73.60	4.45	11.73
12.	Grain yield/plant (g)	95.40	100.80	80.97
13.	Shelling %	88.90	7.71	10.06
14.	100-seed weight (g)	97.60	15.16	46.88
15.	Biological yield/plant (g)	95.20	275.60	75.64
16.	Harvest index (%)	68.20	8.00	23.85

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