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Genetic analysis of yield and its component traits in maize (*Zea mays* L.)

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Abstract

Maize (*Zea mays* L.) a member of grass family, poaceae (gramineae) having $2n = 2x = 20$ chromosomes is one of the most important cereal crops of India. Mexico and Central America are the origin place of this crop. It has more than thirty-two thousand genes in its genome and the size of genome is about 2.3 gigabase. The objective of this study was to evaluate seventy-seven maize genotypes in relation to heritability and genetic advance for fourteen quantitative traits. The estimates of heritability provide information regarding to possibility and extent to which improvement is possible through selection. In this experiment it was found that the mean sum of squares due to genotypes were highly significant for all the characters under study. Indicated that significant amount of variability was available in the genotypes for all the traits. Majority of the traits were found to exhibit moderate to high estimates of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV), however some traits such as days to 50% tasseling, days to 50% silking, days to 75% dry husk, cob diameter and shelling% had low estimates of GCV and PCV. Highest estimate of GCV was reported for grain yield per plant (36.706) followed by kernels per cob (32.136) cob weight (31.066) and kernels per row (27.087) while the lowest estimate of GCV was reported for days to 75% dry husk (3.162). High estimates of heritability in broad sense (>61%) were reported for all the fourteen characters under study but among them nine traits such as grain yield per plant (75.452), kernels per cob (66.191), cob weight (63.952), kernels per row (55.639), cobs per plant (37.46), 100-kernel weight (27.718), cob length (27.529), kernel rows per cob (23.856) and plant height (20.957) had high estimates of genetic advance in percent of mean (>20%). High estimates of heritability coupled with high estimates of genetic advance are the indicative of additive gene effects in the inheritance of above-mentioned traits. Therefore, selection will be rewarding for the improvement of these traits.

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops of India. It is a member of grass family, poaceae (gramineae) has $2n = 2x = 20$ chromosomes. It originated in Mexico and Central America. It possesses over 32,000 genes on ten chromosomes with a genome size of 2.3 gigabase (Hossain *et al.*, 2016) [9]. It has assumed greater significance due to its demand for food, feed and industrial utilization. It is the third most important cereal crop of India after rice and wheat. In India the annual production of cereals is around 252.02 mt from an area of 124.30 m ha. with productivity level of 2028 kg/ha, Maize contributed around 24.17 mt productions from an area of 9.19 m ha. with productivity level of 2632 kg/ha during 2014-15 (Agricultural statistics at a glance 2016, DAC&FW). Hybrid cultivars have played a vital role in increasing acreage and productivity of maize but continuous increasing demand of maize required specific attention in maize breeding to develop high yielding maize cultivar suitable for different agroclimatic zones. However, the breeding objective in maize improvement program is to obtain genetic progress in yield component traits along with maintaining a high amount of variability (Hallauer, 1973) [7]. Welsh, 1981 emphasized the importance of variability and stated that genetic variability is key to any crop improvement programme. Efficiency of selection and genetic improvement of yield and other agronomic traits also depend upon the nature and magnitude of variability and the proportion of total variability

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which is heritable in nature. Heritability alone has no reliable for remark of genetic progress from individual genotype selection. Hence knowledge about heritability along with genetic gain is very useful (Johnson *et al.*, 1955) [10]. Therefore, the present investigation carried out to evaluate maize genotypes in relation to heritability and genetic advance.

Materials and Methods

Fifty-four single cross hybrids (obtained through the crossing of 18 lines (females) with 3 testers (males) in line x tester design during *Kharif* 2018) along with their parental lines and 2 check varieties evaluated at Student Instructional Farm, CS Azad University of Agriculture and Technology, Kanpur-208002 (U.P.), India during *Rabi* 2018-19 in Randomized complete block design. Each treatment grown in a single row of 4m length with 60x25cm spacing and replicated three times. Data on various quantitative traits such as plant height, number of cobs/plant, number of kernel rows/cob, number of kernels/row, cob length (cm), cob diameter (cm), cob weight (g), number of kernels/cob, 100-kernel weight (g), grain yield/plant (g) and shelling percentage (%) were recorded on 5 randomly selected plants per entry per replication while, data on days to 50% tasselling, days to 50% silking, days to 75% dry husk, were recorded on plot basis. All the recommended cultural practices were followed to raise a good crop. The mean values of recorded data were used for Analysis of variance for Randomized Complete Block Design (Panse and Sukhatme 1985) [16].

Phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for different characters were estimated by following formulae suggested by Burton and de Vane (1953).

Phenotypic coefficient of variation (PCV) $= \dfrac{\sqrt{\text{Phenotypic variance}}}{\overline{X}} \times 100$

Genotypic coefficient of variation (GCV) $= \dfrac{\sqrt{\text{Genotypic variance}}}{\overline{X}} \times 100$

Environmental coefficient of variation (ECV) $= \dfrac{\sqrt{\text{Environmental variance}}}{\overline{X}} \times 100$

Where, $\overline{X}$ = Mean of the characters.
As suggested by Sivasubramanian and Menon (1973) [22], GCV and PCV were categorized into
Low = Less than 10%
Moderate = 10-20%
High = More than 20%
Heritability in broad sense (h^2b) was calculated as suggested by Hanson, 1963.

$$h^2b\,(\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
$\sigma^2 g$ = genotypic variance
$\sigma^2 p$ = phenotypic variance
As suggested by Robinson *et al.*, 1949, heritability in broad sense h^2 (b) estimates were categorized into
Low = 0 – 30 per cent,
Moderate = 31- 60 per cent,
High = 61 per cent and above
The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.*, 1955 [10].

$$Ga = h^2b \times \sigma\,p \times K$$

Where,
h^2b = Heritability
σ p = Phenotypic standard deviation
K = Standardized selection differential (2.06) a constant at 5% selection intensity.
Now Genetic advance as per cent of mean (Ga) was worked out as

$$(\overline{Ga})\,(\%) = \frac{GA}{\overline{X}} \times 100$$

Where,
Ga = Genetic advance
$\overline{X}$ = Mean of the character
The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.,* 1955 [10].
Low = Less than 10 per cent, Moderate = 10-20 per cent, High = More than 20 per cent

Result and Discussion

Efficiency of selection and genetic improvement of yield and other agronomic traits depend upon the nature and magnitude of variability and the proportion of total variability which is heritable in nature. The analysis of variance for different quantitative traits was done and presented in table 1 which revealed that the mean sum of squares due to genotypes were highly significant for all the characters under study. Indicated that significant amount of variability was available in the genotypes for all the traits. Muhammad *et al.*, 2010, Thakur *et al.*, 2016, Patil *et al.*, 2016, Kumar *et al.*, 2017, Beulah *et al.*, 2018 and Dar *et al.*, 2018 has also reported highly significant variation for all the characters under study. Devkota *et al.*, 2020 has also observed significant variation for grain yield, silking and tasseling, number of kernels per cob and cob length in the genotypes. Adhikari *et al.*, 2018 has reported significant differences among the genotypes for days to tasseling, days to silking, plant height, ear height, ear length, ear diameter and grain yield. Sharma *et al.*, 2018 has also reported significant differences for all growth, yield and yield attributing characters in the genotypes. Considerable genotypic variability among the genotypes for different traits have also observed by Turi *et al.*, 2007.

The estimates of heritability provide information regarding to possibility and extent to which improvement is possible through selection. Heritability alone has no reliable for remark of genetic progress from individual genotype selection. Hence knowledge about heritability along with genetic gain is very useful (Johnson *et al.*, 1955) [10]. The estimates of GCV, PCV, heritability and genetic advance presented in table 2. Critical analysis of the table showed that three types of GCV and PCV estimates (high GCV and high PCV, moderate GCV and moderate PCV and low GCV and low PCV) could be observed for various traits under study in this investigation. Such type of estimates has also been reported by Beulah *et al.*, 2018, Dar *et al.*, 2018, Thakur *et al.*, 2016 and Shengu, 2017. High estimates of GCV and PCV (>20%) were exhibited by grain yield per plant, kernels per cob, kernels per row, cob weight and kernels per row. Bisen *et al.*, 2018 has also reported high GCV and PCV for the traits such as grain yield, stover yield, cob weight and cob/ plant. Beulah *et al.*, 2018 has reported such estimates for grain yield per plant. Moderate estimates of GCV and PCV were observed for cobs per plant, cob length, 100-kernel weight, kernel rows per cob and plant height. Sandeep *et al.*, 2015 has also reported moderate GCV and PCV for cob length, 100-

kernel weight and kernels per row. Pandey *et al*., 2017 has reported such estimates for 100-kernel weight and Thakur *et al*., 2016 has reported such estimates for cob length. In this way majority of the traits were found to exhibit moderate to high estimates of GCV and PCV, however some traits such as days to 50% tasseling, days to 50% silking, days to 75% dry husk, cob diameter and shelling% had low estimates of GCV and PCV. Similar results have also been reported by Sandeep *et al*., 2015, Maruthi and Rani (2015) [13], Patil *et al*., 2016, Pandey *et al*., 2017 and Adhikari *et al*., 2018. High estimates of heritability in broad sense (>61%) were reported for all the fourteen characters under study but among them nine traits

such as grain yield per plant (75.452), kernels per cob (66.191), cob weight (63.952), kernels per row (55.639), cobs per plant (37.46), 100-kernel weight (27.718), cob length (27.529), kernel rows per cob (23.856) and plant height (20.957) had high estimates of genetic advance in percent of mean (>20%). Similar results have also been reported by Maruthi and Rani (2015) [13], Kinfe and Tsehaye (2015) [11] and Thakur *et al*., 2016. High estimates of heritability coupled with high estimates of genetic advance are the indicative of additive gene effects in the inheritance of above-mentioned traits. Therefore, selection will be rewarding for the improvement of these traits.

Table 1: Analysis of variance for different quantitative traits in maize

Source of variation	d.f.	Days to 50% tasseling	Days to 50% silking	Days to 75% dry husk	Plant height (cm)	Number of cobs/plant	Cob length (cm)	Cob diameter (cm)
Replication	2	2.082	1.403	4.727	10.014	0.003	0.898	0.887
Treatment	76	50.727**	49.319**	65.921**	1362.876**	0.130**	15.573**	3.437**
Error	152	2.780	2.091	3.153	3.799	0.001	0.287	0.293
Source of variation	d.f.	Cob weight (g)	Number of kernel rows/cob	Number of kernels/row	Number of kernels /cob	100-Kernel weight (g)	Shelling percentage (%)	Grain yield/plant (g)
Replication	2	2.501	0.263	0.726	9.205	0.697	3.638	2.824
Treatment	76	2965.804**	8.463**	124.560**	35182.710**	30.300**	123.575**	3030.838**
Error	152	1.326	0.112	0.239	3.058	0.233	3.156	4.339

*, ** significant at 5% and 1% level, respectively

Table 2: Estimates of GCV, PCV, heritability and genetic advance for different quantitative traits in maize

	Range Lowest	Range Highest	General Mean	GCV	PCV	h² (Broad Sense)	Ga 5%	Gen. Ad. As% of Mean (5%)
Days to 50% tasseling	**101.67**	**117**	**108.095**	**3.698 L**	**4.007 L**	**85.2 H**	**7.601**	**7.032 L**
Days to 50% silking	105	120.67	112.247	3.535 L	3.762 L	88.3 H	7.679	6.842 L
Days to 75% dry husk	134	157.33	144.675	3.162 L	3.392 L	86.9 H	8.784	6.072 L
Plant height (cm)	157.93	262.62	208.352	10.216 M	10.258 M	99.2 H	43.663	20.957 H
Number of cobs/ plant	1	1.78	1.123	18.443 M	18.706 M	97.2 H	0.421	37.46 H
Cob length (cm)	10.47	21.83	16.435	13.734 M	14.115 M	94.7 H	4.525	27.529 H
Cob diameter (cm)	9.53	14	11.683	8.764 L	9.912 L	78.2 H	1.865	15.96 M
Cob weight (g)	34.13	187.68	101.189	31.066 H	31.086 H	99.9 H	64.713	63.952 H
Number of kernel rows/ cob	10.88	18.73	14.126	11.811 M	12.046 M	96.1 H	3.37	23.856 H
Number of kernels /row	7.62	39.75	23.766	27.087 H	27.165 H	99.4 H	13.223	55.639 H
Number of Kernels/cob	106.83	625.7	336.972	32.136 H	32.14 H	100 H	223.047	66.191 H
100-Kernel weight (g)	16.74	30.99	23.259	13.611 M	13.768 M	97.7 H	6.447	27.718 H
Shelling percentage (%)	51.6	87.65	76.471	8.285 L	8.604 L	92.7 H	12.567	16.433 M
Grain yield/plant (g)	26.84	160.7	86.531	36.706 H	36.785 H	99.6 H	65.29	75.452 H

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