



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2020; 9(2): 1276-1278

Received: 13-01-2020

Accepted: 15-02-2020

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Genetic divergence for yield and yield contributing traits in yellow corn (Maize, *Zea mays* L.)

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Abstract

The experiment was conducted with twenty six maize genotypes collected in *Rabi* 2014 in randomized block design. Wide range of variability was present in the maize genotypes under study. The range of GCV and PCV was 6.49% to 58.04% and 10.20% to 66.31%, respectively. The estimates of phenotypic, genotypic and environmental variances revealed that phenotypic variances were higher in magnitude over the respective genotypic variances for all the characters under study. PCV and GCV were high for anthesis silking interval and grain yield per plant, respectively. The broad sense heritability ranged from 34.43% to 90.69%. The genetic advance and genetic advance as percent of mean was ranged from 3.50% to 93.96% and 8.50% to 104.63% respectively. Heritability along with genetic advance is more useful for selection than the heritability alone.

Keywords: Maize, genotypic variance, phenotypic variance, yield, randomized block design

Introduction

Maize (*Zea mays* L.; $2n = 20$) belongs to the family poaceae and is grown as a multipurpose crop in the world. It is considered as the queen of the cereal and is one of the most important cereal crops in the world next only to rice and wheat. The unique energy capturing capacity and efficient use of CO₂ as C₄ plant have made it capable of producing maximum grain yield per unit area when compared to all other cereal crops. At present, the yield level is much lower than the potential of our existing varieties. A main constraint to enhance maize productivity is the selection of unsuitable cultivars under a given set of environments. The adoption of hybrids was the most important task in the cultivation of maize. The first commercial sale of hybrid seed was initiated in 1984. Increased production per unit area is the prime objective in many maize breeding programs. Of these, grain yield is the most important and complex trait with which the maize breeders work. Maize displays an orderly sequence of development of yield components namely number of cobs /plant, number of kernel rows per cob and kernel weight (Viola *et al.* 2003) [13]. Genetic variability, which is a heritable difference among cultivars is required in an appreciable level within a population to facilitate and sustain an effective long term plant breeding programme. Progress from selection has been reported to be directly related to the magnitude of genetic variance in the population (Tabanao and Bernardo, 2005) [11]. Genetic variation is an important agronomic trait, especially about the earliness to sufficiently justify the initiation of the selection programme (Abayi *et al.*, 2004, Turi *et al.*, 2007 and Salami *et al.*, 2007) [1, 12, 10]. Breeders have developed thousands of hybrids of which one or more can flourish in almost any combination of soil and climate found in farming areas. The appropriate knowledge of interrelationship between grain yield and its contributing components can significantly improve the efficiency of breeding programs through the use of appropriate selection indices (Mohammadia *et al.*, 2003) [8]. One of the goal of this study was to confirm correlation between grain yield and yield attributing traits. The present study also aimed to determine the genetic variability of yield and yield contributing traits in different maize hybrids and to formulate the genotypic and phenotypic correlations among the important traits of maize hybrids.

Materials and Methods

The field experiment conducted at Oilseed Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, U.P. during *Rabi* season of year 2014. The experimental material for the present study consisted of 26 genotypes of yellow corn (maize) maintained in the gene bank of Research Centre of oilseed farm, Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur were used as base material.

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Twenty six varieties/genotypes were planted during *Rabi* season of 2014 in a complete Randomized Block Design with 3 replications at the oilseed research farm of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur. Each genotype was sown in two rows of 5.0 m long spaced at 60 cm apart. While plant to plant distance 20 cm. All the recommended package of practices were followed along with plant protection measure were taken into consideration during crop growth. Data were recorded with respect of eight traits which are given in table 1, viz., Days to 50% tasselling, Days to 50% silking, Anthesis silking interval, Ear length, Ear placement ratio, Plant height, 1000 kernel weight and Grain yield per plant for their analysis and interpretation to determine the correlation coefficient, path coefficient analysis, heritability, genetic advance and genetic divergence.

The variability was estimated as per procedure suggested by Fisher (1955) [9]. PCV and GCV were calculated by the given formula by Burton and De Vane (1953) [3], broad sense heritability (h^2_b) by Lush (1949) [7] and genetic advance *i.e.* the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955) [5]

Result And Discussion

The outcome of analysis of variance indicating that there is significance differences among the genotypes thus, genotypes were suitable for genetical studies (Table 1).

The highest phenotypic coefficient of variation (PCV) was observed for Anthesis silking interval (66.31) followed by Grain yield per plant (40.03), Ear length (29.43), 1000 kernel weight (23.04), Ear Placement Ratio (16.64), Plant height

(12.97), Days to 50% silking (10.75) and Days to 50% tasselling (10.20) respectively (Table 2). While, The maximum value of genotypic coefficient of variability (GCV) was observed for Anthesis silking interval (58.04), followed by Grain yield per plant (38.63), 1000 kernel weight (21.94), Ear length (19.35), Ear Placement Ratio (14.00), Plant height (7.61), Days to 50% silking (7.57) and Days to 50% tasselling (6.49) respectively. High GCV indicated high genetic variability within the test genotype.

The broad sense heritability ranged from 34.43% to 90.69% (Table 3). The maximum heritability value was observed for 1000 Kernel weight (90.69) and minimum heritability value was observed for Plant height (34.43). However all the characters under study showed high heritability *viz.*; Grain yield per plant (73.12), Anthesis silking interval (76.60), Ear placement ratio (70.79), Days to 50% silking (49.57), Ear length (43.23) and Days to 50% tasselling (40.67) respectively. Also, the highest value of genetic advance in percent of means were recorded for Anthesis silking interval (104.63) followed by Grain yield per plant (76.78), 1000 kernel weight (43.04), Ear length (26.20), Days to 50% silking (10.97), Ear placement ratio (10.97), Plant height (9.20) and lowest in Days to 50% tasselling (8.50). Similar finding of PCV, GCV, heritability and genetic advance have also been reported by Gupta and Salgotra (2005), Abriami *et al.* (2005) [2] and Kumar (2014) [6]. This is not possible to conclude the genetic progress of genotypes for selection based on heritability. High heritability with high genetic advance were taken into consideration. High heritability estimates with high genetic advance were notice for 1000 Kernel weight, Grain yield per plant and plant height.

Table 1: ANOVA for 8 characters in maize

Title	df	Days to 50% tasselling	Days to 50% silking	Anthesis silking interval	Ear length	Ear Placement ratio	Plant height	1000 Kernel weight	Grain Yield per plant
Replication	2	50.67	380.70	646.8	259.6	222.4	16.20	3287	216.50
Treatment	25	31.90**	924.00**	1575**	74.33**	53.41*	12.47**	7118**	647.00**
Error	50	3.828	28.38	44.69	18.83	17.58	1.152	235.6	15.55
Total	77	1.184	8.947	13.75	5.517	5.651	0.358	72.73	4.98

Table 2: Estimates of Coefficients of variability of 8 characters in Maize

Sr. No.	Characters	PCV	GCV	Difference
1	Days to 50% tasselling	10.20%	6.49%	3.71%
2	Days to 50% silking	10.75%	7.57%	3.18%
3	Anthesis silking interval	66.31%	58.04%	8.28%
4	Ear length	29.43%	19.35%	10.08%
5	Ear Placement ratio	16.64%	14.00%	2.64%
6	Plant height	12.97%	7.61%	5.36%
7	1000 Kernel weight	23.04%	21.94%	1.10%
8	Grain Yield per plant	40.03%	38.63%	1.40%

Table 3: Heritability, Genetic advance and Genetic advance in % over mean for 8 characters in Maize

Sr. No.	Characters	h^2 (Broad Sense) (%)	Genetic Advance	Genetic Advance as % of Mean
1	Days to 50% tasselling	40.46	4.5284	8.50
2	Days to 50% silking	49.57	6.2381	10.97
3	Anthesis silking interval	76.60	3.5012	104.63
4	Ear length	43.23	7.1206	26.20
5	Ear Placement ratio	70.79	0.1233	10.97
6	Plant height	34.43	9.6741	9.20
7	1000 Kernel weight	90.69	93.9593	43.04
8	Grain Yield per plant	73.12	28.8398	76.78

Conclusion

The experiment shows that yield is complex character and controlled by grain yield per plant and yield contributing characters. PCV as well as GCV can be use appropriate

selection procedure for improvement of yield and otheryield contributing characters in general since high heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive

gene action in their expression. High heritability with low genetic advance was indicated the presence of non-additive gene action. The heritability provide the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone.

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