

Assessment of Genetic Variability and Selection Parameter For Yield Contributing Traits In Maize (*Zea mays* L.)

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Abstract: In the present study, ten parents of maize were crossed in half diallel fashion to evaluate, 45 F₁s and 45 F₂s and ten parents for assessment of genetic variability and selection parameters in grain yield and related attributes during *Kharif* 2015 in Complete Randomized Block Design with three replication at C. S. Azad University of agriculture and Technology, Kanpur. Analysis of variance was recorded significant differences for all the traits revealing the genetic diversity among the maize genotype. The moderate PCV as well as GCV were observed for cob diameter (11.43 and 12.89 per cent) and cob length (12.61 and 13.50 per cent) in F₁ generation. The moderate PCV as well as GCV were observed for cob diameter (13.33 and 12.10 per cent) and cob length (12.55 and 13.65 per cent) in F₂ generation. High heritability estimates were observed for cob diameter in both generations. Moderate heritability estimates were found for days to 50% tasselling, days to 50% silking, physiological maturity, plant height (cm), cob length (cm), kernel rows per cob and kernels per row in both the generations. These results are in agreement which indicated the greater role of non-fixable genetic effect. Moderate heritability with moderate genetic advance was found for days to physiological maturity and plant height in both the generations

Key word: Genetic variability, GCV, PCV, Heritability and Genetic advance in maize

Date of Submission: 09-08-2018

Date of acceptance: 24-08-2018

I. INTRODUCTION

Maize (*Zea mays* L.; 2n=20) is the third most important crop in the world. Maize is a major source of starch, maize flour is ingredient in home cooking, corn oil, cornflakes, gluten and in many industrial food products. Maize starch can be hydrolyzed treated to produce syrups, particularly high-fructose corn syrup as a sweetener also fermented and distilled to produce grain alcohol. Grain alcohol from maize is traditionally the source of Bourbon whiskey and beer. The systematic breeding programme involves three important steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. Estimates of heritability and genetic advance will play an important role in exploitation of these steps. Heritability is a good index of the transmission of character from parents to their offspring (**Falconer, 1981**). The narrow sense heritability is estimated from additive genetic variances, which requires crossing in a definite fashion and becomes useful in selection of elite types from segregating populations.

Direct and indirect selection may be judged by their genetic gain. The effective improvement in the attributes would be based on the quantum of genetic advance. Hence, the estimate of heritability (h^2) is a parameter of high importance. Whereas genetic advance has no independent identify but it has added advantage over heritability as a guiding factor to the plant breeder during selection programme, where the character is to be improved through series of segregating generation. **Johnson et al. (1955)** reported that without genetic advance, the estimates of heritability would not be of practical importance based on phenotypic expression and emphasized the concurrent use of genetic advance along with heritability. **Hanson (1963)**, stated that heritability and genetic advance are two complementary concepts. According to **Kung (1977)**, genetic advance would be overestimated in either of the following situations (i) low selection proportion with high heritability (ii) high selection proportion with low heritability. Genetic gain would be under estimated, where both selection proportion and heritability are high or low.

II. MATERIAL AND METHOD

In the present study, ten parents of maize were crossed in half diallel fashion to evaluate, 45 F₁s and 45 F₂s and ten parents for assessment of genetic variability and selection parameters in grain yield and related attributes during *Kharif* 2015 in Complete Randomized Block Design with three replication at C. S. Azad University of agriculture and Technology, Kanpur. The breeding material used in this experiment comprised of

10 inbred lines viz. CIMMYT (K-13), TSK-44, TSK-27, TSK-29, TSK-109, TSK-110, TSK-10, TSK-79, TSK-99 and TSK-39. The observation were taken for days to 50% tasseling, days to 50% silking, physiological maturity, plant height (cm), cob length (cm), kernel rows per cob and kernels per row on five randomly selected competitive plant of each entry in each replication.

Analysis of variance was carried out to establish the level of significances among genotypes using the Panse and Sukhatme (1967) method.

The narrow sense heritability was estimated by the following formula. Thomas and Tapsell (1983)

$$h^2 n.s = \frac{\sigma^2 A}{\sigma^2 P}$$

Where

$h^2 n.s$ = Heritability in narrow sense

$\sigma^2 A$ = additive genetic variance

$\sigma^2 P$ = phenotypic variance (genetic and environment variance).

The genetic advance of the character was calculated according to the following formula:

$$\Delta G = h^2 n.s . \sigma P . K$$

Where:

ΔG = Genetic improvement

K = selection intensity 10% = 1.76

σP = standard deviation of phenotype

After that the expected genetic advance as percent (%) calculated according to the following equation

Where:

$$\Delta G = \frac{\Delta G}{y \dots} \times 100$$

$y \dots$ = Mean of concerned character

III. RESULT AND DISCUSSION

Analysis of variance indicated significant differences among the genotypes for all the traits evaluated (Table 1). It's indicated that experimental genotype had sufficient genetic variability for all the characters evaluated.

General mean range was varied from (4.52 to 197.66) in F_1 and (4.44 to 193.41) in F_2 generations (Table 2). In F_1 and F_2 generation general mean for days to 50% tasseling (57.57) and (61.35), days to 50% silking (63.81) and (68.49), physiological maturity (87.57) and (91.45), plant height (197.66) and (193.41), cob length (20.62) and (19.69), cob diameter (4.52) and (4.44), kernel rows per cob (12.91) and (12.11) and kernels per row (37.75) and (34.25).

In both F_1 and F_2 generations the estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters. The moderate PCV as well as GCV were observed for cob diameter (11.43 and 12.89 per cent) and (13.33 and 12.10 per cent) and cob length (12.61 and 13.50 per cent) and (12.55 and 13.65 per cent). While the low PCV as well as GCV were observed for remaining characters. The values for ECV were low for almost characters. **Sharma et al. (2014)**, **Kanagarasu et al. (2013)** also reported.

High heritability estimates were observed for cob diameter in both generations. Higher estimates of heritability for these traits were also reported by earlier workers, **Maruthi and Rani (2015)** ear girth indicating additive gene action for these traits.

Moderate heritability estimates were found for days to 50% tasseling, days to 50% silking, physiological maturity, plant height (cm), cob length (cm), kernel rows per cob and kernels per row in both the generations. This indicated the greater role of non-fixable genetic effect. Moderate heritability estimates were also reported by **Kanagarasu et al. (2013)** heritability indirectly indicates that selection may be effective for these traits, **Viola et al. (2003)** moderate heritability with low to medium genetic advance as percentage of mean was recorded for number of cob per plant, cob height, plant height and number of seed rows per cob.

The heritability estimates in F_2 generation were comparatively higher than F_1 for plant height and cob diameter. Selfed seeds of F_1 s could improve the yield contributing characters and further improvement may be expected in advanced generation by suitable selection.

The high heritability coupled with high genetic advance was not observed for any character in both the generations. Moderate heritability with moderate genetic advance was found for days to physiological maturity and plant height in both the generations, indicating that selection in later generations would not be much rewarding. Similar results were observed **Nayak et al. (2013)** showed moderate heritability with moderate genetic advance, **Satyanarayana et al. (2003)**, **Singh and Dash (2000)**.

Heritability was computed as per method suggested by **crumpacker** and **Allard (1962)** in F₁ and **verhalen and Murray (1969)** in F₂ generation. High heritability character was observed in cob diameter in both generations, whereas medium heritability were observed in characters like days to 50% tasseling, days to 50% silking, physiological maturity, plant height (cm), cob length (cm), kernel rows per cob and kernels per row.

In order to ascertain the relative merit of different attributes, genetic advance in percent of mean varied from both (11.58 to 24.27) in F₁ and (11.68 to 23.78) in F₂ generations. In both F₁ and F₂ generations characters like days to 50% tasseling, days to 50% silking, physiological maturity, plant height (cm), cob length (cm), cob diameter, kernel rows per cob and kernels/ row exhibited moderate value of genetic advance.

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Table 1: analysis of variance for eight characters of diallel crosses in maize

source of variation	d. f.	Days to 50% tasseling	Days to 50% silking	Days to physiological maturity	Plant height (cm)	Cob length (cm)	Cob diameter (cm)	Kernel row/cob	Kernel/row
Replication	2	0.11	0.77	0.24	18.97	0.09	0.02	0.20	0.90
Treatment	99	39.93**	59.11**	83.08**	723.28**	20.54**	0.77**	3.41**	16.48**
Error	198	1.40	1.40	1.32	24.48	1.06	0.05	0.73	1.47

Table 2: Grand mean, heritability (narrow sense) and genetic advance for 8 characters in maize

Source of variance	generations	Days to 50 (%) Tassling	Days to 50(%) Silking	Days to physiological Maturity	Plant Height (cm)	Cob Lenght (cm)	Cob Diameter (cm)	Karnel Rows/ Cob	Karnels/ Row
General Mean	F ₁	57.57	63.81	87.57	197.66	20.62	4.52	12.91	37.75
	F ₂	61.35	68.49	91.45	193.41	19.69	4.44	12.11	34.25
GCV	F ₁	5.97	6.57	7.01	7.74	12.61	11.43	8.47	5.92
	F ₂	6.00	6.53	6.56	8.16	12.55	11.33	7.80	7.17
PCV	F ₁	6.34	6.82	7.14	7.94	13.50	12.89	10.68	6.91
	F ₂	6.34	6.77	6.69	8.70	13.65	12.10	10.56	7.86
h ² (narrow Sense)	F ₁	26.43	17.01	16.45	13.26	22.11	40.12	29.59	21.02
	F ₂	23.63	15.05	14.84	15.80	15.94	49.46	11.75	14.31
Genetic Advancement 5%	F ₁	6.67	8.33	12.40	30.69	5.00	0.94	1.71	3.95
	F ₂	7.16	8.90	12.12	30.47	4.68	0.97	1.53	4.61
Gen.Adv as % of Mean 5%	F ₁	11.58	13.05	14.16	15.53	24.27	20.87	13.84	10.46
	F ₂	11.68	12.99	13.25	15.75	23.78	21.87	11.86	13.47

Vishwanath”, Assessment of Genetic Variability and Selection Parameter For Yield Contributing Traits In Maize (*Zea mays L.*)” *IOSR Journal of Pharmacy (IOSRPHR)*, vol. 8, no. 8, 2018, pp. 01-03.