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Dharmateja Palapartha

Department of Genetics and Plant Breeding, College of Agriculture, UAS, Dharwad, Karnataka, India

Mruthunjaya C Wali

Department of Genetics and Plant Breeding, College of Agriculture, UAS, Dharwad, Karnataka, India

Genetic variability and heritability for yield and its traits in diverse S₂ populations developed through reciprocal recurrent selection in maize (*Zea mays* L.)

Dharmateja Palapartha and Mruthunjaya C Wali

Abstract

The present study was carried out at College of Agriculture, University of Agricultural Sciences, Dharwad during *khariif*, 2017 to determine the various parameters of genetic variability, broad sense heritability and genetic advance estimates in newly developed S₂ progenies through reciprocal recurrent selection. Analysis of variance revealed that the mean sum of squares due to genotypes showed significant differences for all the 12 characters studied. High to moderate estimates of GCV and PCV were recorded for Grain yield, number of kernels per row, 100-grain weight, ear length and plant height which represents considerable variability and offers scope for genetic improvement through selection. High estimates of genetic advance coupled with high heritability was recorded for Grain yield, 100-grain weight, ear height and plant height which further leads to improvement of traits under selection. This provides better opportunities for selecting plant material for these traits in maize breeding program.

Keywords: Maize, broad sense heritability, PCV, GCV, genetic advance

Introduction

Maize is the third most important food crop of the world, after wheat and rice, providing 15% of the protein, and 19% of the calories for the developing countries (Shakoor *et al.* 2007) ^[15]. The grain yield is influenced by several genes which also interact with various environmental conditions. Thus, the yield has a multiplicative effect on the end product of many factors otherwise referred to as yield components (Zeeshan *et al.* 2013) ^[20]. These yield components are simply inherited with minimal environmental deviations, and hence selection based on them is more appropriate as opposed to the yield per se (Nagabhushan *et al.* 2011) ^[10]. The assessment of performance of parental lines based on the yield components could aid in the selection of superior parents for the production of better yielding hybrids. This can successfully be achieved if the genetic parameters which govern inheritance of important agronomic traits are established. In addition, the proper characterization of the physiological traits and their relationships with maize yield and yield components coupled with utilization of the revealed genetic variability could lead to improvement and broadening of the diversity of the maize gene pool (Al-Tabbal *et al.* 2012) ^[21]. The mean values, genotypic and phenotypic coefficient variances and heritability of agronomic traits are some of the key parameters which determine the efficiency of a breeding program. The phenotypic variance explicates the total variance among phenotypes tested in different environments of interest to the plant breeder while the total genotypic variance explains the portion of phenotypic variance attributable to the failure of homogeneity among genotypes in different environments (Sujiprihati *et al.* 2003) ^[17].

The heritability measures the value of selection for a particular trait in various types of progenies (Al-Tabbal *et al.* 2012; Lule *et al.* 2012) ^[2, 8]. The knowledge of heritability establishes appropriate selection methods coupled with the prediction of any gains from selection while also helping to establish the magnitude of the genetic effects. Larger genotypic variance is most preferred given that high heritability values can be obtained with genotypes with either small or large genetic progress. High heritability is associated with additive gene effect whereas low heritability is due to dominance and epistasis. The coefficient of variation shows the extent of variability represented by the different characters, but it excludes the heritable portion. This study aimed at understanding the genetic parameters which govern the inheritance of maize yield and other agronomic traits.

Correspondence

Dharmateja Palapartha

Department of Genetics and Plant Breeding, College of Agriculture, UAS, Dharwad, Karnataka, India

Materials and Methods

Plant Materials

The experimental material in the present study was generated by diallel crossing, using elite single cross hybrids. Based on the yield performance, superior selected lines are used to initiating reciprocal recurrent selection. First cycle of reciprocal recurrent selection is completed, during 2015. These S₁ lines are used to produce S₂ progenies. The experiment consisting of 48 S₂ progenies each from populations A and B with commercial checks CP-818, NK-6240, GH-0727 and an inbred tester CI-4 for evaluation of Variability were laid out by Augmented RCBD (Federer 1975).

Data on days to 50% tasseling (X₁), days to 50% silking (X₂), plant height (X₃), ear height (X₄), days to maturity (X₅), cob length (X₆), cob girth (X₇), number of kernel rows per cob (X₈), number kernels per cob (X₉), 100 grain weight (X₁₀), shelling percentage (X₁₁) and yield (q/ha) (X₁₂) were recorded.

Experimental site location

College of agriculture, Dharwad is located in Northern transition zone (Zone VIII) of Karnataka. Geographically, Dharwad lies between 15°26' N latitude and 70°26' E longitude and at an altitude of 678 m above mean sea level. The experiment were laid at College of Agriculture, University of Agricultural science, Dharwad during *khari* 2017.

Statistical analysis

Five plants were selected randomly and data on individual mean for each trait was subjected to statistical analysis. The data was analysed using INDOSTAT software Programme version 9.1). For the analysis of the data the following statistical methods were employed. Analysis of variance (ANOVA) for augmented design-II as per Federer (1975) was carried out for each character.

Coefficients of variability

Both genotypic and phenotypic coefficients of variability were computed as per the method suggested by Burton and Devane (1952).

a. Genotypic coefficient of variability (GCV)

$$GCV = \frac{sg^2}{X} \times 100$$

b. Phenotypic coefficient of variability (PCV)

$$PCV = \frac{sp^2}{X} \times 100$$

GCV and PCV values were categorized by Shivasubramanian and Menon (1973) as follows,

0-10%	: Low
10.1 -20%	: Moderate
20.1% and above	: High

Heritability (h²_{bs})

Heritability in broad sense was computed as the ratio of the total phenotypic variance to genotypic variance as suggested by Lush (1949) was expressed as percentage.

$$\text{Heritability (h}^2_{bs}) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability percentage was classified by Robinson *et al.* (1949) as follows,

0-30 per cent	: Low
30.1-60 per cent	: Moderate
60.1 per cent and above	: High

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{X} \times 100$$

Genetic advance as per cent mean was categorized by Johnson *et al.* (1955) as follows,

0-10 per cent	: Low
10.1-20 per cent	: Moderate
20.1 per cent and above	: High

Results and discussion

Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied. Partitioning the variance and co-variance into genotypic, phenotypic and environmental components. The results obtained from analysis of variance for all entries, including checks for 12 characters revealed that the treatment variances were highly significant for all the characters. This indicates the presence of substantial variability among the S₂ progenies (Table 1 & 2).

Table 1: Analysis of variance for twelve quantitative characters in S₂ progenies of pop A

Source of variation	D.F	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂
Block (Eliminating Check + Var.)	5	5.941	4.291	49.081	31.1	17.009	0.721	0.025	0.645	4.031	4.556	2.898	0.659
Entries (Ignoring Blocks)	51	74.3 **	83.2**	530.8**	237.5**	65.5**	8.7**	0.31**	6.1**	47.5 **	43.8**	28.21**	7.31**
Checks	3	91.58**	106.13**	1703**	388 **	700.73**	23.9**	0.72**	2.926 *	53.56 *	53.18**	170.31**	29.63**
Varieties	47	10.08 *	12.7 **	455 **	229.9*	25.06 *	3.13 **	0.16 **	4.11**	28.8*	39.8**	19.38**	0.992 **
Checks vs. Varieties	1	3043.3**	3325**	570.9**	147.2*	65.3 *	227.2**	6.40 **	109.2 **	909**	201.6**	16.9 *	237.6 **
ERROR	15	3.425	2.764	65.635	31.345	11.033	0.953	0.034	0.768	12.409	5.656	3.288	0.301

*- significant at 5% level, **-significant at 1% level, days to 50% tasseling (X₁), days to 50% silking (X₂), plant height (X₃), ear height (X₄), days to maturity (X₅), cob length (X₆), cob girth (X₇), number of kernel rows per cob (X₈), number kernels per cob (X₉), 100 grain weight (X₁₀), shelling percentage (X₁₁) and yield (q/ha) (X₁₂) were recorded.

Table 2: Analysis of variance for twelve quantitative characters in S₂ progenies of pop B

Characters	D.F	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂
Block (eliminating Check+Var.)	5	5.941	4.29	49.081	15.275	9.599	0.721	0.025	0.645	4.031	4.555	3.64	0.659
Entries (ignoring Blocks)	51	84.6 **	77.4**	643**	334.7**	64.0**	7.0**	0.34**	4.46**	48.26**	46.3**	29.02**	7.3**
Checks	3	91.5**	106.1**	1703**	2405**	609.6**	23.9**	0.72**	2.92 *	53.05 *	53.18**	245.9**	29.63**
Varieties	47	22.0**	8.16*	571.6**	197.8**	29.0 *	2.96 *	0.17**	3.12 **	37.38 *	43.31 **	15.27**	0.74*
Checks vs. Varieties	1	3006**	3249**	812**	558.5**	69.44*	148.8**	6.83**	71.9**	545.6**	168.7**	24.6**	248.9**
ERROR	15	3.425	2.764	65.635	15.72	12.684	0.953	0.034	0.768	12.409	5.657	2.501	0.301

*- significant at 5% level, **-significant at 1% level, days to 50% tasseling (X₁), days to 50% silking (X₂), plant height (X₃), ear height (X₄), days to maturity (X₅), cob length (X₆), cob girth (X₇), number of kernel rows per cob (X₈), number kernels per cob (X₉), 100 grain weight (X₁₀), shelling percentage (X₁₁) and yield (q/ha) (X₁₂) were recorded

High PCV and GCV recorded for 100 grain weight (21.6 and 19.4%), yield (27.61 and 21.7%) in both the populations A and B respectively. In population B, high PCV and GCV observed for 100 grain weight (22.2 and 20.1%) and yield (25.02 and 17.9%). Moderate PCV and GCV for plant height, ear height, cob length, number of kernel rows per cob, number kernels per cob were recorded in both the populations A and B (Table 3 & 4), Suggesting sufficient variability existing among populations and offers scope for selection. Similar results of PCV and GCV values for grain yield and other traits were reported by Zahid Mahmood *et al.* (2004)^[19] Abirami *et al.* (2005)^[1] and Patil *et al.* (2016)^[12]. Traits like days to 50 per cent tasseling, silking, ear height, plant height and shelling percentage exhibited low PCV and GCV in pop A as well as B.

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Heritability was found to be high for grain yield (62%), 100-kernel weight (81%), number of kernel rows per ear (75%), cob girth (72%), days to 50 per cent silking (72%), cob length

(62%), ear height (81%), shelling percentage (77%) and plant height (79.11%). Moderate heritability for number of kernels per row (48%), days to 50 per cent tasseling (58%) and days to maturity (59%) observed for these traits in pop A. With respect to pop B high heritability exhibited by 100-kernel weight (82%), number of kernel rows per ear (75%), cob girth (72%), days to 50 per cent tasseling (58%), cob length (60%), ear height (88%), shelling percentage (78%) and plant height (84%). Moderate heritability for number of kernels per row (58%), days to maturity (57%), days to 50 per cent silking (59%) and grain yield (51%). High values of heritability in broad sense indicate characters are less influenced by environmental effects. Similar results were reported by Satyanarayan and Kumar (1995)^[14] and Ojo *et al.* (2006)^[11].

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about genetic advance coupled with heritability is most useful. Character exhibiting high heritability may not necessarily give high genetic advance. High heritability should be accompanied with high genetic advance to arrive more reliable conclusion. Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method. High genetic advance were observed for grain yield, plant height, ear height, number of kernels per row, 100-kernel weight, cob length, cob girth and number of kernel rows per ear. Moderate and low estimates of genetic advance were observed for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity and shelling percentage in both the populations A and B were observed (Table 3&4).

Table 3: Estimates of variability, heritability and genetic advance as per cent of mean for grain yield components in S₂ progenies of pop-A

Characters	Mean	Range	PCV%	GCV%	h ² (bs)	GAM
Days to 50% tasseling	59.79	54-71	4.77	3.64	58	5.7
Days to 50% silking	60.92	56-74	5.16	4.38	72	7.6
Plant height (cm)	146.6	95-185	12.63	11.35	80	21.04
Ear height (cm)	72.47	48-111	18.13	16.4	81	30.58
Brown husk maturity	98.0	96-108	4.56	3.14	59	8.8
Cob length (cm)	12.93	8.5-16.7	12.25	9.65	62	15.06
Cob girth (cm)	3.65	2.88-4.56	9.67	8.24	72	14.14
Number of kernel rows /cob	12.54	8.4-16.4	14.15	12.31	75	22
Number of kernels/ row	25.51	15-37.4	19.24	13.4	48	19.2
100 grain weight	25.35	12.5-38.0	21.6	19.4	81	36.13
Shelling percentage (%)	82.00	68.8-88.1	4.6	4.12	77	7.49
Grain yield (q/ha)	3.22	1.08-5.04	27.61	21.7	62	35.2

GCV = Genotypic Coefficient of variation, h² (bs) = Heritability (Broad Sense)

PCV = Genotypic Coefficient of variation, GA= Genetic advance and

GAM (%) = Genetic advance as percent of mean

Table 4: Estimates of variability, heritability and genetic advance as per cent of mean for grain yield components in S₂ progenies of pop-B

Characters	Mean	Range	PCV%	GCV%	h ² (bs)	GAM
Days to 50% tasseling	60.8	46- 70	6.89	6	79	11.6
Days to 50% silking	61.08	48- 72	4.2	3.2	59	5.04
Plant height (cm)	145.4	101- 187	14.1	13	84	24.7
Ear height (cm)	71.71	45- 102	16.8	15.8	88	30.8
Brown husk maturity	95.2	92- 108	4.8	3.3	57	6.01
Cob length (cm)	13.64	9.9- 17.4	11.3	8.7	60	14
Cob girth (cm)	3.62	2.82-4.62	10.15	8.7	74	15.6
Number of kernel rows /cob	13.03	9.2- 16.4	11.9	9.93	69	16.9
Number of kernels/ row	27.20	14.8-42.2	20.19	15.5	58	24.5
100 grain weight	25.65	13.5- 40	22.2	20.1	82	37.7
Shelling percentage (%)	81.91	69.3-88.5	4.15	3.6	78	6.7
Grain yield (q/ha)	3.134	1.6- 3.13	25.02	17.9	51	26.3

GCV = Genotypic Coefficient of variation, h² (bs) = Heritability (Broad Sense)

PCV = Genotypic Coefficient of variation, GA= Genetic advance and

GAM (%) = Genetic advance as percent of mean

Characters like grain yield, plant height, ear height, number of kernels per row, 100-kernel weight exhibited moderate to high heritability along with high GCV and Genetic advance indicating additive gene action and provides scope for improvement of traits through selection. Similar results were reported by Zahid Mahmood *et al* (2004) [19], Thanga Hemavathy *et al* (2008) [18], Jawaharlal *et al* (2011) [6] and Anshuman *et al* (2013) [3].

Conclusion

High estimates of PCV and GCV, heritability coupled with genetic advance were recorded for grain yield and 100-grain weight, which provides considerable variability and offers scope for genetic improvement through selection. Thus provides better opportunities for selecting plant material for these traits in maize breeding program. Further high heritability coupled with genetic advance were observed for ear length and plant height indicating careful selection leads to improvement of traits.

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