Estimation of Components of Genetic Variance in Maize (*Zea mays* L.)

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Abstract

An investigation was undertaken to estimate the components of genetic variance in the biparental progenies (BIP F_3 progenies) of two F_2 populations of maize derived from crosses HKI-26-2-4-(1-2) × CML 358 (C-I) contrasting for ASI and CML 41 × CM 500 (C-II) contrasting for grain yield. Higher magnitude of additive genetic variance than dominance genetic variance was noticed in BIP F_3 progenies for plant height, cob length and 100 grain weight in both the crosses, indicating effectiveness of simple selection for improving these traits in desired direction. However, dominance genetic variance was higher than additive genetic variance for cob circumference kernel rows cob^{-1} and kernels row^{-1} in both the crosses indicating the improvement of these traits through heterosis breeding. Further, prevalence of over dominance was noticed for grain yield plant^{-1} and cob shelling per cent in C-I and for the traits such as days to anthesis, days to silking and ASI in C-II.

Maize (*Zea may* L.; 2n= 20) the sole cultivated member of the genus *Zea* and tribe Maydeae is a versatile crop and is cultivated at all the altitudes and fertility conditions, making it a remarkable cereal crop having global importance (FAO, 2012). Maize ranks third in the world after rice and wheat among cereals and provides about 30 per cent of the food calories for more than 4.5 billion people in 94 developing countries (Thomas, 2012).

Estimates of additive and dominance genetic variance help to choose the most effective breeding procedure for the improvement of a crop species. In the present investigation genetic analysis of a random mating heterozygous maize population was undertaken to estimate the components of genetic variance and to study its genetic architecture using North Carolina Design-I to derive information on relative magnitude of additive and dominance variance and dominance ratio.

Material and Methods

The basic material for the experiment comprised of two F_2 populations derived from crosses involving parents HKI-26-2-4-(1-2) and CML 358 (designated as C-I) contrasting for Anthesis-silking interval (ASI) and from the parents CML 41 and CM 500 contrasting for grain yield (designated as C-II).

Experimental material (biparental progenies): Each F_2 population was raised to develop biparental progenies during summer 2013 at the experimental site of K-Block, Department of the Genetics and Plant Breeding (GPB), University of Agricultural Sciences (UAS), Gandhi Krishi Vignana Kendra (GKVK), Bengaluru. From each of the F_2 population of both the crosses (C-I and C-II), eight plants were selected randomly and were designated as male parents. Each male parent was crossed to three different randomly selected plants designated as female parent. A female plant crossed with a given male plant was not involved in the mating with any another male parent. A group of progenies having one male parent in common was called as a male group. In all there were eight such male groups generated. These eight male groups were further divided into two sets each with four male groups. Thus, in all 24 (8×3) progeny families (here after designated as BIP F_3 progenies) were developed. Simultaneously, the plants designated as males were selfed to generate the F_3 progenies.

Evaluation of experimental material : Seeds of 24 BIP F_3 and eight F_3 progenies were sown in randomized complete block design with two replications at the experimental plots of the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Gandhi Krishi Vignana Kendra, Bengaluru, during 2013 *kharif* season. Each

of the BIP F_3 and F_3 progeny was grown in three rows each of 3 m length with row spacing of 0.60 m and 0.3 m between plants within a row.

Data collection :   Observations were recorded on 20 competitive random plants (avoiding border plants) for 11 quantitative characters on each of the 24 BIP F_3 progenies and F_3 progenies.

Statistical Analysis : Statistical analysis was carried out to estimate the components of genetic variance in BIP F_3 progenies of maize for 11 quantitative characters as per Comstock and Robinson (1952). A separate ANOVA was performed to partition the total variation in F3 progenies into sources attributable to 'between' and 'within F3 progeny' variances as per Van Ooijen (1989).

Analysis of variance :   Analysis of variance of BIP F_3 progenies revealed highly significant mean sum of squares due to sets for all the characters except for cob length, cob circumference, grain yield plant^{-1} and cob shelling per cent in C-I (Table I) and except for kernel rows cob^{-1} and cob shelling per cent in C-II

(Table II). A highly significant mean sum of squares due to males in sets and females in males in sets were observed for days to silking, ASI, plant height, cob circumference, kernel rows cob^{-1}, kernel rows and 100 grain weight in the cross in C-I (Table I) and for ASI, plant height, cob length, kernel rows cob^{-1}, kernel rows and grain yield plant^{-1} in C-II (Table II) indicating substantial contribution of males and females towards variability for most of the traits.

Higher magnitudes of mean sum of squares due to males in sets than those due to females in males in sets indicated the predominant contribution of males (Comstock and Robinson, 1952). Significant variability in BIP F_3 progenies adequately provide statistical and genetic validity for comparative assessment of BIP F_3 progenies and F_3 progenies for the traits investigated in the present study. Non significance of mean sum of squares due to males in sets and females in males in sets in both the crosses suggested lack of evidence for influenciable effect of edaphic factor and / or micro environment associated with the expression of the traits.

TABLE I

Analysis of variance of BIP F_3 progenies derived from the cross C-I involving the parents contrasting for ASI in maize

Source of variation	df	Mean Sum of Squares										
		Days to anthesis	Days to silking	ASI (days)	Plant height (cm)	Cob length (cm)	Cob circumference (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100 grain weight (g)	Grain yield plant^{-1} (g)	Cob shelling per cent
Sets	1	15.41**	21.47**	2.95**	413.89**	0.69	0.03	1.08**	28.14**	6.49**	499.55	2.83
Replication in sets	2	0.84	0.05	0.16	4.72	0.75	0.13	0.02	0.65	0.03	360.46	0.05
Males in sets	6	2.65	4.24**	1.21**	254.21**	2.17	0.30**	0.79**	7.33**	4.06**	376.81	4.61
Females in males in sets	16	1.33	1.97**	0.54**	81.96**	1.20	0.20**	0.47**	3.47**	1.42**	175.38	2.51
Error	22	1.05	0.63	0.11	15.06	0.96	0.06	0.01	0.23	0.13	201.40	2.61

* Significant @ P=0.05;   ** Significant @ P=0.01

C-I: HK1-26-2-4-(1-2) × CML 358

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Analysis of variance of BIP F₃ progenies derived from the cross C-I involving the parents contrasting for grain yield in maize

Source of variation	df	Mean Sum of Squares										
		Days to anthesis	Days to silking	ASI (days)	Plant height (cm)	Cob length (cm)	Cob circumference (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100 grain weight (g)	Grain yield plant^{-1} (g)	Cob shelling per cent
Sets	1	8.88**	13.81**	6.02**	222.96**	0.36	1.44**	1.49	4.50**	0.41**	482.03**	3.48
Replication in sets	2	4.48*	5.95	0.26**	1.83	0.01	0.05	0.25	0.02	0.14	92.79	3.62
Males in sets	6	2.42	2.72	0.72**	174.25**	2.93**	0.42*	2.68**	21.24**	0.29**	552.27**	10.41
Females in males in sets	16	1.63	2.00	0.35**	53.75**	1.05**	0.30	2.02**	8.80**	0.11	158.84**	6.55
Error	22	0.96	2.34	0.04	2.12	0.01	0.15	0.37	0.01	0.07	46.44	5.02

* Significant @ P=0.05;   ** Significant @ P=0.01

C-I: (HK1-26-2-4-(1-2) × CML 358)

Analysis of variance of F₃ progenies revealed highly significant mean sum of squares due to 'between F₃ progenies' for all the traits except cob circumference in C-I (Table III). A significant mean sum of squares due to 'between F₃ progenies' were documented for all the traits except for days to anthesis, ASI and cob length in C-II (Table IV) indicating adequate variation in F₃ progenies.

Components of genotypic variance : Higher magnitude of additive genetic variance than dominance genetic variance was noticed for traits such as plant height, cob length and 100 grain weight in BIP F3 progenies in both the crosses (Table V). However, the magnitude of dominance genetic variance was noticed to be higher than additive genetic variance for cob circumference, kernel rows cob^{-1} and kernels row^{-1} in both the crosses. The magnitude of additive genetic variance was higher for days to anthesis, days to silking and ASI in the C-I and the magnitude of dominance genetic variance was higher for days to anthesis and days to silking in the C-II. Higher dominance genetic variance in C-I and high additive genetic variance in C-II was documented for grain yield plant^{-1} and cob shelling per cent, respectively. Over dominance

appeared to be controlling the inheritance of cob circumference, kernel rows cob^{-1} and kernels row^{-1} in both the crosses. For the traits such as grain yield plant^{-1} and cob shelling per cent in C-I and for the traits such as days to anthesis, days to silking and ASI in C-II, the over dominance prevailed. For the remaining traits, preponderance of partial dominance was detected in both the crosses.

The F₂ population is expected to be in linkage disequilibrium (LD) which cause biases in the estimates of genotypic variance. The estimates of dominance variances are biased upward and additive variances are biased upward or downward in the presence of coupling or repulsion phase linkages, respectively (Comstock and Robinson, 1952). In the present study, BIP F₃ progenies of both the crosses manifested greater magnitudes of additive genetic variance than dominance genetic variance in the inheritance of traits such as plant height, cob length and 100 grain weight. Further, higher magnitudes of additive genetic variance for days to anthesis, days to silking and ASI in the C-I and for cob shelling per cent in C-II indicated effectiveness of simple selection for improving these traits in desired direction (Narendra Kumar *et al.*,

TABLE III

Analysis of variance of F₃ progenies derived from the cross C-I involving the parents contrasting for ASI in maize

Source of variation	df	Mean Sum of Squares										
		Days to anthesis	Days to silking	ASI (days)	Plant height (cm)	Cob length (cm)	Cob circumference (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100 grain weight (g)	Grain yield plant^{-1} (g)	Cob shelling per cent
Between F₃ families	14	3.59**	8.56**	2.48**	523.22**	1.58**	2.10	2.01&&	18.01**	14.39**	179.35**	19.40**
Within F₃	14	1.17	1.23	0.03	63.24	0.25	1.74	0.13	2.21	0.38	16.84	2.13

* Significant @ P=0.05; ** Significant @ P=0.01

C-I: (HK1-26-2-4-(1-2) × CML 358)

TABLE IV

Analysis of variance of F₃ progenies derived from the cross C-II involving the parents contrasting for grain yield in maize

Source of variation	df	Mean Sum of Squares										
		Days to anthesis	Days to silking	ASI (days)	Plant height (cm)	Cob length (cm)	Cob circumference (cm)	Kernel rows cob^{-1}	Kernels row^{-1}	100 grain weight (g)	Grain yield plant^{-1} (g)	Cob shelling per cent
Between F₃ families	14	1.53	4.37**	1.96	501.65**	0.46	0.62***	0.67**	4.54**	5.75**	232.34**	20.55**
Within F₃	14	1.04	0.84	1.13	120.61	0.23	0.07	0.16	0.94	0.23	9.91	2.11

* Significant @ P=0.05; ** Significant @ P=0.01

C-II: (CML41× CM500)

TABLE V

Estimates of components of genotypic variance in BIP F₃ progenies derived from two crosses (C-I and C-II) involving parents contrasting for ASI and grain yield, respectively, in maize

Traits	σ^2_A		σ^2_D		σ^2_D / σ^2_A	
	C-I	C-II	C-I	C-II	C-I	C-II
Days to anthesis	0.88	0.53	0.32	0.81	0.36	1.55
Days to silking	1.51	0.48	1.15	1.16	0.76	2.40
ASI (days)	0.45	0.24	0.40	0.37	0.89	1.53
Plant height (cm)	114.83	80.33	18.97	22.94	0.17	0.29
Cob length (cm)	0.76	1.25	0.63	0.85	0.83	0.68
Cob circumference (cm)	0.07	0.08	0.21	0.22	3.05	2.74
Kernel rows cob^{-1}	0.22	0.44	0.70	2.86	3.23	6.52
Kernels row^{-1}	2.57	8.29	3.90	9.29	1.51	1.12
100 grain weight (g)	1.76	0.12	0.82	0.03	0.47	0.22
Grain yield plant^{-1} (g)	134.28	262.29	186.32	37.48	1.39	0.14
Cob shelling per cent	1.40	2.58	1.60	0.47	1.14	0.18

C-I : (HKI-26-2-4-(1-2) × CML 358) involving parents contrasting for ASI
C-II : (CML 41 × CM 500) involving parents contrasting for grain yield

2013). Dominance genetic variance was predominant for cob circumference, kernel rows cob^{-1} and kernels row^{-1} in both the crosses. Days to anthesis, days to silking and ASI in the C-II and grain yield plant^{-1} in C-I were noticeably under higher dominance genetic variance. These traits being the most important yield contributing traits they could be improved through heterosis breeding.

Studies on different maize population by Zdunic *et al.* (2008) and Khodarahmpour (2011) have also reported the preponderance of dominance genetic variance in the inheritance of several traits in maize. Prevalence of over dominance for cob circumference, kernel rows cob^{-1}, kernels row^{-1} in both the crosses was noticed. Prevalence of over-dominance was noticed for the traits such as grain yield plant^{-1} and cob shelling per cent in C-I and for days to anthesis, days to silking and ASI in C-II. For the remaining traits, preponderance of partial dominance was detected in both the crosses. Similar reports were reported in maize by Irshad-Ul-Haq *et al.* (2010) and Narendra Kumar *et al.* (2013).

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