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Genetic components analysis in maize (*Zea mays* L.)

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Abstract

The result of Analysis of variance revealed highly significant difference among treatments as well as its components for almost all the traits. In most of the traits the magnitude of dominance component was higher than additive component. The observed estimate of average degree of dominance indicated presence of over dominance for all the traits.

Keywords: degree of dominance, maize and over dominance

1. Introduction

Maize (*Zea mays* L.) is third most important cereal crop of the world after wheat and rice. It belongs to grass family and important to human being because of their role as staple food in many areas of the world. It is also used to produce animal feed, oils, starch, flour, sugar, syrup, processed foods, malt, alcoholic beverages and renewable energy. Approximately 50% of the world's calories are provided by rice, wheat and maize, but in many parts of Africa and Asia, people really depends on grains such as sorghum or millet. Maize, is also utilized in USA in brewing industry and ethanol production. Maize (*Zea mays* L.) is also called "The queen of cereals" which includes eight genera, five of these (*Coix*, *Schlerachne*, *Polytoca*, *Chinonachne* and *Trilobachene*) are relatively unimportant while the three as important American genera are: *Zea*, *Tripsacum* and *Euchalaena* (Teosinte). Five species of genus *Zea* viz, *maxicana*, *perennis*, *luxuriant*, *diploperenis* and *mays*. First four species are wild and commonly called Teosinite and the last species *Zea mays* is only cultivated. The diploid chromosome number of maize is 20. The wild species *Z. perennis* is tetraploid ($4n=40$) rest are diploid. On the basis of kernel characteristics maize are classified in different groups (Kipps-1959) viz., *Z. mays everta* (popcorn), *Z. mays saccharata* (sweet corn), *Z. mays amyloacea* (soft corn), *Z. mays tunicata* (pod corn) and *Z. mays cerantinakulesh* (waxy corn).

2. Materials & Methods

The present experiment was carried out at Oilseed Research Farm, Kalyanpur of C.S.A. University of Agriculture and Technology, Kanpur during Rabi 2013-14. Experimental material consisting 45 genotypes (9 parents namely; CIM 78, KURARA, TSK 109, TSK 36, TSK 92, TSK 27, HK1-193-1, TSK 10 and NEW BLUE II and their possible 36 F_1 s crosses, were developed by using diallel mating design excluding reciprocal) were evaluated in three replication using Randomized Block Design (RBD) Each parent and cross was planted in 5m single row length spaced at 60 x 25 cm between rows and plants, respectively. All the recommended package of practices were adopted according to the recommended by agronomical practices. The observations are recorded for 13 traits namely; Days to 50% tasseling, Days to 50% silking, Days to 75% dry husk, Plant height, Cob height, No. of cobs/plant, No. of grain rows/cob, No. of grains/row, Cob weight, 100 grain weight, Grain yield/cob, Grain yield/plant and shelling percentage. The components of variance in diallel cross were computed by the use of equation given by Hayman (1954, a).

3. Results & Discussion

The analysis of variance was carried out for all the 13 characters to test the significance of differences among the treatments means and its components, the results are presented in Table-1. Highly significant differences among the treatments involving parents and F_1 s for all the characters. Interaction between as a group of parents and hybrids also revealed highly significant difference for all traits except number of cobs per plant indicating heterotic effects in the hybrids with differential magnitude. Similar findings were also observed by Gul *et al.*

Geetha *et al.* (2001) [5], Haddadi Appunu *et al.* (2006) [6], Patel *et al.* (2010) [9], Asif *et al.* (2010) [2], Bharathiveeramani

et al. (2012) [3], *et al.* (2012), Nayak *et al.* (2013) [8], Quarban *et al.* (2013) and Rajesh *et al.* (2014) [11].

Table 1: ANOVA for Parents and F₁ of 13 characters in 9- parents- diallel- cross of maize (*Zea mays* L.): mean sum of square.

Source of Variation	d.f	Days to 50% tasseling	Days to 50% silking	Days to 75% dry husk	Plant height (cm)	Cob height (cm)	No. of cobs/ plant	No. of grain rows/ cob
Replication	2	0.051	0.14	0.27	0.118	1.918*	0.0025	0.13
Treatments	44	11.73**	11.26**	57.10**	196.88**	76.09**	0.022**	2.09**
Parents	8	10.81**	10.41**	23.70**	247.00**	19.25**	0.0102**	0.64**
F ₁ s	35	6.01**	6.85**	46.94**	190.04**	89.14**	0.026**	1.97**
Parents Vs F ₁ s	1	219.14**	172.26**	680.06**	35.26**	74.07**	0.0032	18.05**
Error	88	0.30	0.39	0.44	0.61	0.50	0.0031	0.160

Table 1: Continue.....

Source of Variation	d.f	No. Of grains/ row	Cob weight at 15% moisture(gm)	100 grain weight (gm)	Grain yield/ cob(gm)	Grain yield/ plant (gm)	Shelling percentage
Replication	2	0.433	21.792	0.69*	2.406	0.268	0.046
Treatments	44	31.627**	761.648**	14.50**	537.85**	658.20**	3.30**
Parents	8	11.655**	480.52**	19.96**	271.34**	525.43**	6.303**
F ₁ s	35	7.29**	412.44**	13.45**	297.79**	359.67**	2.53**
Parents Vs F ₁ s	1	1043.11**	15232.79**	7.63**	11072.13**	12168.64**	6.30*
Error	88	0.309	8.107	0.185	2.28	2.40	0.911

*Significant at 5% level, **significant at 1% level

Analysis of genetic components of variance was carried out for all the 13 characters based on F₁ generation (Table-2). Regression coefficient ‘b’ deviated significantly from zero and unity for no. of grains/ row indicates presence of non-allelic gene interaction (epistasis) while the regression coefficient deviate significantly from zero and unity was found with differential significance for remaining trait, which indicated that validity of the hypothesis. The value of ‘t²’ were observed highly significantly for cob weight and number of grains per row which indicated that allelic interaction in the expression of these traits. The estimates of all genetic components viz, \hat{D} , \hat{H}_1 , \hat{H}_2 , \hat{E} , \hat{F} and \hat{h}^2 along with their standard error were calculated. These estimates are presented in Table-3. The estimate of additive component (\hat{D}) was significant for days to 50 % tasseling, days to 50% silking, plant height, cob weight, 100 grain weight, grain yield per cob, grain yield per plant and shelling percentage. The estimate value of dominant component (\hat{H}_1) and (\hat{H}_2) were highly significant for all the traits. The relative magnitude of component \hat{H}_2 was lower than component \hat{H}_1 for all the traits. The values of \hat{F} were positive and highly significant for days to 50% tasseling and significant for days to 50% silking, 100 grain weight and shelling percentage. It indicated the excess of dominant genes for controlling these characters. The negative and non-significant value of \hat{F} were observed for number of grain rows per cob, which indicated that recessive alleles for the expression of these traits. The estimate of \hat{h}^2 were positive and significant for days to 50% tasseling, days to 50% silking, days to 75 % dry husk, cob weight, no. of grain rows per cob, no. of grains per row, grain

yield per cob and grain yield per plant, exhibits the mean direction of dominance in F₁ generation. The value of \hat{E} component was significant for shelling percentage only showing environmental influence in the expression of this trait. The estimate of mean degree of dominance (\hat{H}_1/\hat{D})^{0.5} were more than unity for all the traits, which indicated that over dominance for these traits. The proportion of genes with positive and negative effects ($\hat{H}_2/2\hat{H}_1$) was lesser than theoretical value (0.25) for all the traits which indicated that positive and negative genes to be asymmetrically distributed among the parents for these attributes. The ratio of dominant and recessive alleles i.e., $(4\hat{D}/\hat{H}_1)^{0.5} + \hat{F}/(4\hat{D}/\hat{H}_1)^{0.5} - \hat{F}$ were more than one for all traits except no. of grain rows per cob which revealed that dominant genes were more frequent than recessive genes in these traits. While no. of grain rows/ cob exhibited nearly equal distribution (0.98) of dominant and recessive alleles in the parents. The ratio (\hat{h}^2/\hat{H}_2) which measures the number of major gene group showing the value less than unity for plant height, cob height, number of cobs/ plant, 100 grain weight and shelling percentage reflecting involvement of one major gene group in inheritance of these characters. The coefficient of correlation (r) between parental order of dominance and parental measurement was found negative for days to 75 % dry husk, and cob height, while it was positive for all the other traits. Similar findings were also observed by Gul *et al.* (2000) [5], Geetha *et al.* (2001), Haddadi Appunu *et al.* (2006) [6], Patel *et al.* (2010) [9], Asif *et al.* (2010) [2], Bharathiveeramani *et al.* (2012) [3], *et al.* (2012), Nayak *et al.* (2013) [8], Quarban *et al.* (2013) and Rajesh *et al.* (2014) [11].

Table 2: Uniformity test by regression coefficient and t² for 13 traits in 9X 9 parents diallel crosses in maize.

S. No.	Characters	b	SE(b)	b-0/SE(b)	b-1/SE(b)	t ²
1	Days to 50% tasseling	0.693	0.207	3.347*	1.48	0.285
2	Days to 50% silking	0.473	0.287	1.648	1.83	0.120
3	Days to 75% dry husk	-0.235	0.295	-0.796	4.18**	0.322
4	Plant height	0.105	0.395	0.265	2.26	0.017
5	Cob height	-0.146	0.118	-1.23	9.71**	13.90**
6	No. of Cobs/plant	0.119	0.200	0.595	4.40**	3.095

7	Cob weight at 15% moisture (gm)	0.398	0.247	1.61	2.43*	0.712
8	No. of grain rows/ cob	0.105	0.203	0.517	4.40**	2.977
9	No. of grains/ row	0.315	0.101	3.11*	3.37*	16.97**
10	100 grain weight (gm)	0.171	0.395	0.432	2.09	0.023
11	Grain yield/ cob (gm)	0.46	0.25	1.84	2.16	0.38
12	grain yield/ plant(gm)	0.015	0.493	0.030	1.99	0.509
13	Shelling percentage (%)	0.676	0.259	2.610*	1.25	0.021

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

Table 3: Estimates of genetic components and related parameters of breeding value for 13 characters in 9X 9 diallel cross in maize.

S. No.	Characters	\hat{D}	\hat{H}_1	\hat{H}_2	\hat{F}	\hat{h}^2	\hat{E}	$(\hat{h}_1/D)^{1/2}$	$(H_2/4H_1)$	$\sqrt{(4DH_1) + F} / \sqrt{(4DH_1) - F}$	\hat{h}^2 / \hat{H}_2	R
1	Days to 50% Tasseling	3.50**	17.58**	12.71**	7.89**	32.02**	0.10	2.24	0.18	3.02	2.51	0.78
	SE ±	0.61	1.35	1.16	1.43	0.78	0.19					
2	Days to 50% silking	3.34**	16.98**	12.26**	7.37*	25.15**	0.12	2.25	0.18	2.91	2.05	0.52
	SE ±	0.85	1.87	1.61	1.98	1.08	0.26					
3	Days to 75% dry Husk	7.75	82.89**	71.62**	15.84	99.44**	0.14	3.26	0.21	1.90	1.38	-0.28
	SE ±	6.70	14.78	12.71	15.63	8.51	2.11					
4	Plant height	82.13*	308.61**	240.44**	128.92	5.08	0.20	1.93	0.19	2.36	0.021	0.10
	SE ±	26.85	59.27	50.95	62.65	34.13	8.4					
5	Cob height	6.23	111.48**	79.43**	18.26	10.76	0.18	4.22	0.17	2.05	0.13	-0.42
	SE ±	8.47	18.69	16.07	19.76	10.76	2.67					
6	Cobs/plant	0.0023	0.035**	0.028**	0.007	0.00006	0.001	3.88	0.20	2.26	0.002	0.21
	SE ±	0.0026	0.005	0.004	0.006	0.0033	0.0008					
7	Cob weight at 15% at moisture	157.37*	886.66*	803.41**	186.11	2227.74*	2.80	2.37	0.22	1.66	2.77	0.52
	SE ±	56.74	125.24	107.66	132.37	72.12	17.94					
8	No. of grain rows/ Cob	0.16	2.46**	2.39**	-0.012	2.62*	0.05	3.89	0.24	0.98	1.094	0.19
	SE ±	0.20	0.46	0.39	0.488	0.26	0.06					
9	No. of grains/ row	3.78	33.58**	29.78**	6.27	152.58*	0.104	2.98	0.22	1.77	5.12	0.76
	SE ±	2.10	.64	3.99	4.90	2.67	0.66					
10	100 grain weight (gm)	6.58**	18.64**	15.12**	7.47*	1.09	0.065	1.68	0.20	2.01	0.072	0.16
	SE ±	1.32	2.92	2.51	3.09	1.68	0.419					
11	Grain yield/ cob (gm)	89.68*	621.50**	573.41**	98.38	1619.76*	0.76	2.63	0.23	1.52	2.82	0.56
	SE ±	34.74	76.69	65.92	81.05	44.16	10.98					
12	grain yield/ plant	174.35*	790.93**	698.01**	220.00	1780.19*	0.78	2.13	0.22	1.84	2.55	0.012
	SE ±	53.27	117.59	101.09	124.29	67.72	16.84					
13	Shelling percentage	1.80**	4.41**	3.01**	2.89*	0.80	0.29*	1.56	0.17	3.11	0.267	0.70
	SE ±	0.38	0.85	0.73	0.90	0.49	0.12					

*Significant at 5% level, **significant at 1% level

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