

QUANTITATIVE GENETIC ANALYSIS OF GRAIN YIELD AND SOME OTHER AGRONOMIC TRAITS IN MAIZE

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A nine parent diallel set of maize (*Zea mays* L.) inbreds was studied for combining ability and nature of inheritance of grain yield, ear length, ear diameter, kernel rows per ear, number of kernels per row and 1000-kernel weight. Both additive and non-additive genes were important for all characters except 1000-kernel weight where only non-additive genes were important. Combining ability as well as component analysis revealed the presence of overdominance or predominant role of non-additive genes in the inheritance of all traits studied. The parental performance seemed to be a good indicator of general combining ability effects. Out of nine lines, two were good general combiners for grain yield, ear diameter and number of kernels per row. Desirable significant specific combining ability effects for grain yields were observed in three crosses. Variance component analysis correlated with those of combining ability analysis.

Key words: *Zea mays*, Diallel cross, Grain yield, Genetic analysis.

INTRODUCTION

Maize, with its manifold utilization both as human food and feed for animals and also as the raw materials of some industrial products, is one of the leading cereals whose high per hectare yield will play an important role in reducing world food crisis. A through knowledge on the genetics of the parents and the nature of gene action for grain yield and its contributing characters is a prerequisite for maize improvement programme. The present study was, therefore, undertaken to understand the nature and magnitude of genetic variation governing grain yield and some other agronomic traits in a 9 x 9 half diallel of maize inbreds.

MATERIALS AND METHODS

Nine maize inbreds (Table 1) were crossed in a half diallel, making 36 cross-combinations. Thirty six cross-combinations and nine parents were raised in a randomized block

Table 1. Pedigrees and codes of the parental maize lines.

Pedigree*	Code
1. Eto 25-f-#-1-f-#-#-#-#	P1
2. CM 201: G715-A1-2-#	P2
3. CM 105: Peru 330-#-23B-1-f-f	P3
4. Eto 81-#-2-#-1-#-2B-f-#-#-#	P4
5. Eto 297-f-#-#-#-6-#-#-1bulk-#-#-#	P5
6. Eto 182-(C)-1-2-1-f-4-4-1-#-1-f-f-#	P6
7. Syn C(8b)-#-#-1-1-f-#	P7
8. Cuba 43-#-1-3-#-2-f-f-#-#	P8
9. CM 110: PH3-A6-#-1-#-#-1-1-f-#-#	P9

*All these lines were further selfed for at least two generations.

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design with three replications during summer. Each plot consisted of two rows, 5 m long, spaced 75 cm between rows and 25 cm within rows. Observations were recorded on grain yield per plot (kg) (adjusted for shelling percentage and 15% moisture), ear length (cm), ear diameter (cm), kernel rows per ear, number of kernels per row and 1000-kernel weight (g). Data on grain yield were taken on the basis of whole plot whereas, the rest of the data were recorded from ten random plants in each plot. Statistical analysis was made on entry mean basis. The combining ability analysis was carried out following model I (fixed effect model) and method 2 (parents and one set of F_1 'S) described by Griffing [1]. Relative importance of general combining ability (g.c.a.) and specific combining ability (s.c.a.) was calculated by the ratio $2\sigma_g/(2\sigma_g+\sigma_s)$ given by Baker [2] for fixed effect model, where σ_g and σ_s are the equivalent component of g.c.a. and s.c.a., respectively. Heritability in narrow sense was estimated as suggested by Prem Narain *et al.* [3].

$$\text{Heritability in narrow sense} = \frac{V_A}{V_A + V_D + V_E}$$

where, $V_A = 2\sigma_g$; $V_D = \sigma_s$ and V_E error variance in the absence of epistasis.

Simple correlation between g.c.a. effects and the parental means was calculated for all characters using standard procedure. Variance component analysis was based on the diallel cross technique of Hayman [4].

RESULTS AND DISCUSSION

The mean performance of the parental lines (Table 2) indicated considerable amount of genetic variability for all characters studied. Mean squares due to g.c.a. and s.c.a.

Table 2. Mean performance of the parental lines for various characters.

Parent	Characters					1000-kernel weight (g)
	Grain yield (kg)	Ear length (cm)	Ear diameter (cm)	Kemel rows/ear	No. of kernels/row	
P1	2.41	10.52	3.42	14.27	23.17	139.40
P2	2.50	10.90	3.60	15.13	24.33	136.83
P3	3.02	13.88	3.70	14.03	28.90	145.50
P4	2.02	9.48	2.96	11.33	15.27	179.50
P5	2.67	12.61	3.30	13.90	25.87	141.63
P6	2.20	11.11	3.50	12.23	20.30	202.80
P7	3.12	12.79	3.69	13.13	27.53	124.80
P8	2.15	11.17	3.37	14.00	22.07	140.13
P9	3.56	12.46	3.47	13.37	25.53	140.10
S.E.(±)	0.39	0.55	0.10	0.32	1.40	20.47

(Table 3) indicated the importance of both additive and non-additive components of variation in the inheritance of all characters except 1000-kernel weight where only non-additive genes were important. Importance of both additive and non-additive components of variation in the inheritance of grain yield and other agronomic traits was also reported by other authors [5, 6].

The values of the ratio $2\sigma_g/(2\sigma_g + \sigma_s)$ for all characters were less than 0.5, indicating more importance of s.c.a. in the inheritance of these characters (Table 4). Similar results were also reported by some other authors [7-11] for grain yield and/or its contributing characters. The heritability estimates was lowest for 1000-kernel weight and it was followed by grain yield (Table 4). Highest percentage of narrow sense heritability was shown by number of kernels per

Table 3. Analysis of variance for combining ability.

Source	d.f.	Mean squares					
		Grain yield	Ear length	Ear diameter	Kemel rows/ear	No. of kernels/row	1000-kernel weight
G.c.a.	8	0.49**	3.52**	0.123**	1.88**	41.31**	524
S.c.a.	36	0.50**	2.19**	0.051**	0.66**	12.68**	842**
Error	88	0.15	0.31	0.009	0.11	1.96	419

**Significant at 1% level.

Table 4. Estimates of components of g.c.a. (σ_g) and s.c.a. (σ_s) alongwith relative importance of g.c.a. and s.c.a. $\{2\sigma_g/(2\sigma_g + \sigma_s)\}$ and heritability percentage (h^2) in narrow sense.

	Characters					
	Grain yield	Ear length	Ear diameter	Kemel rows/ear	No. of kernels/row	1000-kernel weight
σ_g	0.03	0.29	0.01	0.16	3.58	9.55
σ_s	0.34	1.88	0.04	0.55	10.71	405.02
$2\sigma_g/(2\sigma_g + \sigma_s)$	0.15	0.24	0.32	0.37	0.40	0.05
h^2	10.91	20.94	24.99	32.65	36.11	2.27

row followed by kernel rows per ear, ear diameter and ear length. Hence, selection for these characters will confer rapid improvement compared to grain yield and 1000-kernel weight. Low heritability for grain yield in maize was also reported by Nawar [12].

Combining ability analysis showed that the present P7 was a good general combiner for grain yield, ear diameter and number of kernels per row (Table 5). P9 was a good general combiner for all characters except kernel rows per ear and 1000-kernel weight. These two parents appeared

Table 5. G.c.a. effects of the parental lines and the correlation coefficients (r) between g.c.a. effects and parental means for various characters.

Parent	Characters					
	Grain yield	Ear length	Ear diameter	Kemel rows/ear	No. of kernels/row	1000-kernel weight
P1	-0.26*	-0.50**	-0.02	0.57**	0.03	-14.30
P2	-0.04	0.01	0.04	0.62**	0.69	-2.64
P3	0.12	0.77**	0.11**	0.02	1.61**	-4.55
P4	-0.24*	-0.96**	-0.23**	-0.69**	-3.65**	7.08
P5	0.07	0.49**	-0.09**	-0.27**	1.39**	4.38
P6	-0.04	-0.34*	0.00	-0.19*	-1.89**	7.64
P7	0.34**	0.27	0.07**	-0.23*	1.46**	2.30
P8	-0.20	-0.27	0.03	0.02	-1.54**	2.87
P9	0.24*	0.54**	0.09**	0.17	1.91**	-2.78
C.D.	0.22	0.31	0.05	0.18	0.79	-
(g) at 5%						
C.D.	0.29	0.42	0.07	0.24	1.05	-
(g) at 1%						
C.D.	0.33	0.47	0.08	0.28	1.19	-
(g-g) at 5%						
C.D.	0.44	0.62	0.11	0.36	1.58	-
(g-g) at 1%						
r	0.87**	0.97**	0.92**	0.91**	0.95**	0.53

*Significant at 5% level; (++) Significant at 1% level.

worthy of exploiting in practical plant breeding utilizing fixable component of variation.

The correlation coefficients between the g.c.a. effects of the parents and the parental means for all characters except 1000-kernel weight were positive and highly significant (Table 5). This indicates that the *per se* performance of the parents bear direct reflection of their respective g.c.a. effects for grain yields and most of its contributing characters.

Table 6 represents the s.c.a. effects of the crosses. The crosses showing significantly positive s.c.a. effects are listed in Table 7 along with the best five hybrids on the basis of *per se* performance. The crosses P4XP7, P4XP8 and P3XP8 possessed significant and positive s.c.a. effects for grain yield and one or more agronomic traits. Out of them, P4XP7 and P3XP8 were also among the best five hybrids on the basis of *per se* performance for grain yield. Hence, these two crosses may be considered best and the inbreds P3, P4, P7 and P8 can be utilized in future breeding programme to exploit non-additive component of variation.

Table 6. S.c.a. effects of the crosses for various characters.

Cross	Characters					
	Grain yield	Ear length	Ear diameter	Kernel rows/ear	No. of kernels/row	1000-kernel weight
P1XP2	-0.33	0.55	-0.11	-0.48	2.46	20.15
P1XP3	0.20	0.25	0.22*	1.39**	1.15	-24.68
P1XP4	0.16	0.44	0.07	0.23	1.87	25.79
P1XP5	0.10	1.45**	0.07	-0.59*	5.00**	8.23
P1XP6	0.18	1.12*	0.10	0.83**	0.55	-30.23
P1XP7	0.28	0.85	-0.06	-0.66*	0.33	9.57
P1XP8	-0.23	-0.68	0.02	-0.88**	-1.21	-23.23
P1XP9	0.45	1.00	0.36**	1.97**	1.81	19.78
P2XP3	0.65	1.53**	0.04	-0.33	2.62*	-18.47
P2XP4	0.22	1.84**	0.27**	0.98*	3.67**	38.10*
P2XP5	0.36	0.80	0.16	-0.14	2.61*	-33.76
P2XP6	0.47	0.88	0.10	-0.06	0.22	16.31
P2XP7	-0.27	-0.29	-0.01	-0.18	-1.04	-13.42
P2XP8	0.30	0.76	0.06	0.27	1.60	11.45
P2XP9	0.07	0.17	0.03	0.19	0.11	36.79
P3XP4	-0.45	-1.32*	0.04	0.31	-4.78**	-4.56
P3XP5	-0.49	-0.60	0.02	-0.04	-0.71	10.67
P3XP6	0.59	0.77	0.03	0.01	2.57*	26.81
P3XP7	0.40	0.55	0.18*	0.79**	0.45	41.78*
P3XP8	0.93+	1.32*	0.24**	0.13	1.45	-6.85
P3XP9	-0.07	0.83	-0.13	-2.21**	4.06**	7.50
P4XP5	0.49	0.58	-0.04	-0.40	1.91	12.84
P4XP6	0.22	0.42	0.07	0.65*	2.12	-55.29**
P4XP7	1.06**	0.93	0.03	-0.31	3.33*	-6.85
P4XP8	1.01**	1.68**	0.14	0.04	3.87**	-6.81
P4XP9	-0.38	0.63	0.15	0.56	1.05	7.50
P5XP6	0.32	-0.01	0.14	0.83**	0.62	-24.15
P5XP7	0.45	0.80	0.09	-0.19	0.40	32.42
P5XP8	0.68	0.73	0.06	-0.58	-0.13	52.39**
P5XP9	0.34	1.01*	0.16	0.28	2.28	17.00
P6XP7	-0.68	0.36	-0.02	0.26	1.51	30.96
P6XP8	-0.35	0.45	0.00	0.07	0.08	13.23
P6XP9	0.64	0.45	0.16	0.26	2.33	-11.29
P7XP8	-0.19	-0.26	0.22*	0.65*	1.53	33.07
P7XP9	0.20	0.58	0.04	0.50	2.44	-26.55
P8XP9	0.07	0.58	0.24**	0.45	0.68	-0.65
C.D. (s_{ij}) at 5%	0.71	1.01	0.17	0.59	2.55	37.27
C.D. (s_{ij}) at 1%	0.94	1.34	0.23	0.78	3.38	49.43
C.D. ($s_{ij}-s_{ik}$) at 5%	1.05	1.49	0.26	0.87	3.76	54.95
C.D. ($s_{ij}-s_{ik}$) at 1%	1.39	1.97	0.34	1.15	4.99	72.88
C.D. ($s_{ij}-s_{kl}$) at 5%	0.99	1.41	0.24	0.82	3.57	52.13
C.D. ($s_{ij}-s_{kl}$) at 1%	1.32	1.87	0.32	1.09	4.73	69.13

*Significant at 5% level; **Significant at 1% level.

The t-test showed non-significant t-values for all characters except number of kernels per row thereby suggesting, in general, the validity of the postulated hypotheses for all traits except number of kernels per row (Table 8). Thus the conclusion made for number of kernels per row will not be valid though the parameters for all characters are presented in Table 8. Both additive (D) and dominance (H_1) components were involved in the control of all characters except grain yield and 1000-kernel weight. Significant h^2 suggested a net of dominant effects in all cases. The ratio $(H_1/D)^{1/2}$ was greater than one for all traits suggesting that overdominance was involved in their inheritance. Overdominance as well as predominant role of non-additive

Table 7. Good hybrid combinations with significant and positive s.c.a. effects and the best five hybrids on the basis of *per se* performance arranged in order of magnitude.

Character	Crosses with significant and positive s.c.a. effects	Best five hybrids on the basis of <i>per se</i> performance
Grain yield	P4XP7, P4XP8, P3XP8	P4XP7, P6XP7, P3XP7, P3XP8, P5XP7
Ear length	P2XP4, P4XP8, P2XP3, P1XP5, P3XP8, P1XP6, P5XP9	P2XP3, P3XP9, P5XP9, P3XP8, P3XP7
Ear diameter	P1XP9, P2XP4, P3XP8, P8XP9, P1XP3, P7XP8, P3XP7	P1XP9, P3XP8, P3XP7, P8XP9, P1XP3
Kernel rows/ear	P1XP9, P1XP3, P2XP4, P5XP6, P1XP6, P3XP7, P7XP8, P4XP6	P1XP9, P1XP3, P1XP6, P2XP9, P2XP4
No. of kernels/row	P1XP5, P3XP9, P4XP8, P2XP4, P4XP7, P2XP3, P2XP5, P3XP6	P3XP9, P1XP5, P7XP9, P5XP9, P2XP3
1000-kernel weight	P5XP8, P3XP7, P2XP4	P5XP8, P2XP4, P6XP7, P3XP7, P5XP7

Table 8. Analysis of genetic variation for various characters.

Component of variation/derived values	Characters					
	Grain yield	Ear length	Ear diameter	Kernel rows/ear	No. of kernels/row	1000-kernel weight
D	0.11 ±0.10	1.56** ±0.29	0.042** ±0.009	1.04** ±0.38	15.01** ±2.02	188.91 ±195.85
H_1	0.77** ±0.22	4.47** ±0.64	0.102** ±0.019	2.34** ±0.84	27.04** ±4.46	1566.28** ±432.27
H_2	0.81** ±0.19	4.46** ±0.55	0.099** ±0.016	1.90** ±0.72	26.38** ±3.84	1312.30** ±371.60
h^2	46.93** ±0.13	245.43** ±0.37	5.369** ±0.011	11.43** ±0.48	1306.18** ±2.57	18708.97** ±248.94
F	-0.05 ±0.23	0.48 ±0.67	0.005 ±0.020	0.85 ±0.89	1.41 ±4.72	392.02 ±456.88
E	0.15** ±0.03	0.31** 0.09	0.09** ±0.003	0.11 ±0.12	1.96** ±0.64	419.13** ±61.93
$(H_1/D)^{1/2}$	2.60	1.69	1.552	1.50	1.34	2.88
$H_2/4H_1$	0.27	0.25	0.241	0.20	0.24	0.21
$(4DH_1)^{1/2}+F$	0.84	1.20	1.071	1.75	1.07	2.13
$(4DH_1)^{1/2}-F$	0.84	1.20	1.071	1.75	1.07	2.13
h^2/H_1	57.62	55.01	54.536	6.02	49.52	14.26
r	-0.86**	-0.85**	-0.877**	-0.59	-0.60	-0.41
t	1.25	2.21	0.577	2.35	2.39*	0.06

*Significant at 5% level; **Significant at 1% level.

gene effects were also observed for all characters in combining ability analysis (Table 4). Similar results were also obtained from W_r , V_r graphs for all traits except kernel rows per ear which showed partial dominance [13]. The insignificant positive values of F for all characters except grain yield indicated almost symmetrical gene distribution with a small excess of dominant genes in the parents. This was also confirmed by the ratio $\{(4DH_1)^{1/2}+F\}/\{(4DH_1)^{1/2}-F\}$. Grain yield showed a slight excess of recessive alleles. The ratio $H_2/4H_1$ indicated equal distribution of negative and positive alleles among the parents for all traits except

kernel rows per ear and 1000-kernel weight. Highest number of genes or gene groups exhibiting dominance was shown by grain yield whereas kernel rows per ear had the lowest number followed by 1000-kernel weight. Positive genes were mostly dominant for grain yield, ear length and ear diameter. The rest of the characters exhibited equal importance of both dominant and recessive genes. The influence of environment on all characters except kernel rows per ear was drastic.

Results from the present study indicates that over dominance or predominant role of non-additive gene effects were important for all characters in the present material. Therefore, the combined improvement of all characters should be based upon exploitation of non-additive component of genetic variation. Breeding method such as recurrent selection for specific combining ability may be followed to exploit the non-additive component in the population derived from these parents.

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