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GENERATION MEAN ANALYSIS FOR EAR CHARARCTERS IN MAIZE

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ABSTRACT

The choice of an efficient breeding procedure mainly depends upon the knowledge of the type of gene action controlling the inheritance of a particular trait to be improved. Present study was conducted to ascertain genetic parameters for ear characters using generation mean analysis. Analysis of variance showed significant differences among all the crosses of each character. Generation mean analysis suggested that non additive genetic effects were responsible for the inheritance of ear height, ear length and number of grain rows per ear. Dominance x dominance type of allelic interaction was observed for ear height while both additive x additive and dominance x dominance interaction played significant role in the manifestation of ear length and number of grain rows per ear. The opposite sign of h and l indicated the presence of duplicate epistasis. Significant role of dominance variance along with duplicate epistasis favour the use of research material for the development of hybrid varieties.

Key words: Maize, *Zea mays* L., gene action, dominance, additive and generation mean analysis.

INRODUCTION

Maize has gained a significant position in the crop husbandry of Pakistan due to its high yield potential. Currently, the area under maize crop in Pakistan is 950 thousand hectares with total production of 3487 thousand tones having average yield of 3670 Kg/ha (Govt. of Pakistan, 2010). Its production showed a record increase of 47 % during 2004-05 as compared to 2003-04 (Govt. of Pakistan, 2005) which is mainly due to the cultivation of high yielding varieties. In maize, ear characters contribute significantly toward grain yield, hence, knowledge regarding the inheritance pattern of this character is very essential for the development of high yielding variety. Various studies (Kumar *et al*., 1998, Azizi *et al*., 2006, Sufi *et al*., 2006 and Ravikant *et al.*, 2006) successfully reported generation mean analysis for the said purpose.

Present study was designed keeping in view to determine the gene action and contribution of epistasis in the phenotypic expression of ear characters in maize.

MATERIAL AND METHODS

Six maize inbred lines (viz., FR-37, NYP-8, NYP-8-1,NCQPM-1, NCQPM-2, NCQPM-4) sown during spring 2005 at National Agricultural Research Centre, Islamabad were crossed to produce F_1 generation. Two rows of five meter length of each F_1 hybrid and their parents were sown during first week of July 2005. Parental lines were crossed to develop fresh F_1 hybrids. To produce F_2 generation, four F_1 plants in each cross were selfed. At the same time BC_1 and BC_2 generations were also developed by crossing two F_1 hybrid plants with either of the parents.

Seeds of hybrid generations i.e., F_1, F_2, BC_1 and BC_2 along with parents were sown during February 2006 in a randomized complete block design replicated thrice at National Agricultural Research Center, Islamabad. A single row for parental lines and F_1 hybrids, two for each back cross and four for F_2 generations were planted in each replication. In a five meter row inter row and inter plant distances were kept as 75 cm and 25 cm, respectively. Recommended dose of NPK fertilizers and cultural practices were adopted to meet the nutritional requirements of the crop and weed control respectively. Furadan granules at the time of sowing and six week after sowing was used to control borer attack.

At maturity data for ear height, ear length and number of grain rows per ear were recorded from ten plants in F_1s and parents each, on 70 plants in F_2 progenies and 15 in BC_1 and BC_2 in each repeat. Average values of individual cross for each character were used to find the significant differences among different generations following Steel and Torrie (1980) method. A computerized program based on the procedures outlined by Singh and Narayanan (2000) and Singh and Chaudhary (2004) was used in the present study.

RESULTS AND DISCUSSION

The ultimate objective of any successful breeding program is to develop genetically improved high yielding varieties with wider adaptability. This can be achieved through hybridization and utilization of germplasm having sufficient genetic diversity. Therefore, the precise information regarding the gene action controlling the inheritance of particular traits to be incorporated. Generation mean analysis has successfully been used to obtain information on the above said purpose.

EAR HEIGHT

The results of analysis of variance showed significant differences among genotypes which implies, that there was substantial amount of variability for further study(Table 1). Six parameter model was used to determine the type and magnitude of gene action involved in the inheritance of ear height. The results of scaling tests (Table 2) showed the importance of epistasis as all four tests i.e. A, B, C, and D were significant in all the crosses except NYP-8-1 x FR-37 and FR-37x NCQPM-1 in which "C" scaling test was non significant.

Table 1. Mean square values of various plant characteristics in different crosses of maize.

Crosses	S.O.V	d.f	MS value for ear height	MS value for ear length	MS value for number of grain rows per ear
NCQPM-2X NYP-8	Generations	5	142.31**	16.08**	5.15**
	Error	10	12.23	0.58	0.014
NCQPM-2X NYP-8-1	Generations	5	511.11**	24.55**	13.42**
	Error	10	4.73	0.30	0.02
NCQPM-2X FR-37	Generations	5	525.08**	12.11**	11.87**
	Error	10	16.72	1.18	0.008
NCQPM-2X NCQPM-4	Generations	5	393.28**	14.38**	6.06**
	Error	10	6.80	0.50	0.005
NCQPM-2X NCQPM-1	Generations	5	651.17**	27.92**	8.60**
	Error	10	4.98	0.74	0.037
NYP-8 X NYP-8-1	Generations	5	270.25**	12.56**	10.62**
	Error	10	6.06	0.25	0.032
NYP-8 X FR-37	Generations	5	431.69**	12.01**	5.88**
	Error	10	5.44	0.32	0.021
NYP-8 X NCQPM-4	Generations	5	423.26**	17.03**	5.11**
	Error	10	6.01	0.68	0.029
NYP-8 X NCQPM-1	Generations	5	323.63**	13.41**	6.47**
	Error	10	4.04	0.19	0.004
NYP-8-1 X FR-37	Generations	5	480.47**	9.78**	7.36**
	Error	10	2.66	0.24	0.024
NYP-8-1 X NCQPM-4	Generations	5	335.63**	5.28**	9.38**
	Error	10	2.22	0.28	0.026
NYP-8-1 X NCQPM-1	Generations	5	296.14**	16.74**	8.72**
	Error	10	2.14	0.43	0.013
FR-37 X NCQPM-4	Generations	5	274.73**	6.58**	7.99**
	Error	10	2.16	0.46	0.015
FR-37 X NCQPM-1	Generations	5	365.66**	6.48**	5.86**
	Error	10	5.31	0.29	0.024
NCQPM-4 X NCQPM-1	Generations	5	431.57**	15.10	5.54**
	Error	10	2.72	0.43	0.011

**, * = Significant at 1% and 5% probability level, respectively.

Estimates of generation means presented in Table 3 revealed that dominant genetic effect (h) was significant in all the crosses under study. Presence of maximum number of dominant genes was evident from higher value of dominant estimates in all the crosses. These results are in accordance with the findings of Abdel *et al.* (1998), Amer

(2004) and Balc *et al.* (2004). In contrary to this, additive variance was important for ear height as indicated by Amer *et al*. (2002), Mousa (2004) and Suryia and Ganguli (2004). The results also showed that additive x additive interaction (i) contributed significantly in all the crosses except NYP-8-1 x FR-37, NYP-8-1 x NCQPM-1, FR37 x NCQPM-4 and FR-37 x NCQPM-1. Dominance x dominance type of gene interaction was significant in all the crosses. Sign of the dominance effect (h) was positive while sign of dominance x dominance (i) was negative which suggested that duplicate type of gene interactions was present confirming the importance of dominance effects.

Table 2. Scaling tests for ear height in different generations of maize hybrids.

Cross	A	B	C	D
NCQPM-2xNYP-8	6.72±1.26*	12.62±1.22*	-53.96±1.86*	-36.65±1.04*
NCQPM-2xNYP-8-1	26.88±1.17*	23.81±1.13*	-21.88±1.71*	-36.28±0.92*
NCQPM-2xFR-37	21.26±1.27*	21.96±1.21*	-28.17±1.93*	-35.69±1.10*
NCQPM-2xNCQPM-4	21.23±1.19*	21.26±1.22*	-22.5±1.85*	-32.50±1.09*
NCQPM-2xNCQPM-1	28.69±1.22*	26.55±1.18*	-13.92±1.77*	-34.58±1.08*
NYP-8xNYP-8-1	21.14±1.13*	11.51±1.16*	-21.57±1.83*	-27.11±1.03*
NYP-8xFR-37	21.51±1.17*	18.88±1.09*	-10.18±1.85*	-25.28±1.02*
NYP-8xNCQPM-4	23.12±1.33*	19.63±1.24*	-18.62±1.92*	-30.69±1.13*
NYP-8xNCQPM-1	17.22±1.22*	18.10±1.15*	-28.39±1.91*	-31.85±1.09*
NYP-8-1xFR-37	23.77±1.24*	22.26±1.21*	-2.94±1.93*	-24.48±1.09*
NYP-8-1xNCQPM-4	16.5±1.26*	24.57±1.27*	-17.87±2.02*	-29.47±1.20*
NYP-8-1xNCQPM-1	15.14±1.52*	15.17±1.33*	-17.45±2.26*	-23.88±1.37*
FR-37xNCQPM-4	18.5±1.33*	17.91±1.32*	-7.16±1.94*	-21.78±1.16*
FR-37xNCQPM-1	20.51±1.37*	20.36±1.28*	-3.25±2.21*	-22.06±1.29*
NCQPM-4xNCQPM-1	16.84± 1.29*	21.11±1.27	-7.31±1.83	-22.63±1.16

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

Table 3. Estimates of generation mean parameters, mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) dominance x dominance (l) for ear height in different generations of maize hybrids.

Cross	M	D	H	I	J	l
NCQPM-2xNYP-8	45.62±5.38	-0.33±4.93	84.42±23.87*	73.30±23.66*	-2.95±5.72	-92.65±29.88*
NCQPM-2xNYP-8-1	62.01±4.57	2.27±4.47	96.67±20.59*	72.57±20.34*	1.53±5.23	-123.25±26.33*
NCQPM-2xFR-37	59.2±5.80	3.60±5.08	99.43±25.50*	71.38±25.33*	-0.35±5.85	-114.59±31.40*
NCQPM-2xNCQPM-4	-62.84±5.73	-0.58±5.02	88.47±25.17*	65.00±25.03*	-0.01±5.76	-107.49±30.93*
NCQPM-2xNCQPM-1	65.55±5.52	3.47±5.10	99.70±24.44*	69.17±24.32*	1.07±5.80	-124.41±30.47*
NYP-8xNYP-8-1	56.93±5.57	2.93±4.62	73.24±24.28*	54.22±24.13*	4.82±5.44	-86.87±29.47*
NYP-8xFR-37	60.85±5.58	2.67±4.51	78.18±24.24*	50.56±24.08*	1.32±5.35	-90.95±29.25*
NYP-8xNCQPM-4	61.42±5.80	-1.43±5.36	85.29±25.72*	61.37±25.56*	1.75±6.05	-104.11±32.13*
NYP-8xNCQPM-1	54.63±5.82	-0.62±4.87	84.92±25.41*	63.71±25.25*	-0.44±5.59	-99.03±30.89*
NYP-8-1xFR-37	64.05±5.76	3.82±4.97	75.26±25.26*	48.96±25.08	0.76±5.74	-94.99±30.10*
NYP-8-1xNCQPM-4	62.13±6.44	-5.33±5.38	80.13±28.05*	58.93±27.93*	-4.03±6.05	-100.00±33.97*
NYP-8-1xNCQPM-1	60.17±5.93	1.69±6.20	70.83±32.03*	47.76±31.91	-0.01±6.78	-78.07±38.86*
FR-37xNCQPM-4	60.09±5.93	-4.22±5.56	61.75±26.34*	43.57±26.19	0.29±6.39	-79.98 ±33.00*
FR-37xNCQPM-1	60.90±7.09	-1.29±5.60	67.68±30.62*	44.11±30.48	0.08±6.40	-84.98±36.57*
NCQPM-4xNCQPM-1	64394±5.83	0.87±5.57	70.20±25.97*	45.27±25.85	-2.13±6.06	-83.23±32.64*

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

EAR LENGTH

The analysis of variance given in Table 1 showed significant genotypic differences suggesting that reasonable amount of genetic variability was present for further study. The results of scaling test (Table 4) confirmed the presence of additive x additive, additive x dominance and dominance x dominance types of epistasis for ear length.

Six parameter model of owing to its greater statistical power was used to determine the type and magnitude of gene interactions involved in the inheritance of ear length.

Estimates of generation means presented in Table 5 revealed that non-additive component was involved in the inheritance of ear length in all crosses due to significant value of h. High value of dominance estimates in all crosses suggested the presence of maximum number of dominant alleles in the hybrid combinations. Similar results have been reported by Abdel *et al.* (1998), Balc *et al.* (2004), Mousa (2004), Sofi *et al.* (2006) and Singh and Roy (2007). However, Mahmood *et al.*, (1990), Amer (2004), Bujak *et al.* (2006), Chattopadhyay and Dhiman (2006) and Ishfaq (2011) did not agree by reporting additive genetic variance for the same trait.

As for as interaction components i, j, and l are concerned, the additive x additive and dominance x dominance types of interactions were equally important in crosses NCQPM-2 x NYP-8-1, NCQPM-2 x FR37, NCQPM-2 x NCQPM-1, NYP-8 x NCQPM-1, NYP-8-1 x NCQPM-1 and FR-37 x NCQPM-4. Dominance x dominance type of interaction contributed significantly in all other crosses. The opposite signs of h and l proposed the duplicate type of epistasis in the inheritance of ear length. Therefore, heterosis breeding would be advantageous.

Table 4. Scaling tests for ear length in different generations of maize hybrids.

Cross	A	B	C	D
NCQPM-2xNYP-8	2.02±0.43*	1.79±0.44*	-10.27±0.64*	-7.04±0.35*
NCQPM-2xNYP-8-1	3.87±0.40*	4.15±0.38*	-8.64±0.62*	-7.12±0.31*
NCQPM-2xFR-37	0.98±0.38*	3.55±0.40*	-8.64±0.59*	-6.59±0.30*
NCQPM-2xNCQPM-4	2.35±0.38*	4.95±0.36*	-4.46±0.55*	-5.88±0.29*
NCQPM-2xNCQPM-1	4.84±0.36*	6.22±0.35*	-0.79±0.56*	-5.93±0.27*
NYP-8xNYP-8-1	3.41±0.34*	4.02±0.32*	-3.41±0.49*	-5.42±0.25*
NYP-8xFR-37	2.04±0.38*	4.44±0.38*	-4.19±0.58*	-5.33±0.30*
NYP-8xNCQPM-4	1.79±0.39*	3.82±0.36*	-6.05±0.53*	-5.83±0.29*
NYP-8xNCQPM-1	1.25±0.49*	3.52±0.38*	-9.15±0.60*	-6.96±0.31*
NYP-8-1xFR-37	1.36±0.38*	2.46±0.39*	-9.87±0.59*	-6.84±0.32*
NYP-8-1xNCQPM-4	1.13±0.35*	0.99±0.37*	-9.04±0.54*	-5.58±0.28*
NYP-8-1xNCQPM-1	2.71±0.39*	3.25±0.40*	-8.88±0.60*	-7.42±0.31*
FR-37xNCQPM-4	2.55±0.39*	2.46±0.38*	-8.09±0.57*	-6.55±0.30*
FR-37xNCQPM-1	2.13±0.38*	2.10±0.38*	-7.87±0.58*	-6.06±0.30*
NCQPM-4xNCQPM-1	3.91±0.36*	2.73±0.35*	-4.85±0.53*	-5.74±0.28*

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

Table 5. Estimates of generation mean parameters, mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) dominance x dominance (l) for ear length in different generations of maize hybrids.

Cross	M	D	H	I	J	l
NCQPM-2xNYP-8	15.35±1.74	-0.10±1.70	19.08±7.83*	14.08±7.74	0.11±2.02	-17.90±10.03*
NCQPM-2xNYP-8-1	16.54±1.61	0.12±1.48	20.56±7.18*	14.25±7.08*	-0.14±1.83	-22.27±9.05*
NCQPM-2xFR-37	13.91±1.49	2.11±1.46	17.02±6.73*	13.17±6.63*	-1.29±1.83	-17.70±8.64*
NCQPM-2xNCQPM-4	15.20±1.45	-0.24±1.42	16.09±6.55*	-11.75±6.46	-1.31±1.79	-19.05±8.38*
NCQPM-2xNCQPM-1	17.31±1.35	0.17±1.26	18.8±6.08*	11.86±5.98*	-0.69±1.67	-22.93±7.74*
NYP-8xNYP-8-1	16.38±1.28	0.17±1.24	14.99±5.72*	10.84±5.64	-0.30±1.67	-18.27±7.33*
NYP-8xFR-37	15.18±1.54	0.07±1.43	14.40±6.89*	10.66±6.80	-1.2±1.84	-17.14±8.70*
NYP-8xNCQPM-4	15.40±1.45	0.26±1.43	16.76±6.53*	11.66±6.46	-1.01±1.82	-17.27±8.35*
NYP-8xNCQPM-1	14.34±1.59	-0.07±1.50	18.06±7.12*	13.92±7.03*	-1.14±1.88	-18.68±9.03*
NYP-8-1xFR-37	12.83±1.65	0.24±1.50	16.52±7.32*	13.69±7.24	-0.55±1.84	-17.51±9.15
NYP-8-1xNCQPM-4	12.93±1.40	0.87±1.35	13.78±6.32*	11.16±6.23	0.07±2.93	-13.28±8.06
NYP-8-1xNCQPM-1	14.33±1.56	2.22±1.49	19.44±7.02*	14.84±6.93*	2.22±1.82	-20.81±8.93*
FR-37xNCQPM-4	12.45±1.48	0.04±1.46	15.86±6.70*	13.10±6.61*	0.05±1.87	-18.11±8.60*
FR-37xNCQPM-1	12.59±1.44	-0.19±1.44	14.64±6.70*	12.10±6.61	0.02±1.85	-16.34±8.57
NCQPM-4xNCQPM-1	14.47±1.42	0.39±1.35	16.27±6.36*	11.49±6.29	0.59±1.76	18.14±8.07*

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

Table 6. Scaling tests for grain rows per ear in different generations of maize hybrids.

Cross	A	B	C	D
NCQPM-2xNYP-8	2.16±0.39*	0.78±0.39*	-9.49±0.57*	-6.21±0.30*
NCQPM-2xNYP-8-1	2.76±0.40*	4.73±0.37*	-5.93±0.60*	-6.71±0.33*
NCQPM-2xFR-37	3.04±0.37*	4.38±0.36*	-4.48±0.65*	-5.95±0.32*
NCQPM-2xNCQPM-4	1.98±0.38*	2.62±0.38*	-6.68±0.57*	-5.64±0.30*
NCQPM-2xNCQPM-1	1.8±0.38*	2.48±0.39*	-0.77±0.61*	-7.53±0.30*
NYP-8xNYP-8-1	0.53±0.38*	2.99±0.37*	-0.14±0.57*	-6.84±0.28*
NYP-8xFR-37	-0.29±0.38	2.07±0.38*	-9.41±0.59*	-5.59±0.27*
NYP-8xNCQPM-4	0.53±0.38	2.38±0.38*	-7.90±0.38*	-5.40±0.28*
NYP-8xNCQPM-1	-0.11±0.39	-0.71±0.40*	-2.73±0.59*	-5.96±0.28*
NYP-8-1xFR-37	2.73±0.38*	1.82±0.40*	-7.84±0.58*	-6.20±0.30*
NYP-8-1xNCQPM-4	3.64±0.39*	2.22±0.40*	-7.54±0.60*	-6.70±0.30*
NYP-8-1xNCQPM-1	3.22±0.39*	2.11±0.41*	-6.78±0.60*	-6006±0.30*
FR-37xNCQPM-4	1.87±0.40*	1.09±0.39*	-10.9±0.62*	-6.94±0.31*
FR-37xNCQPM-1	2.47±0.39*	1.64±0.39*	-7.30±0.62*	-5.71±0.29*
NCQPM-4xNCQPM-1	2.53±0.39*	2.49±0.39*	-7.03±0.59*	-6.03±0.30*

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

Table 7. Estimates of generation mean parameters, mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) dominance x dominance (l) for grain rows per ear in different generations of maize hybrids.

Cross	M	D	H	I	J	l
NCQPM-2xNYP-8	12.50±1.51	0.09±1.49	13.89±6.81*	12.42±6.73	0.69±1.87	-15.35±8.73
NCQPM-2xNYP-8-1	12.93±1.74	0.04±1.51	17.26±7.65*	13.42±5.59*	-0.99±1.88	-20.91±9.43*
NCQPM-2xFR-37	13.65±1.82	-0.007±1.32	15.7±7.828	11.90±7.74	-0.67±1.72	-19.32±9.27*
NCQPM-2xNCQPM-4	12.71±1.53	0.04±1.43	13.71±6.84*	11.28±6.75	-0.32±1.83	-15.88±8.64
NCQPM-2xNCQPM-1	11.72±1.56	-0.03±1.92	17.42±6.93*	15.05±6.83*	-0.34±1.79	-19.33±8.67*
NYP-8xNYP-8-1	11.71±1.37	0.40±1.35	15.98±6.21*	13.68±6.10*	-1.23±1.83	-17.21±8.028
NYP-8xFR-37	11.78±1.37	0.09±1.31	12.52±6.21*	11.19±6.08	-1.18±1.79	-12.97±7.98
NYP-8xNCQPM-4	12.61±1.39	0.04±1.36	12.44±6.29*	10.81±6.18	-0.92±1.82	-13.72±8.11
NYP-8xNCQPM-1	11.13±1.41	1.20±1.40	12.88±6.41*	11.91±6.29	0.300±1.86	-11.09±8.30
NYP-8-1xFR-37	11.26±1.47	0.09±1.45	15.16±6.66*	12.39±6.56	0.46±1.85	-16.95±8.57*
NYP-8-1xNCQPM-4	11.78±1.49	0.04±1.44	16.48±6.73*	13.41±6.63*	0.71±1.84	-19.28±8.63*
NYP-8-1xNCQPM-1	12.04±1.50	-0.18±1.48	15.18±6.81*	12.11±6.70	0.56±1.88	-17.45±8.78*
FR-37xNCQPM-4	11.85±1.56	0.09±1.45	16.65±6.99*	13.88±6.89*	0.39±1.89	-16.83±8.87*
FR-37xNCQPM-1	11.92±1.51	0.04±1.39	13.78±6.78*	11.42±6.63	0.41±1.85	-15.53±8.60
NCQPM-4xNCQPM-1	11.94±1.48	-0.04±1.43	13.72±6.69*	12.05±6.59	0.02±1.88	-17.07±8.55*

* = Significant (if the value of parameter divided by its standard error exceeds 1.96)

NUMBER OF GRAIN ROWS PER EAR

Results of analysis of variance indicated the presence of significant genetic variability among genotypes for further genetic study. Significance of four scaling tests i.e. A, B, C and D was observed in almost all the crosses except NYP-8 x FR37 and NYP-8 x NCQPM-1 in which “A” scaling test was non significant (Table 6). Presence of epistasis is important for the expression of number of grain rows per ear. Therefore, six parameter model was used to explain the genetic effects as well as the nature and magnitude of inter genic interactions. Perusal of estimates of generation mean parameters presented in Table 7 revealed the significance of non additive genetic effects (h) in all crosses under study. Number of rows per ear being governed by non additive genetic effects was also reported by

Abdel *et al.* (1998), Kumar *et al*, (1998), Sofi *et al.* (2006) and Singh and Roy (2007). While the findings of Amer *et al.* (2002), Amer (2004), Mousa (2004) Bujak *et al.* (2006) and Ishfaq (2011) who reported additive genetic effects are not in conformity with the present studies. Regarding epistatic interactions, the estimates of generation mean analysis predicted that both type of interactions i.e. additive x additive and dominance x dominance are equally important for the expression of rows per ear in crosses NCQPM-2 x NYP-8-1, NCQPM-2 x NCQPM-4, NYP-8-1 x NCQPM-4 and FR-37 x NCQPM-4. In other crosses only dominance x dominance (l) type of interaction was noticed which highlighted the important contribution of epistasis for the expression of the said character. Duplicate epistasis was found due to the positive and negative signs of “h” and “l” respectively, thus heterosis breeding may be helpful for the improvement of number of grain rows per ear in maize.

REFERENCES

Amer, E. A., A. A. El-Shenawy, and H. E. Mosa (2002). Evaluation of some new inbred lines of maize for combining ability. *Annals Agr. Sci. Moshtohor,* 40(2): 791-802.

Amer, E. A. (2004). Combining ability of new white inbred lines of maize with three testers tested over two locations. *Annals Agr. Sci. Moshtohor*, 42(2): 461-474.

Azizi, F., A. M. Rezai, and G. Saeidi (2006). Generation mean analysis to estimate genetic parameters for different traits in two crosses of corn inbred lines at three planting densities. *J. Agr. Sci. and Tech*., 8(2): 153-169.

Bujak, H., S. Jedynski, J. Karczmarek, C. Karwowska, Z. Kurczych and A. Damczyk (2006). Evaluation of breeding value of inbred lines of maize on the basis of multi trait analysis. *Biuletyn-Instytutu-Hodowli-i-Aklimatyzacji-Roslin*, (240/241): 211-216

Chattopadhyay, K. and K. R. Dhiman (2006). Characterization of two landraces of maize from Tripura, India and genetic study of a few selected morphological traits. *Pl. Genet. Res. Newsletter*, (145): 61-63

Government of Pakistan. (2005). *Agricultural Statistics of Pakistan (2004-05).* Ministry of Food, Agriculture and Livestock, Government of Pakistan, Islamabad.

Government of Pakistan. (2010). *Agricultural Statistics of Pakistan (2009-10).* Ministry of Food, Agriculture and Livestock, Government of Pakistan, Islamabad.

Ishfaq. A (2011). Generation mean analysis of reproductive and yield traits in maize (*Zea mays* L.). *SAARC J. Agri*., 9 (2) : 37-44.

Mosa, H. E. (2004). Comparison between two types of testers for evaluating new white inbred lines of maize. *Annals Agr. Sci., Moshtohor,* 42(2): 475-487.

Ravikant, R. Prasad, and Chandrakant (2006). Gene effects for metric traits in quality protein maize (QPM) (*Zea mays* L.*).* Crop Improvement 33(1): 94-101.

Singh, P. and S. S. Narayanan. (2000). *Biometrical techniques in plant breeding.* 2nd ed., Kalyani Publishers, New Delhi (India).

Singh, R. K. and B. D. Chaudhry (2004). *Biometricamethods in quantitative genetic analysis*. Kalyani Publishers, New Delhi, (India).

Kumar, A., M. G. Gangashetti and A. Kumar (1998). Gene effects in some metric traits of maize (*Zea mays* L.). *Annals Agri. Bio. Res*., 3(2): 139-143.

Prakash, S. and D. K. Ganguli (2004). Combining ability for various yield component characters in maize (*Zea mays* L.*). J. Res., Birsa Agric. Univ*., 16(1): 55-60.

Sofi, P., A. G. Rather, and S. Venkatesh (2006). Detection of epistasis by generation means analysis in maize hybrids. *Pak. J. Biol. Sci.,* 9(10):1983-1986.

Singh, P. K. and A. K. Roy (2007). Diallel analysis of inbred lines in maize (*Zea mays* L.*). Int. J. Agri. Sci*., 3(1): 213-216.

Steel, R. G. D. and J. H. Torrie. (1980). *Principles and Procedures of Statistics, A Biological approach*. 2nd ed., McGraw Hill Inc., NewYork.

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