Gene effects controlling earliness, yield and their components in maize using generations means analysis

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ABSTRACT

Six populations of three maize crosses were grown during the three growing seasons, 2016-2018 at Ghazalla Agricultural Experimental Station, Fac. of Agric., Zagazig Univ. were evaluated for earliness characters and yield characters. The adequacy of genetic model of gene effects for the evaluated characters were estimated.

Scaling tests provided evidence of non-allelic interaction in controlling most studied the genetic model was found to be adequate for explaining the inheritance of number of ears/plant in all crosses, ear diameter and number of rows/ear in the third cross as well as days to 50% silking in the first cross.

The genetic model indicated that the additive, dominance and epistatis gene effects were significant for some earliness and yield characters among the three crosses. Additive and additive x additive gene effects were negative and significant for days to 50% tasselling and days to 50% silking in the third cross.

The dominance and dominance x dominance gene effect were significant for days to 50% tasselling in second and third crosses crosses; and days to 50% silking and plant height in third cross.

Duplicate type of epistasis was detected for some earliness and yield characters in all crosses. Complementary type of epistasis was also detected the first cross for number of grains/row.

Keywords: Maize, yield, Six population, Gene effects, earliness.

Introduction

Maize is one of principal cereal crops in Egypt and all over the world. It is used as feed for cattle and poultry. Also, it is considered as a main component in several important industries such as corn oil, starch, fructose sugar and other products. In the last period, maize is used for human feed in Egypt by mixing 20% with wheat flour in bread making to lessen wheat imports by 2.4 million tons annually and to save hard currency.

The choice of an efficient breeding program depends largely on the knowledge of gene action involved in the expression of the character.

Different genetic cross designs such as generation mean, line × tester and diallel analyses are used to estimate gene action of yield and its components in maize.

Generations means analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit laying in the ability to estimate epistatic gene effects. Besides gene effects, breeders will also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable, since efficiency of selection mainly depends on additive genetic variance.

Many researchers observed the important role of non-allelic interactions in the inheritance of quantitative traits in maize (Shahrokhi *et al.,* 2013; Dorri *et al.,* 2014 and Wannows *et al.,* 2015). Haq *et al.* (2013) found that generations means analysis showed the superiority of non- additive gene effects for most yield and its components in maize. Ravikant *et al.* (2006) reported epistatic gene effects for several traits including grain yield in maize. Azizi *et al.* (2006) suggested that both additive and dominance effects were important for most of evaluated traits in maize, but dominance had a more pronounced effect. Kumar *et al.* (2005) also reported over-dominance effects for plant height, ear height and grain yield/plant. The additive genetic variance was significant for all traits except ear

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diameter, however, the dominance genetic variances were significant for all traits except ear length and number of kernels/row (El-Badawy, 2011). Hussain and sabre (2017) and Hussain *et al.* (2017) showed significant differences among generations in plant height, number of Kernels/row, 100 kernel weight and grain yield in maize. Al-Naggar *et al.* (2016) found that additive and dominance variances were significant, but the magnitude of dominance was much higher than additive variance for all studied traits.

The present study was carried out to estimate the type of gene effects in three maize crosses derived from four parental maize inbred lines using six populations model.

Materials and Methods

The present study was conducted during the summer growing seasons 2016, 2017 and 2018, at Ghazalla Agricultural Experimental Station, Fac. of Agric., Zagazig Univ., Four white maize in bred lines were used as parents which were differed in earliness and yield components. The origin and pedigree of the used maize inbred lines are presented in Table (1).

In the first summer growing season of 2016, the parental inbred lines (L 120, L 74, L 144 and L 56) were grown and crossed in such a way to produce three crosses i.e. (L120 x L74), (L144 x L120) and (L 56 x L74).

Table 1: The origin and pedigree of the used maize inbreds.

Inb. lines	Origen	Pedigree
120	Locally developed	L. 57-B
74	(PI 221866 x 307) (Sc.14)	Rg. 31
144	Locally developed	L. 226 -A
56	g.s (Beida x ci .64) (Sc. 14)	Rg – 11

In the second summer growing season of 2017, the three F_1's grains were sown to produce F_1 plants, and were back crossed to their respective parents to produce three backcrosses. In the meantime, same F_1 plants were selfed to produce F_2 grains.

In the third summer growing season of 2018, the obtained grains of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each of the three crosses were sown in rows in randomized complete block design with three replicates. All recommended culture practices were applied at proper time as in maize production.

Data were recorded on ten plants for parents or F_1 crosses, 20 plants for each back cross and 40 plants for each F_2 population per replicate. The following earliness characters: days to 50 % tasselling, days to 50% silking, plant height, ear height and the following yield characters, ear length, ear diameter, number of ears/ plant, number of rows/ear, number of grains/row, 100- grain weight and grain yield/plant.

The collected data were statistically analyzed using six populations model and A, B and C scaling tests were estimated as Hayman and Mather (1955). The analysis was proceeded to compute the gene effects involved in the six parameters genetic model.

Results and Discussion

1-1-Earliness characters:

Table (2) show mean performances of the six populations of three maize crosses for earliness characters. The results indicated that, the F_1's means tented towards the earlier parent for days to 50% tasselling and silking in first and second crosses, providing evidence for the presence of partial dominance mode of inheritance.

The F_1's means were lower than the earlier parent for days to 50% tasselling and days to 50% silking in the third cross. This result revealed the presence of over-dominance mode of inheritance.

The F_2 means were more than the F_1 means for days to days to 50% tasselling and days to 50% silking in all crosses, suggesting accumulation of increasing alleles for earliness.

Table 2: Mean performances of the studied six populations of the three maize crosses for earliness characters.

Populations	Days to 50% tasselling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)
			I- L$_{120}$ x L$_{74}$			
P$_1$	58.00 $\pm$ 0.20	61.00 $\pm$ 0.28	228.43 $\pm$ 0.58	112.73 $\pm$ 0.64	14.28 $\pm$ 0.28	3.7 $\pm$ 0.05
F$_1$	59.00 $\pm$ 0.20	61.33 $\pm$ 0.22	312.5 $\pm$ 0.84	170.06 $\pm$ 0.61	17.66 $\pm$ 0.47	3.94 $\pm$ 0.05
F$_2$	62.00 $\pm$ 0.56	64.66 $\pm$ 0.76	240.43 $\pm$ 3.74	141.9 $\pm$ 3.5	12.92 $\pm$ 0.68	3.4 $\pm$ 0.1
BC$_1$	59.00 $\pm$ 0.38	61.66 $\pm$ 0.29	262.03 $\pm$ 2.75	132.43 $\pm$ 2.35	15.37 $\pm$ 0.56	3.65 $\pm$ 0.07
BC$_2$	61.66 $\pm$ 0.54	65.00 $\pm$ 0.7	245.6 $\pm$ 3.19	124.83 $\pm$ 2.81	14.37 $\pm$ 0.55	3.5 $\pm$ 0.07
P$_2$	66.66 $\pm$ 0.16	69.66 $\pm$ 0.17	169.66 $\pm$ 0.57	109.3 $\pm$ 0.61	11.48 $\pm$ 0.08	3.26 $\pm$ 0.04
			II- L$_{144}$ x L$_{120}$			
P$_1$	66.00 $\pm$ 0.11	69.33 $\pm$ 0.15	219.14 $\pm$ 0.91	144.4 $\pm$ 0.50	10.13 $\pm$ 0.05	3.1 $\pm$ 0.02
F$_1$	59.00 $\pm$ 0.29	61.33 $\pm$ 0.15	304.53 $\pm$ 0.1	170.7 $\pm$ 0.801	18.48 $\pm$ 0.32	4.4 $\pm$ 0.05
F$_2$	61.00 $\pm$ 0.74	64.66 $\pm$ 0.6	267.03 $\pm$ 4.55	147.53 $\pm$ 3.57	13.93 $\pm$ 0.62	3.6 $\pm$ 0.1
BC$_1$	60.66 $\pm$ 0.49	62.66 $\pm$ 0.47	298.6 $\pm$ 3.53	162.3 $\pm$ 3.00	15.83 $\pm$ 0.58	3.78 $\pm$ 0.11
BC$_2$	58.33 $\pm$ 0.61	60.66 $\pm$ 0.43	284.63 $\pm$ 3.61	144.5 $\pm$ 2.68	14.90 $\pm$ 0.5	3.82 $\pm$ 0.7
P$_2$	58.00 $\pm$ 0.2	61.00 $\pm$ 0.28	228.43 $\pm$ 0.58	121.73 $\pm$ 0.64	14.28 $\pm$ 0.28	3.7 $\pm$ 0.05
			III- L$_{56}$ x L$_{74}$			
P$_1$	64.66 $\pm$ 0.16	68.00 $\pm$ 0.07	180.23 $\pm$ 0.6	107.6 $\pm$ 0.61	11.21 $\pm$ 0.13	3.42 $\pm$ 0.05
F$_1$	61.33 $\pm$ 0.23	63.00 $\pm$ 0.19	306.56 $\pm$ 0.89	174.93 $\pm$ 0.78	18.65 $\pm$ 0.4	3.95 $\pm$ 0.03
F$_2$	63.66 $\pm$ 0.43	67.33 $\pm$ 0.48	278.53 $\pm$ 3.44	146.83 $\pm$ 3.66	13.76 $\pm$ 0.47	3.56 $\pm$ 0.089
BC$_1$	62.00 $\pm$ 0.42	65.00 $\pm$ 0.41	286.13 $\pm$ 2.04	150.46 $\pm$ 2.07	15.26 $\pm$ 0.45	3.75 $\pm$ 0.083
BC$_2$	63.33 $\pm$ 0.15	66.66 $\pm$ 0.39	283.63 $\pm$ 3.08	143.8 $\pm$ 3.72	14.28 $\pm$ 0.41	3.66 $\pm$ 0.083
P$_2$	66.66 $\pm$ 0.16	69.66 $\pm$ 0.17	169.66 $\pm$ 0.57	109.3 $\pm$ 0.61	11.48 $\pm$ 0.08	3.26 $\pm$ 0.04

1-2- Yield characters:

Mean performances of the six population of the three maize crosses for yield and its components are given in Table (3). The three studied crosses varied greatly in yield and its components. Such wide variation indicated the presence of appreciable amount of genetic variability. The results revealed that, the F_1's exceeding the high performing parent for most studied yield characters in all crosses. These results provided evidence for the presence of over dominance gene effects.

F_2 means were lower than the F_1 means for most yield characters in the three studied crosses, indicating the presence of inbreeding depression.

The backcross populations means were between the F_1 and the parental genotypes for all characters in the studied crosses, suggesting absence of dominance.

1- Gene effects:

2-1- Earliness characters:

Scaling tests and gene effects for earliness characters in three maize crosses are shown in Table (4). The results indicated significant non-allelic interactions for days to 50% tasselling in the three crosses and for days to 50% silking in the second and third crosses. These results indicated the presence of epistasis. In this respect, Hussain and Sabra (2017) explanted the genetic variation for days to tasselling and days to silking.

Also, insignificant non-allelic interaction was observed for days to 50% silking in the first indicating cross, that the simple additive-dominance genetic model proved to be satisfactory in explaining the inheritance of such character.

The adequacy of genetic model, Table (4) indicated that all gene effects were significant for days to 50% silking in the second cross and days to tasselling in the first cross. In this respect Shahrokhi *et al.* (2013), Dorri *et al.* (2014) and Wannows *et al.* (2015) confirmed gene effects that inheritance of tasselling date.

Moreover, the additive (d) and additive x additive (i) gene effects were negative and significant for days to tasselling and days to 50% silking in the third cross. In this connection, negative and significant gene effects were reported in the inheritance of tasselling date by Awaad and Hassan (1997).

Whereas, the dominance (h) dominance x dominance (L) gene effects were significant and involved in the inheritance of days to 50% tasselling in second and third crosses and days to 50% silking in the third one.

Meanwhile, the additive x dominance (j) type of interaction was negative and significant for days to 50% tasselling in the second cross, as well as the additive (d) and dominance (h) were significant for days to 50% silking in the first cross.

It is important to mention that additive (d), dominance (h) gene effects and their interactions were negative and significant for earliness characters in first and third cross.

Interestingly the dominance (h) and dominance x dominance (L) gene effects were significant and have different signs in all crosses for days to 50% tasselling and days to 50% silking, revealing that the interaction is predominantly of duplicate type.

2-2- Yield and its components:

The results in Tables (5 and 6) indicated significant non-allelic interactions for most yield characters in all crosses; ear diameter and number of grains/row in first and second crosses; number of rows/ear in first cross; number of rows/ear in second cross and number of grains/row in third one. These results indicated the presence of epistasis and the digenic model was adequate to explain the genetics of yield characters which agreed with those reported by Haq *et al.* (2013).

The insignificancy of non –allelic interaction tests were observed in number of ears/plant in all crosses, ear diameter and number of rows/ear in third cross. These results might indicate that, the simple additive-dominance genetic model proved to be satisfactory in explaining the inheritance of

Table 3: Mean performances of the studied six populations of the studied three maize crosses for yield characters.

Populations	Number of ear/plant	Number of rows/ ear	Number of grains/row	100- grain weight (gm)	Grain yield / plant (gm)
			I- L $_{120}$ x L $_{74}$		
P_1	1.2 ± 0.074	13.46 ± 0.21	26.73 ± 0.51	27.42 ± 0.19	46.427 ± 0.68
F_1	1.2± 0.074	14.33 ± 0.38	35.8 ± 0.62	34.18 ± 0.17	115.94 ± 0.07
F_2	1.03± 0.12	11.86 ± 0. 4	24.53 ± 1.31	23.664 ± 0.7	69.879 ± 1.4
BC_1	1.1 ± 0.11	12.93 ± 0.43	30.46 ± 0.99	28.2 ± 0.68	79.024 ± 1.13
BC_2	1.06 ± 0.08	11.93 ± 0.26	27.83 ± 1.00	25.412 ± 0.34	71.802 ± 1.4
P_2	1.00± 0.00	12.2 ± 0.22	19.86 ± 0.37	11.203 ± 0.3	21.768 ± 0.29
			II- L $_{144}$ x L $_{120}$		
P_1	1.2 ± 0.074	14.6 ± 0.23	18.16± 0.31	18.38 ± 0.19	26.947 ± 0.28
F_1	1.23 ± 0.078	14.8 ± 0.28	40.6 ± 0.55	36.476 ± 0.25	159.417 ± 1.16
F_2	1.1 ± 0.11	12.86 ± 0.45	26.23 ± 1.04	25.729 ± 0.77	88.287 ± 2.44
BC_1	1.13 ± 0.03	13.93 ± 0.33	36.23 ± 1.04	27.165 ± 0.07	103.999 ± 2.33
BC_2	1.06 ± 0.106	13.2 ± 0.41	29.8 ± 0.71	28.24 ± 0.67	98.529 ± 2.01
P_2	1.2 ± 0.074	13.46 ± 0.21	26.73 ± 0.51	27.42 ± 0.19	46.427 ± 0.68
			III- L $_{56}$ x L $_{74}$		
P_1	1.23 ± 0.07	12.2 ± 0.24	19.03 ± 0.36	23.137 ± 0.26	33.968 ± 0.51
F_1	1.26 ± 0.08	13.00 ± 0.26	41.86 ± 0.36	32.975 ± 0.4	145.353 ± 0.81
F_2	1.06 ± 0.116	12.4 ± 0.4	26.7 ± 1.03	22.031 ± 0.52	79.307 ± 2.78
BC_1	1.1 ± 0.11	12.6 ± 0.38	28.56 ± 0.91	26.869 ± 0.55	86.913 ± 1.86
BC_2	1.00 ± 0.09	12.53 ± 0.31	25.4 ± 0.74	22.648 ± 0.39	80.89 ± 2.21
P_2	1.00± 0.00	12.2 ± 0.22	19.86 ± 0.37	11.203 ± 0.3	21.768 ± 0.29

Table 4: Scaling tests and gene effects for earliness characters, plant height and ear height in three maize crosses.

Cross \ Scaling	Days to 50% tasselling			Days to 50% silking			Plant height (cm)			Ear height (cm)		
	I	II	III	I	II	III	I	II	III	I	II	III
A	1.00	-3.68**	-1.99*	0.99	-5.34**	-1.00	-16.87**	73.51**	85.47**	-26.93**	9.5*	18.39**
	±0.82	±1.02	±0.86	±0.67	±0.97	±0.84	±5.59	±5.27	±4.23	±4.79	±4.35	±4.26
B	-2.34*	-0.34	-1.33**	-0.99	-1.01	0.66	9.04	36.3**	91.04**	-29.7**	-3.43	3.37
	±1.1	±1.26	±0.51	±1.02	±0.90	±0.81	±6.47	±7.33	±6.25	±5.7	±3.93	±6.62
C	5.34*	2.00	0.66	5.32	5.65*	5.66**	-61.37**	11.47	151.11**	-3.55	-17.41	20.56
	±2.27	±3.02	±1.76	±2.96	±2.46	±1.95	±15.08	±18.34	±13.9	±14.12	±14.41	±14.77
Six – parameters model												
m	62.00**	61.00**	63.00**	70.65**	64.66**	67.33**	240.43**	267.03**	278.53**	141.9**	147.53**	146.83**
	±0.56	±0.74	±0.43	±3.28	±3.28	±0.48	±3.74	±4.55	±3.44	±3.5	±3.57	±3.66
d	-2.66**	2.33**	-1.33**	-4.33**	2.00**	-1.66**	16.43**	13.97**	2.5	7.6*	17.8**	6.7
	±0.66	±0.78	±0.46	±0.16	±0.63	±0.56	±4.21	±5.06	±3.7	±3.67	±4.02	±3.87
h	-10.01**	-9.02**	-8.31**	-14.64**	-15.95**	-11.83**	166.99**	179.07**	326.67**	1.46	61.11**	67.68**
	±2.66	±3.36	±1.95	±7.39	±2.75	±2.23	±17.2	±20.86	±15.65	±15.86	±16.43	±16.61
i	-6.68**	-6.02	-3.98*		-12.00**	-6.00**	53.54**	98.34**	25.4	-53.08**	23.48	1.2
	±2.59	±3.35	±1.93		±2.74	±2.22	±17.17	±20.83	±15.62	±15.84	±16.41	±16.58
j	1.67*	-1.67*	-0.33		-2.16**	-0.83	-12.95**	18.6**	-2.78	1.37	6.46	7.51*
	±0.67	±0.79	±0.47		±0.65	±0.57	±4.23	±5.08	±3.72	±3.69	±4.04	±3.89
I	8.02*	10.04*	7.3**		18.35**	6.34*	-45.11*	-208.15**	-201.91**	109.71**	-29.55	-22.96
	±3.49	±4.35	±2.57		±3.72	±2.99	±22.62	±27.32	±20.31	±20.37	±21.16	±20.13

Table 5: Scaling tests and gene effects for three maize crosses.

Cross / Scaling	Ear length (cm)			Ear diameter (cm)			Number of ears / plant			Number of rows / ear		
	I	II	III	I	II	III	I	II	III	I	II	III
A	-1.2	3.05*	0.66	-0.34*	0.06	0.13	-0.2	-0.017	-0.29	-1.93	-1.54*	0.00
	±1.23	±1.20	±0.98	±0.17	±0.23	±0.17	±-0.24	±0.12	±0.24	±0.96	±0.74	±0.84
B	0.4	-2.96*	-1.57	-0.2	-0.46**	0.11	-0.08	-0.31	-0.26	-2.67**	-3.00**	0.14
	±1.21	±1.34	±0.92	±0.15	±0.15	±0.17	±0.17	±0.23	±0.20	±0.64	±0.86	±0.74
C	-9.4**	-5.65*	-4.95*	-1.24**	-1.2**	-0.34	0.48	-0.46	-0.51	-6.88**	-6.22**	-0.8
	±2.88	±2.68	±2.04	±0.41	±0.45	±0.37	±0.5	±0.47	±0.48	±1.78	±1.88	±1.71
Six – parameters model												
m	12.92**	13.93**	13.76**	3.4**	3.6**	2.76**	0.9	1.22*	1.155*	11.86**	12.86**	11.54*
	±0.68	±0.62	±0.47	±0.1	±0.1	±0.42	±0.54	±0.49	±0.54	±0.4	±0.45	±1.88
d	1.00	0.93	0.98	0.15	-0.04	0.08**	0.1**	0.00	0.115**	1.00*	0.73	0.00
	±0.78	±0.76	±0.60	±0.1	±0.13	±0.02	±0.03	±0.00	±0.03	±0.5	±0.41	±0.15
h	12.92**	12.02**	11.34**	1.16**	1.8**	5.96**	0.22	0.74	0.485	3.78*	3.59	1.98
	±3.17	±2.94	±2.27	±0.45	±0.51	±1.01	±0.72	±1.1	±1.26	±1.92	±1.95	±4.37
i	7.8*	5.72	4.04	0.7	0.8					2.28	2.82	
	±3.13	±2.92	±2.23	±0.45	±0.51					±1.88	±1.92	
j	-0.4	3.01**	1.11	0.07	0.26					0.37	0.16	
	±0.79	±0.87	±0.61	±0.08	±0.14					±0.51	±0.39	
I	-6.2	-5.83	-3.13	-0.16	0.4					2.32	0.58	
	±4.27	±4.06	±3.85	±0.53	±0.70					±2.68	±2.37	

Table 6: Scaling tests and gene effects for number of grains/row, 100-grain weight and grain yield /plant in three maize crosses.

Cross / Scaling	Number of grains / row			100 – grain weight (gm)			Grain yield / plant (gm)		
	I	II	III	I	II	III	I	II	III
A	-1.61	14.04**	-3.77*	-5.2**	-0.52	-2.37*	-4.31	21.6**	-5.49
	±2.13	±1.75	±1.89	±1. 38	±1.43	±1.21	±2.46	±4.82	±5.3
B	0.00	-7.73**	-10.92**	5.44**	-7.41**	1.11	5.89*	-8.78*	-5.34
	±2.13	±1.6	±1.58	±0.74	±1.83	±0.92	±2.9	±4.24	±5.07
C	-20.07**	-21.17**	-15.81**	-12.32**	-15.83**	-12.16**	-20.55**	-39.08**	-29.21**
	±5.45	±4.34	±4.21	±2.83	±3.14	±2.26	±5.83	±10.05	±11.26
				Six – parameters model					
m	24.53**	26.23**	26.7**	23.66**	25.72**	22.03**	69.87**	88.28**	79.307**
	±1.31	±1.04	±1.03	±0.68	±0.77	±0.52	±1.4	±2.44	±2.78
d	2.63	6.6**	3.16**	2.78**	-1.07	4.22**	7.22**	5.47	6.023
	±1.41	±1.08	±1.17	±0.76	±0.97	±0.67	±1.8	±3.08	±3.61
h	30.96**	45.63**	23.53**	27.43**	21.47**	20.76**	103.97**	197.62**	135.86**
	±6.02	±4.72	±4.76	±3.19	±3.67	±2.52	6.7	±11.06	±13.30
i	18.45**	27.48**	1.12	12.56**	7.89**	10.91**	22.13**	51.9**	18.37
	±5.95	±4.68	±4.74	±3.18	±3.66	±2.48	±6.6	±11.54	±13.27
j	-0.80	10.88**	3.57**	-5.32**	3.44**	-1.73*	-5.1**	15.19**	-0.07
	±1.19	±1.12	±1.2	±0.78	±0.98	±0.7	±1.84	±3.1	±3.62
I	99.73**	-33.79**	-5.87	-12.8**	0.58	-9.65**	-23.71*	-64.72**	-7.54
	±7.13	±6.12	±5.14	±4.16	±5.00	±3.53	±9.27	±15.91	±18.32

*, ** Significant at 0.05 and 0.01 respectively.

such characters. In this respect, Hassan *et al*. (1993) found that, the simple genetic model was adequate to interpret the genetic control of ear diameter in maize. Also, Awaad and Hassan (1997) observed that the simple genetic model was suitable to explain the inheritance of number of rows/ear in maize.

Likewise, all types of gene effects were significant for plant height in second cross; 100-grain weight in third cross and grain yield/plant in 1ˢᵗ cross; plant height and 100-grain weight in first cross and number of grains/row in second cross. Therefore, recurrent selection procedure could be used for improving such characters. In this connection, Amer and Mosa (2004) and El-Badawy (2011) reported that additive, dominance and epastiatic gene effects were important in the inheritance of plant height, ear height, ear length, number of grains/row, 100-grain weight and grain yield/plant in maize.

Whereas, the additive (d) and, additive x additive gene effects were significant for ear height in first cross, but the dominance (h) and dominance x dominance (L) gene effects were significant and involved in the inheritance of plant height in third cross; number of grains/row in first cross and grain yield/plant in second one.

Morever, the dominance gene effects were significant for ear length in second cross; ear diameter in first and third crosses; number of grains/row in third cross and 100-grain weight in second cross; ear height in second and third crosses, ear length in first and third crosses; ear diameter in second cross; number of rows/ ear in first cross and grain yield/plant in third one. Also, the dominance x dominance type of gene effect was significant for plant height in third cross and ear height in first one. The considerable amount of non-fixable type of gene effects detected in these characters might suggest that improving these characters could be achieved through hybrid breeding method. In this respect, Amer and Mosa (2004) Hussain and sabre (2017) found that the dominance (h) and dominance x dominance gene effect were involved in the inheritance of plant and ear heights, ear length, ear diameter, number of rows/ear, number of grains/row and grain yield /plant in maize.

Meanwhile, the additive x dominance (j) type of gene effects was significant for ear length, 100-grain weight and grain yield/plant in second cross and number of grains/row in third one.

The additive gene effects (d) was significant for number of ears/plant in first and third crosses and ear diameter in third one; ear height and number of rows/ear in second one.

The additive x additive (i) type of gene effects was significant for ear length in first and second crosses; number of grains/row in first cross; 100-grain weight and grain yield/plant in second one.

It is interest to mention that, the dominance x dominance (L) type of gene action was negative and significant for plant height in all crosses and ear height in first cross.

It is noticeable that the dominance (h) and dominance x dominance (L) gene effects were significant and having different signs in all crosses for plant height for 100-grain weight in third cross and for grain yield/plant in first cross for number of grains/row in second cross for 100-grain weight in first cross and for grain yield/plant in second cross. These results might indicate that interaction is predominantly of duplicate type. Whereas, the sign of dominance (h) and dominance x dominance (L) gene effects were similar in first cross for number of grains/row, revealing that interaction is predominantly of complementary type

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