

تقييم بعض المعايير الوراثية لبعض الصفات الكمية في هجينين من الذرة الصفراء (*Zea mays L.*)

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الملخص

نفذ البحث في حقول قسم بحوث الذرة التابع للهيئة العامة للبحوث العلمية الزراعية في دمشق خلال المواسم الزراعية 2010 و2011 و2012 وفقاً لتصميم القطاعات العشوائية الكاملة بثلاثة مكررات بهدف تقييم بعض المعايير الوراثية لصفات الإزهار المؤنث، وارتفاع النبات والعرنوس، وطول العرنوس وقطره، وعدد الصفوف بالعرنوس، وعدد الحبوب بالصف، ووزن المنة حبة، وغلة النبات الفردي في هجينين فرديين من الذرة الصفراء (IL.459-06 × IL.362-06، IL.565-06 × IL.292-06) باستخدام طريقة تحليل متوسطات الأجيال. وقد خلصت النتائج إلى أن الفعل الوراثي التراكمي والسيادي كانا عاليي المعنوية في أغلب الصفات المدروسة مع تفوق قيم الفعل الوراثي السيادي على الفعل الوراثي التراكمي. كما بينت النتائج أن الفعل الوراثي التفوقي ساهم في وراثية معظم الصفات، إذ دل التعاكس بين إشارتي الفعلين الوراثيين السيادي والسيادي × سيادي إلى النوع المزدوج (Duplicate) من الفعل الوراثي التفوقي، مشيراً إلى أن الانتخاب لمثل هذه الصفات يجب أن يتم بعد عدة أجيال. وبيّنت النتائج كذلك أن تأثير البيئة كان كبيراً على وراثية معظم الصفات المدروسة، وذلك لتفوق قيم معامل التباين المظهري على معامل التباين الوراثي، وترافقت القيم العالية المعنوية لقوة الهجين قياساً لمتوسط الأبوين والأب الأفضل مع تدهور وراثي مصاحب للتربية الذاتية في الجيل الانعزالي الأول. كما أوضحت النتائج أيضاً أن معظم الصفات أظهرت قيماً منخفضة إلى متوسطة لدرجة التوريث بمفهومها الضيق، فأكد ذلك أن معظم هذه الصفات خاضعة في وراثتها للفعل الوراثي اللاتراكمي الذي بدوره ينبئ عن قيم منخفضة إلى متوسطة للتقدم الوراثي من خلال عملية الانتخاب.

الكلمات المفتاحية: الذرة الصفراء، الفعل الوراثي، درجة التوريث، قوة الهجين، درجة السيادة.

(1) طالب دكتوراه، (2) أستاذ دكتور في قسم المحاصيل الحقلية كلية الزراعة، جامعة دمشق، (3) دكتور باحث في الهيئة العامة للبحوث العلمية الزراعية.

Evaluation of some genetic parameters for some quantitative traits in two maize hybrids (*Zea mays* L.)

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Abstract

The research was conducted at the Maize Researches Department, General Commission for Scientific Agriculture Researches (G.C.S.A.R.) Damascus, Syria during the summer growing seasons of 2010, 2011 and 2012. Treatments were arranged in a Randomized Complete Blocks Design with three replications. The research aimed to evaluate genetic parameters for some traits like days to 50% silking, plant and ear height, ear length, ear diameter, number of rows per ear, number of kernels per row, 100 kernel weight and grain yield per plant using generations means analysis of two maize hybrids (IL.292-06 × IL.565-06, IL.459-06 × IL.362-06) to detect epistasis and estimates of mean effect [m], additive [d], dominance [h], additive × additive [i], additive × dominance [j] and dominance × dominance [l] parameters. Results showed that the additive - dominance model was adequate to demonstrate the genetic variation and its importance in the inheritance of most studied traits. Non-allelic gene interaction was operating in the control of genetic variation in most studied traits. The signs of [h] and [l] were opposite in most studied traits for the two crosses. Also, the inheritance of all studied traits was controlled by additive and non-additive genetic effects, but dominance gene effects play the major role in controlling the genetic variation of the most studied traits, suggesting that the improvement of those characters need intensive selection through later generations. The phenotypic variations were greater than genotypic variations for all studied traits in the two crosses, indicating greater influence of environment in the expression of these traits. Highly significant heterosis relative to mid and better parents, respectively was found for all characters, and this accompanied with inbreeding depression for all traits. Narrow sense heritability and genetic advance were low in most of the traits due to the dominance of non-additive gene action in controlling the genetic variation of the most studied traits and this predict low to medium values of genetic advance through selection process.

Keywords: Maize, Gene action, Heritability, Heterosis and Potency ratio.

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Introduction

Maize is one of the major cereal crops providing raw material for the food industry and animal feed (Ünay *et al.* 2004). Grain yield is the most important quantitative and complex trait in maize. This means that yield expression is caused, not only by genetic factors, but also by environmental and genotype \times environment interaction effects. Melchinger *et al.* (1986) described how the knowledge about the nature of gene action allows maize breeders to optimize their breeding programs. The choice of selection and breeding procedures for genetic improvement of maize or any other crop depends largely on the knowledge of type of gene action for different characters in the plant materials under investigation. Generation mean analysis, a biometrical method developed by Mather and Jinks (1982), is a useful technique for determining gene effects for polygenic traits. Its greatest merit depends on the ability to estimate epistasis gene effects such as additive \times additive [i], additive \times dominance [j] and dominance \times dominance [l] interactions (Singh and Singh 1992). Breeding for improved varieties requires a thorough understanding of the genetic mechanisms governing yield and yield components (Saleem *et al.* 2002; Ünay *et al.* 2004). In this respect many researchers have reported the importance of non-additive gene action for grain yield and some other agronomic traits (Sofi *et al.* 2006; Iqbal *et al.* 2010; El-Badawy 2012; Shahrokhi *et al.* 2013). On the other hand, heterosis has important implications for both F_1 and for obtaining transgressive segregates in F_2 generation. In succeeding selfing generation, homozygosis increases, vigour and productiveness reduces by 50% due to inbreeding depression (Falconer 1989). Several authors have reported significant heterosis over mid and better parent as well as, inbreeding depression for grain yield and its components (Saleh *et al.* 1993; AL-Ahmad 2004; El-Badawy 2012). Heritability is a measure of the phenotypic variance attributable to genetic causes and has a predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences on the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Waqar-Ul-Haq *et al.* 2008 and Laghari *et al.* 2010). The most important function of heritability in genetic studies of quantitative characters is its predictive role to

indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay 1996). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Najeeb *et al.* 2009). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable conditions for selection. Ramanujam and Thirumalachar (1967) reported the limitation of estimating heritability in narrow sense, as it included both additive and epistatic gene effects, and thereby suggested that heritability estimates in the broad sense will be reliable if accompanied by a high genetic advancement. Different researchers (AL-Ahmad 2004; Rafique *et al.* 2004; Hefny 2011; Nagabhushan *et al.* 2011; El-Badawy 2012 and Ram Reddy *et al.* 2013) have reported high heritability and high genetic advance for different traits controlling the yield of maize. Therefore, availability of good knowledge of these genetic parameters existing in different yield contributing characters and the relative proportion of this genetic information in various quantitative traits is a pre-requisite for effective crop improvement.

Therefore, The present study aimed to obtain useful information and evaluate gene action involved in the inheritance of grain yield and some agronomic characters as well as potency ratio, hybrid vigor, inbreeding depression, phenotypic and genotypic coefficient of variations, broad and narrow sense heritability and genetic advance in two maize crosses.

Materials and methods

The field experiments were conducted at the Experimental Farm of the Maize Researches Department, General Commission for Scientific Agriculture Researches (G.C.S.A.R.) Damascus, Syria during the growing seasons of 2010, 2011 and 2012. In the first season (2010), the four parental lines IL.292-06, IL.565-06, IL.459-06 and IL.362-06 (Table 1) were intercrossed to produce two F₁ crosses i.e. IL.292-06 × IL.565-06 (cross 1), IL.459-06 × IL.362-06 (cross 2). In the second season 2011, F₁ plants of each cross were selfed and backcrossed to the two parents to obtain F₂, BC₁ and BC₂ generations. The six populations, i.e. P₁, P₂, F₁'s, F₂, BC₁ and BC₂ of the two maize crosses were grown during the third season 2012 in a randomized complete blocks design with three replicates in rows with 6 m long

and 70 cm apart with 25 cm between plants. The six populations of each cross were planted in 39 rows, i.e. 4 rows for each of P₁, P₂ and F₁, 7 rows for each of BC₁ and BC₂, and 13 rows for F₂. In each replicate, 60 plants of non-segregating populations and 120 plants of BC₁ and BC₂ and 180 plants of F₂ segregating populations were selected randomly for recording observations of nine traits, namely: days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of rows per ear, number of kernels per row, 100 kernel weight (g) and grain yield per plant (g).

Table 1. Names, origin and source of the inbred lines

Symbol	Inbred lines	Origin	Source
P ₁	IL.292-06	PMX- 1	U.S.A
P ₂	IL.565-06	Gota-1	Syria
P ₃	IL.459-06	Gota-1	Syria
P ₄	IL.362-06	Ideal	France

Statistical and genetic analysis

- To determine the presence or absence of non-allelic interactions, scaling test as outlined by Mather (1949) and Hayman and Mather (1955) was used. The quantities A, B, C and D and their variance have been calculated to test adequacy of the additive-dominance model in each case. Where:

$$A = 2\overline{BC_1} - \overline{P_1} - \overline{F_1}, \quad B = 2\overline{BC_2} - \overline{P_2} - \overline{F_1}, \quad C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2},$$

$$D = 2\overline{F_2} - \overline{BC_1} - \overline{BC_2}$$

The significance of A and B scales indicate the presence of all types of non-allelic gene interactions. The significance of C scale suggests [d × d] type of epistasis. The significance of D scale reveal [a × a] gene interaction, significance of C and D scales indicate [a × a] and [d × d] type of gene interactions (Singh and Narayanan 1993)

- The six parameters of the genetic model: mean effect [m], additive [d], dominance [h], additive × additive [i], additive × dominance [j] and dominance × dominance [l] were computed according to Jinks and Jones (1958) where: $m = \overline{F_2}$, $d = \overline{BC_1} - \overline{BC_2}$, $h = \overline{F_1} - 4\overline{F_2} - 0.5\overline{P_1} - 0.5\overline{P_2} + 2\overline{BC_1} + 2\overline{BC_2}$, $i = 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$, $j = \overline{BC_1} - 0.5\overline{P_1} - \overline{BC_2} + 0.5\overline{P_2}$, $l = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$

- Smith (1952) approaches used to estimate Potency ratio (P) as follows:

$$P = (F_1 - MP) / [0.5 \times (P_2 - P_1)]$$
 where: F_1 = the first generation mean, P_1 = the mean of the first parent, P_2 = the mean of the better parent and MP = mid parents value. Complete dominance is indicated when potency ratio is equal to (+1) or (-1). Partial dominance is the case when ratio between (+1) and (-1). Over-dominance indicated if ratio exceeds (± 1).
- Heterosis was expressed as the percentage deviation of F_1 mean performance from mid-parents and better parent according to Singh and Chaudhary (1977) as follows:

$$HMP = [(F_1 - \overline{MP})/\overline{MP}] \times 100$$
 and
$$HBP = [(F_1 - \overline{BP})/\overline{BP}] \times 100$$
- Inbreeding depression (%) were estimated according to Singh and Chaudhary (1977) as follows: $ID = [(F_1 - F_2)/F_1] \times 100$
- Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula suggested by Singh and Chaudhary (1977) as follows:

$$PCV = (S_{F_2}/\overline{X_{F_2}}) \times 100$$
 and
$$GCV = [(S_{F_2}^2 - S_B^2)/\overline{X_{F_2}}] \times 100$$
- Broad and narrow sense heritability were estimated using the formula proposed by Burton (1951) and Warner (1952): $BSH = S_G^2/S_{ph}^2$ and $NSH = S_G^2/S_{ph}^2$
- The expected genetic advance from selection was calculated using the formulae proposed by Johanson *et al.* (1955).

$$\Delta G = 2.0627 \times NSH \times S_{F_2}$$
 The predicted genetic advance where the expected genetic gain upon selection was expressed as percentage of F_2 mean.

$$\Delta G\% = (\Delta G/F_2) \times 100$$

Results and discussion

The means, variances, variance of means and coefficients of variation of the six generations with the two crosses for nine traits are presented in tables 2, 3, 4. The results indicated that means of the F_1 's were higher than either the highest parent or mid-parent value

indicating over or partial dominance, respectively towards the respective parents for most studied traits, as well as, the transgressive segregation for all traits was also observed in the F₂ generation. Similar results were obtained by AL-Ahmad (2004); Ishfaq (2011); Shahrokhi *et al.* (2011) and El-Badawy (2012).

Table 2. Means, variances, variance of means and coefficients of variation for days to 50% silking, plant and ear height.

Traits	Hybrids	Populations						LSD 5%	
		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂		
Days to 50% silking	(P ₁ ×P ₂)	Number of plants	60	60	60	180	120	120	0.67
		Mean	73.43	74.95	65.32	69.18	70.97	68.50	
		Variance	5.37	6.69	3.78	19.07	16.39	16.29	
		Variance of mean	0.09	0.11	0.06	0.11	0.14	0.14	
		CV%	3.16	3.45	2.98	6.31	5.70	5.89	
	(P ₃ ×P ₄)	Number of plants	60	60	60	180	120	120	0.36
		Mean	88.52	78.05	68.72	73.38	74.59	74.52	
		Variance	3.44	6.32	1.70	13.53	8.88	10.91	
		Variance of mean	0.06	0.11	0.03	0.08	0.07	0.09	
		CV%	2.10	3.22	1.90	5.01	4.00	4.43	
Plant height	(P ₁ ×P ₂)	Number of plants	60	60	60	180	120	120	2.30
		Mean	156.83	175.83	201.47	187.98	177.13	190.13	
		Variance	57.60	114.55	76.52	266.69	209.10	202.30	
		Variance of mean	0.96	1.91	1.28	1.48	1.74	1.69	
		CV%	4.84	6.09	4.34	8.69	8.16	7.48	
	(P ₃ ×P ₄)	Number of plants	60	60	60	180	120	120	1.75
		Mean	158.57	166.82	202.17	176.87	189.33	182.75	
		Variance	85.33	99.07	63.87	148.21	139.89	115.06	
		Variance of mean	1.42	1.65	1.06	0.82	1.17	0.96	
		CV%	5.83	5.97	3.95	6.88	6.25	5.87	
Ear height	(P ₁ ×P ₂)	Number of plants	60	60	60	180	120	120	1.07
		Mean	65.00	70.58	79.48	72.69	74.16	75.34	
		Variance	41.53	56.86	42.80	156.25	114.76	118.21	
		Variance of mean	0.69	0.95	0.71	0.87	0.96	0.99	
		CV%	9.91	10.68	8.23	17.20	14.45	14.43	
	(P ₃ ×P ₄)	Number of plants	60	60	60	180	120	120	1.29
		Mean	81.98	71.47	107.33	91.89	104.67	90.04	
		Variance	67.58	59.61	42.77	121.83	109.97	92.23	
		Variance of mean	1.13	0.99	0.71	0.68	0.92	0.77	
		CV%	10.03	10.8	6.09	12.01	10.02	10.67	

Table 3. Means, variances, variance of means and coefficients of variation for ear length, Ear diameter and Number of rows per ear.

Traits	Hybrids	Populations						LSD 5%	
		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂		
Ear length		Number of plants	60	60	60	180	120	120	
	(P ₁ ×P ₂)	Mean	15.50	16.16	22.48	19.56	18.6	20.37	0.25
		Variance	1.20	1.54	2.22	7.40	5.85	4.56	
		Variance of mean	0.02	0.03	0.04	0.04	0.05	0.04	
		CV%	7.08	7.67	6.63	13.91	13	10.48	
	(P ₃ ×P ₄)	Number of plants	60	60	60	180	120	120	
		Mean	13.98	15.03	20.58	17.97	17.58	18.62	0.27
		Variance	1.64	1.69	1.16	4.38	3.51	2.98	
		Variance of mean	0.027	0.028	0.019	0.024	0.029	0.025	
	Ear diameter		Number of plants	60	60	60	180	120	120
(P ₁ ×P ₂)		Mean	3.49	4.21	4.91	4.57	4.49	4.81	0.08
		Variance	0.14	0.14	0.11	0.17	0.16	0.15	
		Variance of mean	0.0023	0.0023	0.0019	0.0009	0.0014	0.0012	
		CV%	10.57	8.86	6.82	9.03	9.00	8.00	
(P ₃ ×P ₄)		Number of plants	60	60	60	180	120	120	
		Mean	3.59	4.13	5.53	4.94	4.70	5.00	0.07
		Variance	0.14	0.15	0.14	0.27	0.25	0.23	
		Variance of mean	0.0024	0.0026	0.0024	0.0015	0.0021	0.0019	
Number of rows per ear			Number of plants	60	60	60	180	120	120
	(P ₁ ×P ₂)	Mean	13.77	16.77	16.30	16.21	16.02	17.01	0.29
		Variance	2.18	2.32	1.87	4.19	3.33	3.42	
		Variance of mean	0.04	0.04	0.03	0.02	0.03	0.03	
		CV%	10.73	9.08	8.40	12.62	11.39	10.87	
	(P ₃ ×P ₄)	Number of plants	60	60	60	180	120	120	
		Mean	15.07	16.77	21.13	19.98	18.93	20.57	0.34
		Variance	1.52	2.32	2.66	6.12	4.23	4.79	
		Variance of mean	0.03	0.04	0.04	0.03	0.04	0.04	
			CV%	8.18	9.08	7.72	12.38	10.87	10.63

Potency ratio, heterosis and inbreeding depression

Potency ratio, heterosis and inbreeding depression in the two crosses are given in table 5. Potency ratio was calculated to determine the nature and degree of dominance for all studied characters. The results indicated that potency ratio values exceeded the unity in most of the studied traits except number of rows per ear for the first cross. Over dominance towards the higher parent was detected for most studied traits. Generally, potency values followed the same trend as heterotic effects for all traits. These results are in agreement with those obtained by AL-Ahmad (2004) and El-Badawy (2012).

The results in Table 5 denoted highly significant positive heterosis relative to mid and better parent for most studied traits in the two crosses, indicating that dominance direction was toward the best parent, with exception for days to 50% silking trait which showed highly significant negative heterosis relative to mid and better parent indicating that dominance direction was toward to the low respective parent. It is worth noting that heterosis effect for grain yield per plant was larger in magnitude than for any one of its components which is logically expected. The results of heterosis suggested that hybrid vigor is available for the commercial production of maize and selection of desirable hybrids among the crosses having heterosis and heterobeltiotic effects in other characters is the best way to improve the grain yield of maize. The significance of heterosis effects showed that non-additive genetic type of gene action affects such traits. These results were previously reported by Saleh *et al.* (1993); AL-Ahmad (2004) and El-Badawy (2012).

Values of inbreeding depression which are presented in table 5 were positive for all studied traits in the two crosses, except for days to 50% silking. As it is well known both heterosis and inbreeding depression effects are two coincides to a same particular phenomenon (Falconer 1981; Mather and Jinks 1982). Therefore, it is logically to expect that heterosis in F_1 will be followed by an appreciable reduction in the F_2 performance and vice versa due to the direct effect of homozygosis. These results are harmony with previous results obtained by Saleh *et al.* (1993); AL-Ahmad (2004) and El-Badawy (2012).

Table 4. Means, variances, variance of means and coefficients of variability for Number of kernels per row, 100-kernel weight and Grain yield per plant.

Traits Hybrids	Populations						LSD 5%	
	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂		
Number of kernels per row	Number of plants	60	60	60	180	120	120	
	(P ₁ ×P ₂) Mean	22.42	27.77	44.88	32.39	30.70	37.17	0.92
	Variance	9.98	9.06	13.53	50.66	36.95	31.9	
	Variance of mean	0.17	0.15	0.23	0.28	0.31	0.27	
	CV%	14.09	10.84	8.20	21.98	19.80	15.20	
	Number of plants	60	60	60	180	120	120	
	(P ₃ ×P ₄) Mean	23.87	25.73	40.42	33.54	31.63	34.47	0.4
	Variance	9.37	10.91	10.28	30.6	26.2	22.17	
100-kernel weight	Number of plants	60	60	60	180	120	120	
	(P ₁ ×P ₂) Mean	27.64	26.67	35.78	31.86	32.07	32.65	0.78
	Variance	6.41	6.25	5.57	22.23	15.95	15.46	
	Variance of mean	0.11	0.1	0.09	0.12	0.13	0.13	
	CV%	9.16	9.37	6.6	14.8	12.45	12.04	
	Number of plants	60	60	60	180	120	120	
	(P ₃ ×P ₄) Mean	23.4	24.78	31.77	29.09	28.22	27.45	0.42
	Variance	3.27	2.8	2.94	8.57	6.61	7.9	
Grain yield per plant	Number of plants	60	60	60	180	120	120	
	(P ₁ ×P ₂) Mean	72.80	95.58	227.44	128.81	111.27	163.78	3.12
	Variance	151.09	136.83	189.47	610.94	528.83	526.60	
	Variance of mean	2.52	2.28	3.16	3.39	4.41	4.39	
	CV%	16.88	12.24	6.05	19.19	20.67	14.01	
	Number of plants	60	60	60	180	120	120	
	(P ₃ ×P ₄) Mean	57.02	86.11	215.71	146.05	128.82	146.81	2.18
	Variance	235.28	335.72	153.17	1142.33	907.44	832.68	
Variance of mean	3.92	5.60	2.55	6.35	7.56	6.94		
CV%	26.90	21.28	5.74	23.14	23.38	19.66		

Phenotypic and Genotypic Coefficient of Variations, broad and narrow sense heritability and genetic advance

Data of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) for yield and yield component and for plant and ear height traits in the two crosses are presented in table 5. The PCV was greater than GCV for all studied traits in the two crosses. These results indicated that, the environment had an important role in the expression of these traits. There is enough scope for selection based on these characters and the diverse genotypes can provide materials for a sound breeding program. These results are in a harmony with those obtained by Shakoor *et al.* (2007); Hefny (2011) and Nagabhushan *et al.* (2011).

Genetic coefficient of variation indicates the genetic variability present in various quantitative traits without the level of heritability. Genetic coefficient of variation together with heritability estimates would give the best indication of the amount of gain due to selection (Swarup and Chaugale, 1962).

For all studied traits in the two crosses narrow sense heritability values were lower than those of broad sense indicating that most of genetic variance was due to non-additive effects i. e., dominance and/or epistasis. This finding ascertained the previously studies on the nature of gene action where the non-additive gene effects were found to have a great role in these traits. Such results are in agreement with that obtained by several investigators AL-Ahmad (2004); Rafiq *et al.* (2010); El-Badawy (2012) and Ram Reddy *et al.* (2013).

Table 5. Potency ratio (P), heterosis %, inbreeding depression (ID), phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad (H_{BS}) and narrow (H_{NS}) sense heritability, genetic advance (ΔG) and genetic advance as percentage of F₂ mean (ΔG%) for all studied traits in the two crosses.

Traits	Hybrids	P	Heterosis %		ID	PCV	GCV	H _{BS}	H _{NS}	ΔG	ΔG%
			MP	BP							
Silk	(P ₁ ×P ₂)	-11.67	-11.96**	-11.04**	-5.91	6.31	5.37	0.72	0.29	2.59	3.74
	(P ₃ ×P ₄)	-2.78	-17.49**	-11.95**	-6.78	5.01	4.25	0.72	0.54	4.08	5.56
Plant height	(P ₁ ×P ₂)	3.70	21.13**	14.58**	6.70	8.69	7.21	0.69	0.46	15.41	8.20
	(P ₃ ×P ₄)	9.57	24.26**	21.19**	12.51*	6.88	4.57	0.44	0.28	7.02	3.97
Ear height	(P ₁ ×P ₂)	4.19	17.24 ^{NS}	22.28*	8.54	17.20	14.38	0.70	0.51	13.12	18.05
	(P ₃ ×P ₄)	5.82	39.89**	50.17**	14.39	12.01	8.79	0.54	0.34	7.75	8.43
Ear length	(P ₁ ×P ₂)	20.15	42.01**	39.11**	12.99	13.91	12.25	0.78	0.59	3.33	17.02
	(P ₃ ×P ₄)	11.57	41.88**	36.93**	12.68	11.64	9.44	0.66	0.52	2.24	12.44
Ear diameter	(P ₁ ×P ₂)	2.94	27.53**	16.63 ^{NS}	6.92	9.03	4.44	0.24	0.17	0.14	3.16
	(P ₃ ×P ₄)	6.19	43.26**	33.90**	10.67	10.43	7.00	0.45	0.22	0.24	4.83
Number of rows per ear	(P ₁ ×P ₂)	0.69	6.75 ^{NS}	-2.80 ^{NS}	0.55	12.62	8.86	0.49	0.39	1.64	10.11
	(P ₃ ×P ₄)	6.13	32.73**	26.00**	5.44	12.38	9.96	0.65	0.53	2.69	13.47
Number of kernels per row	(P ₁ ×P ₂)	7.40	78.84**	61.61**	27.83*	21.98	19.48	0.79	0.64	9.41	29.05
	(P ₃ ×P ₄)	16.80	62.98**	57.09**	17.02	16.49	13.47	0.67	0.42	4.78	14.26
100-kernel weight	(P ₁ ×P ₂)	17.78	31.76**	29.45**	10.96	14.80	12.61	0.73	0.59	5.71	17.91
	(P ₃ ×P ₄)	11.13	31.88**	28.21**	8.44	10.06	8.11	0.65	0.31	1.86	6.38
Grain yield per plant	(P ₁ ×P ₂)	12.58	170.15**	137.96**	43.37**	19.19	16.50	0.74	0.27	13.89	10.78
	(P ₃ ×P ₄)	9.91	201.42**	150.51**	32.29**	23.14	20.55	0.79	0.48	33.23	22.76

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Johnson *et al.* (1955) reported that effectiveness of selection depends not only on heritability but also on genetic advance. Genetic advance was highest for grain yield per plant in the second cross (33.23) and lowest for ear diameter in the first cross (0.14). The genetic advance as percent of mean was highest in case of number of kernels per row in the first cross (29.05) followed by grain yield per plant in the second cross (22.76), while lowest recorded by ear diameter in the first cross (3.16). The information on heritability and

genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. In general, the characters that show high heritability with high genetic advance are controlled by additive gene action (Panse and Sukhatme 1957) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance. In the present study, high heritability along with high genetic advance was noticed for number of kernels per row trait, other characters showed moderate or low heritability along with moderate or low genetic advance which can be improved by inter-mating superior genotypes of segregating population developed from combination breeding.

Gene Effects:The results of the A, B, C and D scaling tests for assessing the validity of additive - dominance models are given in Table 6. The non-allelic interaction was found to be operating in the control of genetic variation among the six generations for most studied traits. On the other hand, the values of the A, B, C and D scaling tests were not significant in the first cross for ear height indicating the absence of non-allelic interaction and the additive - dominance model was adequate to demonstrate the genetic variation and it is important in the inheritance of this studied trait in such cross. These results are in agreement with those obtained by AL-Ahmad (2004); Azizi *et al.* (2006) and Ishfaq (2011).

The estimates of the six parameters, i.e. additive [d], dominance [h], additive \times additive [i], additive \times dominance [j] and dominance \times dominance [l] and means [m] are presented in Table 6. The mean effects were highly significant for all studied traits in the two crosses, indicating that these traits are quantitatively inherited. Additive effects [d] were significant for all traits in the two crosses, except days to 50% silking for the second cross, Ear height and 100-kernel weight for the first cross. Non-significance in those cases may be ascribed to large error variance (Edwards *et al.* 1975). As is shown in Tables 6, some of the additive effects were negative. The negative or positive

signs for additive effects depend on which parent is chosen as P_1 (Cukadar-Olmedo and Miller 1997 and Edwards *et al.* 1975). Dominance effects were positive and significant in the two crosses for all traits, except days to 50% silking which shows negative and significant values for dominance effects in the two crosses. With regard to the negative value of [h] observed for some studied traits indicated that the alleles responsible for less value of traits were over dominant over the alleles controlling high value (Cukadar-Olmedo and Miller 1997). The dominance gene effect was higher than additive gene effect for all studied traits in the two crosses indicating predominant role of dominant component of gene action in inheritance of these traits, so the selection for these traits should be delayed to later generation when dominant effect is diminished. These results are in agreement with the results of Sofi *et al.* (2006); Iqbal *et al.* (2010); El-Badawy (2012) and Shahrokhi *et al.* (2013).

As it is shown in Tables 6, different types of epistasis interaction effects were found for different traits and crosses, with the exception of ear height in the first cross, as well as, ear diameter and number of kernels per row in the second cross. Our results showed that, besides the additive and dominance genetic effects, epistatic components have also contributed to genetic variations for most of the characters studied. However, their relative magnitudes vary for different traits. In such a situation, the appropriate breeding method is the one that can effectively exploit the three types of gene effects simultaneously. The same finding was also reported by AL-Ahmad (2004); Sofi *et al.* (2006); Shahrokhi *et al.* (2011); El-Badawy (2012) and Sher *et al.* (2012). The signs associated with estimates of [i], [j] and [l] types of epistasis indicate the direction in which the gene effect influence the mean of the population (Mather and Jinks 1982). Most of the signs of the estimates of [l] were opposite to that of [h] in both crosses, indicating duplicate epistasis.

Table 6. Scaling test, parameters of gene effects and types of epistasis for all studied traits in the two crosses.

Traits	Hybrids	Scaling test				Parameters						Type of epistasis
		A	B	C	D	m	d	h	i	j	l	
Silk	(P ₁ ×P ₂)	**	**	-	-	69.18 ^{ns} ± 0.33	2.47 ^{**} ± 0.52	-6.65 ^{**} ± 1.70	2.22 ^{NS} ± 1.67	3.23 ^{**} ± 1.14	-2.14 ^{NS} ± 2.55	Com.
	(P ₃ ×P ₄)	**	**	**	**	73.38 ^{**} ± 0.27	0.07 ^{NS} ± 0.41	-9.86 ^{**} ± 1.39	4.70 ^{**} ± 1.36	-5.16 ^{**} ± 0.91	1.09 ^{NS} ± 2.03	Dupl.
Plant height	(P ₁ ×P ₂)	-	-	**	**	187.98 ^{**} ± 1.22	-13.00 ^{**} ± 1.85	17.74 ^{**} ± 6.28	-17.40 ^{**} ± 6.12	-3.50 ^{NS} ± 4.07	18.48 ^{**} ± 9.30	Com.
	(P ₃ ×P ₄)	**	-	**	**	176.87 ^{**} ± 0.91	6.58 ^{**} ± 1.46	76.16 ^{**} ± 4.85	36.68 ^{**} ± 4.66	10.71 ^{**} ± 3.40	-51.11 ^{**} ± 7.38	Dupl.
Ear height	(P ₁ ×P ₂)	-	-	-	-	72.69 ^{**} ± 0.93	-1.18 ^{NS} ± 1.39	19.93 ^{**} ± 4.77	8.24 ^{NS} ± 4.65	1.61 ^{NS} ± 3.07	-12.70 ^{NS} ± 7.03	Dupl.
	(P ₃ ×P ₄)	**	-	-	**	91.89 ^{**} ± 0.82	14.63 ^{**} ± 1.30	52.47 ^{**} ± 4.34	21.86 ^{**} ± 4.19	9.37 ^{**} ± 2.98	-43.17 ^{**} ± 6.54	Dupl.
Ear length	(P ₁ ×P ₂)	-	**	-	-	19.56 ^{**} ± 0.20	-1.77 ^{**} ± 0.29	6.35 ^{**} ± 1.03	-0.30 ^{NS} ± 1.00	-1.44 [*] ± 0.63	-1.02 ^{NS} ± 1.50	Dupl.
	(P ₃ ×P ₄)	-	**	**	-	17.97 ^{**} ± 0.16	-1.04 [*] ± 0.23	6.60 ^{**} ± 0.80	0.52 ^{NS} ± 0.78	-0.52 ^{NS} ± 0.52	-2.75 ^{**} ± 1.18	Dupl.
Ear diameter	(P ₁ ×P ₂)	**	**	**	*	4.57 ^{**} ± 0.03	-0.32 ^{**} ± 0.05	1.38 ^{**} ± 0.17	0.32 [*] ± 0.16	0.04 ^{NS} ± 0.12	-1.40 ^{**} ± 0.26	Dupl.
	(P ₃ ×P ₄)	*	**	**	-	4.94 ^{**} ± 0.04	-0.30 ^{**} ± 0.06	1.31 ^{**} ± 0.21	-0.36 ^{NS} ± 0.20	-0.03 ^{NS} ± 0.14	-0.26 ^{NS} ± 0.32	Dupl.
Number of rows per ear	(P ₁ ×P ₂)	**	*	*	-	16.21 ^{**} ± 0.15	-0.99 ^{**} ± 0.24	2.25 ^{**} ± 0.80	1.22 ^{NS} ± 0.77	0.51 ^{NS} ± 0.55	-4.14 ^{**} ± 1.21	Dupl.
	(P ₃ ×P ₄)	**	**	**	-	19.98 ^{**} ± 0.18	-1.64 ^{**} ± 0.27	4.29 ^{**} ± 0.95	-0.92 ^{NS} ± 0.92	-0.79 ^{NS} ± 0.60	-3.98 ^{**} ± 1.41	Dupl.
Number of kernels per row	(P ₁ ×P ₂)	**	-	**	*	32.39 ^{**} ± 0.53	-6.47 ^{**} ± 0.76	25.97 ^{**} ± 2.67	6.18 [*] ± 2.61	-3.80 [*] ± 1.62	-1.97 ^{NS} ± 3.86	Dupl.
	(P ₃ ×P ₄)	-	**	-	-	33.54 ^{**} ± 0.41	-2.84 ^{**} ± 0.63	13.66 ^{**} ± 2.14	-1.96 ^{NS} ± 2.08	-1.91 ^{NS} ± 1.40	-0.20 ^{NS} ± 3.19	Dupl.
100-kernel weight	(P ₁ ×P ₂)	-	**	-	-	31.86 ^{**} ± 0.35	-0.58 ^{NS} ± 0.51	10.63 ^{**} ± 1.78	2.00 ^{NS} ± 1.74	-1.07 ^{NS} ± 1.12	-5.57 ^{**} ± 2.60	Dupl.
	(P ₃ ×P ₄)	*	**	**	**	29.09 ^{**} ± 0.22	0.77 [*] ± 0.35	2.66 [*] ± 1.15	-5.02 ^{**} ± 1.12	1.46 ^{NS} ± 0.76	5.40 [*] ± 1.73	Com.
Grain yield per plant	(P ₁ ×P ₂)	**	-	**	**	128.81 ^{**} ± 1.84	-52.51 ^{**} ± 2.97	178.11 ^{**} ± 9.69	34.86 ^{**} ± 9.46	-41.12 ^{**} ± 6.32	38.30 ^{**} ± 14.58	Com.
	(P ₃ ×P ₄)	*	-	-	**	146.05 ^{**} ± 2.52	-17.99 ^{**} ± 3.81	111.21 ^{**} ± 12.82	-32.94 ^{**} ± 12.63	-3.45 ^{NS} ± 8.22	56.23 ^{**} ± 18.80	Com.

This kind of epistasis generally hinders the improvement through selection and, hence, a higher magnitude of dominance and [I] type of interaction effects would not be expected. It also indicated that selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. This result is supported by the findings of Azizi *et al.* (2006); Sofi *et al.* (2006); Ishfaq (2011) and Sher *et al.* (2012). On the other side, Grain yield per plant, days to 50% silking and Plant height in the first

cross and 100-kernel weight in the second cross revealed Same sign of [h] and [I] components indicated presence of complimentary type of gene action for these traits. Thus, these traits can be exploited through heterosis breeding. Similar results for the traits were reported by Iqbal (2009); Ishfaq (2011) and El-Mouhamady *et al.* (2013).

Conclusion

The traits evaluated in the present study had shown complex genetic behavior. The simple selection procedure in the early segregating generation may not play significant role for the improvement of these traits. The complex genetic behavior, particularly additive and dominance components could be successfully exploited in later generation. It is suggested that selection for the improvement of the examined traits should be delayed to later generation of segregation population in maize. After attaining homozygosis for maximum heterozygous loci in bulk method of selection is recommended.

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