GENERATION MEAN ANALYSIS USING GENERATION VARIANCE IN MAIZE TRAITS

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ABSTRACT

This study was conducted to evaluate the effect of gene action on grain yield and yield components of maize(*Zea mays* L.) using generation mean analysis method for six generations (P_1, P_2, F_1,F_2, Bc_1 and Bc_2)of two crosses of maize (H40×un44052)and (Ik8×Hs). The analysis of variance shows significant differences between generation means. Generation mean analysis revealed that the non-additive effect for plant height, No.of kernels row^{-1}, 300- kernel weight and grain yield plant^{-1}. In addition the result showed that complete and additive × additive variance were positive values for all traits, This is an indicator of the presence of complete dominance for those characteristics. The results indicated that the broad sense heritability values were more than the narrow sense heritability values. Positive heterosis was revealed for plant height and kernel yield plant^{-1} in both crosses.

Key word: Generation mean maize, variance, dominance, additive

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تحليل متوسطات الاجيال بأستعمال تباينات الاجيال في صفات الذرة الصفراء

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المستخلص

طبقت تجربة لتقدير تأثيرالفعل الجيني لصفات حاصل الحبوب ومكوناته للذرة الصفراء باستعمال طريقة متوسطات الاجيال لستة اجيال (الاب الاول والثاني والجيل الاول والثاني والتهجين الرجعي الاول والثاني) في تضريبين للذرة الصفراء (*Zea mays* L.) (OH40×un44052) و(IK8×HS). أظهر تحليل التباين وجود فروقات معنوية بين الاجيال كما أشار التحليل الى وجود أرجحية للتأثيرات غير الاضافية لأرتفاع النبات وعدد الحبوب في الصف ووزن 300 حبة و حاصل النيات. كما أظهرت النتائج ان قيم التباينات السيادية والاضافية × الاضافية كانت موجبة لجميع الصفات مما يدل على وجود سيادة تامة لهذه الصفات. كانت قيم التوريث بالمعنى الواسع عالية وبالمعنى الضيق منخفضة وسجلت الصفات أرتفاع وحاصل النبات أعلى قوة هجين موجبة في كلا التهجينين.

كلمات مفتاحية: متوسطات الاجيال، الذرة الصفراء، التباين، السيادة والاضافة.

INTRODUCTION

Maize is one of main cereal crop providing raw material for food industry and animal feed (18). In the past, considerable efforts were made to discuss maize productive ; however, further studies required to exploit the genetic potential of maize. Grain yield and yield components are two quantitative traits controlled by large number of genes in maize. The phenotypic expression of these traits depends upon the type of gene action, the choice of selection and breeding procedures for genetic improvement of maize depends largely on the acknowledge of type of gene action for different traits in the plant materials. The generation mean analysis is a useful technique used to determine gene effects of polygenic traits (12). Several researchers have reported the role gene action in yield, and other agronomic traits (8, 16, 9, 5 and 14). In addition, heterosis has important implication for both F_1 and for obtaining transgressed segregates in F_2 generation.(2 and 5), On other hand, heritability is a measure of the phenotypic variance attributable to genetic function and has a predictive in plant breeding. Knowledge about heritability affected the choice of selection procedures that used by the plant breeders to determine the best methods could be most useful to improve the trait and so that this parameters study from many researchers (19, 11, 7 and 13). The experiment was conducted to get information and evaluate gene action involved the inheritance of grain yield and its components in two maize crosses.

MATERIALS AND METHODS

A field experiment was carried out at the field of College of Agriculture, University of Duhok during the spring and fall seasons 2014. In spring season, the four inbred lines parents (Table-1) were inter crossed to produce two F_1 crosses (OH40×Un44052) and (IK8×HS). In the fall season 2014, F_1 plants of each cross were self pollinated and back crossed to the two parents to obtain F_1, Bc_1 and Bc_2 generations. The genetic materials were P_1, P_2, F_1, F_2, Bc_1 and Bc_2 of two maize crosses, were grown during spring season 2015, was used a randomize Complete Block design (RCBD) with three replications in rows with 3m long and 0.75m between the rows and 0.25m within the rows .Field was fertilized with (N.P.K.,27:27:0)at rate 400kg per ha.As first doses at planting date and 200 kg per ha .of urea(46%)were added. Weed control and other cultivate practices were performed according to plant requirement. The six generation of each cross were planted in 2 rows for each P_1 and P_2, 6 rows for F_1, 16 rows for F_2 and 12 rows for Bc_1 and Bc_2. In each replication, 20 plants of non-segregating generation and 120 plants of Bc_1, Bc_2 and 160 plants of F_2 segregating generation were selected randomly for recording data for four traits namely, plant height (cm),No. of kernels row^{-1}, 300-kernel weight and grain yield plant^{-1}.

Table1. Symbol, original and source of inbred lines

Symbol	inbred lines	origin source
P_1	OH40	USA
P_2	Un44052	Greece
P_3	Ik8	IPA
P_4	HS	USA

Generation means analysis was performed for crossing using the genetic model described by Mather and Jink(12) and notation by Hyman (6) to study the six parameters model, and heterosis estimate according to the following formula.

$$H\% = \frac{F_1 - M\bar{P}}{M\bar{P}} \times 100$$

RESULTS AND DISCUSSION

The results of the analysis of variance and mean square four traits for crosses and their generation are presented in Table 2. The result showed that all generation within crosses had significant differences of four traits, indicating the existence of genetic variation and possibility of selection for yield and yield components. This is finding indicates that further portion of genetic variance to its components and the comparisons between means are valid with respect to the traits under study. The development of any plant breeding program is dependent upon the existence genetic variation (17, 15, 3 and 1).

Table 2. Analysis of variance for traits of six generation for cross $_1$ and cross $_2$.

sov	Df	hybridization	MS of traits Plant height (cm)	No. Kernel Row^{-1}	300 grain Weight (g)	Grain yield Plant^{-1} (g)
Replication	2	Cross $_1$	396.81	20.11	20.04	968.47
		Cross $_2$	742.36	230.19	46607.66	11354.3
Generation	5	Cross $_1$	** 31603.56	** 3310.70	** 16896.85	** 206099.14
		Cross $_2$	** 25445.28	** 5735.25	** 427306.70	** 319373.05
Experimental error	10	Cross $_1$	3891.77	66.45	5.45	2505.56
		Cross $_2$	390.04	225.02	31320.95	4487.34
Sampling Error	1484	Cross $_1$	1265.94	20.57	- 6.58	20652.54
		Cross $_2$	71.52	18.97	190.61	1371.33
Total	1501					

***, ** significant difference at level 0.05 and 0.01, respectively**

Mean values and their standard errors for the four traits of two crosses are presented in Table 3. The mean values of the four traits for F_1 generation were derived four the (OH40 ×Un44052) cross and gave higher mean of mid parents and the values reached 193.02, 42.33, 88.44 and 196.69, while the mid parents had 169.18, 36.64, 79.35 and 144.73 respectively. The results of the second cross of the F_1 and P_1 and P_2 were the same results for cross$_1$. The mean values of F_2 generation gave lower than the of values for the four traits compare with Bc_1 and Bc_2 in both crosses, furthermore, the transgressed in the F_2 generation for all traits was also observed in F_2 generation. These results were previously reported by other researcher (2, 9, 14).

Table 3. Generations mean and standard error (SE) of for traits in two crosses of corn inbred Lines.

Generation	Traits (Mean ± SE) Plant height (cm)	No. Kernel Row^{-1}	300- grain Weight (g)	Grain yield Plant^{-1} (g)
	Cross$_1$:(OH40 × Un44052)			
P_1	141.20 ± 0.62	36.71 ± 0.45	86.98 ± 0.55	142.74 ± 3.10
P_2	197.16 ±1.35	36.28 ±0.53	71.73 ±1.60	146.72 ±2.17
F_1	193.02 ±0.85	42.33 ±0.50	88.44 ±0.64	196.69 ±2.45
F_2	180.66 ±1.08	32.14 ±0.55	66.79 ±0.70	110.24 ±2.17
Bc_1	183.29 ±1.04	38.21 ±0.62	72.21 ±0.80	140.54 ±2.68
Bc_2	188.82 ±9.91	37.29 ±0.71	79.67 ±0.90	148.24 ±2.30
	Cross$_2$: (IK8 × HS)			
P_1	138.46 ±1.25	34.73 ±039	73.18 ±0.60	123.43 ±1.20
P_2	181.35 ±1.31	32.13 ±0.43	67.43 ±0.93	136.00 ±1.81
F_1	190.29 ±0.59	44.98 ±0.26	84.93 ±0.77	222.90 ±2.06
F_2	176.22 ±1.02	30.58 ±0.37	67.30 ±1.10	115.37 ±3.68
Bc_1	178.33 ±1.01	32.91 ±0.23	68.57 ±0.59	140.53 ±7.68
Bc_2	181.08 ±0.49	34.18 ±0.36	57.30 ±0.30	142.92 ±1.24

The estimation of the variance of the six parameters mean(m), additive (d), dominance(h), additive × additive(i),Additive × dominance(j) and dominance × dominance (I) are presented in Table 4. The mean effects were highly significant for all studied traits in the two crosses, indicating that these traits are quantitatively inherited. Dominance effects were significant for all traits in the two crosses and non-significant effect for additive, excepted 300-kernel weight. The dominance gene effect was higher than additive gene effect for all traits, except plant height in $cross_1$, indicating the predominant role of dominate component of gene action inheritance of these traits, therefore the hybridization would be more effective than population selection. Similar results in maize were reported by (16, 9, 5 and 14). The results in the same table were shows that the additive × additive(i) interaction were significant for the four traits. Thus, additive gene action was most important in the inheritance of these traits while, the significant additive × dominance(j) effects were positive, indicating that dominance was words direction of increasing the studied traits. Also the results in Table 4 Shows the dominance and additive × additive gave positive value for all traits this mean complementary gene effect controlling various traits in maize. The results are in agreement with the results reported by several Researchers (15, 2 and 1).

Table 4. Variance of six generation parameters for cross $_1$ and cross $_2$

Genetic parameters	Traits			
	Plant height (cm)	No. Kernels Row $^{-1}$	300-kernel Weight (g)	Grain yield Plant $^{-1}$ (g)
	Cross $_1$: (OH40 × Un44052)			
M	1.2 ** ±1.8	0.3 * ±0.55	0.5 ** ±0.70	4.70 ** ±2.16
D	99.2 ±9.96	0.9 ±0.94	1.5 ** ±11.21	64.23 ±8.01
H	24.20 ** ±4.92	6.84 * ±2.61	11.5 ** ±3.39	570.91 ** ±23.89
i	415.57 * ±20.39	8.45 * ±2.91	13.60 ** ±3.69	332.12 ** ±18.22
j	99.88 ±9.99	1.05 ±1.03	2.24 ** ±1.50	570.87 ±23.89
I	1611.53 ±40.14	20.58 ±4.54	35.58 ±5.97	2142.50 ±46.28
	Cross $_2$: (IK8 × HS)			
M	1.1 ** ±1.04	0.13 ±0.36	1.2 ** ±1.10	13.15 3.67
D	1.3 ±1.12	0.18 ±0.4	11.30 ** ±3.35	60.49 ±7.77
H	22.5 * ±4.74	2.54 ±1.59	21.30 ** ±4.61	457.44 ±21.38
i	22.30 ±4.72	2.92 ±1.72	64.29 ** 8.02	458.18 ±21.40
J	2.47 ** ±1.57	0.30 ±0.55	11.64 ** 3.41	62.02 ±7.87
I	42.14 ±6.49	5.76 ±2.40	202.93 ** ±14.25	1205.77 34.72

***, ** significant difference at level 0.05 and 0.01, respectively**

For most traits, dominance variance (H) was more than additive variance (D), (Table 5) therefore hybridization would be more effective than population selection, furthermore all traits gave the positive values for dominance except grain yield in $cross_1$ and kernel no row^{-1} in $cross_2$ negative value of F for some traits, such as 300- kernel weight and grain yield in $cross_1$ and grain yield in cross $_2$. For average degree of dominance (H/D) ½, the traits were not gave values except grain yield plant^{-1} in cross $_1$ and plant height in $cross_2$.

Table 5. Variance of the components of variation, dominance ratio, F/ (D×H) ½ ratio and degree of dominance for four traits of cross $_1$ and cross$_2$

Traits	D	H	F	EW	(H/D)½ Average Degree of dominance
		CROSS $_1$: (OH40 × Un44052)			
Plant height (cm)	** - 193.82	** 24226.83	6004.02	25.56	_______
No. Kernels Row^{-1}	- 0.55	_______	_______	7.40	_______
300-kernel Weight (g)	- 0.97	** 179.81	- 1.04	22.48	_______
Grain yield Plant^{-1} (g)	- 7692.70	** - 3727.42	- 3965.02	5191.47	0.69
		CROSS $_2$ (IK8 × HS)			
Plant height (cm)	1.78	** 42.48	- 98.16	23.54	4.90
No. Kernels Row^{-1}	20.14	- 4.48	3.89	3.04	_______
300-kernel Weight (g)	- 17.68	_______	649.40	18.48	_______
Grain yield Plant^{-1} (g)	- 4075.36	** 1249.96	- 4211.09	107.99	_______

D, H, EW is the variance of additive, dominance and environment, respectively. F is correlation between H and D in all loci and (H/D) ½ is degree of dominance.

Regarding broad and narrow sense heritability, the results indicate that plant height, kernel No. row^{-1}, 300 kernel weight and grain yield had the highest broad sense heritability (0.99, 0.99, 0.96, 0.99) respectively, (Table 6). However narrow sense was low for the same traits in cross$_1$. while the broad sense and narrow sense In cross$_2$, the results exhibited the highest values for broad sense heritability in the same traits and the values (0.88, 0.88, 099, and 0.99) respectively), and the all traits recorded low values for narrow sense heritability except plant height and No. of kernels row^{-1} because the additive value was low compare to the dominance value. For the heterosis, the plant height and yield plant^{-1} recorded positive heterosis and the value were 23.84 and 51.96, respectively in cross $_1$ while, the cross $_2$in the same traits had the highest positive heterosis with value 30.38 and 92.18. It could be conclude that the hybridization method syerained to selection (18).

Table 6. Estimation heritability broad, narrow sense and heterosis for four maize traits

Genetic Parameters	Hybridization	Plant height (cm)	No. Kernel Row $^{-1}$	300 kernel Weight (g)	Grain yield Plant^{-1} (g)
$h_{.b.s}$	CROSS $_1$	0.99	0.99	0.96	0.99
	CROSS $_2$	0.88	0.88	0.99	0.99
$h_{.n.s}$	CROSS $_1$	0.00	0.00	0.00	- 0.93
	CROSS $_2$	0.625	0.84	0.00	0.00
Heterosis%	CROSS $_1$	23.84	5.83	9.08	51.96
	CROSS $_2$	30.38	11.54	14.45	92.18

Cross $_1$: (OH40 × Un44052) and cross $_2$: (IK8 × HS)

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