

ESTIMATION GENE EFFECTS BASED ON JOINT SCALING TEST AND SOME GENETIC PARAMETERS IN FOUR MAIZE CROSSES.

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ABSTRACT

In order to estimate the components of genetic variation, phenotypic (PCV), genotypic (GCV) coefficient of variation, genetic gain and its percentage, an experiment was conducted at the field of Field Crop Dept. College of Agric.-Univ. of Baghdad four crosses (FI01301×Rustico), (AntignaoHi39×Nostred), (Lo1391×Rustico) and (Rusticocangini×Rustico) produced from crossing of genetically different six inbred lines of maize (*Zae mays* L.). Genetic parameters were estimated according to the Joint scaling test using the randomized complete block design with four replications. The components genetic variance, Additive and dominance of the maize grain and other trait, were estimated. The results showed that the values of chi square was significant for all traits of all crosses, thus the simple additive – dominance model in four crosses exhibited lack of good fit for all traits, indicates the role of non-allelic interaction. Dominance gene action was higher than additive for most traits. Therefore the hybridization would be more effective than population selection to improve these traits for these crosses.

Key word : *Zae mays* L., Chi-square, additive, gene action, yield.

Introduction

The aims of many maize breeding programs usually includes the development of maize hybrids or varieties with high grain yield potential. Grain yield and its components are quantitative traits controlled by huge number of genes in maize. The phenotypic expression of these traits depends mainly on the type of gene action (dominance and additive) effects and effects due to the interaction of genotype and environment. Many genetic models have been proposed for the estimation of gene action, most of these genetic models were developed to estimate relative importance of additive and dominance gene effects. In order to choose the best hybrids combinations, a large number of inbred lines are crossed with each other (12,17). Generation mean analysis is a simple, but it useful technique

for estimating genetic effects for polygenic traits. Gamble (5) indicated that the estimate of genetic effects can help the plants breeders to decide the breeding procedures better suited for the improvement of the trait being analyzed. The estimates of gene effects indicate that the dominance effect were higher than mean and additive effects for all traits and all crosses, indicated the importance role of dominance component of gene action in inheritance traits (19). The value of PCV and GCV were indicating the important of the environment and the genetic interaction in the inheritance of the traits (7). The objectives of experiment was estimate gene action via joint scaling test and best fit model of generation mean analysis.

Materials and Methods

Six inbred lines of maize (AntignaoHi39, FI1301, Rusticocangini, Rustico, L01391, Nostred) were tested in Field crops Dept. College of Agric. Univ. of Baghdad. The homozygous inbred have crossed to produce F₁ (First generation). Four superiors crosses were selected (FI01301×Rustico), (AntignaoHi39× Nostred), (Lo1391×Rustico) and (Rusticocangini× Rustico). F₁' planted in spring 2012 with parents to produce Bc₁ and Bc₂. F₁'s were selfed to produce F₂ in fall 2012. The six generation P₁, P₂, F₁, Bc₁, Bc₂ and F₂ of four cross were grown at 2013 in a randomized complete block design with four replications in rows with 5 m long and 70 cm between rows and 25 cm within rows. The data from six generations were analyzed in dependently using (spar2.) to obtain Joint scaling test (2) were used to test the adequacy of the additive – dominance model. [m](mid parents effect), [d] additive effect, [h](dominance effect). Estimation of Phenotypic coefficient of variation PCV and genotypic coefficient of variation GCV were estimated using formula suggested by Sing and chudhary (16) as follows:

$$PCV = (SF_2 / \overline{XF_2}) \times 100$$

$$GCV = [(SF_2 - S^2E) / \overline{XF_2}] \times 100$$

SF₂ = second generation variance

The expected genetic advance from selection was calculated using formula proposed by Johnson et al. (10).

$$\Delta G = 2.0627 \times h^2_{n.s} \times SF_2$$

The predicted genetic advance where the expected genetic gain upon selection was expression percentage of F₂ mean

$$\Delta G\% = (\Delta G / \overline{F_2}) \times 100.$$

Result and Discussion

Phenotypic and genotypic coefficient

Table 1. illustrate the data of phenotypic coefficient of variation (PCA) and genotypic coefficient variation (GCV) for some traits in four crosses of maize. The PCV values were close to PCV values for ear weight of cross 1, leaves area for cross 2, 3 and 4, number of ears per plant of cross 3, indicated these traits were genetically controlled and the phenotypic of plant represents the genotype. Other traits, the GCV values were much less than PCV, indicated that the environment had important role in the expression of these traits. This result agrees with those obtained by (8,14).

The genetic coefficient of variation expresses a genetic variability in the quantitative traits.

Genetic advance and its percentage.

The effectiveness of selection depends not only on heritability but also on genetic advance (10). The genetic advance is a best indicative of the progress that can be expected from selection on the population are presented in table 1. The highest value of genetic advance was 58.84 for the plant height of cross 4, it range between 0.031 for leaves area of cross 4, to 17.52 for grain yield of cross 1. As well as, the value of genetic advance percentage for number of ears per plant was high (65.22) for cross 4, followed by leaf area (50.03), number of ears/plant 49.96 for cross 2 and plant height 49.17 for cross 4. Other traits showed moderate or low genetic advance percentage.

Table1. Phenotypic and genotypic coefficient of variability (PCV), (GCV) , Genetic advance (ΔG) and genetic percentage of F2 means ($\Delta G\%$) for several traits in four crosses.

Crosses	Traits	PCV%	GCV%	ΔG	$\Delta G\%$
FI01301×Rustico	Plant height(cm)	4.81	2.81	10.39	6.89
	No. of leaves	15.87	8.62	2.32	20.22
	Leaf area (m²)	16.56	13.57	0.098	21.81
	No. branches/tassel	16.42	10.27	0.842	9.40
	No. ears/plant	58.14	17.28	0.245	20.83
	Ear weight (gm)	19.05	17.23	8.45	23.53
	Grain yield (gm)	19.3	11.5	17.52	25.05
AntignaoHi39× Nostred	Plant height(cm)	5.57	1.75	4.52	4.79
	No. of leaves	18.25	9.92	2.85	28.57
	Leaf area (m²)	38.02	36.86	0.152	50.03
	No. branches/tassel	27.45	3.45	3.73	29.29
	No. ears/plant	31.52	28.55	0.589	49.96
	Ear weight (gm)	14.48	6.36	16.53	19.53
	Grain yield (gm)	16.92	5.39	15.59	21.46
Lo1391 × Rustico	Plant height(cm)	10.89	5.25	13.53	11.14
	No. of leaves	11.81	7.80	1.82	15.82
	Leaf area (m²)	22.13	21.57	11.92	29.89
	No. branches/tassel	23.82	4.278	4.413	32.05
	No. ears/plant	16.60	15.77	0.303	24.20
	Ear weight (gm)	7.98	2.54	16.05	9.87
	Grain yield (gm)	13.45	5.78	14.27	15.74
Rusticocangini× Rustico	Plant height(cm)	22.86	11.13	58.84	45.17
	No. of leaves	17.32	9.52	2.063	23.75
	Leaf area (m²)	9.28	9.20	0.0305	8.74
	No. branches/tassel	23.80	3.56	5.25	36.84

	No. ears/plant	70.24	58.24	2.063	65.22
	Ear weight (gm)	10.26	4.35	9.99	9.10
	Grain yield (gm)	8.22	3.32	9.60	10.41

Components of Variation

Three parameters m, d and h components and their standard error are presented in tables 3

Cross 1 : Three parameters ;m,d and h components and their standard error are presented in table 3. The table illustrate that most traits have high significant values for parameters m .Number of ears per plant was significant only. The trait plant height have highest value (121.49) , followed by grains yield (85.79) and ear weight (77.60). All values of additive were positive but its lower than dominance for all traits .Plant height ,number of branches per tassel ,ear weight and grains yield were highly significant , number of leaves, and number of ears per plant were non-significant .All dominance values were highly significant except leaves area was significant .It is illustrate that this case

Table 2. Estimation of gene effects of joint scaling test and best fit model applied for various traits in maize cross1.

Traits	M	[d]	[h]	X ²
Plant height(cm)	121.49±1.04**	16.31±1.05**	20.46±2.12**	868.44**
No. of leaves	9.71±0.23**	0.31±0.23 ^{n.s}	2.06±0.56**	14.17**
Leaf area (m ²)	0.359±0.003**	0.003±0.0028 ^{n.s}	- 0.036±0.006*	89.81**
No. branches/tassel	10.24±0.13**	3.38±0.13**	4.14±0.028**	3336.73**
No. ears/plant	0.57±0.228*	0.45±0.234 ^{n.s}	1.23±0.539**	6.64 ^{n.s}
Ear weight (gm)	77.60±2.23**	6.66±2.24**	202.23±6.47**	973.94**
Grain yield (gm)	85.79±0.461**	1.69±0.44**	7.36±0.98**	950.66**

could resulted of over dominance ($\delta^2h > \delta^2d$).

A six parameters model was applied to accommodate epistasis for these traits. Thus hybridization would be more effective than population selection. Dorri et al (3) found significant differences among generations for all traits. Dominance variance was more important than additive variance for most of traits. Hadi (6) found that both of genetic effects additive d, and dominance h were significant for all crosses, but the dominance variation was more important than the additive variation in the ear length, grain weight and yield of unit area. As well wannows et al . (18) reported that dominance gene effect play the major role in controlling the genetic variation of the most studied traits.

cross 2

The values of m for plant height, number of leaves ,number of branches per tassel, ear weight, and grain yield were highly significant, only leaves area was significant(table 3), the remaining traits were non significant. The high value was(112.50) for plant height followed by (75.85) for ear weight (65.14) for number of leaves and (59.09) for grains yield .Three traits only were highly significant ,the other were non significant; for additive variance ,Number of branches per tassel was negative .All these values of additive are less than dominance variance ,whose

values are highly significant. thus hybridization would be more effective than population selection. This case could resulted from over dominance. Significant dominance effects were indicated in all crosses for plant height and these effects were much higher in magnitude than their corresponding additive effects (9). The estimates of gene effects indicate that the dominance gene effects were quite important in the inheritance of yield. Estimates of additive gene effects were of low magnitude and many were non-significant (5).

Table 3. Estimation of gene effects of joint scaling test and best fit model applied for various traits in maize cross2.

Traits	M	[d]	[h]	X ²
Plant height(cm)	112.50±0.653^{**}	2.67±0.642^{**}	9.61±1.12^{**}	140.93^{**}
No. of leaves	65.14±0.135^{**}	0.07±0.124^{n.s}	2.26±0.27^{**}	5.35^{n.s}
Leaf area (m²)	0.276±0.135[*]	0.001±0.133^{n.s}	0.07±0.354^{n.s}	0.04^{n.s}
No. branches/tassel	9.93±0.253^{**}	-0.002±0.242^{n.s}	2.42±0.52^{**}	154.63^{**}
No. ears/plant	3.87±0.138^{**}	0.084±0.138^{n.s}	1.34±0.277^{**}	41.62^{**}
Ear weight (gm)	75.85±0.827^{**}	4.52±0.83^{**}	85.15±1.765^{**}	505.37^{**}
Grain yield (gm)	59.09±0.66^{**}	5.97±0.651^{**}	57.73±1.39^{**}	86.09^{**}

Cross 3.

Most chi-square values for this cross were significant for all traits according to joint scaling test. Also, all values of m were positive and highly significant. The value of (d) close to the value of (h) for trait plant height. This mean, hybridization after selection can used to improve this trait. The additive values (d) for number of leaves, number of ears/plant, were non-significant and very low, whereas the dominance value was more than it and highly significant. This indicate that the trait controlled by dominance effect and

non-allelic interaction was present and therefore the analyze of six parameter must done. While both of leaf area was a contrary of this, the additive value was more than dominance. Amer et al. (1) reported that the additive genetic variance was predominant in the inheritance of plant height and ear height. As well Singh and Roy (15) observed that plant height and days to maturity were governed by the additive types of gene effects. Number of branches/tassel, ear weight, grain yield/plant and no.of grains/row, all were high significant for (d) and (h), but the (h)

values were highest values than (d) values indicate that dominance effect controlled these traits, therefor, the significant heterosis in these traits of this cross is result of over dominance or the dispersion of dominant increasing alleles in the parental lines. Hadi (6) found that the

dominance variation was more important than the additive variation in the grain weight and yield ton/ha. El-Badawy(4) and Shahrokhi et al (13) reported the importance of non-additive gene action for grain yield and some other agronomic traits.

Table 4. Estimation of gene effects of joint scaling test and best fit model applied for various traits in maize cross3.

Traits	M	[d]	[h]	X ²
Plant height(cm)	126.28±0.76**	12.91±0.77**	12.62±1.66**	45.31**
No. of leaves	9.89±0.16**	0.11±0.164 n.s	1.93±0.288**	36.99**
Leaf area (m ²)	0.379±0.004**	0.0195±0.005**	-0.0057± 0.10 n.s	102.65**
No. branches/tassel	10.31±0.11**	3.25± 0.12**	3.84±0.12**	3641.15**
No. ears/plant	1.14±0.013**	-0.046±0.043 n.s	0.405 ±0.074**	32.35**
Ear weight (gm)	97.58±0.618**	29.57±0.639**	82.77±1.39**	3267.98**
Grain yield (gm)	66.56±0.503**	22.37±0.515**	78.46±1.158**	274.4**

Cross 4.

All values of chi-square were highly significant for all traits indicated the according to joint scaling test, thus the three parameters model to explain the genetic variability for these traits were inadequacy. For this, a six parameters model must be applied to accommodate epistasis (This model has been presented in a paper in The Iraqi Journal of Agricultural Sciences(6). All values of m were highly significant. All traits for this

cross exhibited dominance variance more than additive except the trait of plant height which the additive gene effect was more than dominance, indicating that the additive gene action was important type of gene action. The dominance effect of the generation means was greater than the additive effect for all traits indicated that the non-allelic interaction was exist.

Table 5. Estimation of gene effects of joint scaling test and best fit model applied for various traits in maize cross4.

Traits	M	[d]	[h]	X ²
Plant height(cm)	131.09±0.43**	8.20±0.44**	3.39±0.623*	67.49**
No. of leaves	9.81± 0.17**	0.309±0.198 ^{n.s}	1.39±0.57**	30.79**
Leaf area (m ²)	0.35±0.004**	0.013±0.0036**	0.066±0.01**	141.57**
No. branches/tassel	7.51±0.239**	0.544±0.278*	15.69±0.537**	229.31**
No. ears/plant	1.135±0.029**	-0.063±0.031*	0.215±0.043**	11.32*
Ear weight (gm)	112.00±0.868**	13.83±0.924**	47.39±1.35**	223.75**
Grain yield (gm)	74.52±0.5557**	14.28±0.575**	38.96±0.916**	148.02**

The simple additive-dominance model exhibited lack of good fit for all the traits in all crosses which indicated the presence of non-allelic interaction in all traits. Thus, the joint scaling test of five parameters model and six parameters must be done (its done and publish in other paper in The Iraqi Journal of Agricultural Sciences, (6)

In this research, three parameters model m, d and h was found to exhibit the lack of good fit for all traits in all crosses studied, showing the significant of chi-square value, which revealed the presence of non-allelic interactions.

All traits in all crosses, the dominance variance (h) were more than additive variance (d) whether highly significant or just significant or not. Thus hybridization would be more effective than population selection. Only traits plant height , additive effect greater than dominance effect, in this case selection would more effective to improve the trait. Estimate of additive gene effects would be expected to be larger if random unselected inbred lines were used.

If additive effects have only minor importance in the total variation of yield performance, more rapid advance will be

made in a breeding program for the improvement of yield performance in maize by using a breeding procedure which emphasizes the dominance and epistatic gene effects.

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تقدير التأثيرات الجينية باستعمال تحليل joint scaling وبعض المعايير الوراثية لاربعة تضريبات من الذرة الصفراء

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المستخلص

من اجل تقدير مكونات التباين الوراثي ، ومعامل التباين الوراثي والمظهري والتحصيل الوراثي ونسبته من المتوسط ، طبقت تجربة في حقل قسم المحاصيل الحقلية - كلية الزراعة - جامعة بغداد لاربعة تضريبات $\text{Rustico} \times \text{FI01301}$ و $\text{Nostred} \times \text{AntignaoHi39}$ و $\text{Rustico} \times \text{Lo1391}$ و $\text{Rustico} \times \text{Rustico}$ ناتجة من تضريب ست سلالات مختلفة وراثيا من الذرة الصفراء. تم تقدير مكونات التباين الوراثي وفقا لاختبار Joint باستخدام تصميم القطاعات الكاملة المعشاة باربعة مكررات. قدر التباين الوراثي بمكونيه المضيف والسيادي لحاصل حبوب الذرة الصفراء وبعض الصفات الاخرى. اوضحت النتائج معنوية قيم اختبار مربع كاي لكل الصفات المدروسة ولكل التضريبات وهذا يوضح عدم كفاية هذا التحليل ووجوب اجراء تحليل معالم اخرى (ست معالم وراثية) لوجود تداخلات جينية غير اليلية. اظهرت النتائج ان قيم فعل الجين السيادي كانت اكثر من المضيف لمعظم الصفات لذا فان التهجين يكون اكثر فعالية من الانتخاب لتحسين هذه الصفات لهذه التضريبات .

كلمات مفتاحية: الذرة الصفراء ، مربع كاي ، فعل الجين المضيف ، الحاصل