ESTIMATION GENE EFFECTS BASED ON JOINT SCALING TEST AND SOME GENETIC PARAMETERS IN FOUR MAIZE CROSSES
1-YIELD COMPONENTS

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ABSTRACT

The objective of this study 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.Coll. Agric.-Univ. Baghdad, using four crosses (FI01301×Rustico), (AntignaoHi39× Nostred), (Lo1391× Rustico) and (Rusticocangini× Rustico) which developed from crossing of genetically different of six inbred lines for maize *(Zae mays* L.), introduced from Italy. Genetic parameters were estimated according to the Joint scaling test using the randomized complete block design with four replications. The components of genetic variance; Additive and dominance of the maize grain yield and some trait, were estimated. The results showed that the values of Chi square were significant for all the studied some 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.

تقدير التأثيرات الجينية باستعمال تحليل Joint Scaling وبعض المعايير الوراثية لأربعة تضريبات من الذرة الصفراء
1-مكونات الحاصل

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المستخلص

يهدف البحث تقدير مكونات التغاير الوراثي، ومعامل التغاير الوراثي والمظهري والتحصيل الوراثي ونسبته من المتوسط، طبقت تجربة في حقل قسم المحاصيل الحقلية – كلية الزراعة – جامعة بغداد لاربع تضريبات (FI01301×Rustico) و(AntignaoHi39× Nostred)و(Lo1391 ×Rustico) و(Rusticocangini× Rustico) ناتجة من تضريب ست سلالات مختلفة وراثيا من الذرة الصفراء .تم تقدير مكونات التغاير الوراثي وفقا لاختبار Joint scaling باستخدام تصميم القطاعات الكاملة المعشاة بأربع مكررات. قدر التباين الوراثي بمكونيه المضيف والسيادي لحاصل حبوب الذرة الصفراء ومكوناته فضلا عن صفات اخرى.أوضحت النتائج معنوية قيم اختبار مربع كاي لكل الصفات المدروسة ولكل التضريبات كانت معنوية وهذا يوضح عدم كفاية هذا التحليل ووجوب أجراء تحليل معالم أخرى (ست معالم وراثية) لوجود تداخلات جينية غير الىلية. أظهرت النتائج أن قيم فعل الجين السيادي كانت أكثر 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

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INTRODUCTION

The main objective of maize breeder usually includes the development of maize hybrids or varieties with highest potential of grain yield and its component. Grain yield and its components are quantitative traits controlled by higher number of genes in maize. The phenotypic expression of these traits depends mainly on the type of gene action (dominance and additive) effects and interaction of genotype with environment. Many genetic models have been recommended 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 (10,15). Generation means analysis are a simple, and useful technique for estimating genetic effects for polygenic traits. Gamble (5) indicated that the estimation of genetic effects can help the plant breeders to estimate the breeding procedures favorable for the improvement of the traits being analyzed. The estimates of gene effects indicates that the dominance gene effect were higher than mean and additive effects for all the traits and crosses, indicating the importance role of dominance component of gene action in the traits inheritance (17).The value of PCV and GCV could be indicated the importance of the environment and the genetic interaction in the inheritance of the traits (1).The objectives of this experiment were to estimate the gene action via Joint scaling test and desirable model of generation means analysis.

MATERIALS AND METHODS

Six inbred lines of maize (AntignaoHi39, FI1301, Rusticocangini, Rustico, L01391, Nostred) and several their crosses 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)**) .F_1‘ planted in spring 2012 with parents were to produce Bc_1 and Bc_2 .F_1’s were selfed to produce F_2.The six generation P1, P2, F1, BC1, BC2 and F2 of four crosses were planted during 2013 using randomized complete block design with four replications in rows with 5 m long and 0.7 m between rows and 0.25 m within the 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 Singh and Chuadhary (14) as follows:

$PCV= (SF_2/X\overline{F2}\ ) \times 100$

$GCV=[\ (SF_2- S^2E)/X\overline{F2}\ ] \times 100$

SF_2= Stander deviation of second generation

XF2=Second generation mean

S^2E=Mean variance of error

The expected genetic advance from selection was calculated using formula proposed by Johnson et al.(7).

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

$h^2_{.n.s}$ cited from Wuhaib et al.(18).

The predicted genetic advance where the expected genetic gain upon selection was expression percentage of F_2 mean

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

RESULT AND DISCUSSION

Phenotypic and genotypic coefficient

Table 1. illustrate the data of phenotypic coefficient of variation (PCA) and genotypic coefficient variation (GCV) for the some traits in four crosses of maize . The PCV values were higher than GCV values for all traits in all crosses of maize. The highest one was for grain yield (t.ha^{-1}) for three crosses 1,2 and total dry matter for cross 3. The PCV values were greater than GCV, this shows that the environment had an important role in the expression of these traits, and vice versa for other traits. This result agreement with those obtained by other researchers (17,9.12). The effectiveness of selection depends not only on heritability but also on genetic advance (8). The genetic advance is a best indicative of the progress that can be expected from selection on the population. The highest value of genetic advance was for number of grains of plant for all the crosses, it range 37.42 to 190.33 and it 134.4 for total dry matter for cross3.The data of genetic advance and it's percentage are presented in table 1.The lower value was for

grain yield t\ha, other traits shows lower or moderate genetic advance .The highest value of genetic advance percentage for grains yield t.ha^{-1}.,it's range from 36.50 for cross4 ,to 48.62 for cross3,followed by number of grains . plant^{-1} (38.45) for cross1.Other traits shows moderate or lowest advance percentage.

Table1.Phenotypic and genotypic coefficient of variability (PCV), (GCV), Genetic advance (ΔG) and genetic percentage of F2means $\Delta G\%$) for several traits in four crosses of maize

Crosses	Traits	PCV	GCV	Δ G	Δ G %
FI01301×Rustico	**Ear Length (cm)**	**13.46**	**6.47**	**2.61**	**16.87**
	No. rows.ear^{-1}	**15.21**	**8.23**	**2.63**	**21.92**
	No. grains .row^{-1}	**10.48**	**2.10**	**3.23**	**10.63**
	No. grains.plant^{-1}	**26.62**	**10.62**	**190.33**	**38.45**
	Grain weight(100)	**15.36**	**6.85**	**1.89**	**13.16**
	Total dry matter	**8.82**	**4.52**	**13.73**	**6.35**
	Grain yield(t/h)	**30.34**	**21.51**	**1.53**	**39.43**
AntignaoHi39× Nostred	**Ear Length (cm)**	**18.07**	**8.25**	**3.52**	**25.90**
	No. rows.ear^{-1}	**10.90**	**6.87**	**1.704**	**12.62**
	No. grains .row^{-1}	**21.53**	**5.05**	**4.87**	**21.239**
	No. grains.plant^{-1}	**21.65**	**5.258**	**120.83**	**25.86**
	Grain weight(100)	**19.75**	**4.11**	**4.57**	**28.21**
	Total dry matter	**12.28**	**8.28**	**15.26**	**11.13**
	Grain yield(t/h)	**30.62**	**21.63**	**1.53**	**39.38**
Lo1391 × Rustico	**Ear Length (cm)**	**19.97**	**1.39**	**4.98**	**26.75**
	No. rows.ear^{-1}	**19.68**	**6.02**	**3.55**	**24.95**
	No. grains .row^{-1}	**15.28**	**6.75**	**5.365**	**20.13**
	No. grains.plant^{-1}	**14.55**	**4.66**	**103.06**	**24.04**
	Grain weight(100)	**17.75**	**9.88**	**5.93**	**25.5**
	Total dry matter	**30.98**	**10.53**	**134.40**	**48.62**
	Grain yield(t/h)	**16.94**	**12.48**	**1.261**	**20.29**
Rusticocangini× Rustico	**Ear Length (cm)**	**16.05**	**5.68**	**3.12**	**19.39**
	No. rows.ear^{-1}	**12.17**	**6.85**	**2.66**	**18.20**
	No. grains .row^{-1}	**11.84**	**10.54**	**3.96**	**13.29**
	No. grains.plant^{-1}	**7.82**	**2.37**	**37.42**	**7.31**
	Grain weight(100)	**12.84**	**5.50**	**1.76**	**9.80**
	Total dry matter	**6.31**	**3.92**	**10.47**	**6.89**
	Grain yield(t/h)	**30.96**	**17.75**	**2.006**	**36.5**

Components of Variation

Cross 1: Three parameters components m, d and h and their standard error in Table 2 . This Table reveal that all the values of parameter m were highly significant, number of grains.plant^{-1} produced a highest value (316.79) ,followed by total dry matter which gives 123.73. For all the traits, the dominance component of generation means (h) was more than additive variance (d). This illustrate that this superiority could resulted from overdominance gene action. A six parameters model could be best if gene action applied to accommodate epistasis for these traits.Thus hybridization could 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 the 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. (16) reported that dominance gene effecte play the major role in controlling the genetic variation of the most studied traits.

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
Ear Length (cm)	**$14.39\pm0.125^{**}$**	**$0.79\pm0.125^{**}$**	**$3.74\pm0.124^{**}$**	**228.18^{**}**
No. rows/ear	**$13.18\pm0.203^{**}$**	**$1.047\pm0.215^{**}$**	**$0.571\pm2.23^{*}$**	**$4.05^{n.s}$**
No. grains /row	**$20.48\pm0.369^{**}$**	**$0.558\pm0.334^{n.s}$**	**$22.19\pm0.793^{**}$**	**8.09^{*}**
No. grains/plant	**$266.49\pm2.69^{**}$**	**$31.61\pm2.73^{**}$**	**$151.44\pm6.48^{**}$**	**107.37^{**}**
Grain weight(100)	**$21.79\pm0.163^{**}$**	**$1.16\pm0.164^{**}$**	**$4.28\pm0.035^{**}$**	**370.14^{**}**
Total dry matter	**$136.81\pm1.78^{**}$**	**$9.48\pm1.79^{**}$**	**$121.47\pm3.78^{**}$**	**761.2^{**}**
Grain yield(t/h)	**$4.92\pm0.10^{**}$**	**$0.21\pm0.112^{*}$**	**$3.077\pm0.247^{**}$**	**225.88^{**}**

Cross2

Table3 shows that all the m values of were highly significant .Also, the traits of the number of grain. plant^{-1} and total dry matter have been given high values of m (266.49 and 136.81) respectively. The dominance values for all traits were highly significant, as were higher than additive variance. Thus hybridization would be more effective than population selection.This case could be resulted from overdominance. The estimation of gene effects indicate that the dominance gene effects were quite important in the inheritance of yield. Estimate 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
Ear Length (cm)	14.04±0.183**	0.323±0.193 $^{n.s}$	7.11±0.419**	61.93**
No. rows/ear	12.88±0.361**	0.229±0.373 $^{n.s}$	0.026±0.564 $^{n.s}$	3.48 $^{n.s}$
No. grains /row	18.70±0.322 **	2.65±0.314**	16.21±0.667**	90.08**
No. grains/plant	277.59±0.782**	104.85±0.763**	279.06±1.45**	304.68**
Grain weight(100)	25.34±0.268**	1.17±0.304**	0.622±0.438 $^{n.s}$	168.14**
Total dry matter	201.45±1.195**	44.98±1.20**	76.72±5.92**	350.74**
Grain yield(t/h)	3.97±0.075**	-1.24±0.082**	4.72±0.128**	2623.57**

Cross 3

Most chi-square values for this cross were significant for all the traits according to joint scaling test(Table 4). Also, all values of m were positive and highly significant. The traits number of grains.plant^{-1} and total dry matter have given high value 277.59 and 201.45 respectively. The additive values (d) for ear length was non-significant and very low, whereas the dominance value was more than and highly significant. This indicate that the trait controlled by dominance effect and non-allelic interaction was present and therefor the analyze by six parameter. While, grain weight were contrary of this,the additive value was more than dominance. While number of grains.row^{-1}, number of grains.plant^{-1} ,total dry matter and grain yield ton.ha^{-1}. All these traits were high significant for (d) and (h), but the (h) values were highest values than (d) values indicate that dominance effect controlled these traits, therefore, the significant heterosis in these traits of this cross is result from 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 variance in the ear length, grain weight and yield ton.ha^{-1}. Other researchers (4.11) 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
Ear Length (cm)	14.84± 0.336**	0.581±0.337**	5.79±0.546**	147.91**
No. rows/ear	12.44±0.185**	0.764± 0.193**	2.85±0.385**	24.57**
No. grains /row	21.23±0.226**	0.45±0.216*	16.32±0.643**	13.39**
No. grains/plant	316.79±1.85**	-32.96±1.73**	132.15±3.63**	4349.02**
Grain weight(100)	23.50±0.263**	0.593±0.256*	3.92±0.554**	126.08**
Total dry matter	123.73±1.286**	-23.25±1.281**	263.00±1.55**	4501.64**
Grain yield(t/h)	4.93±0.10**	0.055±0.01$^{n.s}$	2.96±0.243**	219.23**

Cross 4

All values of chi-square were highly significant for all the traits 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 by Hadi(6). All values of m were highly significant .Also ,the same two traits number of grains. Plant^{-1} and total dry matter had highest values 316.79 and 123.73respectively. All traits for this cross exhibited dominance variance more than additive. The dominance effect of the generation means was greater than the additive effect for all the traits. The simple additive-dominance model exhibited lack of good fit for all the traits in all crosses which the presence of non-allelic interaction in all traits. Thus, the joint scaling test of five parameters model and six parameters must be done by Hadi (6). All traits for all the crosses, the dominance variance (h) were more than additive variance (d). Thus hybridization would be more effective than population selection. Only traits number of rows. Ear^{-1} for cross2 and grain weight for cross3, additive effect greater than dominance effect, in this case selection would more effective to improve these traits. 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.

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**
Ear Length (cm)	**14.84±0.336****	**0.58±0.337****	**5.798±0.546****	**147.91****
No. rows/ear	**12.45±0.1846****	**0.76±0.193****	**2.85±0.385****	**24.57****
No. grains /row	**21.23±0.226****	**0.453±0.216***	**16.32±0.64****	**13.39****
No. grains/plant	**316.79±1.85****	**-32.96±1.73****	**132.14±3.63****	**4349.02****
Grain weight(100)	**23.50±0.263****	**0.593±0.256***	**3.92±0.55****	**126.08****
Total dry matter	**123.73±1.286****	**-23.25±1.28****	**263.01±1.55****	**4501.64****
Grain yield(t/h)	**4.93±0.102****	**0.055±0.11$^{n.s}$**	**2.96±0.243****	**219.23****

REFERENCES

1. AL-Hadi, R.A., M.Sabbouh and S.AL-Ahmad. 2013. Genetic analysis of some traits in segregation generation of two maize (*Zea mays* L.) hybrids. Damascus J.of Agric. Sci. 29(2): 117-135

2. Cavalli L.L. 1959. An Analysis of Linkage of Quantities Inheritance .In E.C.R. Reive, & C.H. Waddington (Eds.). London: HMSO.PP:134-144

3. Dorri, P., S.K. Khorasani and M. Shamrock. 2014. Generation mean analysis: Acase study of variance components in KSC 500 generation of maize (*Zea mays* L.). International Research J. of Applied and Basic Sciences. 8(2): 194-200

4. EL Badawy, M. M. 2012. Estimation of genetic parameter in maize crosses for yield and its attributes. Asian J. Crop Sci. 4(4): 127-138

5. Gambel, F.F. 1962. Gene effects in corn (*Zea mays* L.). I. Separation and relative importance of gene effects for yield. Canadian J. Plant Sci. 42: 339-348

6. Hadi, B. H.,. 2016. Generation mean analysis for estimation some genetic parameters for yield and yield components in four maize crosses. The Iraqi J.of Agric. Sci. 47 (1): 246-258.

7. Hefny, M. 2011. Genetic parameter and path analysis of yield and its components in corn inbred lines (*Zea mays* L.) at different sowing dates. Asian J. Crop Sci. 3 (3): 106-117

8. Johanson, H.W., H. F. Robinson and R.E.Comstok. 1955. Estimates of genetic and environmental variability in soy bean. Agron. J. 47: 318-324

9. Nagabhushan, N., M. Mallikarjuno, C.Haradari, M.S.Shashibhaskar and G.D.Prahalada. 2011. Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (Zea mays L.). Current Biotica. 5(2): 157-163.

10. Saleem, M., K. Shazad, M. Javeed and A. Ahmed. 2002. Genetic analysis for various quantitative traits in maize (*Zea mays* L.) inbred lines. International J. of Agric. Biol. 4: 379-382

11. Shahrokhi, M, S. K. Kharasani and A. Ebrahimi. 2013. Study of genetic components in various (*Zea mays* L.) traits, using generation mean analysis method. International J. of Agric. Agron. Plant Prod. 4(3): 405-412.

12. Shakoor, M.S., M. Akbar and A. Hussain. 2007. Correlation and path coefficients studies of some morphophysiological traits in maize double crosses. Pak. J. Agric. Sci. 44(2): 213-216

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

14. Singh, R.K., and B.D. Chaudhary.1985. Biometrical Methods in Quantitative Genetic

Analysis. Kalyani Publishers, New Delhi-Ludhiana .pp.318

15. Unay, A., H.Basal and C.Kanak. 2004. Inheritance of grain yield in a half-diallel maize population. Turkish I. of Agric. And forestry. 28: 293-244

16. Wannows, A. A., M. Y. Sabbouh and S. A. Al-Ahmad. 2015. Generation mean analysis technique for determining genetic parameters for some quantitative traits in two maize hybrids (*Zea mays* L.). Jordan J. of Agric. Sci. 11(1): 59-71

17. Wuhaib, K. M. and B. H. Hadi. 2016. Detection of non allelic interactions via generations mean analysis in maize. The Iraqi J. of Agric. Sci. 47: (special Issue): 44-55.

18. Wuhaib, K. M, B. H. Hadi and W. A. Hassan. 2017. Estimation of genetic variation components, average degree of dominance and several traits of maize in four crosses .ISOR. Agriculture and Veterinary Science.10(10):53-57.