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Gene Number and Heredity of Yeild and Yeild Component of Maize

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Abstract: A field experiment was conducted at the field of Crop Science Department, College of Agriculture – University of Baghdad during spring and fall seasons 2009-2010. Two maize inbreds; Nz25 and B73 were planted to produce single crosses hybrid, F2, F3, BC1, BC2, BC3 and BC4. The 9 genotypes were compared using RCBD with three replicates. The hybrid vigor for the single crosses and inbreeding depression for F2 , F3 ,BC_1 and BC_4,the variances of environment ,additive and dominance and the degree of dominance and heritability, number of genes were estimated ,for number of ears.plant^{-1}(NE.P^{-1}), number of row.ear^{-1}(NRE),number of grain.row^{-1}(NGR), weight for 300 grain (gm)(GW), number grain.ear^{-1}(NGE)and grain yield.plant^{-1}(GY) . The experimental results showed significant differences in all characters. In this study, the highest hybrid vigor especially in GY.P^{-1} of 161.53%. There was a decline in the characters in F2 , F3 , BC1 and BC2 so that we cannot recommend to use seeds for commercial production. The dominance genetic variance was significantly superior in all characters in this study than the additive, which indicate that the genetic variance is very important in influencing the studied traits .The estimations of the average of degree of dominance were more than one for all the studied characters. The broad sense heritability was high which ranged from 0.656 in NE.P^{-1} to 0.978 for GW, while there is a decline in narrow sense heritability which indicates an important dominance genetic superiority in the studied characters. The number of genes which control NE.P^{-1} initiation was accede 5 pairs and 4 for the NKR.E^{-1} imitation 14 for NK.R^{-1} and 18 for theNK.E^{-1} and16 pairs for the GW and more than 34 pairs for the GY.P^{-1}, all these results which indicate that these characters should be improved by crossing followed by selection , for they are quantitative traits.

Key words: Maize, back cross, inbreeding depression genetic parameters, heritability, additive, dominance, number of genes**.**

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Introduction

Maize (*zea may* L.)is one of the most important cereal crops and occupies a prominent position in global agriculture after wheat and rice (27), which used for food and as forage crops with abundant natural diversity. The primary objective of many maize breeding programs usually involves the evolution of maize hybrids or varieties with high grain yield potential (2,3,35). In maize, as in other open –pollinating plants, the predominance of intercrossing among population individuals enables heterozygote types to prevail and deleterious, normally recessive genes to remain hidden in the population by

heterozygosis (32). The frequency of these deleterious alleles which varies from population to population, is called genetic load (41). In spite of the importance of self-pollination in maize breeding relatively results exist on inbreeding depression, a genetic phenomenon first explained in Shull's work in 1908 (20).The well-known gain in hybrid vigor from crossing of inbred line contrasts with the inbreeding depression problem resulting from continuous self-pollination which may greatly restrict frequency of useful line extractable from a population (32,37). Inbreeding depression for any characteristic results from the difference between expressed and total genetic load, where the expressed load is defined under random mating and total load includes one hidden by heterozygosis and revealed by self pollination (13). The genetic basis of inbreeding depression is of interest due to its role in determining plant mating systems, which could potentially be agronomical valuable, along with its potential importance in conservation biology , Further, the out crossing of inbred lines can lead to heteroesis, a finding that can be harnessed to develop vigorous crop species (35). In an effort to support a genetic hypothesis, several studies have been conducted to isolate quantitative trait loci (QTL) contributing to inbreeding depression and heterosis in a variety of species, including maize(1**,** 15, 36) .The number of genes of controlling a character is of great importance for the study of mechanism of heredity and for plant breeding. The observed and expected Mendelian ratios are compared in order to know how many genes are involved in quantitative traits. (30). A number of approaches have been suggested to the number of effective factors, including chromosome assay (26),method of moments assay (10,12,24,29), genotype assay (21), inbred back cross technique (41) and molecular marker-based QTL mapping .Genotype assay and inbred-back cross technique are less dependent on assumption but complicated and time consuming on other hand.QTL mapping ,rapidly being developed, involves the search for associations between segregating molecular markers and quantitative character (11,25,35,38).No breeding method can achieve the desirable goal with precise understanding of gene action involved for increased yield or any plant characters. In addition the understand the additive and dominance variance, degree of dominance and heritability is very important for the breeder to choose a right program for his goal.

The objective of this research was to estimate the hybrid vigor for the single cross between two maize inbreed lines, inbreeding depression for F2 , F3 ,BC1 to BC4, variances of environment, additive and dominance , degree of dominance and heritability and Gene number which controlling the conditioning yield and yield components.

Materials and Methods

This research was conducted in the field of Crop Science Department, College of Agriculture – University of Baghdad during spring and autumn seasons in 2009 and 2010. Two inbreed lines of maize were used: Nz25 and B73. During spring crop season (10/3/2009) the inbreeding line was planted, at the flouring stage crossing was conducted between the parents to produces single cross . Then in the autumn season 2009 the single cross and the parents were planted to produce the F2 generation,

Bc1 (the cross between F1 and Nz25) and Bc2 (the cross between F1 and B73). In the third season (13/3/2010) the material from the last season was planted to the produce the F3 , the Bc2 (the cross between F2 and Nz25) and Bc4 (the cross between F2 and B73). In the autumn season 2010 ,the 9 genotypes (parents, F1, F2, F3, Bc1, Bc2, Bc3 and Bc4) which produced were applied in a field experiment by using Randomized Complete Block Design (RCBD) with three replications, where it was planted in 16/07/2010. Row length was kept 6m with plant to plant spacing of 0.25m and row to row spacing of 0,75m. Fertilizer was applied in the form of calcium super phosphate (P_2O_5) and urea (46% N): 320 and 200 kg/ha^{-1}respectivety. All phosphors fertilizer and half of urea was applied at the time of sowing, while the other half of urea applied when plants were at height stage. The crop was irrigated weekly, the herbicide was applied during the course of experiments and hand weeding was done when necessary.

The data on guarded plants for number of ears.plant^{-1}(NE.P^{-1}), number of row.ear^{-1}(NRE),number of grain.row^{-1}(NGR), weight for 300 grain (gm) (GW), number grain.ear^{-1}(NGE) and grain yield.plant^{-1}(GY). The collected data for various parameters were statistically analyzed using analysis of variance (40). Conducted statistical analysis of the data according to the mathematical model for the hard analysis of variance paradigm, and the following equations:

$Yij = \mu + T_i. + R_{.j} + e_{ij}$

where: Yij = the average seen in the sector μ = general average of community and T_i. = effect of the transactions. $R_{.j}$ = effect of repeaters. eij = experimental error.

Heterosis (H%) was calculated for all studied traits of the average of repeaters on the basis of the average deviation for the best parent according to the equation:

$H. \% = (F1- Hp .Hp^{-1}) \times 100$

By deterioration in the genetic Inbreeding depression (ID) traits in the F2 and F3, BC1, BC2, BC3 and BC4 (6,8,17) according to the equation:

$ID = | (F1-F-2/F1-) \times 100 |$

Where: F2-= main for F2 generation In the case of a decline in its F3 generation and crossbreeding is compensated for the value of F3, BC1 and BC2 and BC3 and BC4 (18,38).

Estimated environmental variance by the following equation (18,39).

$\sigma^2E = (\sigma^2p_1 + \sigma^2p_2 + \sigma^2F1) / 3$

Estimated variance for Additive (A) and Dominance (D) according to following equations:

$\sigma^2F2 = 1/2A +1 / 4D + \sigma^2E$

$\sigma^2BC1 + \sigma^2BC2 = 1/2A +1 / 2D + \sigma^2E$

The degree of dominance by the following equation:

$a^- = (2 \sigma^2D + \sigma^2A) \text{^}0.5$

Calculated the proportion of heritability in the broad sense and narrow according to the equations (17)

$h^2b.s = (\sigma^2G / \sigma^2P) \times 100 = (\sigma^2D + \sigma^2A / \sigma^2D + \sigma^2A\ \sigma^2E) \times 100$

$h^2n.s = (\sigma^2A / \sigma^2P) \times 100 = (\sigma^2A / \sigma^2D + \sigma^2A + \sigma^2E) \times 100$

Estimated number of genes that control traits according the following equation (13).

$N = (p1 + p2)\ 2 / (8 (\sigma^2F2-\sigma^2E)$

σ^2G, σ^2p, σ^2E, σ^2A, σ^2D as the Genetic, phenotypic, environmental, Additive, dominance variance .

σ^2p1- σ^2p2 andσ^2BC1 - σ^2BC4 as first and scanned parent variance and backcross variance.

And $h^2b.s$ and $h^2n.s$ ratio in the broad sense heritability and narrow sense.

a^- = degree of dominance, taking into account the values of a^- as follows: If the value of a^- = zero, it means the no dominance. If the zero> a^- <one, it indicates the presence of partial dominance. And if a^- = one, it means a complete dominance. If a^- <one, it means the high dominance.

Results and Discussion

Number of Ear. Plant^{-1}

Analysis of variance indicated highly significant variations (p>0.01) among the genotype for the NE.P^{-1}. The single cross give high NE.P^{-1} compared with other genotype therefore, given positive hybrid vaguer superior for the best parents, reaching (45.16%) (table.2). These results are comparable with the findings of (5,15,1,23). The result showed in table (1) decrease in average of the second, third generation and all backcrosses members compared with F1, maximum mean value (26.67%) was observed for F2 for ID(table.2). The data presented in table (3) show the higher estimates of dominance variance as compared to additive variance for the NE.P^{-1} probably due to predominance of non-additive gene action suggested the scope of improvement of these character through heterosis breeding program. The estimates of heritability in broad sense was high for this character (0.656) and the heritability in narrow sense were low (0.085), the degree of dominance greater than 1 ,which might enhanced broad sense heritability as dominance variance is a component of genetic variance being used for estimation of heritability. Similar observations have also been reported by (22,28,31) .The number of genes which influence initiation was 7 pairs which indicate that this character is one of quantitative characters and can be improved by crossing followed by selection. These results are agreed with those obtained by (8,14).

Table I. Means for the yield and it's Components a Characteristics of the 9 populations for the Maize

Populations	NE.P^{-1}	NKR.E^{-1}	NK.R^{-1}	NK.E^{-1}	GW	GY.P^{-1}
Nz25	1.00	13.00	24.33	281.17	79.87	74.90
B73	1.03	13.33	24.47	295.78	85.10	83.87
F1	1.50	17.33	42.87	542.03	121.37	219.33
F2	1.27	16.50	38.57	488.88	138.30	216.87
F3	1.10	16.03	36.17	517.59	114.33	197.20
BC1	1.27	18.13	40.53	493.71	117.70	193.70
BC2	1.30	15.70	40.13	514.91	109.33	187.33
BC3	1.17	15.30	37.77	493.01	99.03	162.67
BC4	1.13	15.70	36.00	443.87	98.67	145.67
L.s.d 0.05	0.196**	1.22**	2.10**	76.26**	37.04*	51.71**

*and** indicated significance at 0.05 and 0.01 levels of probability, respectively

Number of kernel Row. Ear^{-1}

Analysis of variance showed that the differences among the genotypes were highly significant. (Table.1) The inbreed B73 was better in this character than Nz25 which gave 13.33 row. The Bc1 was superior compared with the

other hybrids genotype which gave 18.13 row as average which means the Nz25 was inherited its genes for the F1 more than other parent. The single cross gave 17.33 row , and gave positive hybrid vigor (30%) which refer presence high dominance controlled this character(table.2). These results were previously reported by (4,16). Table (2) showed a deterioration in genetic which varied between 4.81 %for F2 and 11.73% for Bc3 while no deterioration napped in Bc1 and there is an increase in this character so that Bc1 can be used as male in the breeding back crossing. These results were harmony with the previous results obtained by (4,7,16). Table (3) shows the genetic analysis that estimated variance for dominance (0.102) higher than the estimated variance for additive (0.04). The average degree of dominance was more than one and that indicated the importance of dominance gene in heritability of the $NKR.P^{-1}$, also the heritability ratio in broad sense was high up to 0.776, while it was low in narrow sense which reached 0.203 and that indicate the decline of dissimilarity in additive genes as compared with non additive genes which indicated the possibility of improvement of this character by hybridization. EL-Hosary (16) and Bhavana *et al.*, (9) have also reported the importance of the additive and non-additive. The number of gene pairs which control the number of kernel of row was 5 pairs which was characterized by its dominance influencies and this number of genes was low as compared with the quantitative characters which indicated that the number of grains in the row was a genetic character which can be used to distinguish the varieties or the genotype.

Table 2.Heterosis for F1 and ID for F2,F3,BC1, BC2 ,BC3 and BC4 of Maize

Populations	$NE.P^{-1}$	$NKR.E^{-1}$	$NK.R^{-1}$	$NK.E^{-1}$	GW	$GY.P^{-1}$
F1	45.16	30.00	75.20	83.25	42.62	161.53
F2	15.56	4.81	10.03	9.81	-13.95	1.12
F3	26.67	7.50	15.63	4.51	5.80	10.09
BC1	15.56	-4.62	5.44	8.92	3.02	11.69
BC2	13.33	9.42	6.38	5.00	9.91	14.59
BC3	22.22	11.73	11.90	9.04	18.40	25.84
BC4	24.44	9.42	16.02	18.11	18.70	33.59

Number of Kernel . Row^{-1}

The $NK.R^{-1}$ directly influenced the $NK.E^{-1}$ and this character will influenced the GY. The experiment results showed a highly significant differences among the genotype in this study. The B73 gave 24.33 grain while Nz25 gave 24.47 grain and there is no significant difference between them. The single cross was significant and superior over its parents and other genotypes and gave 42.87 grain which indicated that combining ability between the parents toward increasing the average of these characters, also the Bc1 and Bc2 were superiority in this characters upon the reciprocal hybrids in F2. The experimental results showed a positive hybrid vigor 75.2% which indicated over dominance in the heritability of the genes. The ID between the F2 and F3 and back crosses was 5.44 in Bc1 and 16.02 in Bc4 which

indicated that the seeds of F2 and Back cross cannot used to grow on economical yield. The results in table (3) indicated that variance for dominance (σ^2D) was higher than variance for additive (σ^2A), and the environment variance (σ^2E) was higher than the variance of additive which indicated the importance of variance of non additive of $NK.R^{-1}$. This trait can be influenced to some extent by the environmental variance. The degree of dominance (a^-) was more than one, which is the character of the $NK.R^{-1}$ .The heritability broad sense 0.776 while it was in narrow sense 0.147,these value indicated the importance of non additive variance more than the additive variance . The $NK.R^{-1}$ which controlled the heritability of number of grain in the row was 14 pairs which indicated that this character was quantitative character in maize .We can concluded that the $NK.R^{-1}$ was a quantitative character which controlled by the non additive genes and can be influenced by the environment and be improved by hybridization followed by selection. Similar conclusions have been recorded by (12,33,38), Also Abed (2) and Bhavana (9) reported that, the magnitude of non-additive variance was higher than additive for the $NK.R^{-1}$.

Table.3 Genetic parameters for the yield and its components traits of maize

Genetics parameter	$NE.P^{-1}$	$NKR.E^{-1}$	$NK.R^{-1}$	$NK.E^{-1}$	GW	$GY.P^{-1}$
σ^2E	0.00010	0.041	0.354	105.193	0.434	2.388
σ^2G	0.00019	0.142	1.229	324.740	20.453	10.409
σ^2D	0.00017	0.102	0.996	255.865	12.566	9.945
σ^2A	0.00003	0.040	0.230	68.870	7.890	0.460
σ^2P	0.00029	0.183	1.583	429.933	20.887	12.798
a^-	3.674	2.373	2.927	2.726	1.785	6.542
$H^2b.s$	0.656	0.776	0.776	0.755	0.979	0.813
$H^2n.S$	0.085	0.203	0.147	0.160	0.378	0.036
Nu. of gene	5.675	4.873	14.363	18.111	16.409	34.876

Number of Kernel Per Ear ($NK.E^{-1}$)

The $NK.E^{-1}$ influence directly the GY. The experimental results showed a highly significant differences among the genotype. Nz25 was superior in this character from the other parent, and gave 295.78 kernel (Table.1). The single ($NZ_{25}xB_{73}$) was significantly superior over the other genotype which gave the highest $NK.E^{-1}$ of 542.03. The hybrid vigor was positive in increasing the $NK.E^{-1}$ in the F1 which was 83.25% (Table 2). The results presented in (Table 2) showed that Bc4 was more deteriorated through the back crossing and the percentage was 18.11 %, while in F3 was less deteriorated. The results in table (3) showed that dominance variance significantly superior over additive variance in influencing $NK.E^{-1}$ and the average degree of dominance which was 2.73, and a declines in percentage of heritability in narrow sense which reached 0.16 and its increasing in broad sense which reached 0.755,so we can use the hybridization method to increasing the $NK.E^{-1}$.The result in Table (3) showed that the number of genes pairs which control

these characters were 18 pairs which indicated that the number of grains was a quantities character which was controlled by a large number of genes varied in their influences, while the highest influence was due to the dominance genes and can be improved by hybridization followed by selection.

Weight for 300 Grains (GW) gm

The grain weight is the component of the grain yield in maize which was controlled by the photosynthesis activity which was influenced by the leaf area, leaf angle, distribution of the leaves, the ability of translocation of substrates and the size and the ability of the snick. The average grain weight was for the dry matter accumulation which influenced by the environmental and genetic factors. The result showed high significant differences among the studied genotypes. The F1, F2, F3 and BC1 were the best genotypes (table.1), so the parents did not differ significantly. The F1 generate showed positive hybrid vigor (42.62%) which might indicate the over dominances active (table.2). ID may decrease in two ways: at the cost of small gains in the F2 mean or increase of the population mean after one generation of salving. These two cases seem to depend on the type of predominant gene action in the population, the genetic frequency, the selection method used in breeding, and the environment chosen for selection and evaluation. Inbreeding depression was found for all the population (F2,F3 and their BC‘s). The reason for sever inbreeding depression for the GW may be due to expression of yield reducing genes in homozygous state or due to reshuffling of genes responsible for this trait which may have masked the yield-increasing genes (table 2). Variance components for all traits are presented in (Table 3), In most of studied traits, dominance variance was more than additive variance and the average degree of dominance were greater than unity for this traits (table 3), The narrow-sense heritability estimation is low 0.38 (table 3) . Thus hybridization would be more effective than population selection. The estimated numbers of genes controlling various traits using different formula are presented in (Table 3). The result shows more than 16 genes which controlled the heredity for the GW in maize. We can conclude that GW was one quantitative trait in maize and can be improved by hybridization.

The Grain Yield Per Plant (GY.p^{-1})

Grain yield of maize is the product of three yield components: the number of ears per unit area, the number of grains per ear and the grain weight (38). The increase or decrease in any one of these components, keeping the size of other components constant, contributes to increase or decrease in grain yield. The results in (table 3) indicate high significant differences among the studied genotypes, the single cross (Nz25 x B73) in F1, F2 and F3 was the Superior in GY and gave 219.33, 216.87,197, 2 (gm), respectively. The BC1 and BC2 also gave high GY: 193.7 and 187.33 gm. The parents showed a loss rote in GY with no significant between them, however, the single cross was given up most positive heterosis in all traits which is (161.53%). Hence, heterotic increase if found in one or more attributes with other attributes being constant would lead to favorable yield increase in hybrids. Results refer the over dominance for the genes which

controlled the trait. These result were previously reported by (2,3,4,6,33). The information about inbreeding depression is useful to test the potentiality of F2 seeds after reducing the heterosis in F2 generation due to the reduction of heterozygosity caused by inbreeding. Thus, it is logical expectation that the expression of heterosis in F1 may be followed by reduction in F2 performance for some of the studied traits especially that have high heterosis values (19). Results in table (2) show the ID rote well increased from the F2 (1.12%) to BC4 (33.59%) ,this value refer to Incidence in mean for F2 to BC4 comparing with the F1 mean. These results are agreed with those obtained by (1,15,32,33). The drastic inbreeding may be attributed to expression of deleterious alleles caused by homozygosity of genotype and environmental interaction, in spite of such severe inbreeding found to be superior to their parents. The results in (table 3) indicated that the environmental variation (σ^2E) was less than genetic variation (σ^2G) and the dominance variation (σ^2D) was more than additive variation (σ^2A). Subsequently the heritability in broad sense given high value (0.81) and the narrow sense given 0.036, also the degree of dominance (a^-) was more than 1 which it (6.54). Such results are in agreement with that obtained by (5,8,14,18,22,23,29) who obtained that the dominance variance was greater than additive component for the GY. The number of gene that controlled this trait was more than 34 pairs (high number of genes). All these results prove the $GY.P^{-1}$ was a complex quantitative trait and is under the influence dominance gene effect. We can conclude that $GY.P^{-1}$ can be improved by using plant breeding program which deal with crossing method.

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