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Estimation of Genetic Variation Components, Average Degree of Dominance and Heritability for Several Traits of Maize in Four Crosses.

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Abstract: *Afield experiment was conducted at the field of Field Crop Science, College of Agriculture, and University of Baghdad. The aimed of experiment were to estimate the genetic variation , average degree of dominance, correlation between additive and dominance in all loci, broad sense and narrow sense heritability. Four crosses resulted from crossing between inbred of maize were evaluated by using randomized complete block design with four replications, for several traits of maize. Results showed that the genetic effects were greater than environment effect for all traits of all crosses. Dominance effects were more than additive effect for some traits, while additive effects were more in other traits. For this the average degree of dominance was different, its less than 1 for first traits and more than one for the other traits. As a results of that the heritability was differ. The narrow sense heritability was range between 0.007 for number of branches per tassel for cross 2 to 0.976 for number for rows per ear in cross 4.It can conclude that all traits were genetically controlled, and can use selection to improve the traits that possess additive variation, and delay the selection to subsequent generations until homozygous for heterozygous loci is achieved for other traits.*

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I. Introduction

The rediscovery of Mendel's laws of inheritance in 1900 was the basis for locating the inheritance of quantitative traits and developing plant breeding and selection schemes. The study of quantitative genetics was importance of continuous versus discontinuous variation in evolution. Of the first who contributed to the development the theory and method for studying the inheritance of quantitative traits were Fisher, Wright, and Haldane. Thereafter, extensive research has been conducted to determine the importance of different genetic effects in the inheritance of quantitative traits for most cultivated plant species (Hallauer,2007). Maize has an important role in quantitative genetics. After 1950 the information, both theory and data was related to the types of genetic effects important in heterosis and breeding methods related to developing lines and hybrids. Then the interaction of alleles either within the same loci or among loci were necessary. Several of the earlier quantitative genetic studies were conducted with maize populations to study the relative importance of additive, dominance, and epistatic effects in the expression of the heterosis; and the yield was plateau has been attained with use of double cross hybrids (Hallauer, 2007). Gamble, 1962 compared different generations from crosses of pure lines detected significant estimates of epistatic effects for all traits . Several researchers have used different methods for estimating the epistatic effects (Crow, 2008), all of these studies used generation mean analysis. Carlborg and Haley, 2008, reported that epistasis: too often neglected in complex trait studies. Despite hugely example of dominance and epistasis, animal and plant breeders have found that almost any trait responds to selection. Almost every population (except inbred) has considerable genetic variation of which a substantial component is additive. Breeders have generally ignored or minimized epistasis and usually without any loss of predictive value. Natural selection depends on additive variance, and in the process of selection additive variance is expected to be depleted, yet populations to continue to respond to selection, the additive variance persist, even with strong selection for most quantitative traits. There are four primary causes (Crow 2008): changing environment, mutation, compensating allele frequency changes, and selection for fitness. There is evidence that the smaller the effect of a gene, the more nearly additive it is (Crow,1992; Temin et al. 1969).

Research aims is to conduct a crossing between several inbred of maize to induce genetic variations and to estimate genetic variations, heritability, and degree of dominance to determine the appropriate breeding method to improve the studies traits.

II. Material and Methods

Six inbred lines maize (AntignaoHi39,FI1301,Rusticocangini,Rustico, L01391,Nostred) were tested in Iraqi at a field of Field Crops Dept. College of Agric. Univ. of Baghdad .The homozygous inbred have crossed to produce F1 (First generation).Four superiors crosses were selected (cross1, cross2, cross3, cross4). F_1's were planted in spring 2012 with parents to produce Bc_1 and Bc_2. F_1's were selfed to produce F_2 in fall 2012.The six generation P1,P2,F1,BC1,BC2 and F2 of four crosses 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 calcium superphosphate 45% P_2O_5 with 200 $kg.ha^{-1}$ were added at soil preparation, Nitrogen fertilizer as urea (46%) was added three times at planting , elongation stage and before flowering . The data from six generation were analyzed independently using Micro software Excel 2010 and Spar2 to obtain three parameters model which is used for estimation of genetic components of variance according to Mather (1949) cited from singh and chuadhry(1985).

E=1\3(VP1+VP2+VF1)
D=2(VF2-VB1-VB2)
H=4(VF2-1/2VD-E)
The degree of dominance is calculated as ratio of dominance variance to additive variance $(H/D)^{1\backslash 2}$
F=BC1-BC2 (Mather and Jinks 1982).
$H^2_{.b.s}$ = (VG/VP)
$H^2_{.n.s}$ = (VA/VP) (Burton,1951)

III. Results

Cross 1

The analysis of variance components for all traits are presented in table 1. The data in table 1 illustrated that all values of environmental effect were low than additive and dominance effects. Indicated that all traits were genetic controlled, except number of ears per plant the environmental effect was more than genetic. Dominance variance (H) was more than additive variance (D) for most traits, so hybridization would be more effective method than selection for improve population. Except for number of leaves per plant, ear weight, number of grains per row, number of grains per plant and total dry matter, the additive variance is greater than dominance effect. In this case, the method of selection is more effective to improve these traits.

The degree of dominance$(D/H)^{1/2}$ was greater than one for most traits indicated that these traits under the influence of over dominance gene action evidence of the decline in narrow sense heritability, which range from 0.061 for number of ears per plant to 0.421 for grain weight. In contrast, the number of leaves, ear weight, number of grains per row, number of grains per plant and total dry matter was less than one and it range between 0.135 for number of grains per plant to 0.975 for ear weight. For this the narrow sense heritability was high. Its range from 0.494 for ear weight to 0.980 for number of grains per plant. This indicating that these traits influences by additive and partial dominance gene action. All broad sense heritability values were high for all traits indicated to be genetically controlled and the environment had little effects on them.

Most values of F (is the correlation between H and D in all loci) for most traits were positive. The positive values indicated that the dominant alleles were more than the recessive alleles in the parents, illustrated the importance of dominance gene action in the inheritance of these traits. In other hand, the F values of number of branches per tassel, number of ears per plant and total dry matter, only were negative.

Table1. Estimation of the components of variation , average degree of dominance and heritability for several traits of maize in cross1.

Traits	E	D	H	$(H\backslash D)^{1/2}$	F	$H^2_{.n.s}$	$H^2_{.b.s}$
Plant height(cm)	9.63	40.95	89.32	6.35	23.19	0.292	0.931
No. of leaves	0.54	2.53	1.033	0.638	0.532	0.616	0.868
Leaf area (m^2)	0.00018	0.0048	0.009	1.41	0.016	0.343	0.987
No. branches/tassel	0.149	1.21	5.62	4.64	-1.78	0.173	0.978

No. ears/plant	0.011	0.0095	0.126	3.64	-0.0425	0.061	0.926
Ear weight (gm)	31.63	448.78	426.76	0.975	46.62	0.494	0.965
Grain yield (gm)	28.79	89.17	437.14	2.21	109.07	0.161	0.948
Ear Length (cm)	0.098	1.868	13.19	2.61	0.521	0.123	0.994
No. rows/ear	0.274	2.68	6.87	1.60	0.34	0.273	0.973
No. grains /row	0.421	10.06	4.75	0.687	8.399	0.661	0.972
No. grains/plant	65.45	34400	627.74	0.135	15.08	0.980	0.998
Grain weight(100)	0.514	15.37	20.66	1.16	1.985	0.421	0.985
Total dry matter	14.59	663.60	65.33	0.313	-5.06	0.892	0.980
Grain yield(t/h)	0.299	0.719	3.25	2.12	0.214	0.168	0.929

Cross 2

Table 2 illustrate the analysis of variance components for all traits .There is little from cross 1. The genetic components for all traits was higher than environmental variance. Except the number of branch per tassel the environment effect was more than genetic variance. This indicated that these traits controlled by genetic and the effect of environment condition is little. The dominance variance (H) was more than additive variance (D)for 7 traits. Hybridization would be more effective to improve the population. The other 7 traits were the opposite; the additive variance was more than dominance. In this case, the method of selection is used to improve these traits for this cross. The degree of dominance was greater than one for first 7 traits , indicated the traits influence by over dominance gene action. For this the heritability narrow sense was low, its range from 0.007 for number of branch per tassel to 0.416 for number of grains per plant. Less than one for the other 7 traits, its range from 0.507 for leaves area to 0.857 for ear length, indicated these traits under the influence of partial dominance. All values of broad sense heritability were high, indicating that these traits genetically controlled. Most values of F were positive indicated that the dominant alleles were more than the recessive in parents, this means the importance of dominance gene action in the inheritance of these traits. The negative values of F means, the additive genetic variation controlled inheritance these traits. Selection methods were effective to improve these traits in this cross.

Table2. .Estimation of the components of variation, average degree of dominance and heritability for several traits of maize in cross2.

Traits	E	D	H	$(H\backslash D)^{1/2}$	F	$H^2_{.n.s}$	$H^2_{.b.s}$
Plant height(cm)	3.72	25.69	44.41	1.31	-11.22	0.348	0.949
No. of leaves	0.195	14.22	5.44	0.619	0.849	0.716	0.990
Leaf area (m^2)	0.0015	0.018	0.016	0.937	0.0019	0.507	0.957
No. branches/tassel	0.43	0.36	46.55	11.36	3.194	0.007	0.991
No. ears/plant	0.0057	0.147	0.244	1.288	0.0101	0.328	0.875
Ear weight (gm)	10.45	93.15	372.61	1.99	47.26	0.195	0.782
Grain yield (gm)	15.74	191.47	158.76	0.91	20.279	0.523	0.956
Ear Length (cm)	0.116	11.03	1.717	0.394	-0.109	0.857	0.991
No. rows/ear	0.287	0.541	6.433	3.44	0.104	0.074	0.960
No. grains /row	0.817	35.09	24.17	0.83	-3.169	0.584	0.986
No. grains/plant	55.77	11867.53	16956.77	1.19	3960.86	0.411	0.998
Grain weight(100)	0.217	15.10	9.118	0.777	-5.443	0.617	0.991
Total dry matter	31.90	351.89	301.67	0.927	6.08	0.513	0.953
Grain yield(t/h)	0.461	0.865	3.952	2.13	0.214	0.164	0.914

Cross 3

The environmental variation in this cross was less than the genetic variation of all traits (Table 3).Also, there are 7 traits dominance gene action was greater than additive gene action, and other 7 traits were the opposite of the previous 7 traits. For this, the values of heritability narrow sense for first 7traits were low, whereas for other 7 traits were high. As the result the average degree of dominance more the one in the first and less than one in the second. It refers to non- additive gene effect controlled the first, and additive gene effect in the second. The correlation between H and D in all loci were positive in 7 traits and negative in other 7 traits, that mean the dominance alleles were more in the first 7 traits and opposite that in other 7 traits.

Table3. .Estimation of the components of variation, average degree of dominance and heritability for several traits of maize in cross3.

Traits	E	D	H	(H\D)$^{1/2}$	F	$H^2_{.n.s}$	$H^2_{.b.s}$
Plant height(cm)	6.15	174.26	326.98	1.37	-59.87	0.343	0.987
No. of leaves	0.271	2.65	1.013	0.618	0.09	0.673	0.931
Leaf area (m²)	0.00014	0.0113	0.0081	0.851	-0.0002	0.579	0.995
No. branches/tassel	0.148	6.14	30.21	2.22	4.831	0.168	0.995
No. ears/plant	0.0053	0.035	0.083	1.55	-0.0052	0.286	0.957
Ear weight (gm)	4.199	67.21	522.49	2.79	131.98-	0.113	0.995
Grain yield (gm)	0.051	0.369	3.496	3.07	14.382	0.094	0.984
Ear Length (cm)	0.245	19.447	15.54	0.893	1.537	0.552	0.992
No. rows/ear	0.148	3.713	22.89	2.483	-5.038	0.138	0.994
No. grains /row	1.059	23.15	15.84	0.827	1.688	0.578	0.973
No. grains/plant	16.41	6256.44	2997.15	0.692	-327.38	0.674	0.998
Grain weight(100)	0.532	23.32	8.23	0.594	0.329	0.726	0.983
Total dry matter	11.47	14071.70	1147.92	0.285	88.83	0.923	0.999
Grain yield(t/h)	0.051	0.369	3.496	3.07	-0.270	0.094	0.986

Cross 4

The data for cross 4 are presented in table 4. In this cross all traits were genetically controlled because the genetic variation was more than environment variation. The additive gene effect was less than dominance gene effect in 9 traits while the dominance gene effect was more than additive gene effect in other traits. So the average degree of dominance differed according to this different in gene effect in traits, The highest value was 5.33 for total dry matter, while the value was less 0.133for number of rows per ear. As the results, the heritability narrow sense ranged from 0.033 for total dry matter to 0.976 for number of rows per ear. All values of heritability broad sense were high.The correlation between H and D in all loci were positive for ten traits indicated that the dominant alleles were more than the recessive alleles in the parents, illustrated the importance of the dominance gene action in the inheritance of these traits, and negative for four others. Hadi,2016 illustrated that the dominance variation was more important than the additive variation in the ear length, grain weight and yield(t/h.), as well as, Wuhaib and Hadi 2016, indicated that the dominance effects were higher than the additive effects for all traits and all crosses, indicated the importance role of dominance components of gene action in inheritance traits. Wuhaib,2012(2), reported that the additive variations for inbred were more than testers for most traits ,so it's more than non-additive gene action. Zdunic et al.,2007 reported that the dominance type of gene action was important in 8 out of 9 crosses for starch content, suggesting a similar pattern of gene action for grain yield. Result obtained by Hallauer and Miranda, 1988 showed that dominance effects for traits are often more important than additive ones, this due to hetrozygosity of those genes for which the parents are differ (Kearsey and Pooni, 1996).In some times the additive gene effects are being underestimated because of the lack of knowledge about parental differences regarding the investigated traits (Wilson et al.2000). Iqbal et al. 2010, found that the dominance gene effects were found in all crosses whereas the additive gene effects were observed in 3 out of 4 crosses involved in the study, and the magnitudes of dominance gene effects were much higher compared to those of additive gene effects. Also, Wannows et al.(2015) reported that the additive effects were significant for most traits in two crosses. Many researchers have reported that both additive and non- additive gene action were important for traits of maize. This discrepancy in results is due to different genotypes and the environment in which the test was conducted.

Hadi and Wuhaib, 2010 reported that the number of grain per ear, dry weight and yield efficiency gave the highest heritability broad sense. The results obtained by Wannows et al. 2010 showed that high narrow sense additive genetic variation in the inheritance of these traits and the effectiveness of selection in early segregating generations of crosses for improving these traits. The heritability narrow sense for some traits were high and in others were low (Shahrokhi et al. 2011). Dorri, et al.(2014) referred that the F values for most traits were positive, suggested that dominant alleles were more abundant than the recessive alleles in the parents and indicated the importance of dominance gene action in the inheritance of the traits under study(Shahrokhi et al. 2011).

Table4. .Estimation of the components of variation, average degree of dominance and heritability for several traits of maize in cross4.

Traits	E	D	H	(H\D)$^{1/2}$	F	$H^2_{.n.s}$	$H^2_{.b.s}$
Plant height(cm)	3.43	1624.97	283.99	0.418	25.572	0.844	0.998
No. of leaves	0.239	1.54	8.87	2.39	0.00000	0.144	0.977
Leaf area (m²)	0.000167	0.00095	0.0098	3.22	0.00085	0.087	0.984

No. branches/tassel	**0.864**	**11.55**	**19.78**	**1.31**	**-0.0245**	0.357	0.973
No. ears/plant	**0.016**	**0.938**	**0.028**	**0.247**	**-0.00023**	0.955	0.983
Ear weight (gm)	**12.74**	**64.37**	**327.92**	**5.09**	**88.95**	0.158	0.968
Grain yield (gm)	**3.45**	**26.91**	**159.8**	**2.44**	**15.006**	0.142	0.981
Ear Length (cm)	**0.263**	**12.37**	**0.93**	**0.274**	**0.451**	0.912	0.980
No. rows/ear	**0.036**	**5.82**	**0.104**	**0.133**	**0.050**	0.976	0.995
No. grains /row	**1.973**	**2.823**	**49.33**	**4.179**	**12.74**	0.052	0.963
No. grains/plant	**47.88**	**2060.79**	**2092.08**	**1.008**	**310.92**	0.491	0.988
Grain weight(100)	**0.23**	**9.02**	**0.27**	**0.24**	**-0.337**	0.947	0.976
Total dry matter	**4.61**	**11.49**	**326.64**	**5.33**	**-23.22**	0.033	0.986
Grain yield(t/h)	**0.236**	**0.914**	**8.81**	**3.105**	**1.863**	0.092	0.976

IV. Conclusion

Dominance gene effects were more than additive for some traits while the other traits were vice versa for all crosses, so the average degree of dominancehas varied, leading to different of heritability of these traits. The correlation between dominance and additive for all loci was positive for some traits and negative for other traits for all crosses. For this the additive and dominance components could be successfully exploited in later generations, therefore, selection must be delayed to later generations after the homozygosus for heterozygous loci of the traits is achieved.

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