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ESTIMATION OF GENETIC PARAMETERS IN IRAQI MAIZE INBRED LINES AND THEIR FULL DIALLEL CROSSES

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Abstract

Studied genotypes differed significantly for all traits except NRE and NKR for reciprocals crosses. Values of $\sigma^2 D$ were greater than those of $\sigma^2 A$. The ratio ($\sigma^2 gca / \sigma^2 sca$) was greater than one. The ($h^2_{b.s}$) was high for most traits, while the ($h^2_{n.s}$) was low in diallels and high in reciprocals for all traits. Small difference observed between GCV and PCV in both diallels and reciprocals. For diallels, the highest GCV and PCV was shown only for GY, on the other hands all PCV and GCV values for reciprocal were low. ART-B21 × ART-B26 and ART-B26 × ART-B21 showed higher heterosis for GY and NKR. Inbreeds were distributed into four separated groups. Lines ART-B46 and ART-B37 occupied one group.

Key words : Full Diallel Cross, gene action, heterosis, heritability.

Introduction

Understanding the nature and magnitude of genotypic and phenotypic variability in crop species is important in breeding programs to evolve superior cultivars. Information on genetic variations, levels of dominance, and the importance of genetic effects have contributed to greater understanding of the gene action involved in the expression of heterosis. Bhatnagar *et al*. (2004) reported general combining ability ($\delta^2 gca$) value of 0.06 and specific combining ability ($\delta^2 sca$) value of 1.3 and the ratio ($\delta^2 gca/\delta^2 sca$) was less than one and additive variation less than the dominance variation, which confirms production of plant grain yield under the control of non-additive gene. Rather *et al*. (2009) found that the inheritance of plant grain yield was under the influence of non-additive gene action and the variation of dominance gene is greater than the additive. Wali *et al*. (2010) reported the act of non-additive gene action in controlling the inheritance of the number of kernels per row and weight of 100 kernels.

Heterosis phenomenon associated with some physiological responses that lead to an increase in hybrids performance over their parents. Doney and Theurer (1979) mentioned that the hybrids are faster than their parents in cell division process, which is known to be controlled by additive gene action. Ojo *et al*. (2007) reported significant positive heterosis for grain yield and yield components in diallel crosses of seven corn inbred lines. Using reciprocal cross could reflect the maternal effect on the hybrid vigor which comes due to genes in the cytoplasm. Many studies showed the influence of cytoplasm on maize traits in reciprocal and backcrosses which could be positive or negative and that depends on genes in carried in the maternal cytoplasm. Vang (1995) proved that cytoplasm is relayed on to affect the presence of many morphological traits of reproductive organs, plant height, and grain yield but in comparison to the impact of nuclei genes and the interaction with cytoplasm then the degree of the later impact would be much less and non-significant. Estimating heritability has been extensively used by plant breeders in order to select for promising genotypes and in the prediction of heritability of desirable traits (Morakinyo, 1996). Amer and Mosa (2004) reported $h^2 n.s$ of 44% for silking date, 39% for plant height, 44% for ear height, 27% for ear length, 31% for ear diameter, 29% for number of rows per ear, 23% for number of

kernel per row and 36% for grain yield. Sughrou and Hallauer (1997) reported h²b.s for the number of rows was 39% and 51% for h²n.s and the average degree of dominance was less than one (0.54), but the degree of dominance for the number of kernels per row was greater than one, and inheritance of this trait was under the influence of over dominance genes, for grain yield per plant the h²b.s was 98% and the h²n.s was 15% and the degree that of dominance was greater than one. Traits with a high coefficient of variation and high heritability coupled with high genetic advance may be controlled by additive genes and can be improved directly through simple plant selection. In contrast, the traits with low GCV, PCV, heritability and genetic improvement might be used in heterosis breeding. The objective of this study was to determine some genetic parameters including estimating heterosis, evaluating the additive and dominance gene action, estimating the degree of dominance rate and heritability in both broad and narrow sense for inbred lines of maize using the full diallel cross.

Materials and Methods

Genetic materials and experimental procedures

The experiment was conducted in the agricultural research Station-Abu Ghraib in mid-March 2013 using six inbred lines of maize (P1 to P6) (P1= ART-B21, P2= ART-B26, P3 = ART-B46, P4= ART-B40, P5 = ART-B37, P6 = ART-B34) obtained from the Public Authority for Agricultural Research. Inbred lines were introduced into the full diallel cross-program according to Model-I, Method-1 of Griffing's (1956). In autumn 2013, genotypes (inbred lines and their crosses) (table 1), were planted in randomized complete block design RCBD in three replicates. All crop management processes were carried out as recommended. Data were collected for number of days from planting to 50% tasseling (DT) and silking (DS), plant height (PH), ear height (EH), number of rows per ear (NRE), number of kernels per row (NKR), weight of 100 kernel (HKW) and grain yield per plant (GY).

Statistical analysis and genetic parameters estimation

General combining ability (GCA), specific combining ability (SCA) were estimated according to the following mathematical model: $Y_{ij} = \mu + g_i + g_j + s_{ij} + r_{ij} + 1/bc \Sigma\Sigma e_{ijkl}$ (Griffing, 1956).

Each of the additive variation ($\sigma^2 A$), dominance variation ($\sigma^2 D$) and environmental variation ($\sigma^2 E$) were estimated using the expected variation components EMS (Griffing, 1956), Genetic variance ($\sigma^2 G$) and phenotypic variation ($\sigma^2 P$), Broad sense heritability (h²b.s) and narrower sense (h²n.s) were evaluated according to Singh and Chaudhary (2007), Dominance degree (ā) of each trait, Genotypic Coefficient Variation (GCV) and Phenotypic Coefficient Variation (PCV). Heterosis was estimated according to the first generation deviation from best parents (BP) as a percentage.

Results and Discussion

Analysis of variance results presented in table 1 showing highly significant differences between all used genotypes for all studied traits. Mean square of GCA was highly significant for all studied traits, while the mean square of SCA was significant for all except the (NRE) and (NKR) for the reciprocal crosses, which raises the importance of both additive and non-additive gene action in the inheritance of those traits, results were consistent with Pavan *et al*. (2011) and Ali *et al*. (2012).

Variance components of general ($\sigma^2 gca$) and specific ($\sigma^2 sca$) combining abilities calculated for each trait, were described in terms of additive ($\sigma^2 A$) and dominance ($\sigma^2 D$), genetic variances according to Griffing (1956), and summarized in table 2. Results indicated that all estimated $\sigma^2 A$, $\sigma^2 D$ were significant for all traits except for NRE and NKR in some reciprocals. However, the magnitude of $\sigma^2 A$ was consistently less than that of $\sigma^2 D$ and the ratio of GCA/SCA was less than one for all traits these findings shows that the dominance genetic variance was more important than the additive genetic variance in the inheritance of most studied traits, indicating the important effect of hybridization in the early segregating generations in the studied hybrids for improving such traits. Results also showed that the degree of dominance (ā) was greater than one, for all traits, indicating the control of over dominance genes on the traits. These results agreed with the findings of Hallauer and Filho (1981), El-Hosary (1989) and Soliman *et al*. (2005).

In Converse the magnitude of $\sigma^2 A$ was consistently larger than that of $\sigma^2 D$ for the reciprocals and the value of GCA/SCA ratio was more than one for all traits this finding indicates that the additive genetic variance was more important 87.9 than the dominance genetic variance in the inheritance of most studied traits, which presenting the importance of using selection and its effect on the early segregating generations of the studied hybrids for improving such traits. The Same table shows that the degree of dominance (ā) was less than one, for all the traits, indicating the control of partial dominance of gene on the traits.

Table 1 : Analysis of variance for ordinary analysis and combining ability for studied traits.

S.O.V	DF	DT	DS	PH	EH	NRE	NKR	HKW	GY
BLOCK	2	1.62	6.37	14.3	12.95	0.054	0.929	0.705	12.79
GENOTYPES	35	29.25**	38.83**	149.32**	176.5**	5.60**	49.41**	19.32**	3401.2**
GCA	5	17.36**	21.13**	31.3**	123.7**	1.178**	26.79**	10.03**	1438.6**
SCA	15	14.24**	19.75**	101.2**	87.86**	3.89**	28.87**	11.11**	2132.5**
RECIPROCAL	15	2.72**	3.41**	4.49*	8.17**	0.077	0.629	0.571**	33.38**
ERROR	70	2.37	2.67	6.37	9.95	0.118	0.876	0.587	20.39

Table 2 : Estimates Variability,the ratio of GCA/SCA and degree of dominance for the studied traits.

	DT	DS	PH	EH	NRE	NKR	HKW	GY
σ^2A	2.762	3.37	4.87	20-07	0.190	4.42	1.64	238.64
$\sigma^2\bar{e}$	0.791	0.89	2.123	3.317	0.039	0.292	6.797	0.196
σ^2gca	1.381	1.69	2.434	10.03	0.095	2.21	119.3	0.820
Diallel crosses								
σ^2D	13.45	18.86	99.08	84.54	3.847	28.58	10.92	2125.68
σ^2G	16.21	22.23	103.95	104.61	4.036	32.99	12.56	2364.31
σ^2P	17.003	23.12	106.08	107.93	4.076	33.28	12.75	2371.1
σ^2gca/σ^2sca	0.103	0.089	0.025	0.119	0.025	0.077	0.075	0.056
$\bar{a}$	3.12	3.344	6.38	2.903	**6.36**	3.59	3.65	4.22
Reciprocal crosses								
σ^2D	0.965	1.26	1.185	2.43	0.019	0.169	0.188	13.29
σ^2G	3.73	4.64	6.052	22.49	0.209	4.59	21.83	251.92
σ^2P	4.52	5.52	8.175	25.81	0.248	4.88	2.02	258.72
σ^2gca/σ^2sca	1.43	1.34	2.054	4.138	5.00	13.07	4.36	8.98
$\bar{a}$	0.836	0.87	0.698	0.491	0.447	0.277	0.479	0.334

Heritability

Results presented in table 3 shows the values of both broad and narrow sense heritability. The highest values of h²b.s recorded for diallel crosses were (95.35%) for DT, (96.16%) for DS , (97.99%) for PH, EH was (96.93%), NRE (99.01%), NKR(99.12%), (98.46%) for HKW and (99.71%) for GY per plant. Highest values of estimated h²b.s for most traits revealed that the variations were transmitted the progeny and indicated the potential for developing high yielding varieties through as election of desirable plants in succeeding generations.

However, low h²n.s values were obtained for traits like DT (16.24%), DS (14.59%), PH (4.59%), EH (18.59%), NRE (4.66%), NKR (13.27%), the HKW (12.85%) and GY per plant (10.06%). Thus, this character is controlled by non-additive genes (dominance and epistasis). Obtained results agreed with those of Abd El-Sattar (2003). For reciprocal crosses, in the present study h²b.s was high (greater than 80%) for all studied trait which were 82.49% for DT, DS gave value of (83.92%), 87.15% for EH, NRE (84.27%), NKR (94.01%), HKR (90.31%) and GY per plant (97.37%) with the exception

of the PH that gave (74.03%). High heritability indicates that the environmental influence is mini-impact on traits, any of the traits can be used for selection. On the other hand results showed that high h²n.s estimated were detected for the DT (61.13%), DS (72.79%), PH (59.54%), EH (77.75%), NRE (76.61%), NKR (90.55%), HKR (80.87%) and GY (92.23%) emphasizing that the additive genetic variation was the major component of genetic variation in the inheritance of these traits and the effect of selection in the early segregating generations of the studied hybrids for improving these traits. High heritability estimates were also reported by Yasien (2000) and Abd El-Sattar (2003).

Coefficients of variation

The comparison of characters as regards to the extent of genetic variation could be better judged by the estimation of the genotypic coefficient of variation (GCV) in relation to their respective phenotypic coefficient of variation (PCV). Amongst the yield traits; very small difference between GCV and PCV was observed for the traits in both crosses (diallel and reciprocal) (table 3). It indicates that the observed variations for the traits were

Table 3 : Heritability and coefficient of variation for the studied traits.

	DT	DS	PH	EH	NRE	NKR	HKW	GY
Daillel Crosses								
h²b.s	95.35	96.16	97.99	96.93	99.01	99.12	98.46	99.71
h²n.s	16.24	14.59	4.59	18.59	4.66	13.27	12.85	10.06
GCV	7.103	7.89	5.61	11.72	12.56	15.47	14.44	32.37
PCV	7.27	8.05	5.66	11.91	12.62	15.54	14.25	32.42
Reciprocal crosses								
h²b.s	82.49	83.92	74.03	87.15	84.27	94.01	90.31	97.37
h²n.s	61.13	72.79	59.54	77.75	76.61	90.55	80.87	92.23
GCV	3.49	3.70	1.35	5.36	2.99	5.78	5.44	10.85
PCV	3.84	4.04	1.57	5.75	3.14	5.97	5.72	11.00

mostly due to genetic factors. However, the environment played a little role in the expression of these traits. For diallel crosses, the high GCV and PCV was observed only for one trait (GY) while, the traits EH, NRE, NKR and HKW showed moderate GCV and PCV value, which rest traits, DT, DS and PH exhibited low GCV and PCV estimates. For reciprocal crosses, the small difference between PCV and GCV of all traits indicated the existence of genetic variability and the traits are least influenced by environmental effects.

Heterosis

Heterosis results presented in table 5 showed values of heterosis for the diallel crosses and reciprocals which evaluated according to the increased and decreased percentage over the best parent (BP%). Significant differences were noted in heterosis values between diallel and reciprocal crosses. Most of the diallel crosses showed negative heterosis for the DT and DS. The hybrid P3 × P5 was superior and gave the lowest negative percentage of heterosis (-13.83 DT and -15.42 DS) followed by the hybrid P1 × P3, which gave -11.83 DT and -13.20 DS referring to the existence of over dominance of gene action effect by the early parent, while the hybrids P1 × P5 showed heterosis of 0.00 for DS and P4×P6 gave 0.00 for DT showing the effect of the complete dominance of genes in those crosses. For PH the hybrid P2×P3 showed the highest positive percentage of heterosis reached 11.70, followed by P1×P6 which gave 10.84. For the EH; P1 × P3 had the highest heterosis of 30.22. Heterosis of NRE showed P3 × P4 as the highest reached 30.07 percent for the hybrid vigor followed by hybrid P2 × P3 (29.99). For the NKR, hybrid P1 × P2 was superior by giving values of 43.15. The P1 × P5 cross demonstrated the highest positive heterosis for the weight of 100 grain reached 39.45 outperforming the rest of the hybrids. For grain yield per plant, most hybrids showed positive heterosis values reached the top (124.82) for P1 × P2

cross which already distinct by giving the highest heterosis for the number of kernels per row, P3 × P4 came after and gave 113.96, which was superior for the number of rows per ear. The heterosis values estimated for most of the crosses were positive and crosses were superior compared to their best parent. For PH (10.13) was recorded for P5×P1, EH (28.92) was the highest recorded for P3 × P1, the cross P4 × P3 was superior for the NRE (30.00), heterosis value of 40.25 was the highest for the NKR that presented by P2 × P1. The hybrid P5 × P1 showed highest heterosis (38.16) value of HKW, the highest value of GY was 111.39 reported for the cross P2 × P1, which gave highest hybrid vigour for the NKR (40.25). These results clearly show the effect of over dominance gene action in crosses, which gave a positive hybrid vigour. These results agreed with the results of many researchers (Saleh *et al.*, 2002 and Muraya *et al.*, 2006 and Amiruzzaman *et al.*, 2011).

Reciprocal crosses results presented in table 4 showed that reversing parents didn't change heterosis results of diallel crosses, where all reciprocals of superior diallels were superior as well for all studied traits except for the PH, where the reciprocal hybrid P5 × P1 gave the highest value with no significant difference compared to P3 × P2 the reciprocal cross of the diallel P3 × P2. However, differences were highly significant between diallels and their reciprocals and completely changed the result in some crosses. These outcomes clearly show the maternal effect and presuming the interaction between genes in cytoplasm and genes in the nucleus. Parent lines P1 and P3 appeared and repeated in superior crosses, and all crosses had P1 in their genotype gave high heterosis value for all traits; whether, it was paternal or maternal except in two crosses that contain P4 and P6. This may refer to the dominant gene action of parent's genes. Likewise, crosses (dialles and reciprocals) that showed the lowest heterosis values all shared the same

Table 4 : Heterosis for the traits expressed as percentage of increase over and decrease under better parent (BP %).

F1	DT	DS	PH	EH	NRE	NKR	HKW	GY
P1×P2	-9.61	-11.57	5.11	25.32	28.75	43.15	22.06	124.82
P2×P1	-9.03	-10.52	4.10	25.76	29.26	40.25	16.59	111.39
P1×P3	-11.83	-13.20	3.49	30.22	16.42	37.46	26.23	102.44
P3×P1	-13.44	-14.22	4.76	28.92	17.42	30.54	26.23	90.32
P1×P4	-2.89	-4.31	7.50	13.81	16.53	22.89	1.61	57.11
P4×P1	-4.63	-6.98	4.49	10.69	18.82	15.73	13.54	62.40
P1×P5	0.532	0.00	7.51	15.79	25.86	21.78	39.45	113.73
P5×P1	-10.76	-12.18	10.13	16.05	23.79	23.08	38.16	110.61
P1×P6	-3.23	-3.56	10.84	9.52	18.75	20.66	21.28	74.99
P6×P1	-7.53	-8.13	8.84	16.06	17.97	23.48	23.03	76.11
P2×P3	-7.92	-10.20	11.70	24.78	29.99	-1.12	24.32	68.45
P3×P2	-9.61	-11.57	9.94	23.51	19.75	1.60	13.16	47.67
P2×P4	1.14	-1.61	7.79	11.91	17.05	27.42	27.27	106.46
P4×P2	-5.20	-7.53	9.55	7.08	16.83	24.88	26.06	99.96
P2×P5	-5.64	-7.89	2.53	-0.85	11.41	19.72	21.71	67.16
P5×P2	-7.92	-10.52	4.29	13.59	8.78	20.79	25.04	72.62
P2×P6	-2.25	-3.16	6.59	9.53	22.38	17.84	16.39	68.64
P6×P2	-2.25	-3.68	5.81	15.88	21.65	14.84	11.43	55.75
P3×P4	-6.94	-8.06	9.16	11.28	30.07	21.54	25.61	113.96
P4×P3	-7.53	-10.21	8.77	13.52	30.00	17.52	22.62	97.64
P3×P5	-13.83	-15.42	10.53	10.47	25.63	14.59	18.26	71.31
P5×P3	-16.49	-17.91	9.36	9.57	25.33	19.43	16.69	75.89
P3×P6	-8.52	-9.96	6.35	13.57	11.57	8.67	11.25	36.03
P6×P3	-11.17	-11.94	6.74	7.71	11.03	11.78	11.59	35.16
P4×P5	-1.73	-3.23	3.91	15.99	19.59	24.29	12.52	76.08
P5×P4	-0.859	-2.15	5.85	18.75	19.59	24.49	12.52	76.38
P4×P6	0.00	-1.61	4.09	9.98	20.12	17.84	9.21	57.75
P6×P4	-0.572	-1.61	6.43	9.53	19.89	19.59	4.74	56.14
P5×P6	-7.36	-3.46	10.13	12.36	19.95	3.62	14.78	50.47
P6×P5	-8.94	-9.86	9.55	16.66	19.72	5.45	16.42	52.63
L.S.D	2.17	2.31	3.56	4.45	0.48	1.32	1.08	6.37

two parent lines, which were P2 and/or P4, and P2 appeared mostly. Referring to the existence of the effect of over dominance of gene for early parent.

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