

EVALUATION OF GENETIC BEHAVIOUR OF VEGETATIVE AND EARLINESS TRAITS IN MAIZE HYBRIDS AT TWO LOCATIONS.

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ABSTRACT

This investigation was carried out to evaluate the genetic behaviour of earliness and vegetative traits of maize at two locations. Therefore, 11 inbred lines of maize were crossed among them according to factorial arrangement to obtain 30 F₁ hybrids. Five inbred lines were used as male parents while six inbred lines were used as female parents. All genotypes (41) were evaluated at two locations. The first location was the farm of Genetic Department, Faculty of Agriculture, Mansoura University (L₁) while the second location (L₂) was the farm of Faculty of Agriculture, Sohag University. Different earliness and vegetative traits were studied. These traits were: plant height in centimeters (P.H.), number of leaves per plant (No. L./P.), leaf area (L.A.), number of days to 50% tasseling (No. D. 50%.T.) and number of days to 50% silking (No. D. 50% S.).

The results of the combined analysis indicated that all studied vegetative and earliness traits showed significance among evaluated genotypes. Similarly, the interaction between genotypes and location (g x L.) were also significant for all studied traits except P.H. The results also revealed that P.H. and N.L./P. showed positive and highly significant values of heterosis versus the mid-parents. On the other hand, the two earliness traits (No. D. 50%. T.) and (No. D. 50%. S.) showed significant and negative (desirable) values. The results cleared that the variances of male, female and M. x F. were significant for most studied traits. The results indicated that the values of heritability in broad and narrow senses were medium for most studied traits.

INTRODUCTION

Many investigators studied the manifestation of heterosis and nature of gene action in maize. Galal *et al.* (1994), Shehata *et al.* (1997), Metawei (2002), Alvi *et al.* (2003) and Welcker *et al.* (2005) evaluated different F₁ hybrids of maize and obtained variable estimations of heterosis versus the mid-parents or the better parent for vegetative and earliness traits.

Melchinger *et al.* (1990), El-Hosary and Sedhom (1990), Shafey (1993), Amer *et al.* (1998), Mostafa (2000), Abd El-Hadi *et al.* (2005) and Brandon *et al.* (2007) studied the nature of gene action in maize. Their results illustrated the importance of general combining ability (GCA) and/or specific combining ability (SCA) for different traits OF maize.

Yassien (1999), El-Kahal (2002), Siriani *et al.* (2003) and Leilani *et al.* (2006) estimated heritability values and indicated that heritability in broad sense (h²_b%) were always larger than the corresponding of heritability in narrow sense (h²_n%).

MATERIALS AND METHODS

Eleven inbred lines of maize were used in this investigation. These lines were : Inb.L. 2, Inb.L. 21, Inb.L. 51, Inb.L. 56 , Inb.L. 59 , Inb.L. 76, Inb.L. 81, Inb.L. 122, Inb.L. 133, Inb.L. 144 and Inb.L. 147

The seeds of all parental inbred lines were obtained from National programme of maize, Agricultural Research Center (ARC), Egypt. The parental inbred lines: Inb.L. 2, Inb.L. 21, Inb.L. 51, Inb.L. 56 and Inb.L. 59 were used as male parents. While, the other six parental inbred lines: Inb.L. 76, Inb.L. 81, Inb.L. 122, Inb.L. 133, Inb.L. 144 and Inb.L. 147 were used as female parents. The crosses among males and female inbred lines were made according to factorial arrangement to obtain 30 F₁ hybrids at the growing season of 2005. All genotypes (41) which included 30 F₁ hybrids and 11 parental lines were evaluated in a randomized complete blocks design (RCBD) with three replications at two locations. The first location was Mansoura University, Faculty of Agriculture, Farm of Genetic Department (L₁). The second location was the Farm of Faculty of Agriculture, Sohag University (L₂). The analysis of variances for (RCBD) as outlined by Cochran and Cox (1957). In the same time, the analyses of variance of factorial mating design were made according to Comstock and Robinson (1952). The standard error (S.E.) of the variance components were calculated as outlined by Anderson and Bancroft (1952).

The results were recorded on the following earliness and vegetative traits:

Plant height in centimeters (P.H. cm.), number of leaves per plant (No. L./P.), Leaf area in centimeters² (L.A. cm²), number of days to 50% tasseling (No. D. 50% T.) and number of days to 50% silking (No. D. 50% S.).

Heterosis values were made as the deviation of the mean of F₁ hybrids from the mid -parents and the better parent. The differences were tested for significance through estimating LSD values as outlined by Steel and Torrie (1960). Heritability values in broad and narrow senses were estimated as follows:

$$h^2_{b.s}\% = \frac{\sigma^2_m + \sigma^2_f + \sigma^2_{mf}}{\sigma^2_m + \sigma^2_f + \sigma^2_{mf} + \sigma^2_e} \times 100$$

$$(h^2_{n.s})_m = \frac{2 \sigma^2_m}{\sigma^2_m + \sigma^2_{mf} + \sigma^2_e} \times 100$$

$$(h^2_n)_f = \frac{2 \sigma^2_f}{2 \sigma^2_m + \sigma^2_{mf} + \sigma^2_e} \times 100$$

$$(h^2_n)_{m+f} = \frac{\sigma^2_m + \sigma^2_f}{\sigma^2_m + \sigma^2_f + \sigma^2_{mf} + \sigma^2_e} \times 100$$

where: (F = 1)

$$2 \sigma^2_m = 2 \text{Cov}_{HS(m)} = VA + \frac{1}{4} VAA + \frac{1}{16} VAAA$$

$$2 \sigma^2_f = 2 \text{Cov}_{HS(f)} = VA + \frac{1}{4} VAA + \frac{1}{16} VAAA \dots$$

$$\sigma^2_m + \sigma^2_f = \text{Cov}_{\text{HS}(m)} + \text{Cov}_{\text{HS}(f)} = \text{VA} + \frac{1}{4} \text{VAA} + \frac{1}{16} \text{VAAA} \dots$$

$$\sigma^2_{mf} = \text{Cov}_{fs} - (\text{Cov}_{\text{HS}(m)} + \text{Cov}_{\text{HS}(f)}) = \text{VD} + \frac{1}{2} \text{VAA} + \frac{1}{4} \text{VDD} \dots$$

The combined analysis of variances were made for all studied traits over two locations.

RESULTS AND DISCUSSION

The analysis of variances of all earliness and vegetative traits were made for each location and over both locations and the results are presented in Table 1. The results indicated that the mean squares of locations showed highly significance for all studied traits indicating the great effects of different environments on the expression of different genotypes. The results also indicated that the genotypes mean squares were significant or highly significant for all studied traits. The same trend were also found for genotypes mean squares. These findings cleared the importance of choice of genotypes for suitable locations.

Table 1: The results of the combined analyses of variance and the mean squares of earliness and vegetative traits over both locations.

S.V.	d.f.	P.H.	No. L/P	L.A. cm.		
Loc.	1	5477.5**	13.21**	232497.7**	2536.99**	5766.18**
R(L.)	4	2635.8	1.43**	12535.2	51.663**	43.337**
gen.	40	4986.7**	5.71**	8982.6*	41.90**	29.45*
g x L	40	939.4	2.54**	16795.9**	11.78**	17.37**
Error	160	286.4	0.30	5920.9	6.82	9.31

The mid-parents (M.P.), ranges, mid of F₁ hybrids (F₁), heterosis values against the mid-parents and heterosis values versus the better parent were calculated and the results are presented in Table 2.

The results revealed that the mean of F₁ hybrids significantly exceeded the mid-parents for all studied traits. The highest values of heterosis versus the mid-parents were 33.18% for plant height trait followed by 15.16% for number of leaves per plant. It could be also noticed that the two traits number of days to 50% teaseling and number of days to 50% silking showed negative and significant values of heterosis versus the mid-parents. These negative values were desirable and expected where these traits were the indicator of earliness.

The results also revealed that heterosis from the better parent were 16.34%, 3.33%, - 10.38%, 8.93% and 1.61% for P.H., N.L./P., L.A., No. D. 50% T. and No. D. 50% S., respectively. The hybrids, which exceeded the better parent, could be used as promising hybrids. Similar results were o

The analysis of variances for factorial mating design were made for each location over both two locations and the results are presented in Table 3. The result, revealed that the mean squares of crosses showed highly significance for all studied traits. In the same time, the interactions between crosses and locations were significant for all studied traits. This finding indicated the effect of different environments on the expression of genotypes. It could be noticed from the same table that the mean squares of both males and females were significant for all studied traits. The obtained significant values of males and females indicated that the mean squares of males were

more important than those the mean squares females in the significance of crosses and crosses x locations interactions.

Table 2: Mid-parents, ranges, F₁ hybrids, ranges and heterosis values estimated versus the mid-parents (MP) and better parent (BP) for traits at two locations and from the combined, data.

S.V.	d.f.	P.H.	N.L./P.	L. A.	No. D. 50% T.	No. D. 50% S.
M.P.	L ₁	170.27	13.82	607	61	60.64
	L ₂	182.18	13.09	464	65.64	70.37
	Comb.	176.46	13.46	535.55	63.18	65.36
Range	L ₁	140-188	12 – 15	506-679	55 – 64	57 – 63
	L ₂	149-222	12 – 15	356-564	58 – 69	66 – 77
	Comb.	152-202	12 – 15	490-607	56 – 66	62 – 67
F ₁	L ₁	243	15	560	57	58
	L ₂	226	16	528	64	68
	Comb.	235	15.5	544	61	63
Range	L ₁	210-269	13 – 16	395-708	53 – 62	54 – 63
	L ₂	198-262	14 – 17	434-614	59 – 69	64 – 73
	Comb.	213-265	15 – 16	454-627	57 – 65	60 – 67
H (M.P.)	L ₁	42.72**	8.54**	-7.74	-6.56**	-4.35**
	L ₂	24.05**	22.23**	13.79**	-2.50**	-3.37**
	Comb.	33.18**	15.16**	1.58	-3.45**	-3.61**
H (B.P.)	L ₁	29.26	0.00	-17.53	3.64	1.75
	L ₂	1.80	6.67	-6.38	10.35	3.03
	Comb.	16.34**	3.33	-10.38**	8.93**	1.61
L.S.D. 0.05 M.P.	L ₁	7.02	0.26	40.64	1.27	1.55
	L ₂	6.67	1.18	16.94	0.79	0.80
	Comb.	6.81	0.22	30.98	1.05	1.23
L.S.D. 0.01 M.P.	L ₁	9.31	0.34	53.91	1.68	2.07
	L ₂	8.85	0.24	22.47	1.05	1.06
	Comb.	8.98	0.29	40.83	1.38	1.62
L.S.D. 0.05 B.P.	L ₁	20.23	0.74	117.12	3.65	4.47
	L ₂	19.23	0.52	48.82	2.29	2.31
	Comb.	19.63	0.64	89.27	3.03	3.54
L.S.D. 0.05 B.P.	L ₁	26.83	0.98	155.38	4.84	5.93
	L ₂	25.51	0.69	64.76	3.04	3.06
	Comb.	25.88	0.84	117.68	3.99	4.67

The variance components of males (σ^2_m), females (σ^2_f), male x female (σ^2_{mf}), males x location ($\sigma^2_m \times L.$), females x locations ($\sigma^2_f \times L.$) and males x females x locations ($\sigma^2_{mf} \times L.$) and their standard error were determined and the results are shown in Table 4. The results illustrated that the comparisons of the variance components σ^2_m , σ^2_f , σ^2_{mf} , $\sigma^2_m \times L.$, $\sigma^2_f \times L.$ and $\sigma^2_{mf} \times L.$ with their standard error values showed significant or highly significant values for all studied earliness and vegetative traits except $\sigma^2_f \times L.$ for number of leaves per plant (No. L./P.). These results indicated the effectiveness of locations on the variance components for all studied traits. The obtained results also indicated the importance of both σ^2_m and σ^2_f as indicator to additive genetic variances for many traits. In addition, the results also indicated the importance σ^2_{mf} as indicator of non-additive genetic variances including dominance for some traits.

Table 3: The combined analyses of variance and the mean squares of the factorial mating design for earliness and vegetative traits from the combined data over the two locations.

S.V.	d.f.	E.W.	E.L.	E.D.	No. R/E.	W 100/K
Loc.	1	13028.8**	38.46**	44979.0**	2226.05**	4147.20**
Rep. (L.)	4	2810.2**	2.16**	16522.0*	50.64**	42.41**
Crosses	29	868.6*	0.96**	9686.2	27.33**	22.45**
M.	4	3519.9**	1.90**	34011.6**	81.65**	96.63**
F.	5	852.8*	2.25**	10035.0	58.42**	20.98*
M. x F.	20	342.3	0.45*	4734.0	8.69	7.97
Cross. x L.	29	594.1**	1.82**	13982.0**	10.51	15.56**
M. x L.	4	1860.9**	8.47**	39713.1**	36.62**	52.30**
F. x L.	5	176.0	0.42	18326.8	2.76	25.67**
M.x F.x L.	20	445.3	0.83**	7749.7	7.23	5.68
Error	116	248.5	0.22	5482.6	6.08	7.66

Table 4: The estimated values of variance components from the factorial mating design and their standard errors for earliness and vegetative traits over the two locations.

S.V.	P.H.	No. L/P	L.A.	No. D-50% T.	No. D-50% S.
σ^2_m	49.0 ± 1.20	-0.17 ± 0.052	-74.6 ± 4.45	1.21 ± 0.18	1.17 ± 0.20
σ^2_f	156.0 ± 3.18	0.07 ± 0.031	-176.0 ± 3.20	1.81 ± 0.15	-0.23 ± 0.13
$\sigma^2_{m \times f}$	20.6 ± 1.82	-0.07 ± 0.057	-503.0 ± 5.62	0.25 ± 0.21	1.38 ± 0.19
$\sigma^2_{m \times L}$	-4.55 ± 1.25	0.424 ± 0.095	1776.0 ± 6.56	1.63 ± 0.20	2.59 ± 0.24
$\sigma^2_{f \times L}$	27.0 ± 2.36	-0.028 ± 0.03	705.0 ± 5.14	-0.30 ± 0.10	1.33 ± 0.19
$\sigma^2_{m \times f \times L}$	69.9 ± 2.05	0.207 ± 0.094	756.0 ± 9.41	0.38 ± 0.29	-0.66 ± 0.27

The values of heritability in broad and narrow senses were estimated for each location and over two locations and the results are cleared in Table 5. The results cleared that the highest calculated values of heritability in narrow sense from σ^2_m , σ^2_f and from $\sigma^2_m + \sigma^2_f$ were: 34.2, 49.5 and 41.3% for P.H. and No. D. 50% T., respectively.

Table 5: The estimated percent values of heritability in broad and narrow senses for vegetative and earliness traits at the two locations and combined.

S.V.	d.f.	P.H.	N.L./P.	L. A.	No. D. T.	No. D. S.
%h ² _{n,m}	L ₁	34.7	-	33.2	2.24	8.2
	L ₂	58.5	65.7	54.0	74.4	79.0
	Comb.	34.2	-	-	33.1	31.9
%h ² _{n,f}	L ₁	9.97	32.1	5.05	15.2	16.9
	L ₂	-	1.74	49.5	55.1	37.8
	Comb.	37.0	28.11	-	49.5	-
%h ² _{n,m+f}	L ₁	25.7	1.91	21.5	9.17	12.7
	L ₂	41.3	49.1	51.8	69.4	68.6
	Comb.	35.6	14.1	-	41.3	15.9
%h ² _{b,m+f+mf}	L ₁	31.6	41.6	23.2	16.6	12.7
	L ₂	59.9	76.5	63.4	71.7	68.6
	Comb.	35.6	14.1	-	44.7	21.1

In the same time, the values of heritability in broad sense ranged from 14.1% to 44.7% for No. L./P. and No. D. 50% T., respectively. The obtained quit values of heritability indicated the possibility of improving of genotypes of maize through suitable selection programme in promising hybrids of maize.

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تقييم السلوك الوراثي لبعض الصفات الخضرية والتبكير في بعض هجن الذرة في منطقتين مختلفتين •

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أجريت هذه الدراسة لتقييم السلوك الوراثي لبعض الصفات الخضرية في هجن مختلفة من الذرة في منطقتين مختلفتين • وقد استخدم إحدى عشر سلالة نقية من الذرة تم الحصول على بذورها من البرنامج القومي للذرة الشامية - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية • تم التهجين بين السلالات النقية الإحدى عشر طبقاً لنظام التزاوج العامي للحصول على ٣٠ هجين جيل أول حيث تم استخدام ٥ سلالات نقية كأباء و ٦ سلالات نقية كأمهات • وقد تم تقييم التراكيب الوراثية (٤١) تركيب وراثي والتي اشتملت على الأباء والجيل الأول) في منطقتين مختلفتين الأولى هي مزرعة قسم الوراثة - كلية الزراعة - جامعة المنصورة - (موقع أول)، والثانية هي مزرعة كلية الزراعة - جامعة سوهاج (موقع ثان) •

أظهرت نتائج تحليل التباين وجود فروق معنوية بين التراكيب الوراثية لكل الصفات التي درست، وكذلك وجود فروق معنوية للتفاعل بين التراكيب الوراثية والبيئة، وقد كان هذا متوقعاً حيث أن متوسط مربعات المواقع كان عالي المعنوية لجميع الصفات التي درست • وقد أظهرت النتائج أيضاً أن صفات طول النبات، وعدد الأوراق/نبات، ومساحة الورقة قد أعطت قيم معنوية موجبة لقوة الهجين حساباً من متوسط الأباء، بينما أعطت صفتي التبكير وهما عدد الأيام لظهور ٥٠% من النورة المذكورة وعدد الأيام لظهور ٥٠% من الحريرة قيم معنوية سالبة • وهذا أمر مرغوب فيه ويبحث عنه المربي •

أظهرت النتائج أيضاً أهمية كل من التباين ا لراجع للأباء وكذلك التباين الراجع للأمهات (تباين تجمعي)، وكذلك التفاعل بين الأباء والأمهات (التباين التجمعي) وأيضاً التفاعل بين هذه المكونات الثلاثة والمواقع • وقد كانت قيم معامل التوريث المتحصل عليها في نطاق المتوقع • والنتائج السابقة توضح إمكانية إنتاج هجن في الذرة وتحسين هذه الصفات من خلال الانتقاب في نسل الأجيال الإنعزالية لبعض الهجن المباشرة •