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Genetic parameters and combining ability of corn lines for grain

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Abstract

The general combining ability (GCA) and the specific (SCA) are used to identify hybrid combinations between parents with higher or lower yield than the expected average behavior of the progenitor lines. The objective of this study was to evaluate the GCA of 7 lines as female (H) and 4 male lines (M); as well as the SCA of the 28 crosses made; as a hypothesis it was proposed that crosses between lines with contrasting characteristics will produce outstanding hybrids. The obtaining of the lines with an inbreeding level of S3, the crosses and evaluation of the latter was carried out in the Experimental Field of the Faculty of Agronomy of the Autonomous University of Nuevo León, Mexico, the simple crosses were evaluated in an experimental design of complete blocks at random with three repetitions. Genetic analysis was performed with Comstock and Robinson's North Carolina mating design II. The parents that presented the highest yields were M2 (8.12 t ha⁻¹) and M4 (7.9 t ha⁻¹) considered as males and as H3 and H5 females (8.13 t ha⁻¹) both with the same yield; however, the greatest effects of GCA were in M2 (0.19), M1 (0.08), H4 (0.14) and H2 (0.13) in grain yield. The greatest effects on SCA were observed in the crosses H4xM2 (1.17 t ha^{-1}) , H6xM3 (0.84 t ha^{-1}) and H2xM3 (0.58 t ha^{-1}) . In the genetic parameters for grain yield, the environmental variance exceeded the additive and dominance variance, the heritability in the broad and narrow sense were 87.14 and 52.15%, respectively.

Keywords: combinatorial capacity, crosses, inbred lines, males and females.

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Introduction

Genetic improvement programs dedicated to the formation of hybrids and commercial varieties of corn require the generation of lines with high yield potential, agronomic behavior and combining ability. The lines that meet these characteristics present satisfactory results in hybrid combinations (Fan *et al.*, 2008). The concepts of general (GCA) and specific (SCA) combining ability allow to express the average behavior of a line in its hybrid combinations and designate the hybrid combinations that are superior, or not, to those expected in relation to the average of the GCA of the two parent lines. These are frequently used to estimate effects and variances of GCA and SCA (Sprague and Tatum, 1942).

An important purpose of the genetic improvement of maize by hybridization is to generate crosses that surpass in grain yield to the native varieties, improved and commercial hybrids. If in a population the effects of general combining ability are more important than the specific effects, it is recommended to improve the population by recurrent selection; on the contrary, if the effects of specific combining ability are the most important, the population should be improved by hybridization (Reyes *et al.*, 2004).

The knowledge of the genetic action that controls the traits of economic interest is basic for the planning of a genetic improvement program through the combinatorial aptitude of the parents, the breeder obtains greater achievements in his improvement program because it allows to select parents with an average behavior acceptable in a series of crosses and identify specific combinations with a behavior higher than expected, based on the average of the parents (De la Cruz *et al.*, 2005; Guillen *et al.*, 2009).

Much of the genetic diversity of Mexican native maize can still be found in agricultural fields in the form of creole varieties, since only 23% of the maize area uses improved seed (Polanco, 2008). In addition, farmers have identified characteristics that are favorable to their needs and preferences, so it is necessary to search for new genetic combinations in a creative way to generate greater variation (Louette and Smale, 1996).

The objective of this study was to identify an alternative that improves the yield of hybrids, generated from crossing between inbred lines derived from the Pinto Amarillo and Liebre groups collected in the north-central part of Nuevo Leon, Mexico. The hypothesis was that crosses between parents with contrasting characteristics from the Pinto Amarillo and Liebre populations will produce hybrids with high levels of heterosis for grain yield and its components.

Materials and methods

The study was carried out under irrigation conditions in the Experimental Field of the Faculty of Agronomy of the Autonomous University of Nuevo Leon, located at km 17.5 of the Zuazua-Marin highway in the municipality of Marín, Nuevo León, Mexico, which is It is located at 25° 53' north latitude, 100° 03' west longitude, with an altitude of 375 m, average annual temperature of 22 °C and average annual rainfall of 573 mm (INEGI, 2013). 11 lines were used (Table 1) with an inbreeding level of S3, which were crossed in a North Carolina design II, 7 parents were used as female (H) and four as male, for which 28 crosses were generated. simple.

Line	Municipality	Formation and characteristics of the line
H-1	Los Ramones	Population 24 of Pinto Amarillo. Drought tolerant early
H-2	Mina	Population 13 of Pinto Amarillo. Intermediate with wide adaptability
H-3	Paras	Population 71 of Pinto Amarillo. Drought tolerant intermediate
H-4	Pesqueria	Population 11 of Pinto Amarillo. Intermediate with wide adaptability
H-5	China	Population 50 of Pinto Amarillo. Drought tolerant intermediate
H-6	García	Population 46 of Pinto Amarillo. Intermediate with wide adaptability
H-7	Bustamante	Population 16 of Pinto Amarillo. Drought tolerant early
M-1	Pesqueria	Population 10 of Liebre. Intermediate with wide adaptability
M-2	Los Ramones	Population 19 of Liebre. Drought tolerant early
M-3	Los Ramones	Population 37 of Liebre. early drought tolerant
M-4	Cadereyta	Population 63 of Liebre. early with wide adaptability

Table 1. Origin and description of the maize lines with the S₃ inbreeding level participating as parents in the formation of 28 hybrids.

The Pinto Amarillo lines present acceptable yields (Table 2) and yellow semi-dent grain, the Liebre lines are early, tolerant to water deficit and semi-crystalline white grain and tolerant to water stress. The 11 lines were selected based on the results of a cluster analysis (Rodríguez *et al.*, 2012). Six rows of each parent inbred line were planted (Table 1) and 35 plants were used to perform the crosses between females and males.

The 28 hybrids were evaluated in a randomized complete block design with three replications, in an experimental plot of 4 rows of 5 m long and 0.8 m wide, with seven plants per linear meter to obtain a density of 87 500 plants ha⁻¹. The variables studied were: plant height (AP), ear height (AM), days to female flowering (FF), ear length (LM), ear diameter (DM), ear diameter (DO), number of rows per ear (HM), number of grains per row (GH) and grain yield (RG). All the plants of the plot were harvested and the grain was weighed in kg to transform the data into t ha⁻¹, adjusting to 13% humidity.

The genetic analysis was done with the North Carolina mating design II of Comstock and Robinson (1948), whose linear model was the following: $Y_{ijk} = \mu + M_i + H_j + \phi_{ij} + \varepsilon_{ijk}$. Where: i = 1. 2 m (males); j = 1. 2 h (females); k = 1. 2 r (rep); Y_{ijk} = observation of the cross between the ith male and the j-th female in the k-th repetition; μ = general mean; M_i and H_j = effect of the i-th male and jth female; ϕ_{ij} = effect of the interaction of the i-th male with the j-th female; ε_{ijk} = experimental error.

The estimation of the effects of general combining ability (GCA) for males and females and of specific combining ability (SCA) for crosses was made according to the proposal of Sprague and Tatum (1942): $g_i = \widetilde{Y}_{i.} - \widetilde{Y}_{...} g_j = \widetilde{Y}_{.j} - \widetilde{Y}_{...} S_{ij} = Y_{ij} - g_j - \widetilde{Y}_{...}$ Where: $g_i \cdot g_j$ and S_{ij} are the effects of GCA and SCA, respectively for the i-males, the j-females and their i and j crosses; $\widetilde{Y}_{i.}$ and $\widetilde{Y}_{.j}$ are the means of males and females; Y_{ij} is the value of the cross i*j y $\widetilde{Y}_{...}$ is the mean of the i*j crosses.

The statistical difference between the GCA of the male and female parents and the SCA of the crosses was determined by the minimum significant difference, (DMS, 0.05 α = EE x t (α 2-1. gl ee), where EE= standard error in the comparison of means; EE= $\sqrt{2}$ CME (RM)-1; R= repetitions; M= males; H= females; gl= degrees of freedom; and ee= experimental error.

The genetic components were estimated according to the values of the expectations of the mean squares of the analysis of variance; male variance ($\delta^2 M = M4 - m2/rH$), female variance ($\delta^2 H = M3 - M2/rM$), male x female variance ($\delta^2 M H = M2 - M1/r$), phenotypic variance ($\delta^2 F = \delta^2 M + \delta^2 H + \delta^2 M H + \delta^2 e$), additive variance ($\delta^2 A = 4 \delta^2 M$), dominance variance ($\delta^2 D = 4[\delta^2 H - \delta^2 M]$, narrow sense heritability ($h^2 = \delta^2 A / \delta^2 F$) and broad sense heritability ($H^2 = \delta^2 G / \delta^2 F$).

Results and discussion

There were statistical differences (Table 2) between hybrids, for grain yield (RG), ear height (AM), female flowering (FF), ear length (LM) and grains per row (GH); for males, in ear height (AM), female flowering (FF), ear length (LM), cob diameter (DO) and grains per row (GH), in females, for grain yield (RG), height of ear (AM) and length of ear (LM); in the MxH interaction it was significant in RG, AM, FF, LM, DO and GH.

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FV	GL	RG	AP	AM	FF	LM	DM	DO	HM	GH
Repetitions	2	0.5	0.06	0.01	10.08	1.16	0.16	0.13	0.68	14.89
Hybrids	27	0.74^{*}	0.81 ns	0.14^{*}	217.38^{*}	9.16*	0.15 ns	0.7 ns	2.25 ns	61.36*
Males	3	1.1 ns	0.02 ns	0.22^{*}	220.57^*	8.47^{*}	0.09 ns	0.23*	1.3 ns	58.01^{*}
Female	6	1.19^{*}	0.03 ns	0.02^*	5.75 ns	5.01**	0.09 ns	0.03 ns	0.19 ns	13.06 ns
M*H	18	0.98^*	0.06 ns	0.03^{*}	25.59^{*}	5.31*	0.11 ns	0.04^*	0.79 ns	22.34^{*}
Error	54	0.82	0.04	0.02	13.53	1.69	0.21	0.07	1.95	14.95
Total	83	0.88	0.04	0.03	94.61	2.95	0.17	0.07	1.52	17.97
CV (%)		11.55	10.45	9.48	4.84	9.37	10.8	5.49	10.74	11.8

 Table 2. Mean squares of the analysis of variance and level of statistical significance of the North Carolina Design II analysis. Marín, Nuevo León.

RG= grain yield AP= plant height; AM= ear height; FF= female flowering; LM= length of ear; DM= ear diameter; DO= cob diameter; HM= rows per ear; GH= grains per row.

These differences are due to the contrasting origin of the genetic material studied, which confirms the results obtained by; De la Cruz *et al.* (2005); De la Rosa *et al.* (2006); Borghi *et al.* (2012) who identified hybrids, males and females in maize genotypes with yield potential and their agronomic components as a result of the high genetic variability between populations from which the lines were derived, and due to the genetic diversity between the lines.

The coefficients of variation used as a measure of precision in conducting the experiments (Kang *et al.*, 1999), for grain yield, was 11.55%, considered acceptable, the coefficients in the yield components fluctuated between 4.84 and 11.80%, because they are characters with less variation.

Yield behavior and its components

In Table 3 the H3 and H5 females presented an average grain yield with 8.13 t ha⁻¹; however, H6, H7, H2 and H1 were in the second statistical group with averages of 8.01, 7.88, 7.84 and 7.54 t ha⁻¹ respectively; The outstanding yield in females could be due to their intermediate cycle and drought tolerance, in males M2 (8.12 t ha⁻¹) and M4 (7.9 t ha⁻¹) stood out. It is probable that the combination between males and females influenced the behavior of the crosses, since the similarity in the yield obtained from the male lines is due to the fact that they are of intermediate cycle, which is reflected in their superior yields to the rest of the males. Wong *et al.* (2007) also related this component which allows a high expression with a higher yield. Therefore, a good yield would be expected when combining these parents in the formation of hybrids (Soengas *et al.*, 2003).

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Progenitor	RG (t ha ⁻¹)	AP (m)	AM (m)	FF (days)	LM (cm)	DM (cm)	DO (cm)	HM	GH
H1	7.54 ab	1.96 a	1.32 b	76 a	12.97 d	4.36 a	2.48 a	13.16 a	31.66 a
H2	7.84 ab	1.99 a	1.39 ab	76.58 a	13.14 cd	4.15 a	2.37 a	13.08 a	31.75 a
H3	8.13 a	1.97 a	1.44 a	76.5 a	14.01 abcd	4.23 a	2.51 a	13 a	33.33 a
H4	7.29 b	1.95 a	1.43 a	76.25 a	13.72 bcd	4.1 a	2.4 a	13 a	32 a
H5	8.13 a	1.93 a	1.4 ab	75.5 a	14.31 ab	4.21 a	2.38 a	13 a	32.91 a
H6	8.01 ab	2.05 a	1.39 ab	75.75 a	14.05 abc	4.31 a	2.4 a	13 a	34.58 a
H7	7.88 ab	1.86 a	1.38 ab	74.58 a	14.82 a	4.23 a	2.4 a	12.75 a	33 a
DMS (0.05)	0.74	0.17	0.11	3.01	1.06	0.37	0.21	12.36	33.21
M1	7.75 a	1.97 a	1.29 c	81.14 a	14.39 a	4.31 a	2.58 a	12.95 a	33 a
M2	8.1 a	1.95 a	1.36 bc	81.19 a	13.22 b	4.21 a	2.35 b	12.66 a	30.38 b
M3	7.58 a	1.91 a	1.39 b	80.67 a	14.42 a	4.15 a	2.36 b	13.19 a	34.24 a
M4	7.89 a	1.98 a	1.53 a	60.52 b	13.41 b	4.23 a	2.39 b	13.19 a	33.38 a
DMS (0.05)	0.56	0.13	0.08	2.28	0.8	0.28	0.16	0.86	2.39

 Table 3. Averages of the yield and agronomic components of the simple crosses grouped by female and male parent. Marín, Nuevo León.

RG= grain yield; AP= plant height; AM= ear height; FF= female flowering; LM= length of ear; DM= ear diameter; DO= cob diameter; HM= rows per ear; GH= grains per row.

For plant height (AP) the females with the highest bearing were H6 (2 m) and H2 (1.99 m), this type of height is ideal for mechanical harvests because they can resist lodging, the females presented on average a height of ear (AM) favorable for mechanical harvests were H3 (1.44 m) and H4 (1.43 m), in female flowering the averages in the seven females fluctuated between 74 to 76 days (d), and they are considered as intermediate cycle , which is an advantage since farmers prefer to sow materials from this cycle, in ear length (ML) the H7 had the largest size with 14.88 cm, while the H5 was in the second statistical group with 14.31 cm, the rest of the females were concentrated in different groups, in ear diameter (DM) females H1, H6 and H3 presented averages of 4.66, 4.31 and 4.23 cm respectively; in rows per ear (HM) and grains per row (GH), there were no statistical differences.

For males there was no statistical significance in (RG), (AP), (DM) and (HM), however, for ear height (AM), M4 presented an average of 1.53 m and M1 obtained the lowest value with 1.29 m, for female flowering, M4 was earlier with 60 d, while the rest of the males obtained averages of 80 d, in ear length and cob diameter there were no marked differences, only 1.2 and 0.23 cm was the range of difference In both variables, respectively, in grains per row, the lowest average was presented in M2 with 30.38 and the highest average was obtained by M3 with 34.24.

By combining, by recombination and selection some contrasting lines, it could result in defined heterotic patterns because, according to Dzib *et al.* (2011), the highly yielding hybrids were due to heterosis and also due to hereditary factors, such as the multiple interaction of additive type genes. This shows the convenience of knowing the relative importance of each genetic component in the production of hybrids. Lines H3 and H5 were the ones that intervened in the most outstanding crosses for their yield, followed by H6 and H7. M2 was the one that appeared most frequently in superior crosses, so lines H6 and M2 would be indicated to separate the rest of the lines into two heterotic groups (Malacarne and San Vicente, 2003).

General combinatorial ability (GCA)

The highest general combining ability effects for RG and DM were found in H4 and H2 females (Table 4); however, H5 and H1 obtained lower and negative values, which suggests that H4 and H2 contain genes with additive effects that are favorably expressed in grain yield (Ávila *et al.*, 2009). For AP, H2 and H3 showed higher effects on FF, H6 and H4 obtained higher values, for LM females H1 and H3 indicated that they had higher expression with positive effects, however, for DO, HM and GH, H3 and H5 obtained on average the maximum values, all with positive effects and also with the maximum values *per se* recorded; that is, on average these populations generated the best combinations.

Line	RG (t ha ⁻¹)	AP (m)	AM (m)	FF (days)	LM (cm)	DM (cm)	DO (cm)	HM	GH
H1	-0.19	-0.49	0.95	0.8	0.8	2.56	-0.29	-0.1	0.02
H2	0.13	0.35	0.9	-0.16	-0.16	1.81	0.3	0.01	0
H3	-0.01	0.23	0.91	1	1	2.06	0.03	0.11	0.01
H4	0.14	0.1	0.89	-0.16	-0.16	0.89	0.8	0.02	0.02
H5	-0.03	-0.13	0.9	-0.04	-0.04	-2.27	0.22	0.07	0.06
H6	0.08	-0.05	0.87	-0.33	-0.33	-3.77	-0.51	-0.04	-0.04
H7	0.04	-0.01	0.85	0.25	0.25	-1.27	-0.55	-0.06	-0.07
M1	0.08	0.12	0.7	-0.06	8.01	8.45	0.02	0.03	0.1
M2	0.19	0.04	0.75	-0.08	7.38	7.79	-0.05	0.04	-0.04
M3	-0.25	-0.32	0.65	0.04	-1.47	-1.55	-0.35	-0.06	0
M4	0.04	0.15	0.85	0.1	-13.93	-14.69	0.37	-0.01	-0.06

 Table 4. Estimated values of general combining ability (GCA) of the maize lines used as males and females, in the North Carolina design II. Marín, Nuevo León.

RG= grain yield; AP= plant height; AM= ear height; FF= female flowering; LM= length of ear; DM= ear diameter; DO= cob diameter; HM= rows per ear; GH= grains per row.

These results indicate that these populations have a high contribution in the expression of the characteristics evaluated in their progeny, and that the additive effects are the most important; therefore, they can be included in a maize genetic improvement program, to contribute with superior alleles (De la Cruz *et al.*, 2005; Preciado *et al.*, 2005; Guillen *et al.*, 2009). It is observed that according to the effects of GCA registered there are other populations with diverse origins that can contribute to the genetic improvement of maize and that until now little attention has been paid to their potential as sources to increase the genetic base of commercial hybrids (Guillen *et al.*, 2009).

The males that expressed the highest combining ability for RG and LM were M2 and M1, in AP, AM, FF, LM, DM, DO, HM and GH, M1, M3 and M4 obtained higher and positive values associated between these variables of GCA, which indicates that not all components of grain yield have similar behavior, but depend on the genetic makeup of each line; in addition, M4 showed higher values in six (60%) of the characteristics, which can be advantageous in improving yield, as mentioned by Wong *et al.* (2007).

In all the characters mentioned above, the effects of GCA were greater than those corresponding to SCA, although it is important to note the presence of dominant genes, but the effects of additive genes contribute in a greater proportion than the non-additive effects in the expression of the phenotype, which coincides with Badawy (2013) for the grain yield variable. However, these results differ from those published by Kanagarasu *et al.* (2010); Borghi *et al.* (2012) who found that the non-additive effects were higher than the additives for grain yield, ear diameter, ear length and plant height.

Specific combinatorial ability (SCA)

In Table 5, the average value and the effects of SCA of the 28 hybrids are shown, observing that the five best combinations for RG (Table 6) were presented in (H4*M2), (H6*M3), (H2*M3), (H5*M4) and (H6*M4); however, the hybrid (H1*M2) turned out to be the one that expressed the lowest aptitude with a negative value, where the maximum value was 1.17 t ha⁻¹, which corresponded to the first listed cross, which was expected since the parent lines of H4xM2 expressed the greatest effects of GCA (Table 5), the above, may be due to the sum of the additive effects of the genes of the parents or a high positive effect of SCA, this result suggests that the manifestation of high yield in the crosses is due to the gene action of additive effects of the lines, as asserted by Springer and Stupar (2007). It was detected that in the crosses with higher magnitude SCA, they combined populations of contrasted geographical origin in the distribution area of the state of Nuevo Leon, and that the dimension of the effects recorded was due to the distance that exists between both populations; H4 belongs to the municipality of Pesqueria and M2 to Los Ramones.

In AP, the best five hybrids that expressed greater SCA effects were: H2xM4, H3xM1, H4*M2, H6*M1 and H5*M2. The populations belonging to the variants of the hybrids had an important influence on the expression of the outstanding crosses for this variable, where said crosses mostly presented both average values and high SCA effects, in AM the best crosses were (H4*M4), (H4*M2), (H5*M2), (H2*M1) and (H7*M4). For FF and LM, the simple crosses H2*M3 and H3*M3, expressed greater effects of SCA; however, in DM, DO, HM and GH, they were H1*M3, H1*M1 and H5*M1.

Marin, Nuevo Leon.										
Crosses	RG (t ha ⁻¹)	AP (m)	AM (m)	FF (days)	LM (cm)	DM (cm)	DO (cm)	HM	GH	
H4xM2	1.17	0.65	0.7	1.41	0.3	0.81	0.18	-0.03	0.41	
H6xM3	0.84	-0.01	-0.29	-13.47	-11.37	-0.98	0	0.09	0.39	
H2xM3	0.58	-0.36	0.32	11.01	10.71	-0.08	-0.24	-0.04	-0.32	
H5xM4	0.58	-0.64	0.25	-3.04	-0.39	-0.46	0.1	-0.01	-0.55	
H6xM4	0.43	0.11	0.34	-0.68	3.77	0.49	0	-0.01	-0.18	
H2xM2	0.4	-0.26	0.25	-1.24	-3.62	-0.25	0.01	-0.12	0.83	
H1xM3	0.32	0.19	-0.19	8.94	7.63	2.26	0.28	0	0.39	
H3xM1	0.14	0.66	-0.23	-0.62	-3.20	1.88	-0.02	-0.04	-0.13	
H5xM2	0.13	0.38	0.49	2	4.13	0.12	0.19	0.15	-0.67	
H4xM1	0.06	-0.63	-0.44	-2.1	-3.7	-1.78	-0.12	0.13	-0.54	
H7xM4	0.03	-0.1	0.46	1.98	4.27	2.11	0.01	-0.04	0.15	
H5xM1	0.03	0.18	0.15	3.51	5.8	0.65	0.03	-0.06	1.04	
H1xM4	0.02	0.3	0.14	1.68	0.11	-1.04	-0.22	-0.13	0.15	
H3xM3	0.02	-0.2	-0.47	11.01	10.46	-1.73	0.12	-0.02	-0.32	
H3xM2	-0.05	-0.29	0.15	1.12	-1.2	0.39	-0.05	0	0.16	
H2xM1	-0.08	-0.17	0.46	-1.51	-3.95	0.04	0.03	0.03	-0.79	
H4xM4	-0.08	-0.29	0.7	1.39	1.44	-0.86	-0.04	0	-0.14	
H4xM3	-0.09	0.26	-0.74	2.46	1.96	1.83	-0.02	-0.09	0.27	
H7xM3	-0.1	0.03	-0.49	-9.93	-9.87	-0.98	0.19	0.16	-0.61	
H7xM1	-0.12	0.27	-0.13	2.03	3.13	-1.23	-0.1	-0.12	0.42	

Table 5. Estimated values of specific combining ability (SCA) of the 20 crosses with the highest
yield and their agronomic components generated by the North Carolina design II.
Marín, Nuevo León.

RG= grain yield; AP= plant height; AM= ear height; FF= female flowering; LM= length of ear; DM= ear diameter; DO= cob diameter; HM= rows per ear; GH= grains per row.

On the other hand, of the eight parents involved in the crosses with the highest SCA effects, H1 and M1 showed high GCA effects (Table 5), which indicates that their parents are suitable to form intervarietal hybrids with high yield potential, or to derive lines that when crossed have a good combination between them. In this regard, it is expected that crosses with higher SCA result from crossing at least one population with high GCA (Legesse *et al.*, 2009; Escorcia *et al.*, 2010).

The parents H4, H2, M1 and M2 were the ones that yielded the most (from 7.3 to 8.1 t ha⁻¹), presented a plant size (from 1.8 to 1.9 m) and ear (from 1.2 to 1.4 m), of a cycle intermediate (from 76 to 81 days at FF), but with greater ear length (13 to 14.3 cm), greater number of rows per ear (12.6 to 13) and greater number of grains per row (30.3 to 33) with respect to the rest of the lines.

This indicates that non-additive genes participated in the inheritance of the crosses. The nonadditive action of the genes was reduced between the crosses of the parents, the participation of non-additive genes in the best crosses may be due to the fact that the parents have wide genetic variation and greater additive effects, as corroborated by the high GCA values found. in the variables RG, AP, AM, LM, DM, DO, HM and GH.

These results coincide with that reported by (Dzib *et al.*, 2011), who reported that non-additive genes contributed more to the expression of ear length and diameter, number of rows to obtain the highest grain yield. Crosses with higher SCA values can be considered as prospects in genetic improvement programs to form hybrids and to introduce genetic variation in recurrent reciprocal selection programs. The values were small compared to those obtained by Reyes *et al.* (2004); Escorcia *et al.* (2010), but similar to those of Legeese *et al.* (2009).

Genetic components

When estimating the genetic components (Table 6), in grain yield and ear length, the variances of hybrids, males, females and interaction between males by females, high values were observed; however, in the environmental variance the variables such as RG, AP, LM, DO and GH were higher with respect to the additive and dominance variance, so that the environmental variance influenced in a greater proportion the expression of the phenotypic variance with respect to these characters. In the case of heritability in the broad sense, the RG, AM and HM stood out, with the exception of the LM, AM and FF for heritability in the narrow sense.

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Component	δ^2 Hybrids	$\delta^2 M$	$\delta^2 H$	$\delta^2 M x H$	$\delta^2 A$	$\delta^2 D$	$\delta^2 F$	H^2	h^2
RG	11.36	15.87	7.2	8.45	3.65	5.71	13.49	87.14	10.1
AP	0.31	4.51	0.87	0.61	0.2	0.7	1.26	65.15	31.05
AM	0.87	0.6	0.52	0.75	0.35	1.15	1.87	86.91	46.25
FF	1.1	4.38	3.7	1.89	1.49	3.2	5.52	63.38	34.7
LM	23.74	19.69	10.15	43.87	1.98	15.46	4.9	55.1	52.15
DM	1.65	5.87	8.1	6.7	1.41	3.93	6.86	65.82	28.14
DO	1.36	0.97	5.05	5.62	3.46	7.11	0.95	63.21	29.34
HM	8.37	15.1	3.84	2.79	1.15	2.1	4.28	73.14	30.16
GH	1.7	3.68	8.6	4.21	3.46	3.98	1.5	63.16	29.37

 Table 6. Estimated values of the genetic variance components for grain yield and its agronomic components. Marín, Nuevo León.

RG= grain yield; AP= plant height; AM= ear height; FF= female flowering; LM= length of ear; DM= ear diameter; DO= cob diameter; HM= rows per ear; GH= grains per row. δ^2 M= variance of males; δ^2 H= variance of females; δ^2 A= additive variance; δ^2 D= variance of dominance; δ^2 F= phenotypic variance and h²= heritability.

These results are attributed to the diversity of the genetic makeup of the progenitor lines, which when mating form individuals of a heterozygous type, which reduce the additive effects. For this reason, it is to be assumed that all the variations are estimated based on the genetic behavior determined as dominance variance, which is to be expected since there is a greater heterotic

expression in the hybrids due to the effect of the SCA of most of the lines in RG, which results in a higher heritability value in the broad sense due to the effect of the dominance variance (Badawy, 2013). Hallauer *et al.* (2010) pointed out that another of the possible reasons for a lower additive variance is the origin of the parents that form the hybrids, since when they come from a single population or related populations, there is a high probability that this type of gene action will stand out, as is the case of kinship between the M2 lines (Population 19 of Liebre, early drought tolerant) and the H4 (Population 11 of Pinto Amarillo, intermediate cycle of wide adaptability) used in this work.

The greatest contribution was found in the environmental variance (σ^2 F), so it is suggested to form superior hybrids in yield and their components, with the selection of lines that complement each other in their characters, as well as increasing the outstanding lines in GCA and SCA, analyze and select for grain yield, with the intention of releasing new hybrids (Preciado *et al.*, 2005). Therefore, it is suggested to form heterotic synthetic varieties (with 8 to 10 lines), for which lines that complement each other in their characters and that form contrasting populations are selected to recombine and extract new lines to form hybrids superior in yield, in schemes of recurrent reciprocal selection (Hallauer *et al.*, 2010) the heritability values in the strict sense (h²) for DM, DO and GH were 28.14, 29.34 and 29.37%, respectively, coincide with that reported by Molina (1992) who he identified them as quantitative traits of intermediate heritability. The h² of the RG also coincided with the classification of the cited author (low heritability character).

Heritability refers to the ability of characters to be transmitted from generation to generation; that is, it can be considered as the degree of similarity between the individuals of one generation and the next, for which it is considered these would be the characters that would be recombined and selected. The components (LM, DO, DM and HM) that most influenced grain yield, presented high h^2 (Molina, 1992). This indicates that they are closely associated with grain yield, which is considered high since they are quantitative traits, except for negative heritability variables whose value seems logical as they are more than qualitative traits. These effects may also be due to the fact that the same group of genes does not control all the responses of the genetic components, as pointed out by Springer and Stupar (2007), or hereditary factors such as additivity, dominance and over-dominance, according to Lippman and Zamir (2007).

Conclusions

The analysis of the results of the crosses suggests that the lines with the highest GCA obtained the best grain yield, which allowed defining the use of the parents through the hybridization system as the most indicated for the genetic improvement program, since their parents are suitable to form hybrids with high yield potential. The lines that obtained the highest GCA will be used for the production of hybrid seed. The lines and crosses with superior yield will be used for grain production in the evaluation location. The low values of the additive variance were obtained in most of the variables, with the exception of grains per row, characteristics that can be improved in the long term. Estimates of heritability in the broad sense ranged from 63.16% to 87.14%.

Cited literature

- Avila, P. M. A.; Rodríguez, H. S. A.; Vázquez, B. M. E.; Borrego, E. F.; Lozano, R. A. J. y López B. A. 2009. Aptitud combinatoria y efectos recíprocos en líneas endogámicas de maíz de valles altos del centro de México. Agric. Téc. Méx. 35(3):285-293.
- Badawy, M. E. M. 2013. Heterosis and combining ability in maize using diallel crossed among seven new inbred lines. Asian J. Crop Sci. 5(1):1-13.
- Borghi, M. L.; Ibañez, A. M.; Bonamico, C. N.; Kandus, V. M.; Gomar, A. D.; Guillin, A. E.; Salermo, C. J. and Renzo A. D. M. 2012. Combining ability of Flint corn inbred lines: Mal del Rio Cuarto Disease tolerance and grain yield. J. Exp. Bot. 81(1):123-131.
- Comstock, R. E. and Robinson F. H. 1948. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. Biometrics. 4(4):254-266.
- De la Cruz, L. E.; Rodríguez, H. S.; Estrada, M. A. B. y Mendoza D. P. J. 2005. Análisis dialélico de líneas de maíz QPM para características forrajeras. Univ. Cienc. 21(41):19-26.
- De la Rosa, L. A.; De León, C. H.; Rincón, S. F. y Martínez, Z. G. 2006. Efectos genéticos. heterosis y diversidad genética entre híbridos comerciales de maíz adaptados al Bajío Mexicano. Rev. Fitotec. Mex. 29(3):247-254.
- Dzib, A. L. A.; Segura, C. C. J.; Ortega, R. P. y Latournerie M. L. 2011. Cruzas dialélicas entre poblaciones nativas de Yucatán y poblaciones mejoradas. Trop. Subtrop. Agroecosys. 14(1):119-127.
- Escorcia, G. N.; Molina, G. J. D.; Castillo, G. F. y Mejía, C. J. 2010. Rendimiento, heterosis y depresión endogámica de cruzas simples de maíz. Rev. Fitotec. Mex. 33(3):271-279.
- Fan, X. M.; Chen, H. M.; Tan, J.; Xu, C. X.; Zhang, Y. D.; Luo, L. M.; Huang, Y. X. and Kang, M. S. 2008. Combining abilities for yield and yield components in maize. Maydica. 53(1):39-46.
- Guillén, D. C. P.; De la Cruz, E. L.; Castañón, N. G.; Osorio, R. O.; Brito, P. M. N.; Lozano, R. A. D. y López, N. U. 2009. Aptitud combinatoria general y específica de germoplasma tropical de maíz. Trop. Subtrop. Agroecosys. 10(1):101-107.
- Hallauer, A. R.; Carena, M. and Miranda, F. J. B. 2010. Quantitative genetics in maize breeding. Springer-Verlag. New York Inc. 664 p.
- INEGI. 2013. Instituto Nacional de Estadística, Geografía e Informática. Modificaciones al sistema de clasificación climática de Köppen para adaptarlos a las condiciones de la República Mexicana. Universidad Nacional Autónoma de México (UNAM). México, DF. 246 p.
- Kanagarasu, S.; Nallathambi, G. G. and Ganesan N. K. 2010. Combining ability analysis for yield and its components traits in maize (*Zea mays* L.). Electron. J. Plant Breed. 1(4):915-920.
- Kang, S.M.; Kushairi, A. D.; Zhang, Y. and Magari, R. 1999. Combining ability for rind puncture resistance in maize. Crop Sci. 39(2):368-371.
- Legesse, B. W.; Pixley, K. V. and Botha, A. M. 2009. Combining ability and heterotic grouping of highland transition maize inbred lines. Maydica. 54(1):1-9.
- Lippman, Z. B. and Zamir, D. 2007. Heterosis: revisiting the magic. Trends in Genetics 23(2):60-66.
- Louette, D. and Smale, M. 1996. Genetic diversity and maize seed management in a traditional Mexican community: implications for in situ conservation of maize. NRG Paper 96-03. Centro Internacional de Maíz y Trigo (CIMMYT). México, DF. 21 p.

- Malacarne, M. F. and San Vicente, G. F. M. 2003. Patrones heteróticos de líneas tropicales blancas de maíz. Agron. Trop. 53(4):32-40.
- Polanco, F. 2008. Bases para una política de I&d e innovación de la cadena de valor del maíz. Foro Consultivo Científico y Tecnológico. AC. México, DF. 244 p.
- Preciado, O. E. R.; Terrón, I. A. D.; Gómez M. N. O. y Robledo, G. E. I. 2005. Componentes genéticos en poblaciones heteróticamente contrastantes de maíz de origen tropical y subtropical. Agron. Mesoam. 16(2):145-151.
- Reyes, L. D.; Molina, D. G. J.; Oropeza, A. R. M. y Moreno, C. P. E. 2004. Cruzas dialélicas entre líneas autofecundadas de maíz derivadas de la raza tuxpeño. Rev. Fitotec. Mex. 27(1):49-56.
- Rodríguez, P. G.; Zavala, G. F. G.; Ojeda, Z. C.; Gutiérrez, D. A.; Treviño, R. J. E. y Rincón S. F. 2012. Diversidad de maíces criollos de Nuevo León. México. Mediante AFLP y caracteres morfológicos. Agron. Mesoam. 23(2):29-39.
- Soengas, P.; Ordaz, B.; Malvar, A. R.; Revilla, P. and Ordaz, A. 2003. Heterotic patterns among. Flint maize populations. Crop Sci. 43(3):844-849.
- Sprague, G. F. and Tatum, A. L. 1942. General versus specific combining ability in single crosses of corn. J. Am. Soc. Agron. 34(10):923-932.
- Springer, N. M. and Stupar, M. R. 2007. Allelic variation and heterosis in maize: how do two halves make more than a whole? Genome Res. 17(3):264-275.
- Wong, R. R.; Gutiérrez, R. E.; Palomo, G. A.; Rodríguez, H. S.; Córdova, O. H.; Espinoza, B. A. y Lozano, G. J. J. 2007. Aptitud combinatoria de componentes de rendimiento en líneas de maíz para grano en la comarca lagunera. México. Rev. Fitotec. Mex. 30(2):181-189.