RECURRENT SELECTION FOR GENERAL AND SPECIFIC COMBINING ABILITY IN MAIZE

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ABSTRACT

This study was aimed to identify efficiency of recurrent selection program to improve maize population. This program was applied to var. Buhooth 106 with var. 5012 Using RGCA with the inbred Zm7 for the production of RSCA. The recurrent selection program was implemented for four consecutive seasons (2020 - 2021) at the Fields Station of the College of Agriculture - University of Anbar. In the spring season 2020, 100 top crosses were obtained from both varieties and progeny. During the fall season 2020, an experiment was carried out to compare the top crosses of each variety RGCA and RSCA using a 10 × 10 partially balanced lattice design.. Six genotypes from each genetic population as well as Buhooth 106 and 5012 and Zm7 inbreds). The genotype-S1-2 RSCA achieved the lowest female flowering period for females 61.50 days, the highest number of rows per ear 17.80 rows, and the highest grain yield 177.82 g. The genotype-S1-3 RSCA achieved the highest leaf area 0.593 m^2 and the highest number of kernels per row 43.11 kernel. The broad sense heritability of the traits of the number of rows and the number of kernels in the row and the yield of the plant reached 53.23%, 73.85% and 41.94%, respectively, and high genetic advance for kernels per row and grain yield of 4.79 and 15.52 respectively.

Keyword: PCV, GCV, genetics, hybrids, GCA,

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الانتخاب التكراري لقابليتي الاتحادية العامة والخاصة في الذرة الصفراء

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المستخلص

بهدف التعرف على برنامج الانتخاب المتبادل لرفع كفاءة اداء المجتمعات النباتية, تم تطبيق هذا البرنامج على صنف بحوث 106 مع صنف 5012 لآنتاج RGCA ومع السلالة Zm7 لانتاج RSCA نفذ برنامج الانتخاب التكراري لأربعة مواسم (2020 – 2021) في محطة حقول كلية الزراعة – جامعة الانبار في الموسم الربيعي 2020 تم الحصول على 100 هجين قمي من كل الصنفين والسلالة, نفذ في الموسم الخريفي 2020 تجربة لمقارنة التضريبات القميه لكل صنف RGCA و RSCA باستخدام التصميم الشبكي الموزون جزئياً 10 × 10 ولمكررين, دورة S2–Progeny وعددها 15 تراكيب وراثي (6 تراكيب من كل مجتمع وراثي فضلاً عن بحوث 106 و5012 والسلالة Zm7. حقق التركيب الوراثي –S1–2 RSCA أقل مدة للتزهير الانثوي 61.50 يوم وأعلى عدد صفوف بالعرنوص 17.80 صف واعلى حاصل للحبوب 177.82 غم وحقق التركيب الوراثي S1–3– RSCA أعلى مساحة ورقية 0.593 م^2 واعلى عدد حبوب في الصف 43.11 حبة. بلغت نسبة التوريث بالمعنى الواسع لصفات عدد الصفوف وعدد الحبوب في الصف وحاصل النبات %53.23 و %73.85 و %41.94 بالتتابع مع تحصيل وراثي عالي لعدد الحبوب في الصف ولحاصل الحبوب بلغ 4.79 و15.52 بالتتاب

كلمات مفتاحية: تربية، جينات، حبوب، عرنوص.

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INTRODUCTION

Plant species are an important and renewable source of human food, raw materials and energy, as well as its importance in maintaining the stability of the ecosystem on the planet. Among these types of grains, the yellow corn kernels are the main component of the food basket of any family (10). Its fluctuating global production coincides with environmental conditions that tend to be less favorable. The magnitude of the threat to global food production is increasing in a wide range (2, 9, 31). Maize (*Zea mays* L.) represents direct food for humans and fodder for animals, and it constitutes an important source of income for millions of people in the countries of the world (11, 35), because its grain contains starch, protein, oil, vitamins and minerals, in addition to its use as a source of biofuels such as the production of ethanol gas (1, 5). Hybrid production was considered as the agricultural revolution and the greatest event in plant breeding (36). The hybrid vigor depends mainly on the genetic difference between the parents, so it suggested several statistical analysis tools that can be used to verify the nature of the genetic material and the gene action controlling the transmission of traits across generations (23, 24). Some researchers have pointed out the possibility of improving and increasing the productivity of maize by following the methods of recurrent selection among genetic populations and producing new genetic populations with a high genetic stock to increase productivity and then inducing genotypes or inbreds involved in the production of hybrids to reach an acceptable consensus (7). The researcher Rangle *et al.* (33) added to the possibility of using statistical and genetic measures to find out the superior genotypes in plant yield. The selection, which depends on the agreement between a set of selection index, can give criteria for improving productivity in maize. Therefore, this research aims to improve several genetic populations of synthetic variety Buhooth 106 and synthetic variety 5012 by using reciprocal recurrent selection in recombining a new one in order to improve and increase the yield, so that it will be a starting point for breeding pure inbreds and producing hybrids.

MATERIALS AND METHODS

First season: Planting populations of maize, the synthetic variety Bohooth 106, as well as synthetic variety 5012 that was developed by introduction, selection and cross-breeding method, and pure line Zm7 in three adjacent fields in the research station fields of the College of Agriculture - University of Anbar on 20/3/2020, and up to 1000 plants of each variety. The field was divided into plots with area of 5 x 7 m, spreading triple super phosphate fertilizer (P_2O_5 46%) at soil preparation at a rate of 200 kg ha^{-1}. Urea fertilizer (46% N) was added at a rate of 400 kg ha^{-1} as a source of nitrogen (4). The process of weeding and irrigation was carried out according to the needs of the field. The seeds were planted in the field with a distance of 90 x 40 cm between the lines and the plants in order to increase the chance of obtaining two effective ears on one plant for the purpose of conducting the crossing process by the second population of the upper ear and self-pollination of the lower ear. From the beginning of flowering, 10% of the plants are selected with a self-pollinating procedure for the selected plants. At the same time, pollen grains are taken from the selected plants and plants from:

1- Synthetic variety 5012 for RGCA

2- A pure inbred Zm7 for the purpose of RSCA

At the end of the season, the selected plants are harvested separately, and the top cross hybrid plants are taken individually.

Second season

A field experiment was carried out on 1/8/2020 which is comparison experiment for the top crosses and for each method of selection RGCA and RSCA using the randomized complete block design RCBD and 4 replicates, the distance between one line and another is 75 cm and between one hill and another 25 cm. All soil and crop service operations were carried out as in the first season, and at 100 top cross per population. The characteristics of the yield and its components were studied for each experiment, and after the statistical analysis, the average of each top cross was compared with the general average for each trait. The S1 inbreds whose top crosses exceeded the overall mean were taken. The top crosses were screened with different selection intensities according to the superiority of the top crosses based on their productivity. The top hybrids superior to the general average were divided into three groups. For the purpose of benefiting from time and progress in genetic homogeneity, the S1 plants were self-pollinated to get S2 while the S1 seeds obtained from the first season were sown in addition to an experiment comparing the top crosses of 100 self-pollinated from each genetic population with Buhooth 106, RGCA and RSCA. At flowering, the best five distinct plants from each line were selected and self-pollinated to produce S2. At the end of the season, the plants that had self-pollinated were harvested, and the best ears were taken. We gave them numbers from 1 to 100 for each population, as they were numbered in the first season. It is expected that the genetic similarity at the end of the season will be 75%.

Top crosses of Buhooth 106 with 5012 (RGCA) and Zm7 (RSCA) inbred

The general average of screening for the top cross hybrids was adopted, and the self-pollinators whose top hybrids outperformed the general average were taken in all traits, except for the female flowering trait, which depended on the crosses that achieved lower averages than the general average, while the pollinators whose averages exceeded the general average were taken. S1 self-pollinated are divided into three classes:

1. The superior inbreds with their apical crosses, which share 7 traits, are superior to the general average, and there are 10 inbreds from each cross, with 15% selection pressure. S1 seeds were mixed to form the nucleus of a new population. They were given -S1-1 RGCA and -S1-1 RSCA.
2. The inbreds whose top crosses achieved an average plant yield of more than 100g, numbering 15 inbreds from each cross, with a 15% selection pressure to form the nucleus of a new population. They were given the symbols 2 RGCA and -S1-2 RSCA.=
3. Inbreds whose top crosses achieved an average plant yield of 140 g or more, 10 inbreds from each cross, with 15% selection pressure, and were given the symbol 3 RGCA and -S1-3 RSCA.

When the process of self-pollination was carried out on S1 plants to produce S2, the superior inbreds took their top crosses in 1, 2 and 3 depending on the performance of their top crosses. 200 seed S1 seeds were mixed together as per the above partition to form the nucleus of three S1 genotyped populations. Codes have been given:

-S1-1 RGCA and -S1-1 RSCA. and -S1-2 RGCA and -S1-2 RSCA. and -S1-3 RGCA and -S1-3 RSCA

Also, 200 seeds of S2 were mixed together and according to the categories that divided the superior S1 with their top crosses mentioned in paragraphs 1, 2 and 3 mentioned above to form the nucleus of populations. The codes were given -S2-1 RGCA and -S2-1 RSCA. and –S2-2 RGCA and –S2-2 RSCA. the S2-3 RGCA and the S2-3 RSCA.

Third season

Planting on March 20, 2021 with 200 plants of each genotype, to perform the randomized manual Panmixia pollination of the 12 genotyped populations. The seeds of each group were mixed to form the nucleus of a new population. The seeds of the genotyped populations obtained from the combination of S1 and S2, which were divided according to their productivity, numbered 12 genotypes, were planted in plots 10 × 6 m, with up to 250 plants for each genotype, All soil and crop service operations were carried out, and when the plants reached the flowering stage, a random manual pollination was carried out, Panmixia, for the best 25 plants (recombined). This completes the first reciprocal recurrent selection cycle and the S2 recombination cycle, after the plants reached physiological maturity, the randomly pollinated plants were harvested from each genotype, each genotype individually, to obtain 12 genotypes.

Fourth season

A field experiment was carried out with RCBD design and with three replications on 1/8/2021 to compare the genotypes selected from first reciprocal recurrent selection cycle and the 15 S2-Progeny cycle genotypes (6 genotypes from each population as well as variety Buhooth 106 and variety 5012 and Zm7 inbreds), planted in lines in plots, the length of the line is 5 m, the distance between the lines is 0.75 m, and the distance between the hills is 0.25 m. All soil and crop service operations were conducted, and some growth characteristics, yield, its components and some genetic parameters were studied. The broad sense heritability was calculated on the following equation:

$$H^2_{b.s} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

It is possible to extract σ^2 g and σ^2 p

$$\sigma^2 g = \frac{mst - mse}{r}$$

$$\sigma^2 e = mse \; \sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where: mst = mean squares of genotypes, mse = mean squares of experimental error

$\sigma^2 p, \sigma^2 g, \sigma^2 e$ phenotypic, genetic, and environmental variance respectively

The coefficient of genetic, phenotypic and environmental variation GCV, PCV and ECV were calculated

$$PCV = \frac{\sigma p}{\bar{x}} \times 100$$

$$GCV = \frac{\sigma g}{\bar{x}} \times 100$$

$$ECV = \frac{\sigma e}{\bar{x}} \times 100$$

GCV and PCV values if less than 10% are considered low, between 10-20% are medium and above 20% are considered high. The percentage of gain of selection per cycle was calculated according to the equation of (1)

$$\%\ Gain\ per\ cycle = \frac{Cycle\ 1 - Cycle\ 0}{Cycle\ 0}$$

Where: Cycle 0: Original population

Cycle 1: First selection cycle

The genetic advance achieved as a result of selection was calculated according to the method (13)

Where: GA: Expected genetic advance

K =Selection intensity = 1.76

σp = Standard deviation of trait

$h^2_{b.s}$ = Heritability in broad sense

Whereas, the expected percentage of genetic progression as a result of selection according to the equation of (14)

$$REGA = \frac{GA}{\bar{X}} \times 100$$

Where: $\bar{X}$: Grand mean

The ranges referred to by Sabri *et al.* (34) were used to calculate the expected genetic advance as follows: less than 10% low, between 10% - 30% medium, more than 30% high. The index variation was calculated according to the equation of (16).

$$I.V = \frac{CVG}{CVE}$$

$$CVG = \frac{\sigma g}{\bar{x}} \times 100$$

$$CVE = \frac{\sigma e}{\bar{x}} \times 100$$

Where: CVG: Genetic coefficient of variation

CVE: Environmental coefficient of variation

σg: Standard deviation of genetic variance

σe : Standard deviation of environmental variance

Characters studied

Female flowering: the number of days from planting up to 50% of female flowering (for all plants of the experimental unit).

The average leaf area m^2 = the square of the length of the leaf under the upper ear leaf x 0.75 if the number of leaves is 14 or more and x 0.65 if the number of leaves is 13 or less (27)

Number of rows per ear

Number of kernels per row

Individual plant yield (g): Calculated by dividing the yield of the five plants by their number after adjusting the humidity to 15%.

RESULTS AND DISCUSSION

There were significant differences for the mean squares of the genotypes for all the studied traits (Table 1), which reflect the amount of genetic differences.

Table 1. The mean squares (MS) for the traits studied

S.O.V	df	Female flowering (day)	Leaf area (m^2)	Row per ear	kernels per row	plant yield (g)
Rep.	2	19.267	0.000514	1.8305	0.268	28.022
Genotype	14	12.249**	0.00869**	2.6343**	33.664**	823.848**
Error	28	1.410	0.003034	0.5967	3.553	260.165
Total	44					

The results indicate significant difference between genotypes (Table 2). The earlier variety 5012 gave the lower number of days for female flowering, which was 64.70 days, and it did not differ significantly with the variety Buhooth 106. The best performance in early female flowering in the recurrent selection cycle was in the selected genotype 1 and 3 and in all the recombination cycles, S1, S2 and S3. The genotype S1-2 RSCA gave a flowering period of 61.50 days and it did not differ significantly with the genotype S1-1 RSCA and -S2-1 RSCA. When comparing the selected genotypes, we note that RSCA genotypes are more responsive in reducing flowering time than RGCA genotypes. The results of a number of researchers (19, 22, 37) confirmed the occurrence of early female flowering for the genotypes obtained from recurrent selection. The results of the same table showed a decrease in the values of C.V and $S_{\bar{y}}$ which amounted to 1.83 and 0.30, respectively, which indicates the homogeneity of the data. The genotypes showed a phenotypic and genetic variance of 5.02 and 3.61, respectively. Where genetic variance formed a high percentage of phenotypic variance, which indicates that the trait is genetically controlled, and this was confirmed by the ratio of genetic variance to environmental variance, which amounted to 2.56. The values of the coefficient of genetic and phenotypic variation were 2.93% and 3.46%, respectively. This confirms the homogeneity of genotypes genetically and phenotypically, and the low environmental impact on the trait. These results match those of (3, 14, 39). The high values of genetic variance compared to the value of phenotypic variance were reflected in the percentage of heritability in the broad sense, which rose to 77.0%. These results are in agreement with those of (3, 6 ,26), and it differed with (25) as they obtained moderate percentages of heritability values. The genetic advance reached 2.56 days towards the early female flowering during the first selection cycle, which is a high percentage in the genetic advance when the female flowering period is reduced compared to the general average. While the advance rate was low, amounting to 4.38%. The high heritability rate accompanied by high genetic advance indicates that selection is effective in improving this trait and good genetic achievement can be expected in future breeding programs, especially if this genetic variation is due to the additive genetic action of the pairs of genes. Emphasizing the importance of high genetic variances between the selected genotypes, and this was indicated by the value of the variation index, which amounted to 1.60. These results agreed with those of (27, 32) and disagreed with (29)

Table 2. Average female flowering (day) with some genetic parameters of maize genotypes after one cycle of reciprocal recurrent selection and one cycle of S2 recombination with the two parent and progeny cultivars

Genotype	Mean	Genetic parameters	Values
S1-1 RGCA	**65.30**	***C.V%***	**1.83**
S1-2 RGCA	**67.50**	$S_{\bar{y}}$	**0.30**
S1-3 RGCA	**68.40**	$\sigma^2 e$	**1.41**
S2-1 RGCA	**63.70**	$\sigma^2 g$	**3.61**
S2-2 RGCA	**64.50**	$\sigma^2 p$	**5.02**
S2-3 RGCA	**63.50**	$\sigma^2 g/\sigma^2 e$	**2.56**
S1-1 RSCA	**62.50**		
S1-2 RSCA	**61.50**	***GCV%***	**2.93**
S1-3 RSCA	**65.60**	***ECV%***	**1.83**
S2-1 RSCA	**62.30**	***PCV%***	**3.46**
S2-2 RSCA	**63.70**		
S2-3 RSCA	**64.70**	$H^2 b.s\%$	**72.00**
Buhooth 106	**66.30**		
5012	**64.70**	***GA***	**2.56**
Zm7	**68.30**	***GAM%***	**4.38**
Mean	**64.78**		
L.S.D 5%	**1.98**	***I.V***	**1.6**

Leaf area (m^2)

The results indicate a significant difference between the genotypes for leaf area (Table 3), when comparing the genotypes with the variety Buhooth 106 and variety 5012, a significant increase in the leaf area was observed in the genotype -S1-3 RSCA. When comparing the selected genotypes from the S2 recombination cycle with the reciprocal recurrent selection cycle, it is noticed that many of the genotypes did not differ significantly with the first selected genotype. Selection in the variety Bohuth 106 and 5012 did not lead to a significant increase in the leaf area of the selected genotypes, as the mean leaf area values decreased significantly in the selection cycles for the RGCA-S3-2 genotype. The results showed that the values of C.V and $S_{\bar{y}}$ amounted to 11.96 and 0.014, respectively, and this difference in the two percentages indicates the lack of similarity of the sample data and the lack of homogeneity among the samples taken from the population. The genetic variance decreased (0.001886) compared to the phenotypic variance (0.004920), and this is evidence of the great influence of the environment in this trait, and this was demonstrated by the low ratio of genetic to environmental variance, which amounted to 0.622. The low value of genetic variance was reflected in the percentage of heritability in the broad sense, which decreased to 38.23%. The value of genetic advance also decreased to 0.0473 and this was reflected in the percentage of genetic advance, which amounted to 10.27. Depending on the genetic criteria for this trait, it is possible to improve the trait through hybridization followed by selection in future breeding programs to increase genetic variations based on selection and this was confirmed by the value of the index of variation, which amounted to 0.789 and that the trait is under the influence of the non-additive of the gene pairs. This agrees with (21).

Table 3. Average leaf area (m2) with some genetic parameters of maize genotypes after one cycle of reciprocal iterative selection and one cycle of S2 recombination with the parent and progeny cultivars

Genotype	mean	Genetic parameters	Values
S1-1 RGCA	0.405	C.V%	11.96
S1-2 RGCA	0.528	$S_{\bar{y}}$	0.014
S1-3 RGCA	0.467	$\sigma^2 e$	0.003034
S2-1 RGCA	0.482	$\sigma^2 g$	0.001886
S2-2 RGCA	0.449	$\sigma^2 p$	0.004920
S2-3 RGCA	0.388	$\sigma^2 g/\sigma^2 e$	0.622
S1-1 RSCA	0.531		
S1-2 RSCA	0.465	GCV%	9.43
S1-3 RSCA	0.593	ECV%	11.96
S2-1 RSCA	0.497	PCV%	15.23
S2-2 RSCA	0.490		
S2-3 RSCA	0.404	H^2b.s%	38.33
Buhooth 106	0.482		
5012	0.496	GA	0.0473
Zm7	0.322	GAM%	10.27
Mean	0.460		
L.S.D 5%	0.092	I.V	0.789

Number of rows per ear

The results indicate that they were significant differences between the genotypes (Table 4). The variety Buhooth 106 did not differ with the variety 5012 as well as the Zm7 inbred significantly. When comparing the selected genotypes, the RSCA-S1-2 genotype, which had 17.80 rows, did not differ significantly with 4 genotypes, where the effectiveness of recurrent selection was in increasing the number of ear rows compared to the varieties, and when comparing the selected genotypes, we note the superiority of the RSCA genotypes over RGCA, as well as the superiority of the genotypes selected from the S2 recombination, most of them did not differ significantly, and this agrees with what was found by (25). The results showed that the values of $S_{\bar{y}}$ and C.V were moderate, and they were 0.42 and 11.88 respectively, which indicates the average homogeneity of the data taken. The genotypes showed a phenotypic and genetic variance of 1.275 and 0.679, respectively. The decrease in genetic variance compared to phenotypic variance indicates a significant impact of the environment on the character of the number of rows in the ear, and this was confirmed by the value of environmental variance, which amounted to 0.5967. The percentage of PCV and GCV as values reached 8.02 and 5.85, respectively, which indicates the average homogeneity of the selected genotypes and that there is an influence of the environment on this trait. It agreed with the results of (26), and the result differed with the results of many previous studies (17, 28) The value of the low genetic variance compared to the value of the phenotypic variance was negatively reflected on the percentage of heritability in the broad sense, which reached 53.23% in the middle ranges. These results confirmed the findings of Bekele and Rao (2014). The values of genetic advance reached 1.057 rows per ear, which is a moderate percentage due to the values of the percentage of heritability in the broad sense and the standard deviation. The percentage of genetic advance was also moderate and amounted to 7.51%. These results of genetic parameters indicate that the trait is under the genetic influence of the non-additive gene (14). As this trait can be improved by hybridization followed by selection between genotypes to increase genetic variations. The variation index value (1.068) indicated that the genetic variations were low among the low genotypes.

Table 4. Average number of rows per ear with some genotypes of maize genotypes after one cycle of reciprocal recurrent selection and one cycle of S2 recombination with the parent and progeny cultivars

Genotype	Mean	Genetic parameters	Values
S1-1 RGCA	15.20	C.V%	11.88
S1-2 RGCA	14.36	$S_{\bar{y}}$	0.42
S1-3 RGCA	15.04	$\sigma^2 e$	0.5967
S2-1 RGCA	16.06	$\sigma^2 g$	0.6792
S2-2 RGCA	15.48	$\sigma^2 p$	1.2759
S2-3 RGCA	15.70	$\sigma^2 g/\sigma^2 e$	1.138
S1-1 RSCA	16.55		
S1-2 RSCA	17.80	GCV%	5.85
S1-3 RSCA	16.82	ECV%	5.48
S2-1 RSCA	16.44	PCV%	8.02
S2-2 RSCA	15.55		
S2-3 RSCA	15.78	H^2b.s%	53.23
Buhooth 106	15.66		
5012	15.43	GA	1.057
Zm7	14.08	GAM%	7.51
mean	14.08		
L.S.D 5%	1.92	I.V	1.068

Number of kernels per row

The number of kernels per row is one of the important components of the yield, which all different breeding methods aim to increase or increase the number of rows or both to increase the number of kernels of the ear and thus increase the kernels of the plant. The results indicate that there was a significant difference between the genotypes (Table 5), where the genotype S1-3 RSCA gave the highest number of kernels amounted to 43.11 kernel and did not differ significantly with 3 genotypes which are (S1-2 RSCA, -S1-2 RGCA and -S1-1 RSCA). When comparing the genotypes selected from the S2 recombination cycle with the genotypes selected from the S1 recombination cycle, a significant superiority of the number of kernels in RSCA crosses was observed over RGCA for the recurrent selection cycle. When comparing the genotypes selected from the S2 recombination cycle with the genotypes selected from the reciprocal recurrent selection cycle, the superiority of the S1-1 RGCA genotypes compared to the S2-2 RGCA genotypes and the S1-3 RSCA genotypes compared to the S2-3 RSCA genotypes. These results proved the efficiency of the recurrent selection program in increasing the number of row kernels of the selected genotype -S1-3 RSCA in comparison with the cycle of resynthesizing S2, and these results agreed with the findings of Haseeb *et al.* (21) and did not agree with (6). The values of $S_{\bar{y}}$ and C.V were moderately homogeneous, amounting to 0.47 and 5.10, the genotypes showed phenotypic and genetic variance of 13.59 and 10,037, and the genetic variance constituted approximately two thirds of the phenotypic variance, which indicates that the genetic influence on the environment in this trait. This is indicated by the ratio of genetic variance to environmental variance, which amounted to 2.82. The phenotypic and genetic coefficient of variation values were 9.95% and 8.55%, respectively. The similarity of these ratios indicates the homogeneity of the genotypes, genetically and phenotypically, and that the environmental impact on the trait is less than the genetic influence (29, 38) The high value of genetic variance was positively reflected on the percentage of heritability in the broad sense, which amounted to 73.85%, and the value of genetic advance reached 4.79 kernels per row, which is a good percentage if added to the general average of 37.06 kernel per row, in addition to the average genetic advance rate of 12.93%, while the value of the variation index reached 1.68. By estimating the values of genetic parameters such as the high percentage of heritability in the broad sense and the value of genetic advance and its good percentage, the trait is under the influence of the additive genes and can be improved by selection during breeding programs (12, 17, 21).

Table 5. Average number of kernels per row with some genotypes of maize genotypes after one cycle of reciprocal recurrent selection and one cycle of S2 recombination with the parent and progeny cultivars

Genotype	Mean	Genetic parameters	Values
S1-1 RGCA	40.88	C.V%	5.10
S1-2 RGCA	37.91	$S_{\bar{y}}$	0.47
S1-3 RGCA	37.48	$\sigma^2 e$	3.553
S2-1 RGCA	35.71	$\sigma^2 g$	10.037
S2-2 RGCA	35.42	$\sigma^2 p$	13.590
S2-3 RGCA	36.95	$\sigma^2 g/\sigma^2 e$	2.82
S1-1 RSCA	40.14		
S1-2 RSCA	41.48	GCV%	8.55
S1-3 RSCA	43.11	ECV%	5.086
S2-1 RSCA	35.71	PCV%	9.950
S2-2 RSCA	37.42		
S2-3 RSCA	35.84	H^2b.s%	73.85
Buhooth 106	33.51		
5012	34.06	GA	4.79
Zm7	31.36	GAM%	12.93
Mean	37.06		
L.S.D 5%	3.15	I.V	1.68

Individual plant yield (g)

Plant yield is a complex function involving a large number of gene pairs and their interactions with the environment and its increase is a goal of many breeding methods to reach the maximum potential of the plant's ability to give the largest possible number of kernels. Yield is affected by a number of other characteristics such as the number of kernels in the ear, competition between grains for metabolic materials, the duration of the grain's filling, the rate of grain filling, the rate of dry matter accumulation, and the environmental conditions surrounding the plant before and after flowering (8, 17). Table 6 shows that there are significant differences between the genotypes under study in the trait of plant yield. The two genotypes -S1-2 RSCA and -S1-3 RSCA of the reciprocal-selection cycle differed significantly from the cultivars Buhooth 106 and 5012, and the superiority of these two genotypes may be attributed to giving them a high leaf area (Table 3), more rows in the ear (Table 4), and a high number of kernels in a row (Table 5). When comparing the genotypes selected from the S2 recombination cycle with the recurrent selection cycle, the two cultivars and the progeny, we find that the genotypes -S1-1 RSCA and -S1-2 RGCA did not differ significantly with cultivar 5012, while they differed significantly with cultivar Buhooth 106, superior to it by 16.59% for both, the genotypes -S1-1 RGCA and -S2-3 RGCA gave the lowest average grain weight. These findings confirm the findings of (3, 37). The genotypes showed phenotypic and genetic variance of 448.065 and 187.90, respectively, and genetic variance constituted a low percentage of phenotypic variance, and this was confirmed by the ratio of genetic variance to the environment, which amounted to 0.722. The value of the phenotypic coefficient of variation was 14.05% and the genetic coefficient of variation 9.10%. This indicates that the trait is genetically and phenotypically heterogeneous, these results are in agreement with those of (1). The high value of phenotypic variance was negatively reflected in comparison with the value of genetic variance, so the percentage of heritability in the broad sense decreased to the moderate ranges, which amounted to 41.94%. These results agree with the findings of (26) in the reciprocal recurrent selection program and (2) in hybrid production and do not match the findings of (8, 33). The value of the genetic advance for the individual plant yield was 15.52 g per plant, which is a high percentage, i.e., around 827.73 kg ha^{-1} in the first cycle, the percentage of genetic advance for the trait decreased and reached 10.37%. We conclude by estimating the values of genetic criteria for the trait of plant yield such as the average heritability, high genetic advance and the great impact of the environment on this trait, that it is one of the complex traits and requires more selection cycles (14).

Table 6. The average yield of an individual plant (g) with some genetic parameters of the genotypes of maize after one cycle of reciprocal recurrent selection and one cycle of S2 recombination with the parent and progeny cultivars

Genotype	mean	Genetic parameters	Values
S1-1 RGCA	129.16	C.V%	10.71
S1-2 RGCA	168.95	$S_{\bar{y}}$	4.03
S1-3 RGCA	145.48	$\sigma^2 e$	260.165
S2-1 RGCA	157.47	$\sigma^2 g$	187.90
S2-2 RGCA	134.91	$\sigma^2 p$	448.065
S2-3 RGCA	127.43	$\sigma^2 g/\sigma^2 e$	0.722
S1-1 RSCA	168.98		
S1-2 RSCA	177.82	GCV%	9.10
S1-3 RSCA	176.94	ECV%	10.75
S2-1 RSCA	151.53	PCV%	14.05
S2-2 RSCA	148.97		
S2-3 RSCA	157.77	H^2b.s%	41.94
Buhooth 106	141.96		
5012	144.91	GA	15.52
Zm7	118.98	GAM%	10.37
Grand mean	150.62		
L.S.D 5%	26.97	I.V	0.85

Conclusion

Despite the good productivity of the two varieties Buhooth 106 and 5012, the cycle of recurrent selection and genetic recombination gave a lower yield than its origins. Therefore, the recurrent selection program must be continued to improve the characteristic of the yield, especially with superior genotypes

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