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EPISTATIC GENE ACTION USING TRIPLE TEST CROSS PROCEEDURE IN *ZEA MAIZE* L.

ЭПИСТАТИЧЕСКИЕ ДЕЙСТВИЯ ГЕНОВ ПРИ МЕТОДЕ ТРОЙНОГО ПЕРЕКРЕСТНОГО ТЕСТА *ZEA MAIZE* L.

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Used the triple test cross method. Genotypes: (pure lines, tester and hybrids) planted (in field Voronezh / Russian Federation) by using randomized complete block design with two replications for the deduction of epistates, to infer the superior gene action, estimated of components of variability and genetic parameters of Plant high\cm Ear Length\cm, Number row\ear, 100-grain Weight\g and Grain yield/g Zea mays L. The results showed that the mean of variance, both genotypes, hybrids, and parents were highly significant to all characters. Analysis of variance to infer the superior gene action, indicated that the mean variability of the pure lines was not significant, this confirms the lack of epistates of all traits. Additional genetic variability has shown an important role in the inheritance of most characters.

Key words: Pure lines, Gene action, Epistates, Test triple method, Maize, Heritability.

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Использовали метод тройного перекрестного теста. Генотипы: (чистые линии, тестер и гибриды) посеяны в поле под Воронежем (Российская Федерация) с использованием рендомизированного полного блочного дизайна с двумя репликациями для оценки превалирующего действия гена, влияющего на компоненты изменчивости и генетические параметры. Проводили оценку структуры урожая (высота растения, длина колоса, число колосков, масса 100 зерен, урожайность зерен) у культуры кукурузы. Показано, что среднее значение дисперсии, как генотипов, гибридов, так и родителей, было очень значимым по всем показателям. Дисперсионный анализ для определения превалирующего действия гена показал, что средняя вариабельность чистых линий не была значимой, что подтверждает отсутствие признаков. Дополнительная генетическая изменчивость показала важную роль в наследовании большинства признаков.

Ключевые слова: чистые линии, действие гена, эпистаты, метод тройного теста, кукуруза, наследственность.

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Introduction

The Cross Test Triple method is one of the mating systems adopted the researcher has information on the genotype of the genetically modified gene function such as maize. It is also possible to estimate the genetic parameters after deducing the superior gene action of this method in order to reach the best method of breeding the crop, we can suppose note superiority ,such as [2,6], Deviation of behavior birth resulting from the mixed (hybridization) between an individual gene (two pure lines) and a tester. If the deviation is significant from the rate of individual hybrid behavior resulting from the mixing of the two pure lines with the tester, The superior deviation is Negative or Positive, If it is equal to zero, it indicates the absence of superiority. Suggested [8,4].Expansion of the third design III in a manner [3] In addition to estimating additional genetic variability and genotyping, it is possible to infer the interferon gene act easily, take a random sample(n) representing number of second generation (F_2),and mixed (hybridization) them as male fathers with three tester (tow pure lines and F_1), We get 3n of the families that repeat in number of pilot units, Which is known as the cross test triple method put [10] a similar model includes the tester (tow pure lines and F_1),these are mixed with a number of other species or pure lines instead of random individuals of the second generation (F_2),suggested from [8].Both models are similar in terms of statistical analyzes and genetic estimates. In the maize, several studies were conducted by researchers to estimate the gene function and some genetic parameters Including what he did [16,7,15,5,11,12,13].

Objective of the study Inferred of superior interference and estimation of genetic function controlling the inheritance of traits and their components and estimation of some genetic parameters using the cross test triple method in maize.

Matereals and Methods:

Introduced tow pure lines of maize in the hybridization program Blue Jade , Blue with some to produce the first generation of hybrids(F_1), (during the season of spring, 2015) were planted (in field Voronezh \ Russian Federation), Three families (P_1= Blue Jade, P_2 = Mays Ornamental, (F_1 = Blue Jade × Mays Ornamental) were obtained as being testers. In spring 2016 were planted seeds of three families (P_1,P_2,F_1) with (Pure lines):[V_1=IK8, V_2=ZP, V_3= ABS27, V_4= ZP-430,V_5= SH, V_6= UN-44052,V_7= DK-17,V_8= ZP-607],.in the same field, during the season of spring , (2016) .

Hybridization were made between three families (P_1, P_2, F_1)as female (♀), and eight pure lines as male (♂),Thus making the number of genotypes (35) Including (3 testers (P_1, P_2, F_1) ,(8 Pure lines), (24 hybrids). (During the spring of 2017) All genotypes were planted (in field Voronezh \ Russian Federation), by using randomized complete block design with two replications, farming was on lines in long 5-centimeter,Distance between them(75\cm), and between plants (25\cm).All crop service operations from agriculture to harvesting were applied according to recommendations Ministry of Agricultur, data were recorded on an individual plant basis (10 plants from each experimental unit randomly selected), for plant height traits(cm), the statistical analysis was conducted (based on the average experimental unit), different genetic tests and estimates by [14]. As follows:-

1 — Analysis of variability of genotypes and splitting the average variance into its components for (Parents, Pure lines and testers).

2 — Test Epistasis.

3 — Estimation the value of each of the eight Pure lines in each replicate depending on the main data table resulting from ($P_1 + P_2 - 2F_2$).

4 — Estimated Variance of Pure lines from the equation:

$S^2 = \Sigma\, Yi^{\,2} - [(\Sigma\, Yi)\ [r]$.

r = Number of replicates.

i = The values of the observances for each Pure lines.

Thus, the total of eight variations was found, which represents the average error variance average for the differentiation analysis of the epistasis test.

5 -Analyzed The new data was by design RCBD to find additional genetic variance D from the relationship between the estimated and expected mean differences of Pure lines.

$MS_{\text{lines (Sum)}} = \sigma^2 e + 2r\, \sigma^2 s$;

$D = 8\, \sigma^2 s$

6 — Analyzed The new data was by design RCBD to find dominantional genetic variance H from the relationship between the estimated and expected mean differences of Pure lines in Zea mays.L.

$MS_{\text{lines (Difference)}} = \sigma^2 e + 2r\, \sigma^2 d$;

$D = 8\, \sigma^2 d$.

7 — The significance of additional genetic variability was determined using a method [9] .

8 — Estimated average dominance degree of sovereignty ā from the following equation:- 9 — Estimate heritability the broad sense H^2_{bs} and narrow sense H^2_{ns} from following equation:

$H^2_{\ bs} = (D + H) / (D + H + E)$

$H^2_{\ ns} = D / (D + H + E)$.

10 — Estimate The expected genetic improvement GA and expected as a percentage GA from the mean of each characteristic.

GA% = (GA / Mean) x 100

The estimate of expected genetic improvement was calculated as a percentage by [1].

Results and discussion

Table(1) shows the results of the analysis of genetic variation in the triple test cross method, Differences in the mean variance of genotypes, crosses, parents, inbreeds, and tester were significant at the 1% for all characters, Except Plant high was significant at the

Table 1.

Analysis of variation of genotypes (Triple test cross) for traits Zea mays L.

S.O.V	df	Plant high\cm	Ear Length \cm	Number row\ear	100 -grain Weight\g	Grain yield\g
Replication	1	91.4	0.18	0,37	2.96	67.82
Genotypes	34	293**	5.12**	3.53**	24.5**	561**
Hybrid	23	166**	3.97**	2.8**	19.2**	164
Parents	10	128.9**	3.13**	1.8**	14.3**	212**
Pure lines	7	43.57	2.93**	0.99**	9.28**	147**
Tester	2	428.2**	2.007*	5.14**	20.9**	324**
(P1,P2) against Hybrid	1	850**	1.76	9.18**	26.1**	601**
(P1) against (P2)	1	6.25	2.25*	1.103	15.6**	46.9*
(Pure lines) against (Tester)	1	128.03	6.77**	1.01	36.7**	444**
(Hybrid) against (Parents)	1	4843**	51.6**	35.8**	248**	1319**
Error	34	34.2	0.52	0.28	1.31	9.87

(*) and(**) significant a probability level(5%),(1%) respectively

Fig. 1. Mean genotypes (hybrids) for five traits in zea mays.L.

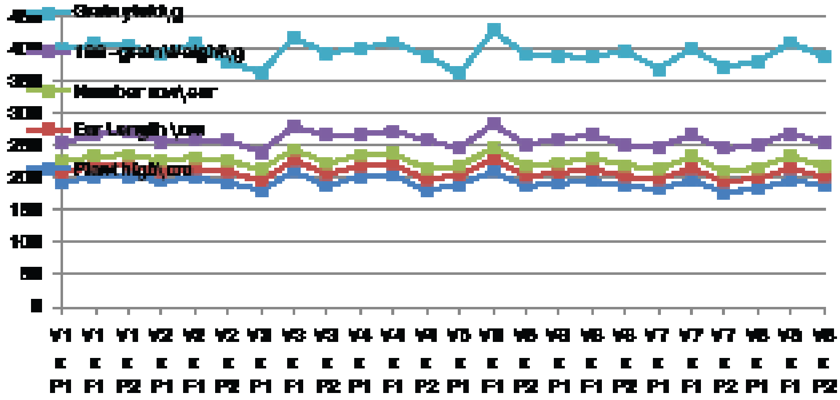


Fig. 2. Mean genotypes **(Pure lines) for five traits in Zea mays. L.**

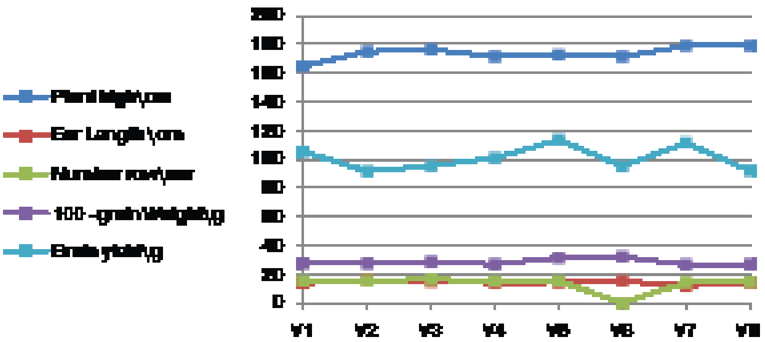


Fig. 3. Mean genotypes (Parents and hybrid between them (tester)) for five traits in Zea mays L.

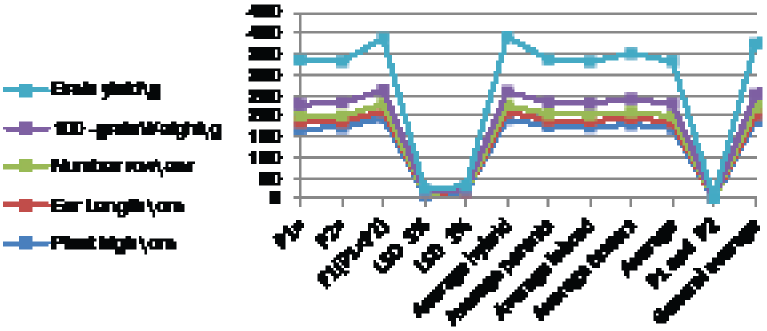
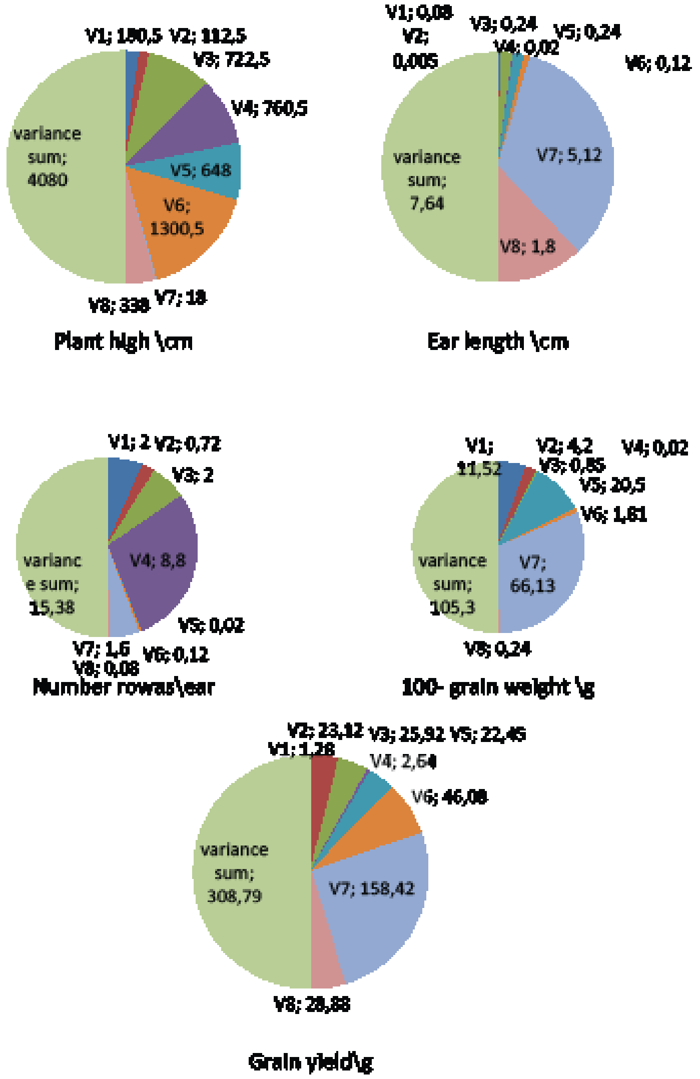


Table 2.
Variation Components and Genetic parameters in Zea mays L.

Variation Components and Genetic parameters	Plant high\cm	Ear Length \cm	Number row\ear	100 -grain Weight\g	Grain yield\g
Additional genetic variation-D	380 ±206,8	1,29 ±1,41	15,49 ±6,96	59,27 ±26,88	475,5 ±212,2
Dominance genetic variation-H	280 ±163,8	14,07 ±6,47	14,32 ±6,3	70,10 ±30,89	723,82 ±324,1
Environment variation- E	34,22 ±15,54	0,52 ±0,22	0,287 ±0,117	1,31 ±0,47	9,87 ±4,55
Heritability broad sense-H2 bs	0,98	0,96	0,99	0,98	0,99
Heritability narrow sense-H2 ns	0,54	0,08	0,51	0,45	0,39
Average dominance degree –a	0,85	3,3	0.96	1,08	1,23
Expected genetic improvement-GA	25,38	0,56	4,97	9,12	24,06
Expected improvement as a percentage of average	13,53	3,61	30,85	28,63	19,46

Fig. 4. Variations of inbred lines and total variation offive traits in Zea mays L.



5% .The average hybrids Superiority in all characters, The mean variance of parents against each other was significant at the 1% for (100 -grain Weight\g), at the 5% for (Ear Length \cm, Grain yield\g) in Zea mays L.

Figure (1) shows that the genetic combination ($V_5 \times F_1$) was the best to the traits: Plant high\cm, Ear Length \cm and 100-grain Weight\g, While excelled the genetic combination ($V_5 \times F_1$),($V_8 \times F_1$) and (F_1) in (Number row\ear, Grain yield\g. (F_1) excelled for all characters over parents (inbred or tester). Indicating the presence of a hybrid force in the desired direction of all characters, Comparison to the higher father or the average parent, The average values of the (tester) showed superiority over the (Pure lines) for all traits, While the mean variance of the hybrid against the parents was of high significance for all traits.

Results (Figure 3) shows average values P_1 were higher for traits: Plant high\cm, 100-grain Weight\g), While the opposite was for the other traits, The average height of the hybrid crosses is higher than the average of the parents in all characteristics.

In (Figure 4) Results indicate to total variance of the eight strains was estimated after estimating the variance of each Pure lines and each characteristic(Table.2) It is noted that the values of the additional genetic variability, the hereditary dominants, and the environmental predictivity differed from zero to all traits except for the ear length\cm ,which no additional genetic variability was deviated from zero, The values of both additional and sovereign genetic variation were greater than the values of the environmental variability of the traits all of them This is consistent with results[15]for all traits,and [5].for all traits except grain yield. It is noted that the values of genetic variation were greater than the additional characteristics: Ear length, 100 -grain weight\g, grain yield per plant in Zea mays. L. The average dominance degree of was greater than one for ear length\cm, 100 -grain weight\g and grain yield in per plant, an indication of the existence of over dominance, less than one for (Plant high\cm),an indication of partial dominance, close to one for number row\ear, an indication of the existence of complete dominance, this is consistent with [11] and [13]. It appears that the broad string was high for all traits,This is due to lower values of environmental contrast compared to their genetic variability values, Inheritance is narrow sense was high for Plant high and middling for(100 -grain weight, grain yield) in *Zea mays* L.

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