Research Journal of Agricultural Science, 42 (2), 2010

GENETIC AND PHENOTYPIC VARIABILITY OF YIELD COMPONENTS IN AN F_3 MAIZE POPULATION

Slaviša STOJKOVIĆ, Nebojša DELETIĆ, Vladan DJURIĆ, Milan BIBERDŽIĆ

University of Priština, Faculty of Agriculture Kosovska Mitrovica – Zubin Potok - Lešak
Jelene Anžujske bb, 38228 Zubin Potok, Serbia,
Corresponding author: slavisass@gmail.com

Abstract: *This paper deals with the investigation of F_3 population 2002-30, created in the Department of Maize, Institute of Field and Vegetable Crops, Novi Sad. During the first year, about 150 plants of the studied population were selfed and simultaneously crossed with the tester 1491x1496, in order to get complementary S_1 and HS progenies. After the harvest, 41 progenies of each type were selected for the trials including three environments, in RCB design. HS progenies had higher average values of the studied traits regarding S_1 progenies. The differences between progeny types were highly significant for all the studied traits, except for root and stalk lodged plants percent. Genetic variances were higher in S_1 progenies, with the exception of root and stalk lodged plants percent and grain number per row. Phenotypic variance followed the same tendency. The obtained values of broad-sense heritability were significantly higher in S_1 than in HS progenies. Low heritability values were calculated only for root and stalk lodged plants percent.*

Key words: *maize, grain yield, genetic variance, heritability*

INTRODUCTION

After starting material for selection is developed, a question arises concerning choice of selection method and intensity, for there is a need to get a quick advance in population improvement, but with simultaneous preservation of sufficiently high variability in order further selection process not to be jeopardized. Having in mind that selection progress and variability preservation are negatively correlated, and depend on the nature of particular population, it is necessary to study quantitative-genetic parameters of every population in order to choose properly the optimal method and intensity of selection (DELETIĆ, 1999; DELETIĆ, 2003). The most frequently used methods are selection based on selfed progenies and half-sib progenies, where meta-analysis of the data from many reports points to a higher genetic gain per cycle given by S_1 method, but also a higher genetic drift in comparison with HS selection (HALLAUER and MIRANDA, 1988).

For that reason, our study has been aimed to investigate genetic variability and other quantitative-genetic parameters of F_3 population 2002-30, created in the Department of Maize, Institute of Field and Vegetable Crops, Novi Sad. The study should be able to estimate suitability of this population for recurrent selection process, as well as to enable proper choice of selection method and intensity.

MATERIAL AND METHODS

The study has been carried out with F_3 population 2002-30, created in the Department of Maize, Institute of Field and Vegetable Crops, Novi Sad. During the first year, about 150 plants of the studied population were selfed and simultaneously crossed with the tester 1491x1496, in order to get complementary S_1 and HS progenies. After the harvest, 41 progenies of each type were selected for the trials, by the random sample method. During the second year trials were set in Aleksinac, and during the third year in Leskovac and Kruševac, as three studied environments, in random complete block design (RCBD) with two replications, where the elementary plot area was 0.7x4.6 m. Sowing distance was 70x46 cm with two plants sown together, which makes seeding rate of 62,112 plants per hectare.

Grain yield is expressed as t*ha^{-1} of grain with 14% of water, and the all plants of a plot were used for calculating grain yield and percent of root and stalk lodged plants. Other traits were established using ten randomly chosen plants, or ears, from each plot. A trait is expressed as a mean value of the all analyzed plants.

RESULTS AND DISCUSSIONS

The average value of grain yield in S_1 progenies was 5.45 t*ha^{-1}, while in HS progenies it was 8.51 t*ha^{-1}. In S_1 progenies, mean values of grain yield and yield components were the highest in the environment Aleksinac (1st year), than in Kruševac (2nd year), while the lowest values of grain yield and the other investigated traits were observed in the environment Leskovac (2nd year). HS progenies followed similar tendencies, but their mean values of grain yield and its components were much higher in regard to the ones of S_1 progenies (tab. 1 and 2).

Table 1

Mean values of the studied traits of S_1 progenies in various environments

Traits	Aleksinac (1st year)	Kruševac (2nd year)	Leskovac (2nd year)	$\overline{X} \pm SE_{\overline{X}}$
Grain yield	7.70	5.80	2.84	5.45 ± 0.18
% of lodged plants	0.10	0.05	0.02	0.05 ± 0.28
Ear height	69.52	76.13	58.41	68.02 ± 0.96
Plant height	206.01	207.35	186.80	200.06 ± 1.28
Ear length	16.80	16.02	10.80	14.54 ± 0.20
Number of grain rows	13.56	13.64	12.51	13.13 ± 0.09
Number of grains	27.48	27.81	16.65	23.98 ± 0.42
1000 grain mass	308.74	305.90	219.23	277.96 ± 3.61

The average value of ear height was 68.02 cm in S_1 progenies and 105.78 cm in HS progenies, while the values of plant height were 200.06 cm and 261.74 cm respectively. Such tendency could be seen for other traits, where HS progenies showed significantly higher values comparing with S_1 progenies (tab. 1 and 2). The respective values for ear length were 14.54 cm (S_1) and 17.22 cm (HS), for number of grains per row 13.13 (S_1) and 15.67 (HS), for number of grains per row 23.98 (S_1) and 32.86 (HS), and for 1000 grain mass 277.96 g (S_1) and 310.72 g (HS).

Table 2

Mean values of the studied traits of HS progenies in various environments

Traits	Aleksinac (1st year)	Kruševac (2nd year)	Leskovac (2nd year)	$\overline{X} \pm SE_{\overline{X}}$
Grain yield	13.21	8.87	3.46	8.51 ± 0.27
% of lodged plants	0.01	0.00	0.03	0.01 ± 0.20
Ear height	127.02	114.83	75.50	105.78 ± 1.56
Plant height	306.65	280.74	197.82	261.74 ± 3.15
Ear length	20.71	17.76	13.20	17.22 ± 0.21
Number of grain rows	16.57	15.63	14.97	15.67 ± 0.09
Number of grains	39.55	33.15	25.91	32.86 ± 0.41
1000 grain mass	364.41	330.48	237.28	310.72 ± 3.83

Differences between the two progeny types (S_1 and HS) were tested by ***t*** test for grain yield and ear length, while for the other traits ***t'*** test was applied, because the test of variance homogeneity showed the variances for those traits were not homogeneous between different progeny types. Based on these two tests, the differences between progeny types were statistically significant for the all traits, except percent of stalk and root lodged plants.

Values of genetic variance, phenotypic variance and heritability were considered as significant if were at lest double than respective standard errors (FALCONER, 1989). Genetic variance in S_1 progenies, as well as in HS progenies, was significant for the all studied traits except percent of stalk and root lodged plants (tab. 3 and 4). Genetic variances of the investigated traits were greater in S_1 than in HS progenies for grain yield (σ_g^2=1.13; σ_g^2=0.35), percent of stalk and root lodged plants (σ_g^2=0.87; σ_g^2=0.55), ear height (σ_g^2=97.63; σ_g^2=13.71), plant height (σ_g^2=200.17; σ_g^2=42.64), ear length (σ_g^2=1.38; σ_g^2=0.35), number of grain rows per ear (σ_g^2=0.94; σ_g^2=0.61), number of grains per row (σ_g^2=5.54; σ_g^2=2.17), and for 1000 grain mass (σ_g^2=696.76; σ_g^2=205.58).

Table 3

Components of variance and genetic parameters of S_1 progenies

Traits	σ_g^{2*}	$SE_{\sigma_g^2}$	CV$_g$%	σ_f^{2*}	$SE_{\sigma_f^2}$	CV$_f$%	h^{2*}	SE_{h^2}
Grain yield	1.13	0.33	19.50	1.64	0.35	23.50	0.69	0.20
% of lodged plants	0.87	1.00	1965.80	3.25	1.25	3797.7	0.27	0.31
Ear height	97.63	24.80	14.53	98.88	24.95	14.62	0.99	0.25
Plant height	200.17	48.54	7.07	209.12	48.74	7.23	0.96	0.23
Ear length	1.38	0.34	8.08	1.67	0.34	8.90	0.83	0.20
Number of grain rows	0.94	0.24	7.40	1.06	0.24	7.82	0.89	0.23
Number of grains	5.54	1.56	9.81	8.23	1.64	11.96	0.67	0.19
1000 grain mass	696.76	172.01	9.50	1056.18	179.38	11.69	0.66	0.16

* - σ_g^2, σ_f^2 and h^2 are significant if have at lest double value than their standard errors.

Hartley tests for comparing genetic variances between progeny types revealed that the differences between the two progeny types in genetic variance were highly significant for grain yield, ear and plant height, ear length, number of grains per row, and 1000 grain mass, while they were not significant for percent of stalk and root lodged plants and number of grain rows per ear. Coefficient of genetic variation was the highest for percent of stalk and root lodged plants in both progeny types, while for the other traits it was within levels from 7.07% to 19.5% in S_1 progenies, and from 2.49% to 6.99% in HS progenies.

Table 4

Components of variance and genetic parameters of HS progenies

Traits	σ_g^{2*}	$SE_{\sigma_g^2}$	CV$_g$%	σ_f^{2*}	$SE_{\sigma_f^2}$	CV$_f$%	h^{2*}	SE_{h^2}
Grain yield	0.35	0.16	6.99	0.81	0.19	10.58	0.44	0.20
% of lodged plants	0.55	0.47	5369.83	2.77	0.65	12083.8	0.20	0.17
Ear height	13.71	7.27	3.50	27.76	8.40	4.98	0.49	0.26
Plant height	42.64	18.58	2.49	84.43	21.23	3.51	0.51	0.22
Ear length	0.35	0.13	3.42	0.46	0.14	3.94	0.75	0.29
Number of grain rows	0.61	0.17	4.98	0.85	0.18	5.89	0.72	0.20
Number of grains	2.17	0.77	4.48	3.64	0.84	5.80	0.60	0.21
1000 grain mass	205.58	64.73	4.61	292.20	68.40	5.50	0.70	0.22

* - σ_g^2, σ_f^2 and h^2 are significant if have at lest double value than their standard errors.

Phenotypic variances also were significant for the all studied traits except for percent of stalk and root lodged plants and number of grain rows per ear in both progeny types. Hartley tests revealed that the differences between the two progeny types in phenotypic variance were significant for grain yield and highly significant for ear and plant height, ear length, number of grains per row, and 1000 grain mass. The differences were not significant for percent of stalk and root lodged plants and number of grain rows per ear.

Coefficients of phenotypic variation were incomparably higher for percent of root and stalk lodged plants than for the all other studied traits. Putting aside percent of root and stalk lodged plants, coefficients of phenotypic variation in S_1 progenies ranged from 7.23% for plant height up to 23.5% for grain yield. The same coefficients in HS progenies ranged within values from 3.51% for plant height up to 10.58% for grain yield.

Values of broad-sense heritability in both progeny types were significant for the all studied traits except for percent of stalk and root lodged plants. That trait was characterized by the lowest value of heritability in both progeny types. Heritability was lower in HS progenies than in S_1 progenies. Grain yield was characterized by lower heritability values in regard to the other investigated traits, because grain yield had been forming from the moment of sowing to the moment of harvest, so it was under the influence of environmental factors during whole vegetation season. Unlike grain yield, yield components were under the effect of environmental factors only during certain stages of plant ontogeny. These results are comparable with the ones presented in previous reports (DELETIĆ, 1999, 2003; NASTASIĆ, 2001; ANĐELKOVIĆ, 2000).

CONCLUSIONS

On the basis of the study, dealing with genetic and phenotypic variability of yield components in S_1 and HS progenies of F_3 maize population 2002-30, we can conclude the following:

– HS progenies had higher average values of the studied traits regarding S_1 progenies. The differences between progeny types were highly significant for all the studied traits, except for root and stalk lodged plants percent.

– Genetic variances were higher in S_1 progenies, with the exception of root and stalk lodged plants percent and grain number per row. Phenotypic variance followed the same tendency.

– The obtained values of broad-sense heritability were significantly higher in S_1 than in HS progenies. Low heritability values were calculated only for root and stalk lodged plants percent.

BIBLIOGRAFY

1. ANĐELKOVIĆ VIOLETA (2000): Identifikacija pokazatelja otpornosti kukuruza (*Zea mays* L.) prema suši kod potomstva sa egzotičnom germplazmom Doktorska disertacija, Poljoprivredni fakultet, Univerzitet u Novom Sadu.
2. DELETIĆ, N. (1999): Genetska i fenotipska varijabilnost komponenti prinosa kod sintetičkih populacija kukuruza. Magistarska teza, Poljoprivredni fakultet, Univerzitet u Novom Sadu.
3. DELETIĆ, N., ĐURIĆ, V., GUDŽIĆ, N. (2000): Genetska i fenotipska varijabilnost prinosa zrna i visine biljke kod dve sintetičke populacije kukuruza. Zbornik izvoda radova sa III JUSEM-a. Zlatibor, 28.05.-1.06.2000., 33.
4. DELETIĆ, N. (2003): Promena aditivne varijanse komponenti prinosa nakon rekurentne selekcije kukuruza (*Zea mays* L.) Doktorska disertacija, Poljoprivredni fakultet, Univerzitet u Novom Sadu.
5. FALCONER, D. S. (1989): Introduction to quantitative genetics. Longman Inc., London and New York.
6. HALLAUER, A.R., MIRANDA, J.B. (1988): Quantitative genetics in maize breeding. (2nd ed.). Iowa State

University Press, Ames, Iowa, USA.

7. NASTASIĆ ALEKSANDRA (2001): Genetička varijabilnost i međuzavisnost prinosa i komponenti prinosa NSB sintetičke populacije kukuruza (*Zea mays* L.). Doktorska disertacija, Poljoprivredni fakultet, Univerzitet u Novom Sadu.
8. STOJKOVIĆ S. (2007): Genetska i fenotipska varijabilnost komponenti prinosa kod S_1 i HS potomstava jedne F_3 populacije kukuruza. Doktorska disertacija, Poljoprivredni fakultet, Univerzitet u Prištini.
9. TRIFUNOVIĆ, S., HUSIĆ, I., IVANOVIĆ, M. (1998): Generation mean analysis for grain yield by RCBD and new experimental design in maize (*Zea mays* L.). Proceedings of the 2nd Balkan Symposium on Field crops, Vol. 1 – Genetics & Breeding, Novi Sad 16-20.06.1998., 303-304.