

**VARIABILITY PARAMETERS FOR YIELD COMPONENTS OF  
DIFFERENT PROGENY TYPES IN AN F<sub>3</sub> MAIZE POPULATION**

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Stojakovic S., N. Deletic, M. Aksic, D. Bekovic and V. Djuric (2012): *Variability parameters for yield components of different progeny types in an F<sub>3</sub> maize population*. Genetika, Vol 44, No. 3, 441-448.

This paper presents the investigation of F<sub>3</sub> population 2002-30, created in the Department of Maize, Institute of Field and Vegetable Crops, Novi Sad. At first, about 150 plants of the studied population were selfed and simultaneously crossed with the tester 1491x1496, in order to get complementary S<sub>1</sub> and HS progenies. After the harvest, 41 progenies of each type were selected by the random sample method for the trials carried out in Aleksinac, Leskovac, and Kruševac, as three studied environments, in RCB design. Genetic variances were significantly higher in S<sub>1</sub> progenies, with the exception of root and stalk lodged plants percent and grain number per row, where these differences were not significant. Phenotypic variances followed the same tendency. The obtained values of broad-sense heritability

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were significantly higher in  $S_1$  than in HS progenies. Low heritability values were calculated only for root and stalk lodged plants percent. Cluster analysis did not show any greater difference between  $S_1$  and HS progenies, neither in distances nor in group definition, although there were significant differences between them in genetic variances. However, one can see a lower degree of distances between HS progenies.

*Key words:* grain yield, yield components, maize, variability

#### INTRODUCTION

Genetic variability, which is a heritable difference among genotypes, is required in an appreciable level within a population to facilitate and sustain an effective long-term plant breeding program. Progress from selection has been reported to be directly related to the magnitude of genetic variance in the population (TABANAO and BERNARDO, 2005; SALAMI *et al.*, 2007). However, reaching selection progress has to be followed by conservation of genetic variability and desirable alleles determining the most important traits. These processes are opposite each other by nature, so the solution ought to be a compromise between them (DELETIĆ *et al.*, 2009; 2011).

Continuous germplasm improvement is still very valuable as a source of new and diverse maize hybrids, but there is a constant need for inbred lines that are new, different and unrelated with the existing ones (BARATA and CARENA, 2006; HALAUER *et al.*, 2010). It forces breeders to create populations with narrow genetic base, in order to get superior material for hybrids through just few selection cycles. Therefore, in short-term breeding programs there is a domination of  $F_2$  and  $F_3$  populations, derived from the best commercial hybrids or from deliberate hybridization of two or several lines (STOJKOVIĆ, 2007; STOJKOVIĆ *et al.*, 2011).

Our study has been aimed to estimate genetic and phenotypic variability of yield components in  $S_1$  and HS progenies derived from  $F_3$  maize population 2002-30.

#### MATERIALS AND METHODS

The object of this study was  $F_3$  maize population 2002-30, created in the Department of Maize, Institute of Field and Vegetable Crops, Novi Sad. During the first year of investigation about 150 plants of the population were selfed and simultaneously crossed with the tester 1491x1496, in order to get parallel  $S_1$  and HS progenies. After the harvest, 41 progenies of each type ( $S_1$  and HS) were selected for trials, by random sample method. Next year, field trials were set in Aleksinac, Leskovac and Kruševac (total three environments), in random complete block design with two replications, where the experimental plot area was 0.7x4.6 m. Number of plants per hectare amounted 62,112.

Data were processed by analysis of variance for RCBD, according to HALLAUER *et al.* (2010). Genetic and phenotypic variances, as well as heritability, and their standard errors were calculated for the all studied traits.

Cluster analysis of both progeny types was carried out according to the all investigated traits. The analysis was based on mean values of the lines per environments. Clustering was done by single linkage, and the distances were Euclidian, according to BRYANT and BERRY (2001).

#### RESULTS AND DISCUSSION

Values of genetic variance, phenotypic variance and heritability were considered as significant if were at least double than respective standard errors (DELETIĆ *et al.*, 2011). 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. 1 and 2). Genetic variances of the investigated traits were greater in  $S_1$  than in HS progenies for grain yield ( $\sigma_g^2=1.13$ ;  $\sigma_g^2=0.35$ ), percent of stalk and root lodged plants ( $\sigma_g^2=0.87$ ;  $\sigma_g^2=0.55$ ), ear height ( $\sigma_g^2=97.63$ ;  $\sigma_g^2=13.71$ ), plant height ( $\sigma_g^2=200.17$ ;  $\sigma_g^2=42.64$ ), ear length ( $\sigma_g^2=1.38$ ;  $\sigma_g^2=0.35$ ), number of grain rows per ear ( $\sigma_g^2=0.94$ ;  $\sigma_g^2=0.61$ ), number of grains per row ( $\sigma_g^2=5.54$ ;  $\sigma_g^2=2.17$ ), and for 1000 grain mass ( $\sigma_g^2=696.76$ ;  $\sigma_g^2=205.58$ ). DELETIĆ *et al.* (2011) also found significant genetic variances for the all yield components except percent of root and stalk lodged plants. Percent of lodged plants is not suitable for common genetic analysis because it follows binominal distribution, which was pointed out by STOJKOVIĆ (2007) and STOJKOVIĆ *et al.* (2011).

Table 1. Componentsof variance and heribility in  $S_1$  progenies

Traits	$\sigma_g^2$	SE ( $\sigma_g^2$ )	$\sigma_r^2$	SE ( $\sigma_r^2$ )	$h^2$	SE ( $h^2$ )
Grain yield	1.13	0.33	1.64	0.35	0.69	0.20
Percent of lodged	0.87	1.00	3.25	1.25	0.27	0.31
Ear height	97.63	24.80	98.88	24.95	0.99	0.25
Plant height	200.17	48.54	209.12	48.74	0.96	0.23
Ear length	1.38	0.34	1.67	0.34	0.83	0.20
Grain rows per ear	0.94	0.24	1.06	0.24	0.89	0.23
Grains per row	5.54	1.56	8.23	1.64	0.67	0.19
1000 grain mass	696.76	172.01	1056.18	179.38	0.66	0.16

\* -  $\sigma_g^2$ ,  $\sigma_r^2$  and  $h^2$  are significant if have at least 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.

Phenotypic variances were significant for the all studied traits 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.

Table 2. Components of variance and heritability in HS progenies

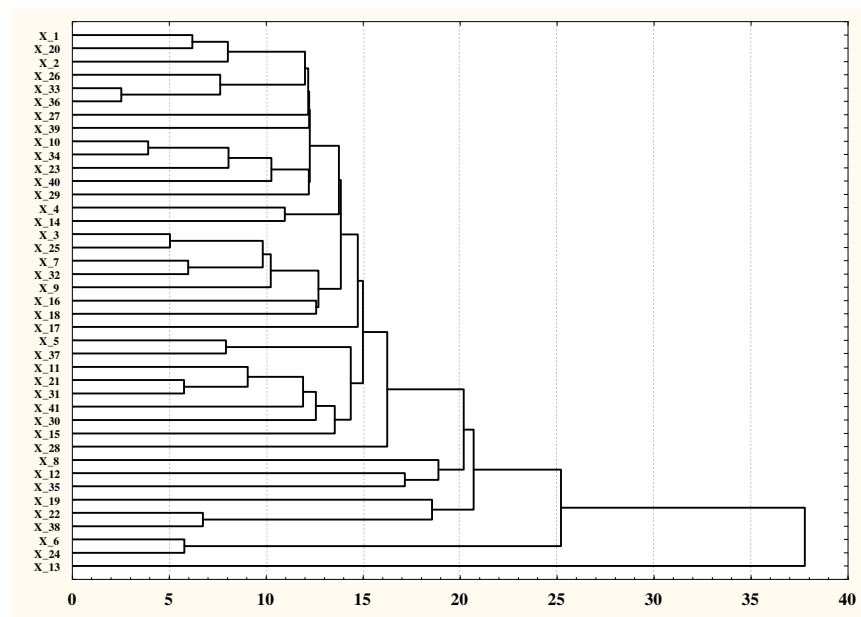
Traits	$\sigma_g^2$	SE ( $\sigma_g^2$ )	$\sigma_r^2$	SE ( $\sigma_r^2$ )	$h^2$	SE ( $h^2$ )
Grain yield	0.35	0.16	0.81	0.19	0.44	0.20
Percent of lodged	0.55	0.47	2.77	0.65	0.20	0.17
Ear height	13.71	7.27	27.76	8.40	0.49	0.26
Plant height	42.64	18.58	84.43	21.23	0.51	0.22
Ear length	0.35	0.13	0.46	0.14	0.75	0.29
Grain rows per ear	0.61	0.17	0.85	0.18	0.72	0.20
Grains per row	2.17	0.77	3.64	0.84	0.60	0.21
1000 grain mass	205.58	64.73	292.20	68.40	0.70	0.22

\* -  $\sigma_g^2$ ,  $\sigma_r^2$  and  $h^2$  are significant if have at least double value than their standard errors

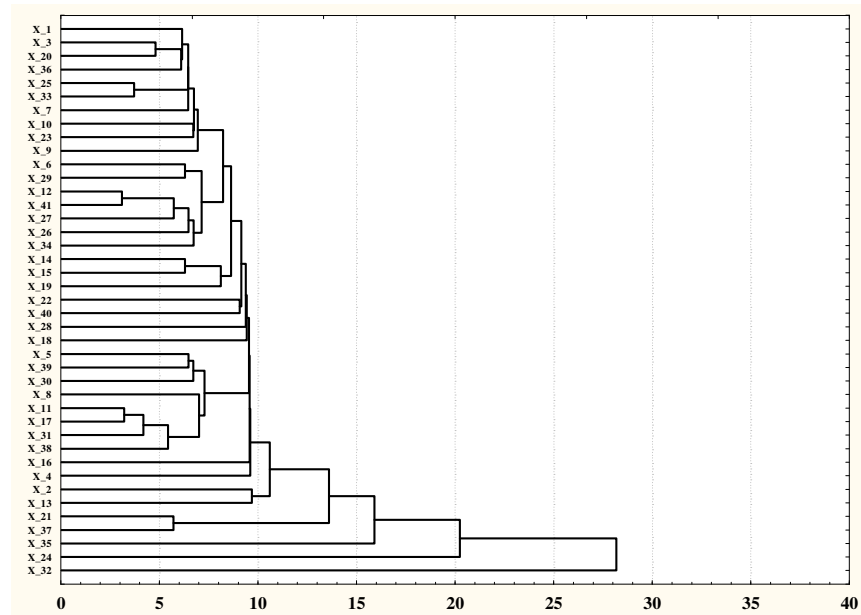
Values of broad-sense heritability in both progeny types were significant for the all studied traits except for percent of stalk and root lodged plants. That trait was characterized by the lowest value of heritability in both progeny types. Heritability was lower in HS progenies than in  $S_1$  progenies. BEKAVAC *et al.* (2008) studied two broad-based maize populations, and also found higher heritability for grain yield in  $S_1$  than in HS progenies. STANISAVLJEVIĆ *et al.* (2010) obtained slightly lower values of heritability for grain yield in two groups of HS progenies of a narrow-based maize population, than observed in this study. 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.

Multivariate cluster analysis was used to group genotypes from both progeny types into clusters according to variation pattern of the all investigated traits, as well as to determine distances among them. Comparison of distances between most of genotypes in each progenies can give valuable information regarding general trends of variability for the traits used to do clustering. In this study clustering has been done on the basis of the all eight investigated traits, by the single linkage method, and distances are expressed as Euclidian values.

Although distances between groups have been lower in half-sib progenies (graph 1 and 2), that difference is not proportional with the observed great differences in genetic and phenotypic variance. Furthermore, groups are slightly less defined in this progeny type. However, this analysis is based on variation of several traits simultaneously, so differences between progeny types in variability of individual traits need not always be clearly visible.



Graph 1. Cluster analysis of the studied S<sub>1</sub> progenies based on the all eight traits



Graph 2. Cluster analysis of the studied HS progenies based on the all eight traits

On the basis of the study, dealing with genetic and phenotypic variability of yield components in  $S_1$  and HS progenies derived from  $F_3$  maize population 2002-30, we can point out to several observations. Genetic variances were significantly higher in  $S_1$  progenies, with the exception of root and stalk lodged plants percent and grain number per row, where these differences were not significant. 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. Cluster analysis did not show any greater difference between  $S_1$  and HS progenies, neither in distances nor in group definition, although there were significant differences between them in genetic variances. However, one can see a lower degree of distances between HS progenies.

#### ACKNOWLEDGEMENT

The investigation published in this paper is a part of the project "The development of new technologies of small grains cultivation on acid soils using contemporary biotechnology" financed by the Ministry of Education, Science and Technological Development of the Republic of Serbia, grant No TR-31054.

Received October 6<sup>th</sup>, 2011

Accepted September 07<sup>th</sup>, 2012

#### REFERENCES

- BARATA, C., M.J. CARENA (2006): Classification of North Dakota maize inbred lines into heterotic groups based on molecular and testcross data. *Euphytica*, 151(3):339-349.
- BEKAVAC, G., B.PURAR, Đ. JOCKOVIĆ (2008): Relationships between line per se and testcross performance for agronomic traits in two broad-based populations of maize. *Euphytica*, 162(3):363-369.
- BRYANT, D., V. BERRY (2001): A structured family of clustering and tree construction methods. *Advances in Applied Mathematics*, 27(4):705-732.
- DELETIĆ, N., S. STOJKOVIĆ, S. GUDŽIĆ, M. BIBERDŽIĆ (2009): The change of genetic and phenotypic variability of yield components after recurrent selection of maize. *Genetika*, 41(2):207-214.
- DELETIĆ, N., S. STOJKOVIĆ, S. GUDŽIĆ, N. GUDŽIĆ, M.AKSIĆ (2011): Additive variance of maize yield components after three cycles of recurrent selection. *Proceedings of the Third International Conference „Research People and Actual Tasks on Multidisciplinary Sciences“*, Lozenec, Bulgaria, 8-10 June 2011, Vol. 1, 71-74.
- HALLAUER, A.R., M.J. CARENA, J.B. MIRANDA FILHO (2010): *Quantitative genetics in maize breeding – Handbook of plant breeding*. Springer, NY-Dodrecht-Heidelberg-London.
- SALAMI, A.E., S.A.O. ADEGOKE, O.A. ADEGBITE (2007): Genetic variability among maize cultivars grown in Ekiti-State, Nigeria. *Middle-East Journal of Scientific Research*, 2(1):09-13.
- STANISAVLJEVIĆ, D., S. TRESKIĆ, B. MITROVIĆ, A. NASTASIĆ, G. BEKAVAC, M.IVANOVIĆ (2010): Genetic variability and correlation analysis for grain yield of a narrow base synthetic maize population NSA15. *Field Veg. Crop Res.*, 47(2):467-472.
- STOJKOVIĆ, S. (2007): Genetic and phenotypic variability of yield components in  $S_1$  and HS progenies of an  $F_3$  maize population. PhD thesis, University of Priština, Faculty of Agriculture.

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- STOJKOVIĆ, S., N. DELETIĆ, M. BIBERDŽIĆ, D. BEKOVIĆ, N. SAVIĆ, M.AKSIĆ (2011): Yield components' variability and genetic gain from selection in a F<sub>3</sub> maize population. Proceedings of the Third International Conference „Research People and Actual Tasks on Multidisciplinary Sciences“, Lozenec, Bulgaria, 8-10 June 2011, Vol. 1, 75-79.
- TABANAO, D.A., R.BERNARDO (2005): Genetic variation in maize breeding population with different numbers of parents. *Crop Sci.*, 45(6):2301-2306.

**PARAMETRI VARIJABILNOSTI KOMPONENTI PRINOSA KOD  
RAZLIČITIH TIPOVA POTOMSTAVA JEDNE F<sub>3</sub> POPULACIJE  
KUKURUZA**

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U radu je ispitivana F<sub>3</sub> populacija kukuruza 2002-30 dobijena u Zavodu za kukuruz Instituta za ratarstvo i povrtarstvo u Novom Sadu. Najpre je oko 150 biljaka navedene populacije samooplođeno i istovremeno ukršteno sa testerom 1491x1496, da bi se dobila naspramna S<sub>1</sub> i HS potomstva. Nakon berbe, metodom slučajnog uzorka odabrano je po 41 S<sub>1</sub> i HS potomstava za oglede koji su obavljeni u Aleksincu, Leskovcu i Kruševcu, što ukupno čini tri okruženja, po RCBD metodi. Genetske varijanse su bile značajno veće kod S<sub>1</sub> potomstava za sva svojstva osim za procenat poleglih i slomljenih biljaka i broj redova zrna, gde te razlike nisu bile značajne. Fenotipske varijanse su pratile isti trend. Dobijene vrednosti koeficijenta heritabilnosti u širem smislu su bile značajno više kod S<sub>1</sub> u odnosu na HS potomstva. Niske vrednosti heritabilnosti dobijene su samo za procenat poleglih i slomljenih biljaka. Klaster analiza nije pokazala veće razlike između S<sub>1</sub> i HS potomstava, ni u distancama ni u definisanosti grupa, iako su postojale značajne razlike u genetskoj varijansi za većinu ispitivanih svojstava. Ipak, primetne su nešto manje distance između HS potomstava.

Primljeno 06. X 2011.

Odobreno 07. IX. 2012.