

**THE CHANGE OF GENETIC AND PHENOTYPIC VARIABILITY OF  
YIELD COMPONENTS AFTER RECURRENT SELECTION OF MAIZE**

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Deletic N., S. Stojković, S. Gudžić, and M.Biberdžić (2009): *The change of genetic and phenotypic variability of yield components after recurrent selection of maize.*– Genetika, Vol. 41, No. 2, 207 - 214.

This paper deals with 31 SSD lines from ZP-Syn-1 C<sub>0</sub> and 37 from ZP-Syn-1 C<sub>3</sub> maize populations. After line selection and seed multiplication in the first year of the study, the trials were set during two years in Kruševac and Zemun Polje, in RCB design with three replications. Additive and phenotypic variances of yield components were calculated, as well as the estimation of genetic variability narrowing by multivariate cluster analysis. The differences in additive and phenotypic variances between the cycles were significant for ear length only and highly significant for grain row number per ear and for percent of root and stalk lodged plants. It means, a significant narrowing of additive and phenotypic variance occurred only for those three traits, and the other traits did not change their variability by selection in a significant manner. However, according to cluster analysis, distances among genotypes and groups in the zero selection cycle were approximately double than in the third one, but group definition was better in the third selection cycle. It

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can suggest indirectly of a total variability narrowing after three cycles of recurrent selection.

*Key words:* cluster analysis, genetic variance, maize, yield components

## INTRODUCTION

The crucial question of recurrent selection is how to reach selection progress together with conservation of genetic variability and without a loss of 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. In order to reach an optimal level of the compromise, the ideal solution would be to explore quantitative-genetic parameters of every new population, and to follow them through the selection process, so the methods and intensity of selection can be properly chosen. Nothing ideal is real in practice, so each particular study can contribute to establishing of general rules. This is especially important in the terms of additive variance, because it has the highest effect to the most important traits, and often could be masked by dominant and epistatic effects (DELETIĆ, 2003; DELETIĆ *et al.*, 2005; DELETIĆ *et al.*, 2006).

Recurrent selection is a long-term process, so the possibility of its duration reduction is often discussed. Advance in improvement of particular traits *per se* and accumulation of desirable alleles for those traits are directly dependent on selection intensity. However, there is a need to be cautious with application of a high selection pressure for getting better gain from selection, because genetic variability can be significantly decreased that way (HALLAUER and MIRANDA, 1988; ROŠULJ, 1999), and genetic drift also can be observed (GUZMAN and LAMKEY, 1999; CEPADA *et al.*, 2000). So the usual way is to apply lower selection intensity in earlier selection cycles, and to increase it after few selection cycles.

## MATERIAL AND METHODS

The ZP Syn 1 maize population was used for the study. It was created by recombination of eight lines – five domestic ones from local populations, one from Lancaster germ-plasm, one Argentinian line from population Colorado, and one line from BS<sub>12</sub>C<sub>5</sub> (ALPH) population. After line recombination and forming of ZP-Syn1-C<sub>0</sub> population, the three cycles of half-sib recurrent selection were done, with selection intensity of 5%, and line A-632 was used as a narrow-base tester (former version of B-14 line from BSSS).

After 150 randomly chosen plants per each selection cycle (C<sub>0</sub> and C<sub>3</sub>) were selfed, selfing continued according to SSD (Single Seed Descent) method to a practically complete homozygosity (12-14 generations). Number of lines decreased during selfing process, mostly because of random factors related with the applied method, and, in some extent, because of the lethal effect of some recessive alleles, so the final number of the studied lines was 31 in C<sub>0</sub> cycle and 37 in C<sub>3</sub> cycle. After seed multiplication, the two-year comparative trials were set in

Krusevac and Zemun Polje, in RCB design, with three replications. Genetic and phenotypic variances of the all studied traits and their standard errors were calculated.

Cluster analysis of the lines from both cycles was carried out according to four (grain yield, plant and ear height, as well as root and stalk lodged plants percent) and five (grain yield and yield components) traits. The analysis was based on mean values of the lines per years and locations. Clustering was done by single interconnectedness, and the distances were Euclidian, according to GOWER and ROSS (1969).

## RESULTS AND DISCUSSION

The all studied traits in lines from both cycles showed significant additive variances, because they were more than double greater regarding respective standard errors, which is, according to FALCONER (1989), the criterium of significance for genetic and phenotypic variance (tab. 1 and 2). Phenotypic variance showed similar tendency, so the all calculated values for lines from both cycles of recurrent selection were significant (tab. 2). It can be seen that both line groups represent a good material for creating new selection cycles from the best ones of them and proceeding process of maize recurrent selection.

Table 1. Components of variance in lines from ZP-Syn-1 C<sub>0</sub> population

Traits	$\sigma_a^{2*}$	$SE_{\sigma_a^2}$	$\sigma_f^{2*}$	$SE_{\sigma_f^2}$
Grain yield	670385	121744	1901875	1152585
% of lodged plants	73.212	14.090	207.989	137.108
Ear height	85.711	15.400	193.846	140.789
Plant height	187.544	33.406	410.226	304.115
Ear length	1.273	0.229	3.180	2.122
Number of rows per ear	1.757	0.313	3.886	2.853
Number of grains per row	10.835	1.945	27.201	17.989
1000 grain mass	600.90	108.38	1452.28	997.98

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

Table 2. Components of variance in lines from ZP-Syn-1 C<sub>3</sub> population

Traits	$\sigma_a^{2*}$	$SE_{\sigma_a^2}$	$\sigma_f^{2*}$	$SE_{\sigma_f^2}$
Grain yield	572313	103707	1423853	192224
% of lodged plants	17.266	3.611	50.524	7.415
Ear height	57.553	10.379	121.068	18.917
Plant height	126.395	22.741	268.424	41.459
Ear length	0.716	0.134	1.567	0.247
Number of rows per ear	0.747	0.137	1.654	0.253
Number of grains per row	8.462	1.550	19.522	2.861
1000 grain mass	804.08	143.21	1726.37	260.65

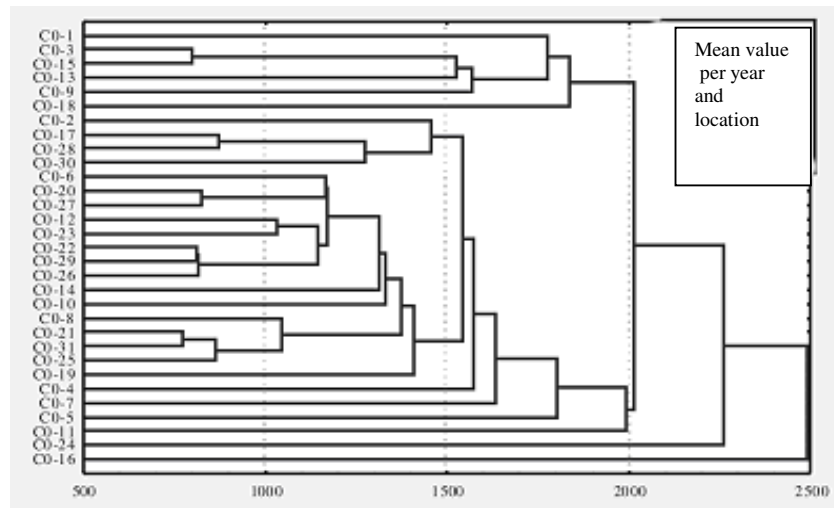
\* -  $\sigma_g^2$  and  $\sigma_f^2$  are significant if have at least double value than their standard errors.

However, among all quantitative-genetic parameters, we paid a special attention to a possible significant reduction of additive variance for yield components after three cycles of HS recurrent selection, with selection intensity of 5%. Hartley tests revealed that differences between the cycles, regarding both additive and phenotypic variances, were significant for ear length only, and highly significant for number of grain rows per ear and percent of root and stalk lodged plants. It means that only those three traits showed a significant reduction of additive and phenotypic variance, while the other traits did not changed significantly under selection.

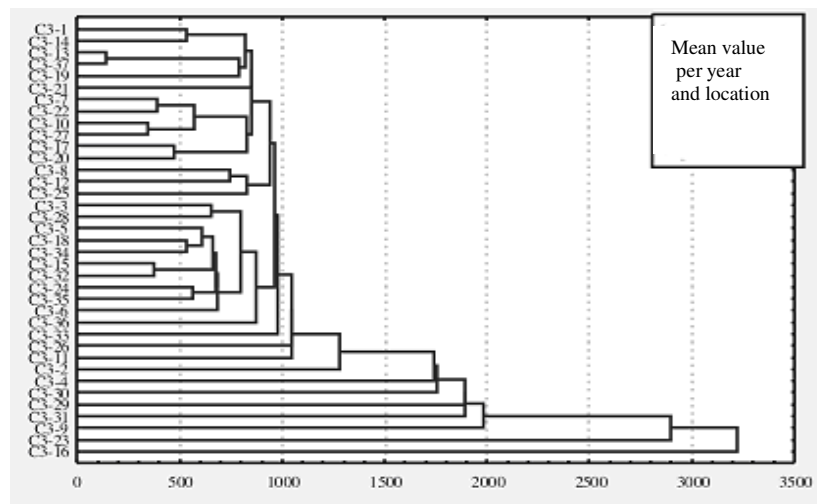
After analysis of additive and phenotypic variability, we tried to reach a broader understanding of the investigated traits variability in lines from two cycles of recurrent selection. Thus, genotypes from the zero and the third selection cycles were clustered according to variation similarity of several traits by multivariate cluster analysis, and the distances among them were determined. Comparison of distances among the majority of lines between the cycles can provide useful information about general variability trends of the traits used for clustering, and group definition and distance between them could point to the existence of line random drift, which was expected here because of the applied SSD method of line creation.

Parameters used for clustering of genotypes ought to be carefully chosen. It is possible to observe variation of one or more traits in different environments, and it is also possible to observe variation similarity of several traits. By the rule, similarity in variation of larger number of traits provides more reliable clustering, but, because of increase of the experimental error, main clustering trends can be hardly visible. That was the reason we used four (% of root and stalk lodged plants, plant and ear height, grain yield) and five traits (grain yield and yield components) for clustering, and the results could be seen in graphs 1-4.

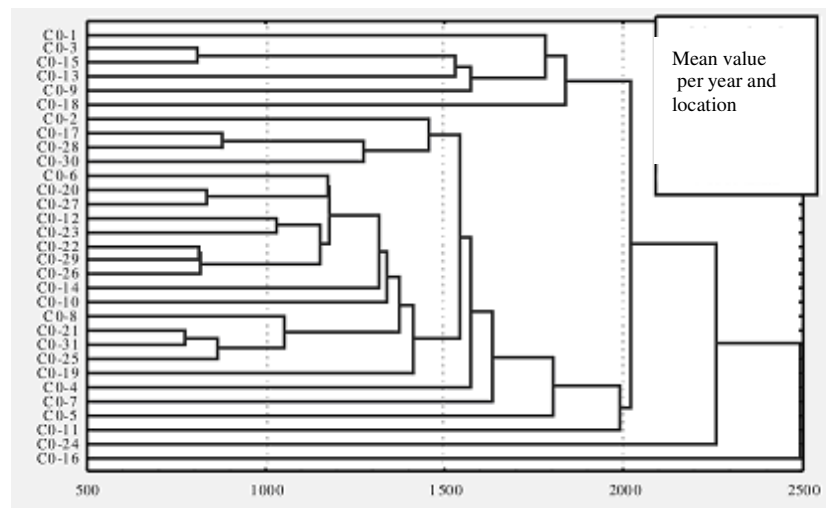
Analysis of tree diagrams based on four traits shows, except few "freelancers" in each cycle lines, that most of lines were clustered in more or less defined and distant from each other groups. In general, lines from the third cycle showed a better definition of groups, and inter-group distance were lower than in lines of the zero cycle (graph 1 and 2). Despite the fact that in clustering based on five traits only grain yield was in common with the previous analysis, trends in group definition and distances between them were almost the same as in analysis based on four traits. Of course, there were certain differences in group composition, but the general impression of variability, as within as between the cycles, was alike in the previous cluster analysis (graph 3 and 4). It can be concluded in general that cluster analysis revealed a narrowing of total variability under recurrent selection.



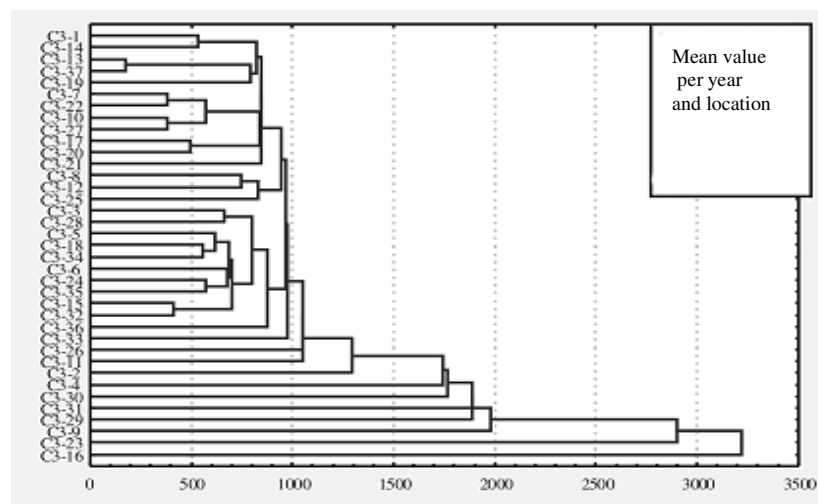
Graph 1. Cluster analysis of lines from ZP-Syn-1 C<sub>0</sub> population on the basis of four traits



Graph 2. Cluster analysis of lines from ZP-Syn-1 C<sub>3</sub> population on the basis of four traits



Graph 3. Cluster analysis of lines from ZP-Syn-1 C<sub>0</sub> population on the basis of five traits



Graph 4. Cluster analysis of lines from ZP-Syn-1 C<sub>3</sub> population on the basis of five traits

## CONCLUSION

On the basis of the presented results one can conclude the following:

- Values of additive and phenotypic variances were significant for the all studied traits in both selection cycles.
- After three cycles there was a significant reduction of additive variability for percent of root and stalk lodged plants, ear length and number of grain rows per ear. Reduction of those values for the other traits was not significant. Phenotypic variances showed the same tendency.
- Cluster analysis showed roughly double distances between genotypes and groups in the zero cycle, and better group definition in the third cycle. It indirectly points to a narrowing of total variability after three cycles of recurrent selection.

Received June 02<sup>nd</sup>, 2009

Accepted August 18<sup>th</sup>, 2009

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**PROMENA GENETSKE I FENOTIPSE VARIJANSE KOMONENTI  
PRINOSA NAKON REKURENTNE SELEKCIJE KUKURUZA**

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Izvod

U radu je ispitivana 31 SSD linija iz ZP-Syn-1 C<sub>0</sub> i 37 iz ZP-Syn-1 C<sub>3</sub> populacije kukuruza. Nakon odabira i umnožavanja semena linija u prvoj godini, ogledi su obavljani tokom dve godine u Kruševcu i Zemun Polju, po RCBD metodi sa tri ponavljanja. Izračunata je aditivna i fenotipska varijabilnost komponenti prinosa, a urađena je i procena suženja varijabilnosti na osnovu multivarijacione *cluster* analize. Razlike između aditivnih i fenotipskih varijansi između ciklusa su bile značajne samo za dužinu klipa, a visoko značajne za broj redova zrna i procenat poleglih i slomljenih biljaka. To znači da je samo kod ova tri svojstva došlo do značajnog smanjenja aditivne i fenotipske varijanse, dok za ostala svojstva nije bilo značajnih promena pod uticajem selekcije. *Cluster* analiza je pokazala, po svim kriterijumima, dvostruko veće distance između genotipova i grupa u nultom ciklusu, a bolju definisanost grupa u trećem ciklusu. Ovo nam na posredan način ukazuje na suženje ukupne varijabilnosti nakon tri ciklusa rekurentne selekcije.

Primljeno 02. VI. 2009.  
Odobreno 18. VIII. 2009.