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## GENETIC ANALYSIS OF DROUGHT ADAPTIVE TRAITS IN MAIZE SYNTHETIC POPULATIONS

Goran BEKAVAC, Božana PURAR, and Đorđe JOCKOVIĆ

Institute of Field and Vegetable Crops, Novi Sad, Serbia

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Maize breeders consider tolerance to drought as an important criterion in commercial breeding programs. Two traits, stay green and anthesis-silking interval seem to be closely associated with drought tolerance. The main objective of this study was to obtain estimates of means, variability, heritability and estimates of genetic correlations for several traits in two maize synthetic populations.  $S_1$  progenies were evaluated in an incomplete block design in four environments. Large genetic variability existed for all traits in both populations but highest variability was found for anthesis-silking interval. Strong, highly significant correlations between drought adaptive traits and grain moisture may cause some undesirable correlative response throughout cycles of selection.

*Key words: maize, variability, correlation*

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*Corresponding author:* Goran Bekavac, Institute of Field and Vegetable Crops, M. Gorkog 30, 21000 Novi Sad, Serbia Tel: +381 21 4898 251; Fax: +381 21 4898 300; e-mail: [gbekavac@ifvcns.ns.ac.yu](mailto:gbekavac@ifvcns.ns.ac.yu)

## INTRODUCTION

Future progress in maize production of south-eastern Europe could be seriously limited by drought. Water deficit during growing season has become a normal occurrence in this region, so maize breeders consider drought tolerance as an important breeding criterion. In the past, breeding for drought tolerance used physiological and morphological traits rather than grain yield as a selection criteria (BLUM, 1988). It remains difficult to identify traits that effectively mark drought-tolerant genotypes. Recent studies have given more attention to flowering traits, such as synchronization of the male and female flowering (anthesis-silking interval) under drought conditions (BOLANOS and EDMEADES, 1988). Also, better stay green is frequently emphasized as a key element of tolerance to drought (ROSENOW et al., 1983; RUSSELL, 1986; DUVICK, 1992; BORRELL et al., 2000). Stay green is characterized by increased photosynthetic activity in older phases of vegetative growth, increased resistance to diseases and pests, and increased tolerance to drought (THOMAS and SMART, 1993).

Population improvement via recurrent selection methodology focuses on two main goals: improving the mean performance of a population through an increase in the frequency of favorable alleles and maintaining adequate genetic variability in the improved population for continued selection and genetic enhancement. To achieve these goals, maize breeders grow a large number of progenies in trials. Such trials are expensive, so any selection procedure that can identify desirable genotypes or eliminate undesirable ones from further consideration is beneficial (CLUCAS and HALLAUER, 1986). Stay green (SG) and anthesis-silking interval (ASI) could be used as selection criteria in breeding for drought tolerance. In order to apply an adequate breeding scheme, it is necessary to know the mean value, variability, heritability and interrelationships between main traits in a breeding material (HALLAUER and MIRANDA, 1988).

The main objective of this study was to obtain estimates of mean values and basic genetic parameters for several agronomic traits in two maize synthetic populations.

## MATERIALS AND METHODS

The materials used in this study were two maize synthetic populations (NS12-SG and NS14-SG) developed at Institute of Field and Vegetable Crops in Novi Sad, Serbia. Both populations were designed to be a source of improved stay green character. The population NS12-SG was obtained by intermating four inbred lines – three domestic ones (NS215-L, NS222-L and NS253-L) and one of US origin (C103). The population NS14-SG was developed in the same manner by intermating the following four inbred lines: NS586-S, NS588-S, NS597-S (domestic origin) and B14 (US origin). The populations were formed by producing all possible single crosses and than all possible double crosses. Equal seed quantities from each double cross were then bulked and randomly mated in the 2000 nursery.

In 2001, approximately 600 plants per population were planted and one half was selfed to produce a random sample of  $S_1$  families. At harvest, 80 ears ( $S_1$  families) per population were randomly chosen. Independent field experiments were set up for each population in 2002 in two environments (Novi Sad and Srbobran, Serbia). Simultaneously, in 2002  $S_1$  families were multiplied with full-sib matings for the succeeding growing season. Approximately 20 plants within each family were used for seed multiplication – this allowed the coefficient of inbreeding within the families to remain unchanged (FALCONER, 1989). In 2003, the same experiments were grown in the same environments. Each experiment was arranged as an incomplete block design with two replications in sets (HALLAUER and MIRANDA, 1988). A total of 80 entries from each population were evaluated in 4 sets. Single-row plots were 0.7 m wide by 4.5 m long, hand planted with 40 seeds (two seed per hill). At the five to seven leaf stages, plots were thinned to 20 plants plot<sup>-1</sup>. Plant density was 63,500 plants ha<sup>-1</sup>. The experiments were grown on a calcareous chernozem soil, and fertilizer application rates were identical for all environments (160 kg N, 80 kg P and 60 kg K ha<sup>-1</sup>).

Data were collected for: (1) Grain yield (mean of 20 hand harvested plants per plot). Plot values were converted to t ha<sup>-1</sup> and adjusted to 14% grain moisture; (2) Stay-green - 1 to 10 rating scale based on the estimated portion of green leaf area in the total plant area, where 1 represents a genotype with less than 10% of green plant tissue area and 10 one with 90%-100% (WALULU et al., 1994); (3) Anthesis-silking interval (ASI, in days) equaled the difference between mid pollination and mid silking; (4) Grain moisture (%) was measured with a moisture meter at harvest.

Analyses for all traits were done on the basis of plot mean data. The data for grain moisture were first transformed with the arcsin of the square root of data. All main effects and interactions in the analysis of variance were considered random. Components of variance ( $\sigma^2_{( )}$ ) and covariance ( $Cov_{( )}$ ) were estimated by using appropriate means squares (products) from analysis of variance and covariance, respectively (Hallauer and Miranda, 1988). Comparison of genetic ( $\sigma^2_g$ ) as well as phenotypic variances ( $\sigma^2_p$ ) between different trials was done with Hartley test (1955).

Heritability on a  $S_1$  progeny mean basis was calculated as the ratio of genetic to phenotypic variance  $h^2 = \frac{\sigma^2_g}{\sigma^2_p}$ . Coefficient of genetic and

phenotypic variation (CV) was obtained as follows  $CV_{g(p)} = \frac{\sqrt{\sigma^2_{g(p)}}}{X} \cdot 100$ .

Genetic correlations among traits within the populations were calculated from the

appropriate variance - covariance components (Falconer, 1989),  $r_{g_{xy}} = \frac{Cov_{g_{xy}}}{\sqrt{\sigma_{g_x}^2 \sigma_{g_y}^2}}$ .

## RESULTS

Analysis of variance (not shown) combined across four environments indicated strong environmental effect for all traits in both populations. Differences among families within sets were highly significant for all traits in both populations. The average stay green was similar in both populations while the mean values for grain yield were somewhat higher in NS12-SG ranging from 4.54 t/ha to 9.58t/ha.

Table 1.  $S_1$  estimates of means evaluated in four environments

Trait	Population	Mean $\pm$ SE	Range	
			min.	max.
Grain yield (t ha <sup>-1</sup> )	NS12-SG	6.91 $\pm$ 0.07	4.54	9.58
	NS14-SG	6.32 $\pm$ 0.06	4.49	8.70
SG (1-10)	NS12-SG	2.73 $\pm$ 0.07	1.00	5.12
	NS14-SG	2.59 $\pm$ 0.07	1.00	4.19
ASI (days)	NS12-SG	2.94 $\pm$ 0.05	1.13	5.75
	NS14-SG	2.21 $\pm$ 0.05	0.88	3.88
Grain moisture (%)	NS12-SG	24.98 $\pm$ 0.06	21.11	29.47
	NS14-SG	19.96 $\pm$ 0.06	16.41	23.18

Anthesis-silking interval was higher in the NS12-SG than in NS14-SG and ranged from 1 to almost 6 days. As these two populations differ in respect to maturity group, significantly higher grain moisture was determined in NS12-SG (Table 1). Genetic and phenotypic variances for all traits and in both populations were significant, but much higher in NS12-SG than in NS14-SG. Differences in genetic and phenotypic variances between the two populations were highly significant ( $P < 0.01$ ). Because the traits studied here were expressed in different units of measurement, comparisons of genetic variability were made with coefficient of genetic variation. Highest genetic variation was determined for ASI followed by stay green. The highest broad sense heritability was determined for grain moisture, the lowest for stay green in both populations (Table 2., 3).

Table 2.  $S_1$  family estimates of components of variance and heritability estimates for grain yield and grain moisture evaluated in four environments

Population	Grain yield		Grain moisture	
	NS12-SG	NS14-SG	NS12-SG	NS14-SG
$\sigma_g^2$	0.909	0.467	1.251	0.727
SE $\sigma_g^2$	0.176	0.096	0.227	0.144
CV <sub>g</sub> (%)	13.80	10.82	3.74	3.22
$\Delta \sigma_g^2$	**		**	
$\sigma_p^2$	1.094	0.593	1.417	0.892
SE $\sigma_p^2$	0.177	0.097	0.228	0.145
CV <sub>p</sub> (%)	15.13	12.18	3.98	3.57
$\Delta \sigma_p^2$	**		**	
$h^2$	0.831	0.788	0.882	0.815
SE <sub><math>h^2</math></sub>	0.161	0.161	0.161	0.161

$\Delta$  - Differences between genetic ( $\Delta \sigma_{g(p)}^2$ ) and phenotypic ( $\Delta \sigma_{g(p)}^2$ ) variances (P $\leq$ 0.01).

Table 3.  $S_1$  family estimates of components of variance and heritability estimates for stay green and anthesis-silking interval evaluated in four environments

Population	Stay green		ASI	
	NS12-SG	NS14-SG	NS12-SG	NS14-SG
$\sigma_g^2$	0.758	0.403	0.923	0.317
SE $\sigma_g^2$	0.157	0.096	0.167	0.068
CV <sub>g</sub> (%)	31.84	24.49	32.65	25.42
$\Delta \sigma_g^2$	**		**	
$\sigma_p^2$	0.970	0.587	1.042	0.422
SE $\sigma_p^2$	0.158	0.097	0.168	0.069
CV <sub>p</sub> (%)	36.02	29.58	34.69	29.33
$\Delta \sigma_p^2$	**		**	
$H^2$	0.781	0.685	0.886	0.751
SE <sub><math>h^2</math></sub>	0.161	0.163	0.160	0.162

$\Delta$  - Differences between genetic ( $\Delta \sigma_g^2$ ) and phenotypic ( $\Delta \sigma_p^2$ ) variances (P $\leq$ 0.01).

Genetic correlation between grain yield and stay green were low and insignificant. Similar interrelationship was found between grain yield and grain moisture in both population. Somewhat higher, negative correlations were obtained between grain yield and ASI. Stay green was positively correlated with ASI and grain moisture in both populations. Highest correlation among the examined traits were obtained between stay green and grain moisture (Table 4).

Table 4. Estimates of genetic correlations among traits in NS12-SG (above diagonal) and NS14-SG (below diagonal) evaluated at four environments

Trait	Grain yield	Stay green	ASI	Grain moisture
Grain yield		0.073	-0.354	-0.076
Stay green	-0.055		0.311*	0.699**
ASI	-0.262	0.171		0.621**
Grain moisture	-0.215	0.497**	-0.043	

\*, \*\* - Significant at the 0.05 and 0.01 level of probability.

## DISCUSSION

Measurement of the mean values and basic genetic parameters in this study was done on the population per se performance. The studied populations differed not only in their genetic background but also in the maturity group they belonged to. While NS12-SG is a mid-late population (FAO 600), NS14-SG is earlier (FAO 400). With the exception of stay green, higher mean values for all traits were determined in NS12-SG. Grain yield of this population was also higher, but not to the extent that could be expected on the basis of its vegetation group. This can be explained by severe drought in 2002 and 2003 coinciding with flowering of NS12-SG. Such conditions resulted in a short pollination period and slow silk growth. Although shorter growing season, NS14-SG had almost the same stay green and a shorter anthesis-silking interval than NS12-SG.

Significant genetic variability was determined in both populations indicating further selection for each trait individually would be effective. Genetic and phenotypic variances for grain yield were similar to the results of ALBRECHT and DUDLEY (1987) and VANČETOVIĆ (1994). However, estimates of genetic variability reported by ĐORĐEVIĆ (1994) and HUSIĆ et al. (1995) do not agree particularly well with our results. As expected, phenotypic variances were higher than corresponding genetic variances for all traits, in both populations. Literature data about basic genetic parameters for stay green are still limited, and discrepancy among studies may be due to the environments in which materials were evaluated and differences in the method of calculating of these parameters. The variance and coefficient of variation for stay green determined in this study were in accordance with our previous results (BEKAVAC, 1994). Differences in genetic and phenotypic variances between these two populations were significant for all traits.

Anthesis-silking interval, followed by stay green had the highest genetic variation, what was expected having in mind the nature of these two populations. The coefficient of genetic variation for grain yield was similar to the results of GOULAS and LONNQUIST (1977), RODRIGUEZ and HALLAUER (1991), HOLTHAUS and LAMKEY (1995a,b), but for grain moisture it was lower than those in the studies of GOULAS and LONNQUIST (1977) and HOLTHAUS and LAMKEY (1995a, b).

Estimation of variances in this study was done on the  $S_1$  family basis, so relatively high heritability estimates were expected for all traits. Heritability estimates for grain yield agree with the results of GOULAS and LONNQUIST (1976), COORS (1988), GROMBACHER et al. (1989), ĐORĐEVIĆ and IVANOVIĆ, (1996), HOLTHAUS and LAMKEY (1995a,b). Somewhat lower heritability estimates were reported by GETSCHMAN and HALLAUER (1991), SMITH et al. (1982), RODRIGUEZ and HALLAUER (1991). Heritability estimates for stay green and anthesis-silking interval agrees with results of our previous studies (BEKAVAC, 1994).

Genetic correlations between grain yield and grain moisture were low and insignificant indicating breeding for grain yield per se to be feasible with no risk of changes in maturity. This agrees with the results of HOLTHAUS and LAMKEY (1995a) and ĐORĐEVIĆ and IVANOVIĆ (1996). Although strong relationship between grain yield and stay green were discovered by FREDERICK et al. (1989), FISHER et al., (1989), and OSAKI (1995), genetic correlations between these two traits in our study were weak and insignificant in both populations. Negative, highly significant correlations between grain yield and stay green were reported by RUSSELL (1985). Several other studies showed strong, positive correlations between the same traits (TOLLENAAR and DAYNARD, 1978; WILLMAN et al., 1987), or quite opposite (ranging from  $r_p = 0.18$  to  $r_p = -0.37^{**}$ ), indicating the dependence of these correlations on the type of studied material, experimental design and calculating method (WALTERS, 1991).

WILLMAN et al. (1987) emphasized that correlations between grain yield and stay green are defines by genetic constitution of the examined material and the length of its vegetation. One is clear, the contrary results obtained in different studies pointed out the complexity of interrelationships between these two traits. Due to competitive relationships for photosynthates between the ear and the vegetative parts of the plant, simultaneous improvement of both traits in a recurrent selection program could be demanding. As expected, the anthesis-silking interval showed a negative effect on grain yield. Similar interrelationships observed by FISHER et al. (1989) and GUEY and WASSOM (1992) proved the importance of close synchronization for pollination and silking. A positive correlation observed between stay green and grain moisture indicated that breeding for stay green can also bring changes in maturity. Such a response would be undesirable in most of applied programs because the main goal is to develop superior hybrids within each maturity group (ETA-NDU and OPENSHAW, 1992).

The observed mean values, genetic variability and heritability estimates confirmed these two populations are interesting sources for breeding. The lack of association indicated that selection for morphological traits alone will not improve grain yield, so the most efficient increase would be achieved by direct selection on grain yield per se. Anyhow, the correlations obtained in this study showed complex interrelationships between traits and the necessity for its paralel improvement. Such a strategy should be applied to avoid an undesirable correlation response throughout the cycles of selection. Finally, this agrees with a general finding among breeders that the single trait model may not be as efficient as multiple trait selection. Results for individual  $S_1$  families (data not shown) indicated possibility to find individual plants with high stay green and short ASI, and also above average grain yield and acceptable low grain moisture. Unfortunately, the frequency of occurrence is rather low, but still enough for breeder usage. Some kind of selection index could probably be the most practical approach for paralel improvement of several traits in a recurrent selection program.

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**GENETIČKA ANALIZA SVOJSTAVA TOLERANTNOSTI PREMA SUŠI  
U SINTETIČKIM POPULACIJAMA KUKURUZA**

Goran BEKAVAC, Božana PURAR i Đorđe JOCKOVIĆ

Institut za ratarstvo i povrtarstvo, Novi Sad, Srbija

**I z v o d**

Oplemenjivači kukuruza smatraju tolerantnost prema suši jednim od najznačajnijih kriterijuma u komercijalnim oplemenivačkim programima. Čini se da su dva svojstva, zakašnjenje u svilanju i stay green tesno povezani sa tolerantnošću prema suši. Cilj ovog rada bio je da se odrede srednje vrednosti, varijabilnost, heritabilnost i genetičke korelacije za nekoliko svojstava u dve sintetičke populacije kukuruza. Vrednosti  $S_1$  potomstava ocenjivane su u nepotpunom blok dizajnu na četiri lokaliteta. Utvrđena je zadovoljavajuća varijabilnost svih svojstava u obe populacije, a najveća za zakašnjenje u svilanju. Visoko signifikantne korelacije između svojstava tolerantnosti prema suši i sadržaja vlage u zrnu mogu biti uzrok nepoželjnih korelativnih odgovora kroz cikluse selekcije.

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