

**INBRED LINES OF DIFFERENT CYCLES OF SELECTION AS DONORS
OF FAVOURABLE ALLELES FOR THE IMPROVEMENT OF F₁ MAIZE
HYBRIDS**

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Eight BSSS and BSCB₁ inbred lines of different cycles of selection were studied with the aim to evaluate which inbreds had the highest relative values of favourable alleles for the improvement of the grain yield trait in an elite single cross maize hybrid. Based on estimated parameters μG , UBND, PTC and NI it was determined that the inbreds B73 (C₅) and B84

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(C₇), originating from the synthetic population BSSS had highest number of favourable alleles for the improvement of the grain yield. Both these inbreds belong to the later cycles of recurrent selections and proved to be better donors of favourable alleles than inbreds belonging to the earlier cycles of selection. The rank correlations of used parameters were positive and highly significant, while the highest values of correlations for yield were determined between μG and NI, that is PTC and NI. The highest grain yield was recorded in the hybrid ZPL2 x B73, which also had the highest value of heterosis (174.9%) in the trial for estimation of loci relative values.

Key words: donor of favourable alleles, heterosis, inbred line, maize, rank correlation

INTRODUCTION

Maize hybrids have a reduced period of the utilisation in the contemporary agricultural production. Therefore, they have to be replaced by new hybrids that will exceed the existing ones in their performances. Ultimately, one of the objectives in maize breeding is to improve different traits in an elite hybrid as well as to improve agronomic traits of parental component without negative effects on grain yield of elite single cross. Classical methods, such as general combining ability (GCA) (SPRAGUE and TATUM, 1942) and predicted three way cross (PTC) (SPRAGUE and EBERHART, 1977), are known to be effective, regardless of the superior or inferior performance of the potential donors and recipients. Numerous statistical methods have been developed for identifying donors to improve elite hybrids, DUDLEY (1984, 1987a, b) developed a statistical procedure for estimation of relative number of loci (μG) for which a donor line is different from each parent of the single cross to be improved. The model starts from the presumption that there is a complete domination $a = 1$ and $z = -\mu$, wherefore the genotypic value $++$, $+ -$ and $--$ of genotypes is $z + 2\mu$; $z + \mu + a\mu$ and z , where z is a value of the least favourable genotype $--$, μ is one half of the difference in genotypic value between $++$ and $--$ genotypes, while a is a degree of domination. Moreover, this model implies that μ is constant for all loci and that there is no epistasis. Dominant alleles (positive value of μG) are favourable for the maize grain yield, and inbreds with the highest value of μG can be considered as a potentially good source of favourable alleles. Positive and high values of μG for donor inbred lines confirm the existence of new favourable alleles in these inbreds that parents of an elite hybrid do not include. The negative values of the relation $\mu G - \mu D$ or $\mu G - \mu F$ point to a number of loci for which inbred lines I_1 and I_2 carry favourable alleles, and I_w carries unfavourable alleles. If this number is higher than the number of loci for which inbred lines I_1 and I_2 carry unfavourable alleles, and I_w carries favourable alleles, it is necessary to perform a backcross of the F_1 generation (parent inbred x donor inbred) to parent inbred I_1 or I_2 . If, on the other hand, the difference $\mu G - \mu D$ or $\mu G - \mu F$ is not significantly different from 0, the direct self-pollination of F_2 generation is recommended in the process of selection. Positive values of the difference $\mu G - \mu D$ or $\mu G - \mu F$ lead to a

conclusion that if the number of loci for which inbred lines I_1 and I_2 carry unfavourable alleles and I_w carries favourable is higher than the number of loci for which inbreds I_1 and I_2 carry favourable alleles and the inbred I_w carries unfavourable alleles, the backcross of the F_1 generation to the donor inbred (I_w) is recommended.

GERLOFF and SMITH (1988a,b) proposed an estimate of a minimum upper bound on μG (UBND). BERNARDO (1990) presented an estimate of the relative number of favourable alleles that can be gained from the inbred minus the relative number of favourable alleles that can be lost from the parents of the hybrid during selection (NI), while METZ (1994) published two estimates of the relative number of loci where favourable alleles can be either gained or lost.

The improvement of existing hybrids, i.e. the improvement of one or both parent inbred lines of an elite hybrid, is one of methods of developing new improved maize hybrids. The procedure implies the introduction of favourable alleles into the existing inbreds, which will result in better agronomic traits and improved yield potential of the new hybrids. Most frequently, inbred lines have been used as donors of favourable alleles for the improvement of qualitative and quantitative traits of single cross hybrids.

The objective of the present study was to estimate which of observed BSSS and BSCB₁ inbred lines of different cycles of selection have the highest relative values as donors of favourable alleles for the improvement of grain yield of an elite maize hybrid. Estimation of number of favourable alleles in inbred donor lines (I_w) that are not present in elite single cross hybrid ($I_1 \times I_2$) was done based on four parameters: μG , UBND (upper bound estimates), PTC (predicted three way cross) and NI (net improvement statistics). For the improvement of grain yield of elite single cross hybrid ZP 580, efficiency of each used parameter was estimated separately. Comparison between used parameters was done using Spearman's rank correlation coefficient. Obtained results can be of importance for the further work on maize breeding, as it is, based on them, possible to select donor inbreds of favourable alleles for the grain yield, which consequently would lead to increased efficiency of breeding.

MATERIALS AND METHODS

Selected maize inbred lines of different cycles of recurrent selection belong to the following two synthetic populations: BSSS and BSCB₁. Inbreds B14(C₀), B37(C₀), B73(C₅) and B84(C₇) were derived from the Iowa Stiff Stalk Synthetic (BSSS), while inbreds B90(C₇), B91(C₈), B97(C₉) and B99(C₁₀) were developed from the Corn Borer Synthetic No.1 (BSCB₁). Inbred lines derived from both synthetics were crossed to parental inbred lines of the hybrid ZP 580 (ZPL1 and ZPL2). During two years, the following two trials in two locations (Zemun Polje and Kraljevci) were set up to estimate the relative value of loci: a trial with hybrids and a trial with donor inbred lines and parental inbred lines of the hybrid ZP 580 which was in the process of improvement. The trials were set up according to the complete

randomised block design with four replications. The elementary plot size was 3.36 m², while crop density was 59,500 plants ha⁻¹.

The estimation of a relative number of favourable alleles of observed inbreds in relation to an elite single cross hybrid (hybrid selected to be improved) for the observed traits was done according to the model developed by DUDLEY (1987a, b).

Besides the parameter μG , the following parameters for inbred lines were used in the study: UBND (GERLOF and SMITH, 1988), PTC (HALLAUER and MIRANDA, 1988) and NI (BERNARDO, 1990 a, b).

UBND estimator is defined as a minimum of the two equations $(I_1 \times I_w) - I_1$ and $(I_2 \times I_w) - I_2$, which have a prediction of $2\mu E + 2\mu G$ and $2\mu C + 2\mu G$, respectively.

PTC is a predicted three way crosses performance that is estimated as $[(I_1 \times I_w) + (I_2 \times I_w)] / 2$ and has a prediction of $N(z + \mu) + \mu(A + B + C + E + G - H)$ where N is a total number of loci that affect observed trait.

Net improvement (NI) estimates the number of loci where favourable alleles can be added (minus the number of loci where they can be lost) in an elite hybrid. This estimator is calculated as a maximum value of the formula $[(I_1 \times I_w) - (I_1 \times I_2)] / 2$ or $[(I_2 \times I_w) - (I_1 \times I_2)] / 2$. The used estimators were compared among themselves by Spearman's rank correlation coefficient (HADŽIVUKOVIĆ, 1991).

Heterosis (H) for grain yield was calculated in relation to a superior parent.

RESULTS

The highest, i.e. lowest grain yield was recorded in the hybrids ZPL2 x B73 (10.908 t ha⁻¹), i.e. the hybrid ZPL2 x B91 (8.730 t ha⁻¹), respectively. The mean values of inbred line yields ranged from 4.932 t ha⁻¹ in the inbred B84(C₇) to 1.783 t ha⁻¹ in the inbred B99(C₁₀) (Table 1.). The inbred line ZPL1 had higher average grain yield (4.394 t ha⁻¹) than the second parent of the elite single cross hybrid, inbred line ZPL2 (3.967 t ha⁻¹, Table 1).

All observed inbred lines have positive and significant values of the parameter μG for grain yield, meaning that they can be donors of new favourable alleles which are not contained by the parents of the elite single cross hybrid ZPL1 x ZPL2. The highest values of this parameter were recorded in the inbreds B73 (C₅), B84 (C₇) and B97 (C₉) of later cycles of selection, while the lowest value of the parameter was detected in the inbred B14 (C₀) that belongs to the initial cycle of selection (Table 2). The significant values of the parameter μG and importance of donors for breeding programmes were presented in studies carried out by DUDLEY (1984 a), MIŠEVIĆ (1989 a, b), ZANONI and DUDLEY (1989 a), METZ (1994), BABIĆ *et al.* (1996), VRAČAREVIĆ (2000), TRIFUNOVIĆ *et al.* (2001), ROSA *et al.* (2001), MALVAR *et al.* (2004), AVILA *et al.* (2005), ŽIVANOVIĆ *et al.* (2006) and SEČANSKI *et al.* (2009).

AVILA *et al.* (2005) reported possibility of improvement of grain yield in three single cross hybrids with use of tropical inbred lines as donors of favourable

alleles. In their research, progenitors of three single cross hybrids were crossed with 23 inbred lines with the purpose of identifying best donor lines for improving grain yield of tropical single cross hybrids. They identified three tropical (CML258, CML264, CML273) and three subtropical inbred lines (CML311, CML312, CML319) as the donors with highest frequencies of favourable alleles.

Table 1. Grain yield ($t\ ha^{-1}$) of 10 inbred lines and 17 maize hybrids and heterosis

Inbred lines and their hybrids (F_1)	Grain yield ($t\ ha^{-1}$)	Heterosis %
ZPL1	4.394	
ZPL2	3.967	
B14(C_0)	2.899	
B37(C_0)	2.256	
B73(C_5)	3.801	
B84(C_7)	4.932	
B90(C_7)	2.078	
B91(C_8)	2.193	
B97(C_9)	4.298	
B99(C_{10})	1.783	
ZPL1 x ZPL2	10.741	144.4**
ZPL1 x B14(C_0)	9.012	105.1**
ZPL1 x B37(C_0)	8.896	102.5**
ZPL1 x B73(C_5)	10.236	132.9**
ZPL1 x B84(C_7)	9.938	101.5**
ZPL1 x B90(C_7)	8.811	100.5**
ZPL1 x B91(C_8)	9.117	107.5**
ZPL1 x B97(C_9)	9.945	126.3**
ZPL1 x B99(C_{10})	9.889	125.1**
ZPL2 x B14(C_0)	8.956	125.8**
ZPL2 x B37(C_0)	9.546	140.6**
ZPL2 x B73(C_5)	10.908	174.9**
ZPL2 x B84(C_7)	10.765	118.3**
ZPL2 x B90(C_7)	9.340	135.4**
ZPL2 x B91(C_8)	8.730	120.1**
ZPL2 x B97(C_9)	9.695	125.6**
ZPL2 x B99(C_{10})	9.670	143.8**

$t_{0.05}=2.042$ $t_{0.01}=2.750$

Genetic relatedness of donor inbreds to parent inbreds was evaluated over the expression $(\mu C + \mu F) - (\mu D + \mu E)$, DUDLEY (1984 a), whereby positive, i.e.

negative, values suggest a greater relatedness to the inbred ZPL1, i.e. the inbred ZPL2, respectively.

The inbred lines B37 (C₀), B73 (C₀), B84 (C₇) and B90 (C₇) had significant and positive values of the expression $(\mu C + \mu F) - (\mu D + \mu E)$ and showed greater relatedness to the inbred line ZPL1. A positive, but not significant value was expressed by the inbred B14 (C₀). The inbreds B91 (C₈), B97 (C₉) and B99 (C₁₀), belonging to the higher cycles of selection of BSCB1, had negative values and expressed greater relatedness to the inbred ZPL2 (Table 2).

Table 2. The estimation of a relative number of favourable alleles for grain yield

Donors (Iw)	μG	Relatedness		Cross method
		$(\mu C + \mu F) - (\mu D + \mu E)$	$\mu G - (\mu D \text{ or } \mu F)$	
B14(C ₀)	0,722*	0,157	-0,892*	(I ₁ x Iw) x I ₁
B37(C ₀)	0,827*	0,863*	-0,597*	(I ₁ x Iw) x I ₁
B73(C ₅)	1,502*	0,885*	0,083	Self
B84(C ₇)	1,392*	1,040*	0,012	Self
B90(C ₇)	0,754*	0,742*	-0,700*	(I ₁ x Iw) x I ₁
B91(C ₈)	0,775*	-0,173	-0,812*	(I ₂ x Iw) x I ₂
B97(C ₉)	1,189*	-0,037	-0,398*	(I ₂ x Iw) x I ₂
B99(C ₁₀)	1,161*	-0,009	-0,426*	(I ₂ x Iw) x I ₂

* > 2SE

Inbred lines B73(C₅) and B84(C₇) expressed high values of the parameter μG but their differences $\mu G - (\mu D \text{ or } \mu F)$ were no significantly higher than 0 (Table 2). This suggests that direct self-pollination and selection of inbred lines from crosses (ZPL1 x B73) and (ZPL1 x B84) can be done, as both donor inbreds showed relatedness to the inbred ZPL1. Other two inbreds, B97 (C₉) and B99 (C₁₀), had positive and significant values of favourable alleles for the grain yield that were not present in the elite hybrid ZPL1 x ZPL2. The number of recessive unfavourable alleles was significantly higher in both inbreds, hence the F₁ generation should, in the process of selection for this trait, be backcrossed to the parent inbred ZPL2, as they showed relatedness to this inbred line (Table 2).

The value of μD was significantly higher than the value of μG for the inbred B14 (C₀), while the value of μF was significantly higher than the value of μG for the inbred B91 (C₈). It means that the number of unfavourable, recessive alleles for grain yield in observed donor inbred lines were significantly higher than the number of favourable, dominant alleles. In order to avoid the introduction of unfavourable alleles, the backcross of F₁ generation ZPL1 x B14 to the inbred ZPL1 that is ZPL2 x B91 to the inbred ZPL2 is recommended. Donor inbred lines B37(C₀)

and B90(C₇) had a significantly higher frequency of unfavourable recessive alleles than a frequency of favourable dominant alleles, hence in this case backcross of F₁ generation should be done to the parent ZPL1 (Table 2).

Ranking of the donor inbred lines on the basis of their values estimated over four used parameters shows a good agreement among parameters μG , UBND, PTC and NI. All four parameters identically ranked the first four best ranked inbred lines (Table 3), even KUMAR *et al.* (2003), reported μG and UBND as the best estimates in ranking donor inbred lines. The stated results are confirmed by high and significant values of the rank correlation (Table 4).

Table 3. The estimation and rank of μG^* , UBND, PTC and NI for grain yield

Donor line	μG	UBND	PTC	NI
B14(C ₀)	0.722 (8)	4.618 (6)	8.984 (7)	-0.864 (8)
B37(C ₀)	0.827 (5)	4.502 (7)	9.221 (5)	-0.597 (5)
B73(C ₅)	1.502 (1)	5.842 (1)	10.572 (1)	0.083 (1)
B84(C ₇)	1.392 (2)	5.544 (3)	10.351 (2)	0.012 (2)
B90(C ₇)	0.754 (7)	4.417 (8)	9.075 (6)	-0.700 (6)
B91(C ₈)	0.775 (6)	4.723 (5)	8.923 (8)	-0.812 (7)
B97(C ₉)	1.189 (3)	5.551 (2)	9.820 (3)	-0.398 (3)
B99(C ₁₀)	1.161 (4)	5.495 (4)	9.778 (4)	-0.426 (4)

Values of the rank are given within the brackets

Table 4. Rank correlation for grain yield

	μG	UBND	PTC	NI
μG^*	*	0.857*	0.928**	0.976**
UBND		*	0.762*	0.786*
PTC			*	0.976**
NI				*

* $p < 0.05$, ** $p < 0.01$

Such results on concordance among parameters μG , UBND, PTC and NI are in accordance with results gained by BERNARDO (1990), and ASORO *et al.* (2007). High correlations among μG , PTC and UBND are presented in the study done by MIŠEVIĆ (1989), while a highly significant rank correlation for grain yield between UBND and PTC are determined by FABROUOIS and OPENSHOW (1994) and REDDY *et al.* (2005).

Possibility of improving agronomic traits of sweet corn hybrids by use field corn inbred lines was reported by MALVAR *et al.* (2004). Objective of their

study was to compare realised results and predictions of methods to identify potential donors for improving agronomic performance of sweet corn hybrids. Yield and three agronomic traits were recorded. Inbred lines A632 and EP42 were identified as the best potential donors for improving yield and several yield components of sweet corn hybrids in their study. The use of EP42 would reduce row number, while the use of W64A would reduce yield and ear length. The estimator μG correctly predicted the best donor of favourable alleles for improving yield and agronomic performance of sweet corn hybrids. Realised response, however, did not coincide with predictions, particularly with ranking of donors, while predictions of best recipient fitted the realised results.

CONCLUSION

The highest grain yield (10.908 t ha^{-1}) was recorded in the hybrid ZPL2 x B73. At the same time, this hybrid, in the trial for the evaluation of relative values of loci, showed the highest heterosis (174.9%).

Based on estimated parameters: μG , UBND, PTC and NI it was possible to evaluate studied inbred lines as donors of favourable alleles for the improvement of the observed hybrid. The donor inbred lines for the improvement of the grain yield in the hybrid ZPL1 x ZPL2 showed greater genetic relatedness to the female parent, inbred line ZPL1. Inbred lines belonging to the higher cycles of recurrent selection of studied synthetics were better donors of favourable alleles than inbred lines belonging to the initial cycles, indicating that the relative number of favourable alleles increased during the selection in both populations (BSSS and BSCB1).

The inbred line B73 (C_5) had the greatest number of favourable dominant alleles for the improvement of the grain yield of the hybrid ZPL1 x ZPL2. Furthermore, the inbred B84 (C_7) was a good donor of favourable alleles for grain yield. As both inbreds showed relatedness to the inbred ZPL1, direct self-pollination and selection of inbreds derived from crosses ZPL1 x B73 and ZPL1 x B84 can be recommended for the process of selection. The inbreds B97 (C_9) and B99 (C_{10}) were closer to the inbred ZPL2 and had positive and significant values of favourable alleles for the grain yield that were not present in the elite hybrid ZPL1 x ZPL2. The number of recessive unfavourable alleles was greater in these inbreds than in the inbreds B73 (C_5) and B84 (C_7), hence the backcross of the F_1 generation (ZPL2 x B97; ZPL2 x B99) should be done to the male parent of the elite hybrid (ZPL2) in the process of selection for grain yield.

The rank correlations among parameters μG , PTC and NI were positive and highly significant, while the rank correlations between UPBND and remaining observed parameters (μG , PTC and NI) were positive and significant.

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INBRED LINIJE IZ RAZLIČITIH CIKLUSA SELEKCIJE DONORI POŽELJNIH ALELA ZA POPRAVKU F₁ HIBRIDA KUKURUZA

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I z v o d

Ispitivano je osam inbred linija različitih ciklusa selekcije poreklom iz BSSS i BSCB₁ izvora sa ciljem da se oceni koja ima najveće relativne vrednosti poželjnih alela za popravku osobine prinos zrna kod elitnog dvolinijskog hibrida kukuruza. Na osnovu izračunatih parametara μG^* , UBND, PTC i NI utvrđeno je da najveći broj poželjnih dominantnih alela za popravku prinosa zrna pokazale su inbred linije B73(C₅) i B84(C₇) iz sintetičke populacije BSSS. Obe ove linije su iz kasnijih ciklusa rekurentne selekcije i pokazale su se kao bolji donori poželjnih alela u odnosu na linije iz ranijih ciklusa. Korelacije ranga između korišćenih parametara bile su pozitivne i visoko značajne, dok su najveće vrednosti korelacije za prinos utvrđene između μG^* i NI, odnosno PTC i NI. Najveći prinos zrna je imao hibrid ZPL2 x B73 koji je u ogledu za procenu relativne vrednosti lokusa pokazao i najveću vrednost heterozisa (174,9%).

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