Turkish Journal of Field Crops, 2012, 17(2):198-202

INBRED LINES OF DIFFERENT CYCLES OF SELECTION - DONORS OF FAVOURABLE ALLELES FOR THE IMPROVEMENT OF THE KERNEL ROW NUMBER OF F_1 MAIZE HYBRIDS

Goran TODOROVIĆ[1], Mile SEČANSKI[1], Tomislav ŽIVANOVIĆ[2], Rade PROTIĆ[3], Miroslav KOSTIĆ[4], Snežana JOVANOVIĆ[1] and Dragan BOŽOVIĆ[5]*

[1]Maize Research Institute, Zemun Polje, Belgrade-Zemun, REPUBLIC SERBIA.
[2]Faculty of Agriculture,University Belgrade, REPUBLIC SERBIA.
[3]Institute for Science Aplication in Agriculture, Belgrade , REPUBLIC SERBIA.
[4]Institute for Medicinal Plant Research "Dr Josif Pančić", Belgrade.
[5]"Agros", Pančevo, REPUBLIC SERBIA.
[*]Corresponding author: gtodorovic@mrizp.rs

Received: 09.07.2012

ABSTRACT

Eight maize inbred lines of different cycles of selection, originating from synthetic populations BSSS and $BSCB_1$, were observed in the present study. The aim of the study was to evaluate inbreds and to determine which ones have the greatest relative values of favourable alleles for the improvement of the kernel row number in the elite single cross maize hybrid. Based on the estimated estimators: μG, UBND, PTC and NI, it was determined that the greatest number of favourable dominant alleles for the improvement of the kernel row number was detected in the inbred lines B73(C_5) and B84(C_7) originating from the synthetic population BSSS and in the inbreds B91(C_8) and B90(C_7) originating from the synthetic population $BSCB_1$. These inbreds are of the later cycles of recurrent selection and have proven to be better donors of favourable alleles than inbreds of earlier cycles of selection. The rank correlations among used estimators were positive and highly significant, while the highest values of correlations for the kernel row number were determined between μG and PTC, μG and UBND and PTC and NI. The greatest kernel row number was determined in the hybrid B73(C_5) x B84(C_7).

Key words: maize, inbred lines, donors, kernel row number, rank correlation

INTRODUCTION

The period of maize hybrids usage in the contemporary agricultural production is limited, meaning they have to be replaced with new hybrids having more favourable traits than the existing hybrids. One of the methods of the development of new hybrids is the improvement of existing hybrids, i.e. the improvement of one or both parental inbreds of the elite hybrid. The procedure involves the introduction of favourable alleles into the existing inbreds, which would be manifested through better agronomic properties of future hybrids.

The presentation and the development of the method for the identification of inbred lines that encompassing the favourable alleles that affected the expression of quantitative traits. These alleles were not present in the elite hybrid were given by Dudley (1984a). The selection of the inbred donors of favourable alleles is provided by the evaluation of the progenies, developed by crossing of each inbred, a potential donor with both parental components of the hybrid under the improvement (P_1 x D and P_2 x D, whereby P_1 and P_2 are parents of the single cross hybrid, while the D inbred is a donor of favourable alleles).

In many commercial programmes new inbred lines are developed from synthetic populations that were derived by crossing of parental inbreds of the existing elite hybrid (I_1 x I_2) to another inbred line, a donor, (Iw). By self-pollination of newly developed F_1 (I_1 x Iw) or after backcrossing, the process of the development of new inbreds begins. These inbreds will be tested with other parent of the elite hybrid (I_2), to isolate new inbreds that will, with an already mentioned inbred line, tester (I_2), result in a new hybrid that is more superior than the existing elite hybrid (I_1 x I_2), Bernardo (1990a). Mišević (1989b) studied 15 inbred lines as donors of favourable alleles for the improvement of seven elite hybrids by three estimators μG, UBND and PTC. Significant differences among inbred donors occurred when all three estimators were used. The greatest values of new favourable alleles were found in inbred lines belonging to heterotic groups different from parents of hybrids under improvement. The correlation among estimators were high, positive and significant, and the highest one exceeded 0.95 (between μG* and PTC).

Bernardo (1990a) estimated that selected Iw inbreds could be crossed to I_1 or I_2 in order to transfer new favourable alleles to a single cross hybrid. However, the favourable alleles already present in the single cross hybrid can be lost in the process of selection. It is important to consider the potential benefit of favourable alleles of Iw, as well as, the loss of favourable alleles already present in I_1 and I_2. The net improvement, i.e. NI statistics estimates the number of loci in which favourable alleles can be obtained minus the number of loci in which favourable alleles can be lost in the single cross hybrid. This estimator was compared with estimators μG, UBND and PTC. Results show a high correlation among all four estimators, whereby ranking of three inbred donors with the most common yield of the F_2 test crossing above the target hybrid was identical with ranking of NI estimator. Trifunović et al. (1999) also determined high rank correlations among four estimators, whereby they emphasised the advantage of the NI statistics within short-term programmes of selection, while the estimator Lplμ* was more advantageous within long-term programmes for the identification of sources of donors of favourable alleles for the improvement of the elite single cross hybrid.

Delić et al. (1996) has studied eight US SC hybrids as donors of favourable alleles for the improvement of grain yield of the elite hybrid Mo17 x L62 by the application of the following three methods: (1) method after Dudley (1987a), by which the value of the estimator Lplμ has been estimated, (2) XTC or the method of the average value of crossing of a donor to both parents of the elite hybrid (Sprague and Eberhart 1997), (3) UBND minimum method (Zanoni and Dudley 1989, Gerloff 1985). The calculated estimators of all three applied methods for the estimation of favourable alleles were compared on the basis of the Spearman's rank correlation coefficient.

According to Malvar et al. (1997), the estimation of favourable dominant alleles present in the donor but absent in the hybrid (μG), predicted three-way cross hybrid (PTC), minimum upper bound estimates (UBND), net improvement (NI) and general combining ability (GCA) are methods for the determination of maize inbred lines with favourable alleles. The correlations amont μG, UBND, PTC, NI and GCA were very high in all traits. Carena (2005) has estimated that improved maize populations and population hybrids could be profitable alternatives to commercial single cross hybrids, as well as, good elite sources of different inbred lines. The improved maize populations and population hybrids were estimated in experiments carried out in 29 environments. Data obtained under different environmental conditions show that at least 20% of estimated population hybrids did not differ from commercial single cross hybrids in relation to grain yield and the percentage of lodged plants. Attempts of selection aimed at elite populations and population hybrids led to the significant improvement of germplasm. These attempts should be supported in order to provide the development of elite sources of different inbred lines and the development of improved population hybrids for various markets.

The objective of the present study was to estimate which of observed inbred lines of different cycles of selections originating from synthetic populations BSSS and $BSCB_1$ had the highest relative values as donors of favourable alleles for the improvement of the commercial maize hybrid. The obtained results will be important in maize breeding programmes in selection inbred donors of favourable alleles for the kernel row number and improving parental components of the commercial single-cross hybrid.

MATERIALS AND METHODS

Maize inbred lines, obtained from different cycles of recurrent selection of two synthetic US populations (BSSS and $BSCB_1$) were selected. The inbred lines B14(C_0), B37(C_0), B73(C_5) and B84(C_7) were derived from the synthetic population Iowa Stiff Stalk Synthetic (BSSS), while the inbred lines B90(C_7), B91(C_8), B97(C_9) and B99(C_{10}) were developed from the synthetic population Corn Borer Synthetic No.1 ($BSCB_1$). Inbred lines derived from both synthetics were crossed to parental inbred lines of the hybrid ZP580 (ZPL1 and ZPL2). Two trials at two locations (Zemun Polje and Kraljevci) carried out during 2007 and 2008 were set up to estimate the relative values of loci. The first trial included the elite hybrid ZP 580 and hybrids developed by crossing parental inbreds of the hybrid ZP 580 to inbred donors from both synthetic populations. The second trial included inbred donors and parents of the hybrid ZP 580 that had been improved. The trial in four replications were set up according to the Randomised Complete-Block Design. The elementary plot size amounted to 3.36 m^2, while the sowing density was 59,500 plants ha^{-1}.

The estimation of a relative number of favourable alleles of studied inbreds in relation to the elite single cross hybrid (the hybrid selected to be improved) for observed traits was done according to the model coined by Dudley (1987 a.b). The model assumes that there is complete dominance $a = 1$ and $z = -\mu$, hence the genotypic value $++$, $+-$ and $--$ of genotypes is $z + 2\mu$; $z + \mu + a\mu$ and z, where z is the value of the least favourable genotype $--$; μ is one half the difference in the genotypic value between $++$ and $--$ genotypes, while a is a degree of dominance. This model implies that μ is constant for all loci and that there is no epistasis.

Dominant alleles are favourable for the kernel row number (μ value is positive). Inbreds with higher value of μG can be considered a good source of favourable alleles. Positive and high values of μG for inbred donors mean the presence of new favourable alleles in inbreds, which are absent in inbred parents of the elite hybrid. Negative values of the relation μG - μD or μG - μF indicate that the number of loci for which inbred lines I_1 and I_2 carry favourable alleles, and Iw carries unfavourable alleles, is higher than the number of loci for which inbred lines I_1 and I_2 carry unfavourable alleles, and Iw carries favourable alleles, hence it is necessary to perform 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 μG - μD or μG - μF is not significantly different from 0, the direct self-pollination of the F_2 generation is recommended in the process of selection. Positive values of the difference μG - μD or μG - μF lead to a conclusion that if the number of loci for which inbred lines I_1 and I_2 carry unfavourable alleles and Iw carries favourable alleles is higher than the number of loci for which inbreds I_1 and I_2 carry favourable alleles and the inbred Iw carries unfavourable alleles, backcross of the F_1 generation to the donor inbred (Iw) is recommended.

UBND (minimum upper bound estimates, Gerlof and Smith, 1988) is defined as a minimum of two expressions: (I_1 x Iw) - I_1 and (I_2 x Iw) - I_2, which have a prediction of $2\mu E + 2\mu G$ and $2\mu C + 2\mu G$, respectively.

PTC (predicted three way cross, Hallauer and Miranda, 1988) is a predicted value of the three-way cross hybrid that is calculated as follows: [(I_1 x Iw) + (I_2 x Iw)] / 2 and have a prediction of $N(z + \mu) + \mu(A + B + C + E + G - H)$, where N is a total number of loci that affect the observed trait.

NI (net improvement statistics, Bernardo, 1990 a, b) estimates the number of loci where favourable alleles can be added (minus the number of loci where they can be lost) in the elite hybrid. This estimator is calculated as a maximum value of the expression [(I_1 x Iw) - (I_1 x I_2)] / 2 or [(I_2 x Iw) - (I_1 x I_2)] / 2.

Heterosis (H) for kernel row number was calculated in relation to a superior parent.

RESULTS AND DISCUSSION

The highest (16.94), i.e. lowest (11.16) means for kernel row number was recorded in the inbred B73 (C_5), i.e. B14(C_0), respectively. The mean values of the kernel row number ranged from 13.53 in the hybrid ZPL2 x B99 to 15.57 in the hybrid ZPL2 x B73. The elite hybrid ZPL1 x ZPL2 had on average 14.04 kernel rows (Table 1).

Table 1. Mean values of the kernel row number of 10 maize inbred lines

Inbred lines	**Kernel row number**
ZPL1	13.19
ZPL2	12.67
B14(C_0)	11.16
B37(C_0)	13.03
B73(C_5)	16.94
B84(C_7)	15.83
B90(C_7)	13.34
B91(C_8)	12.54
B97(C_9)	13.30
B99(C_{10})	11.45

All observed inbred lines, except the inbred B99(C_{10}) of the synthetic population $BSCB_1$ had a significant effect (>2SE) of the estimator μG. The highest values of this estimator were recorded in the inbreds B73(C_5) and B84(C_7) of the synthetic population BSSS and B91(C_8) and B90(C_7) of the synthetic population $BSCB_1$ (Table 2).

The genetic descent of the donor inbreds to one of parents of the elite hybrid was evaluated according to the difference between estimators $(\mu C+\mu F)-(\mu D-\mu E)$, DUDLEY (1984 a). Inbred lines B14(C_0) and B73(C_5) of the synthetic population BSSS had significant (>2SE) positive values, while the inbreds B37(C_0) and B14(C_0) had positive values, which point to their genetic descent to the inbred ZPL1 (Table 2 and Figure 3). The inbred lines B91(C_8), B97(C_9) and B99(C_{10}) of the synthetic population $BSCB_1$ had negative values of the difference between estimators $(\mu C+\mu F)-(\mu D-\mu E)$ and were more related to the inbred line ZPL2, while the inbred line B90(C_7) was more related to the inbred line ZPL1 (Table 2 and Figure 3).

Table 1. Mean values of the kernel row number of 17 maize hybrids and heterosis (%)

Inbred lines	**Kernel row number**	**Heterosis (%)**
ZPL1 x ZPL2	14.04	6.4
ZPL1 x B14(C_0)	14.39	9.1
ZPL1 x B37(C_0)	14.11	6.9
ZPL1 x B73(C_5)	15.50	-8.5
ZPL1 x B84(C_7)	15.15	-4.3
ZPL1 x B90(C_7)	14.49	8.6
ZPL1 x B91(C_8)	14.96	13.4*
ZPL1 x B97(C_9)	14.56	9.5*
ZPL1 x B99(C_{10})	13.91	5.5
ZPL2 x B14(C_0)	14.95	17.9**
ZPL2 x B37(C_0)	14.09	8.1
ZPL2 x B73(C_5)	15.57	-8.1
ZPL2 x B84(C_7)	15.20	-3.9
ZPL2 x B90(C_7)	14.92	11.8*
ZPL2 x B91(C_8)	14.37	13.4**
ZPL2 x B97(C_9)	14.29	7.4*
ZPL2 x B99(C_{10})	13.53	6.8

*, ** significant at the probability levels of 0.05 and 0.01 respectively

The differences between the values of estimators μG and μD in the inbred B37(C_0) were not significant (>2SE), which indicates that self-pollination of the hybrid ZPL1 x B37 will be the better way of the development of the initial population for selection, because the inbred is genetically more related to the inbred ZPL1. The value of the estimator μF did not significantly differ from the value of the estimator μG, hence self-pollination of the hybrid B99 x ZPL2 is the best way to develop the initial population for selection, because the inbred B99(C_{10}) is more related to the inbred ZPL2 (Table 2).

Inbred donors B73(C_5), B84(C_7) and B14(C_0) of the synthetic population BSSS and the inbred line B90(C_7) of the synthetic population $BSCB_1$ had significant values of favourable alleles for the improvement of the kernel row number. These inbreds had significant (> 2SE) difference μG-(μD or μF) in favour of favourable dominant alleles. According to the estimation of relatedness that showed greater relatedness to the parent inbred ZPL1, it is necessary to back cross F_1 generations (ZPL1 x B73, ZPL1 x B84. ZPL1 x B14 and ZPL1 x B90) to inbred donors and then to initiate self-pollination with the aim to improve the inbred line ZPL1 (Table 2).

The inbred lines B91(C_8) and B97(C_9) of the synthetic population $BSCB_1$ show that they had significant values of favourable alleles for the improvement of the kernel row number in the elite hybrid ZP580. Both inbreds had a significant (>2SE) and a positive difference between the number of favourable dominant alleles and unfavourable recessive alleles and therefore they should be back-crossed to the F_1 generation (ZPL2 x inbred donor) with the aim to improve the inbred line ZPL2, parental components of the elite hybrid (Table 2).

Table 2. The estimation of the relative number of favourable alleles for the kernel row number

Donors (Iw)	**μG^{*}**	**Relatedness $(\mu C^{*}+\mu F^{*})-(\mu D^{*}+\mu E^{*})$**	**$\mu G^{*}-(\mu D^{*}$ or $\mu F^{*})$**	**Cross method**
B14(C_0)	0.528^{*}	0.822^{*}	0.456^{*}	(I_1 x Iw) x Iw
B37(C_0)	0.250^{*}	0.234	0.037	Selfing
B73(C_5)	0.962^{*}	0.334^{*}	0.768^{*}	(I_1 x Iw) x Iw
B84(C_7)	0.781^{*}	0.309	0.581^{*}	(I_1 x Iw) x Iw
B90(C_7)	0.545^{*}	0.690^{*}	0.440^{*}	(I_1 x Iw) x Iw
B91(C_8)	0.657^{*}	-0.328^{*}	0.462^{*}	(I_2 x Iw) x Iw
B97(C_9)	0.474^{*}	-0.014	0.262^{*}	(I_2 x Iw) x Iw
B99(C_{10})	0.149	-0.127	-0.063	Selfing

* significant at the level> 2SE (Standard Error)

Inbred donors were ranked according to the values of the estimator μG. Estimators UBND PTC and NI show that the inbred lines B73(C_5) and B84(C_7) were the best carriers of favourable alleles for the kernel row number (Table 3). High and significant values of rank correlation coefficients were determined among mentioned estimators (Table 4). Gained results are in accordance with results obtained by Vračarević (2000) and Trifunovića (2001).

Table 3. Estimation and the rank of μG, UBND, PTC and NI for the kernel row number

Inbred donor	**μG**	**UBND**	**PTC**	**NI**
B14(C_0)	0.528 (5)	1.198 (6)	14.667 (5)	0.454 (4)
B37(C_0)	0.250 (7)	0.925 (7)	14.100 (7)	0.037 (7)
B73(C_5)	0.962 (1)	2.312 (1)	15.537 (1)	0.768 (1)
B84(C_7)	0.781 (2)	1.962 (2)	15.175 (2)	0.581 (2)
B90(C_7)	0.545 (4)	1.300 (5)	14.703 (3)	0.440 (5)
B91(C_8)	0.657 (3)	1.706 (3)	14.670 (4)	0.462 (3)
B97(C_9)	0.474 (6)	1.374 (4)	14.425 (6)	0.262 (6)
B99(C_{10})	0.149 (8)	0.724 (8)	13.718 (8)	-0.063 (8)

Values of the rank are given within the ( )

Table 4. Rank correlation for the kernel row number

	μG	**UBND**	**PTC**	**NI**
μG	-	0.928^{**}	0.976^{**}	0.905^{**}
UBND		-	0.880^{**}	0.905^{**}
PTC			-	0.928^{**}
NI				-

** significant at the p<0.01 level

CONCLUSION

According to the estimators μG, UBND, PTC and NI from both synthetic populations the maize inbred donors of favourable alleles for the improvement of the kernel row number of the parental inbreds of the elite hybrid ZP 580 were identified.

The improvement of the kernel row number of inbred lines, parental components (I_1 and I_2) of the elite hybrid ZP 580 can be done with inbred lines B73(C_5) and B84(C_7) of the synthetic population BSSS and B91(C_8) and B90(C_7) of the synthetic population $BSCB_1$. These inbred lines also had the highest value of the estimator μG. The inbred line I_1 can be improved with inbred lines B73, B84 and B91, while the inbred line I_2 can be improved with the inbred line B91.

High and significant values of rank correlation were determined among observed estimators μG, UBND, PTC and NI.

ACKNOWLEDGEMENT

This paper presents results of the Project TR 31068 *„Improving maize and soya bean traits with molecular and conventional breeding"*, supported by the Ministry of Science and Technological Development of Republic Serbia.

LITERATURE CITED

Bernardo, R., 1990a. An alternative statistics for dentifying lines useful for improving parents of an elite single cross. Theor. Appl. Genet. 80:105-109.

Carena, M. J., 2005. Maize commercial hybrids compared to improved population hybrids for graih yield and agronomic performance. Euphytica. 141: 201-208.

Delić, N., Đorđević, J., Todorović, G., M. Babić, 1996. Ocena komercijalnih hibrida kukuruza *(Zea mays L.)* kao donora poželjnih alela za popravku prinosa zrna elitnog SC hibrida. Genetika. 28 (1): 9-16.

Dudley, J. W., 1984a. A method of indentifying lines for use in inproving parents of a single cross. Crop Sci. 24:355-357.

Dudley, J. W., 1987a. Modification of methods for identifying inbred lines useful for improving parents of an elite single crosses. Crop Sci. 27:944-947.

Gerlof, J. E., 1985. Choice of method for identifying germplasm with superior alleles. Ph. D. Diss. Iowa State Univ., Ames, USA (Diss. Abstr. 85-24656).

Gerlof, J. E. and O. S. Smith, 1988. Choice of method for identifuing germplasm with superior elleles. Theor. Appl. Genet. 76:209-216.

Hallauer, A. R. and J. B. Miranda, 1988. Quantitative genetics in maize breeding, 2nd ed. Iowa State University Press, Ames, Iowa, pp 361-362.

Mišević, D., 1989a. Evaluation of three test statistics used to identify maize inbred lines with new favorable alleles not present in an elite single cross. Teor. Apll. Genet. 77:402-408.

Mišević, D., 1989b. Identification of inbred lines as a source of new alleles for improvement of elite maize single crosses. Crop Sci. 29:1120-1125.

Malvar R. A., Pedro Revilla P., Cartea M. E., Butrón A. M. and A. Ordás, 2001. Cheching performance of field corn inbreds as donors of favorable alleles to improve early vigor and adaptation od sweet corn hybrids to European conditions. Maydica. 46:187-193.

Sprague, G.F. and S.A. Eberhart, 1997. Corn Breeding in Corn and Corn Improvement, Sprague G.F. ed. Am. Soc. Agron. Madison. Wis, pp. 305-363

Trifunović, S., 1999. Procena inbred linija i populacija kukuruza *(Zea mays L.)* kao donora poželjnih alela. Doktorska disertacija, Poljoprivredni fakultet, Novi Sad.

Vračarević, M., 2000. Identifikacija inbridovanih linija, potencijalnih donora poželjnih alela za popravku prinosa i komponenata prinosa hibrida kukuruza *(Zea mays L.)*. Magistarska teza. Poljoprivredni fakultet, Univerzitet u Beogradu.

Zanoni, U. and J. W. Dudley, 1989c. Use of F_2 Generations to Identify Inbreds With Favorable Alleles Not Present in an Elite Hybrid. Crop Sci. 29:583-589.

Zanoni, U. and J. W. Dudley, 1989a. Comparison of Different Methods of Identifying Inbreds Useful for Improving Elite Maize Hybrids. Crop Sci. 29:577-582.