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COMPARISON OF DIFFERENT METHODS FOR IDENTIFICATION OF MAIZE POPULATIONS (*ZEA MAYS* L.) AS SOURCES FOR ELITE HYBRID IMPROVEMENT

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ABSTRACT

Choice of adequate sources of new favorable alleles to be included in elite maize (*Zea mays* L.) hybrids improvement programs is of the main interest for maize breeders. The objectives of this study were: to evaluate potential of seven maize populations as donors of new favorable alleles to improve the hybrid B73 x Mo17 for grain yield, ear length, number of rows, and weight of 1000 kernels, using 5 methods; to compare results obtained by the calculation of rank corellation coefficient (rs) after Spearman, as well as Kendall's coefficient of concordance (W) (Falconer, 1989). All evaluated maize populations had positive values of $1\overline{P}_1\mu$ statistics proposed by Dudley (1987) for all traits. It confirms that broad based sources as favorable allele carriers could be useful in elite hybrid parents improvement. High level of agreement between three applied methods for maize populations evaluation as sources of favorable alleles were obtained for all investigated traits. The strongest corellation relationship between method proposed by Dudley (1987) and $\overline{X}TC$ were calculated for number of rows (rs = 1) and ear length (rs = 0.964**).**

Key words: maize, alleles,yield improvement.

INTRODUCTION

Identification of new sources of favorable alleles for elite hybrid improvement (P_1 x P_2) is of the most interest in maize breeding programs. The objective of this study was to compare different methods of estimating the value of synthetic populations as material for elite hybrid (B73 x Mo17) improvement. Seven populations of maize (*Zea mays* L.) were evaluated for grain yield, ear length, number of rows and weight of 1000 kernels.

Five estimators for determination of population value as elite hybrid enhancer were used:

- method (I): population performance *per se* ($\overline{X}$)**;**
- method (II): (GCA), general combining abilities (Griffing, 1956, method 2, model 1);
- method (III) : estimate of the number of favorable alleles present in an donor population, but not present in an elite hybrid ($1\overline{P}_1\mu$) (Dudley, 1987);
- method (IV): the UBND MINIMUM method (Gerlof and Smith, 1988; Zanoni and Dudley, 1989);
- method (V): mean of crosses of a donor hybrid to both parents of elite single cross ($\overline{X}$TC) (Sprague and Eberhart, 1977).

Significant values of parameters $1\overline{P}_1\mu$ and its usefulness as potential donors for breeding programs were reported by Dudley (1984, 1988), Aldi (2000), Trifunovic (2001) and Zivanovic (2006). Rosa Ana Malvar et al. (1997) reported that correlations between $1\overline{P}_1\mu$, UBND, $\overline{X}$TC i GCA were highly significant for yield and four investigated traits.

MATERIAL AND METHODS

Seven synthetic populations were investigated in three trials at four locations using RCB design:

- First trial: interpopulation crosses and populations *per se* (28 genopypes).

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- Second trial: top crosses (B73 x populations and Mo17 x populations) + elite hybrid (B73 x Mo17) (15 genotypes).
- Third trial: Inbred lines *per se* (B73 and Mo17) (2 genotypes).

- ❑ Analysis of combining abilites and determination of general combining abilities (GCA**)** were calculated by method 2, model 1, after Griffing, (1956) (Falconer, 1989).
- ❑ The estimation of favorable alleles (**$1\bar{P}_1\mu$**) not present in elite hybrid B73 x Mo17 in investigated populations, was calculated by method proposed by Dudley (1987). Because dominance was in positive direction for all investgated traits, frequencies of favorable dominant alleles not present in parental inbreds of elite single cross were used to evaluate potential of seven maize populations as donors for B73 x Mo17 improvement.
- ❑ The minimum upper bound (UBND) was calculated as the minimum of the two expresions (Gerlof and Smith, 1988):

$$\boxed{(P_1 \text{ x } D) - P_1} \quad \text{and} \quad \boxed{(P_2 \text{ x } D) - P_2}$$

- ❑ The mean of crosses of a donor hybrid to both parents of elite single cross ($\bar{\mathbf{x}}$TC) (Sprague and Eberhart, 1977) was computed as:

$$\boxed{[(P_1 \text{ x } D) + (P_2 \text{ x } D)]/2}$$

- ❑ Comparison between the pairs of investigated estimators was calculated by rank correlation coefficient (r_s), after Spearman:

$$r_s = 1 - \frac{6\sum_{i=1}^{n} d_i^2}{n(n^2-1)}$$

d_i = difference between two ranks of investigated trait;
n = number of correlated pairs.

- ❑ To compare more than two variables or estimators (three and four) in all possible combinations Kendall's coefficient of concordance (W) (Falconer, 1989) was applied:

$$W = \frac{\sum_{j=1}^{n} R_j^2 - \frac{(\sum_{j=1}^{n} R_j)^2}{n}}{\frac{k^2(n^3-n)}{12}}$$

- ❑ χ^2 ** values for testing hypothesis of rank independence (for **k** variables) was calculated by the following formula:

$$\chi^2 = k(n-1)W$$

- ❑ *P_1 = mean of the parent B73; P_2 = mean of the parent Mo17; D = mean of the donor population.
- ❑ ** Critical values were used following Friedman χ^2 distribution, because **n ≤ 7.**

RESULTS

Rank correlations of $1\bar{P}_1\mu$ were highest with UBND and $\bar{\mathbf{x}}$TC for ear length and number of kernel rows (Table 1).

Table 1. Comparison of investigated donor populations estimators by pairs using rank correlation after Spearman

Trait	Grain yield	Ear length	Number of rows	Weight of 1000 kernels
Correlated estimators	r_S	r_S	r_S	r_S
$\bar{\mathbf{x}}$ (1) / GCA (2)	0.714	0.857*	0.857*	0.758*
$\bar{\mathbf{x}}$ (1) / $1\bar{P}_1\mu$ (3)	-0.25	0.742	0.742	0.107
$\bar{\mathbf{x}}$ (1) / UBND (4)	0	0.570	0.642	0.285
$\bar{\mathbf{x}}$ (1) / $\bar{\mathbf{x}}$TC (5)	0.357	0.714	0.857*	0.464
GCA (2) / $1\bar{P}_1\mu$ (3)	0.714	0.821*	0.714	0.178
GCA (2) /UBND (4)	0.428	0.714	0.785*	0.392
GCA (2)/ $\bar{\mathbf{x}}$TC (5)	0.607	0.821*	0.785*	0.500
$1\bar{P}_1\mu$ (3) /UBND (4)	0.750	0.964**	0.857*	0.857*
$1\bar{P}_1\mu$ (3) /$\bar{\mathbf{x}}$TC (5)	0.464	0.964**	1.00**	0.892*
UBND (4)/$\bar{\mathbf{x}}$TC (5)	0.587*	0.892**	0.857*	0.785*

Critical values for r_s 0.05 0.750
0.01 0.892

These correlations are expected to be high due to the fact that UBND and $\bar{\mathbf{X}}$TC theoretical values differ from that of $1\bar{P}_{1}\mu$, just for specific combining ability effects. The lowest rank correlations were calculated for $\bar{\mathbf{X}}$ with $1\bar{P}_{1}\mu$ and UBND for all investigated traits. For $1\bar{P}_{1}\mu$ and UBND calculation the population *per se* – mean was not included.

Assuming a new potential line from donor population (D) being homozygous favourable at class **l** locus, the UBND estimates the relative number of favourable alleles in class **l** plus the number of loci in class **j** and **k**. In those classes, the donor population and one of the parental lines have favourable alleles in common, and the other parental line has unfavourable alleles. In the case when large number of favourable alleles in both classes (**j** and **k**) persists, UBND procedure could overestimate the potential value of the donor population (Table 2).

The highest rank correlation of GCA was obtained with $\bar{\mathbf{X}}$ for all estimated traits**.**

Table 2. Comparison of investigated donor populations estimators by triads over coefficient of agreement (W) proposed by Kendall

Correlated estimators	Trait	W	χ^2
(1) $\bar{\mathbf{X}}$ (4) UBND (5) $\bar{\mathbf{X}}$TC	Grain yield	0.603*	10.85
	Ear length	0.841**	15.14
	Number of rows	0.849**	15.28
	Weight of 1000 k.	0.690**	12.42
(2) GCA (3) $1\bar{\mathbf{P}}_{1}\mu$. (4) UBND	Grain yield	0.611*	11.00
	Ear length	0.888**	16.00
	Number of rows	0.857**	15.42
	Weight of 1000 k.	0.615**	11.07
(2) GCA (3) $1\bar{\mathbf{P}}_{1}\mu$. (5) $\bar{\mathbf{X}}$TC	Grain yield	0.587*	10.57
	Ear length	0.920**	16.57
	Number of rows	0.880**	15.85
	Weight of 1000 k.	0.682**	12.28
(2) GCA (4) UBND (5) $\bar{\mathbf{X}}$TC	Grain yield	0.735**	13.57
	Ear length	0.888**	16.00
	Number of rows	0.865**	15.57
	Weight of 1000 k.	0.718**	12.92
(3) $1\bar{\mathbf{P}}_{1}\mu$ (4) UBND (5) $\bar{\mathbf{X}}$TC	Grain yield	0.793**	14.28
	Ear length	0.984**	17.71
	Number of rows	0.920**	16.57
	Weight of 1000 k.	0.753**	13.57

Critical values of the Friedman χ^2 distribution
0.05 = 9.857; 0.01 = 11.762

When relationship between the 5 estimators (grouped three by three) was measured by coefficient of concordance **(W)**, the highest values were computed for the following combinations: $\mathbf{1\bar{P}_{1}\mu}$, UBND, $\bar{\mathbf{X}}$TC; GCA, UBND, $\bar{\mathbf{X}}$TC and $\bar{\mathbf{X}}$, GCA, $\bar{\mathbf{X}}$TC (Tables 3 and 4). Following the same way of comparison, when estimators were grouped four by four, the strongest relationship were calculated for $\bar{\mathbf{X}}$, GCA, UBND**,** $\bar{\mathbf{X}}$TC and GCA, $\mathbf{1\bar{P}_{1}\mu}$, UBND, $\bar{\mathbf{X}}$TC (Table 3).

High and significant concordance among parameters $\mathbf{1\bar{P}_{1}\mu}$, UBND and $\bar{\mathbf{X}}$TC for grain yield in inbred line donors study is in accordance with results obtained by Asoro et al. (2007).

Highly significant rank correlations for grain yield among $1\bar{\mathbf{P}}_{1}\mu$, $\bar{\mathbf{X}}$TC and UBND were reported in inbred line donors investigation by Reddy et al. (2005).

Table 3. Comparison of investigated donor populations estimators by tetrads over coefficient of agreement (W) proposed by Kendall

Combination of the estimators	Trait	W	χ^2
$\bar{\mathbf{X}}$ (1) GCA(2) $1\bar{P}_{1}\mu$ (3) UBND (4)	Grain yield	0.464*	11.14
	Ear length	0.834**	20.03
	Number of rows	0.825**	19.81
	Weight of 1000 k.	0.566**	13.60
$\bar{\mathbf{X}}$ (1) GCA(2) $1\bar{P}_{1}\mu$ (3) $\bar{\mathbf{X}}$TC (5)	Grain yield	0.495*	11.89
	Ear length	0.875**	21.00
	Number of rows	0.866**	20.78
	Weight of 1000 k.	0.616**	14.78
$\bar{\mathbf{X}}$ (1) GCA(2) UBND (4) $\bar{\mathbf{X}}$TC (5)	Grain yield	0.620**	14.89
	Ear length	0.834**	20.03
	Number of rows	0.843**	20.25
	Weight of 1000 k.	0.651**	15.64
$\bar{\mathbf{X}}$ (1) $1\bar{P}_{1}\mu$ (3) UBND (4) $\bar{\mathbf{X}}$TC (5)	Grain yield	0.522*	12.53
	Ear length	0.875**	21.00
	Number of rows	0.861**	20.67
	Weight of 1000 k.	0.665**	15.96
GCA (2) $1\bar{P}_{1}\mu$ (3) UBND (4) $\bar{\mathbf{X}}$TC (5)	Grain yield	0.647**	15.53
	Ear length	0.910**	21.85
	Number of rows	0.866**	20.78
	Weight of 1000 k.	0.691**	16.60

Critical values of the Friedman χ^2 distribution
0.05 = 10.286; 0.01 = 12.714

Trifunovic (1999, 2001) reported significant correlation between $\mathbf{1\overline{P}_{1}\mu}$ and $\overline{\mathbf{X}}$TC for grain yield. The best population for B73 x Mo17 improvement by majority of calculated parameters was Tuxpeno Co (Tables 4 and 5).

Table 4. Calculated values of all estimators per each donor population for grain yield and ear length

Donors	Grain yield					Ear length				
	Estimators					Estimators				
	$\overline{X}$ (1) kg	GCA (2)	$1\overline{\mathbf{P}}_{1}\mu$ (3)	UBND(4) kg	$\overline{X}$ TC (5) kg	$\overline{X}$ (1) cm	GCA (2)	$1\overline{\mathbf{P}}_{1}\mu$ (3)	UBND (4) cm	$\overline{\mathbf{X}}$ TC (5) cm
HCBSA	5.944	-1.09*	0.98	4.587	9.018	15.6	-0.83	0.61	2.8	17.9
Mex.dent	6.572	-0.28	0.54	4.445	9.550	16.9	-0.11	1.16	3.9	18.5
Tuxpeno Co	8.519	0.5	1.69	5.922	10.443	17.8	0.32	1.4	4.4	18.9
AntiquaM (C6)	8.607	-0.1	0.81	4.789	10.085	17.6	0.03	1.32	4.2	18.85
BS12(Hi) C8	6.846	0.23	0.72	4.846	9.914	18.2	0.6	1.6	4.8	19.45
Syn18	9.029	0.48	0.47	3.992	9.415	17.4	0.17	0.82	3.2	17.95
Syn19	8.396	0.25	0.87	4.958	10.154	18.4	0.19	1.19	3.9	18.85
LSD 0.05 0.01	0.63 0.84					0.89 1.18				

Table 5. Calculated values of all estimators per each donor population for number of rows and weight of 1000 kernels

Donors	Number of rows					Weight of 1000 kernels				
	Estimators					Estimators				
	$\overline{X}$ (1)	GCA (2)	$l_{1}\overline{\mathbf{P}}\mu$ (3)	UBND(4)	$\overline{X}$ TC (5)	$\overline{X}$ (1) g	GCA (2)	$1\overline{\mathbf{P}}_{1}\mu$ (3)	UBND (4) g	$\overline{X}$ TC (5) g
HCBSA	279.1	0.08	1.68	1.7	16.4	279.1	-13.1*	4.19	21.1	287.35
Mex.dent	278.3	-0.18	1.14	0.74	15.32	278.3	-7.28	12.7	44.2	296
Tuxpeno Co	301.3	-0.26	1.4	1.24	15.84	301.3	4.56	11.88	41.8	302.7
AntiquaM (C6)	299.8	0.05	1.47	0.79	15.97	299.8	2.47	3.22	13	285.35
BS12Hi	279.1	0.26	1.41	1.32	15.86	279.1	-7.13	3.22	24.4	285.35
Syn18	304.9	0.65	1.54	1.35	16.92	304.9	1.81	9.54	38.9	292.6
Syn19	330.1	-0.61	1.2	0.29	15.4	330.1	18.6**	10.88	98.5	300.7
LSD 0.05 0.01	0.16 0.22					12.65 16.82				

CONCLUSIONS

Estimates of the relative loci number $\mathbf{1\overline{P}_{1}}\mu$ in potential donor population (Dudley, 1987) were highly correlated with the mean of crosses of a donor population to both of parents of elite SC hybrid ($\overline{\mathbf{X}}$TC**)** and UBND for all traits in generally.

Very strong agreement between $1\overline{\mathbf{P}}_{1}\mu$ and $\overline{\mathbf{X}}$TC indicated that the mean of two parents of elite hybrid x donor population could be used as a tool for choosing donor populations for improvement of elite single cross for all investigated traits, except for the grain yield. This statistic is recommendable for traits where dominance is in positive direction and there is no need to grow parental lines. Although this study does not include relatedness parameter in model proposed by Dudley (1987), we can conclude that the main disadvantage of $\overline{\mathbf{X}}$TC statistic compared to $\mathbf{1\overline{P}_{1}\mu}$ is that calculation of genetic similarity between donors and parental lines is not enabled. Our experimental results indicated that ranking by GCA was not always in agreement with ranking by $\mathbf{l\bar{P}_{l}\mu}$, $\bar{\mathbf{X}}$TC and UBND, especially for grain yield and weight of 1000 kernels.The mean of the donor population $\bar{\mathbf{X}}$ was highly correlated only to GCA for all investigated traits (Delic, 1993). Also, the results of all applied models for investigated traits confirmed that a high value of population *per se*, does not qualify this population to be chosen as potential donor of favorable alleles in B73 x Mo17 elite hybrid improvement.

REFERENCES

Aldi, K. and Dudley, J.W., 2000. *Identification of tropical and temperate maize populations having favorable alleles for yield and other phenotypic traits*. Crop Sci., 40: 941-947.

Asoro, F.G., Salazar, A.M., Carpena, A.L. and Altoveros, N.C., 2007. *Identification of donors with favorable alleles for grain yield to improve inbreds in a Philippine maize breeding program.* Philippine Agricultural Scientist, 90(1): 54-63.

Delic, N., 1993. *Ocena sintetičkih populacija kukuruza (Zea mays L.) kao donora poželjnih alela*. Magistarski rad, Poljoprivredni Fakultet, Novi Sad.

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

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

Dudley, J.W., 1988. *Evaluation of maize populations as sources of favourable alleles.* Crop Sci., 28: 486-491.

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

Falconer, D.S., 1989. *Introduction to Quantitative Genetics.* 3rd edn. Longman Scientific & Technical, Harlow.

Malvar, Rosa Ana, Cartea, Aaria Elena, Revilla, P. and Ordas, A., 1997. *Identification of field corn inbreds adapted to Europe to improve agronomic performance of sweet corn hybrids*. Crop Sci., 37: 1134-1141.

Miševic, D., 1990. *Evaluation of commercial maize hybrids as sources of new favourable alleles*. Maydica, 35: 287-295.

Petrovic, R., Filipovic, M., Vidakovic, M., 1992. *Identification of sources containing useful alleles for improving parents of superior maize single crosses (Zea mays L.).* Genetika, 2: 115-126.

Reddy, D.M., Ahuja, V.P. and Mukherjee, B.K., 2005. *Comparison of various statistics for identification of maize inbreds with favourable alleles for the improvement of single cross hybrid in maize (Zea mays L.).* The Indian Journal of Genetics and Plant Breeding, volume 65, issue 4.

Sprague, G.F. and Eberhart, S.A., 1977). *Corn breeding.* In: Corn and Corn Improvement (Sprage, G.F., ed.). American Society of Agronomy, Madison, WI: 305-362.

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

Trifunović, S., Husić, I., Rošulj, M., Stojšin, R., 2001. *Evaluation of U. S. and Yugoslavian maize populations as sources of favorable alleles*. Crop Sci., 41: 302-308.

Zanoni URS and DUDLEY, J. W., 1989. *Comparison of different methods of identifying inbreds useful for improving elite maize hybrids.* Crop Sci., 29, 3: 577-582.