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Comparison of methods to identify donor inbreds with favourable alleles for the improvement of elite maize single cross hybrids

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Abstract

The success of single cross hybrids in maize primarily rests on the economical seed production of its inbred parents. Inbred parental improvement thus holds the key in modern maize breeding programmes. Identification of inbred lines (I_W) as sources of favourble alleles not already present in an elite hybrid ($I_1 \times I_2$) is one of the approaches towards line enhancement in single cross hybrids. In the present study, a minimally biased estimate of the number of favourable alleles present in an inbred but not present in an elite hybrid ($\mu G'$) was compared with minimum upper bound estimates (UBND), net improvement statistic (NI), predicted three-way performance (PTC), an unbiased estimator based on combining ability model ($\mu a[B+G]$), probability of net gain of favourable alleles (PNGg), inbred performance *per se* and general combining ability (GCA). These estimators were applied to grain yield and related characters among 45 F_1's obtained from crossing ten maize inbred lines. The relative efficiency of these estimates was analyzed. The estimates, $\mu G'$ and UBND were found to be the best in ranking the donor inbreds in a select group of five single crosses. A scheme for possible utilization of these estimates for inbred line enhancement of the target crosses is proposed.

Key words: Maize, single cross hybrids, donor inbreds, favourable alleles

Introduction

In maize, considerable success has been achieved in recent years in enhancement of inbred performance by several recycling procedures. In all the methods of recycling, the upgraded inbred lines, though helpful to add elite genes, were unable to preclude the loss of promising alleles already present in the elite single cross. However, the resulting improvement obtained in the single cross due to the accumulation of favourable alleles from the recycled inbreds, represented the net improvement in hybrid performance after accounting for the number of favourable alleles lost during selection.

Dudley (1984) [1] first proposed -a methodology for identification of unique favourable alleles in donor inbred lines for improving the parental constituents in a desirable single cross, alleviating the drawbacks of earlier methods. His first method was followed by several modifications [2-8] devising new parameters for evaluating the donor inbred lines in various aspects like frequency of favourable alleles present, frequency of alleles lacking in the parental inbreds, estimating the relative relationships of the donor inbreds, and estimating the loss of alleles not only in the donor inbreds but also in the single cross hybrids. These parameters evaluate the donor inbreds comprehensively, so that the highest level of heterosis may be attained when a donor inbred replaces/improves a parental inbred in an elite cross. These estimates, in addition, provide information on the likely methods to be followed for the enhancement of inbred performance through the most efficient recycling procedures. The objective of comparing the estimates for their efficiency in ranking the donor inbreds was to obtain a consensus donor with the largest frequency of favourable alleles and to recognize the most efficient estimators for identification of such donors with respect to grain yield and related traits.

Materials and methods

The material consisted of ten second cycle inbred lines namely CM-131, CM-211, LM-5, LM-6, CM-111, AML-102, AML-104, AML-221, AML-224 and AML-226. Of these, two inbred lines (LM-5 and LM-6) are parents of the first single cross hybrid 'Paras' released for Punjab state of India. All these ten inbred lines possessed substantial variation with respect to plant characters, maturity and yield contributing characters. These ten parents were mated in a half diallel fashion, to obtain 45 F_1's, which were evaluated in four identical trials at two locations *viz.*, Rajendranagar and Karimnagar in Andhra Pradesh state of Peninsular India during two winter seasons of 1998-99 and 1999-2000.

In the present experiment, though 45 crosses

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originating from 10 × 10 diallel were included, due to analytical limitations for the identification of unique favourable alleles by various models only 5 crosses were considered for the identification of such alleles. Out of these, the cross, LM-5 × LM-6, was *a priori* projected to be improved, as the inbred parents of the cross already proved their potential in the released hybrid 'Paras'. The other four crosses (AML-221 × AML-226, AML-221 × AML-224, AML-102 × AML-221 and LM-6 × AML-224), may also be considered as target crosses, however, differ from the first one in that these may possess, in combination with different donor inbred lines, variable frequency of favourable and unfavourable alleles as they represented descending levels of yield performance in the trials conducted during 1998-99 and 1999-2000 at two locations *viz.*, Karimnagar and Rajendranagar.

Minimally biased estimates of favourable alleles present in the donor inbred, but lacking in the hybrid to be improved ($\mu G'$), were calculated using the modified procedure given by Dudley (1987) [2]. The other statistics used were minimum upper bound (UBND) estimates [3-4], Predicted three way cross (PTC) means [9], Net improvement [7], Probability of Net gain (PNG_g) of favourable alleles [10], and identification of donor inbreds based on combining ability model [8]. Further, rank correlation coefficients between all different estimates were calculated as per the formulae given by Snedecor and Cochran (1989) [11].

Results and discussion

In the present experiment, comparative analysis of various methods was undertaken as it was expected that none of the methods were free from biases, although the nature and magnitude of these biases might be different. A comparison of the rankings of the donor inbred lines based on different methods reveal interesting findings for the cross LM-5 × LM-6 (Table 1). It appears $\mu G'$ and PTC are two most efficient methods for identification of favourable alleles as each of them have identified six out of eight donors in exactly the same rank order. These two methods, however, failed to show any such pattern in ranking of the donors. In contrast, $\mu G'$ and UBND, NI and PNGg, and UBND and PTC together showed similar consistent pattern of ranking of donors (3 out of 8 donors). Zanoni and Dudley (1989a) [12], Misevic (1989b) [13], Bemardo (1990) [7] and Hohls *et al.*, (1995) [8] also got similar results. Out of eight donor inbreds, AML-102 was ranked first by three methods ($\mu G'$, NI and PTC) for mean grain yield performance, while it was ranked second by PNG_g and GCA. Hence, good agreement was found, in general among $\mu G'$, NI, PTC and mean *per se* for the highest ranked donor inbred, AML-102.

Taking the eight donor inbreds into consideration, the estimators of identification of favourable alleles along with donor mean performance and GCA were also used to rank these eight inbreds for grain yield per plot for the top four superior crosses *viz.*, AML-221 × AML-226, AML-221 × AML-224, AML-102 × AML-221 and LM-6 × AML-224. Significant to highly significant positive correlations were exhibited between $\mu G'$ and other estimates namely UBND, NI, PTC, μa(B+G), PNG_g and GCA for all four crosses, indicating their similarity in identifying the donor inbreds with favourable alleles, though all these methods have conceptual differences (Table 2). Similar high *inter se* correlations among $\mu G'$, UBND and PTC were reported by Zanoni and Dudley (1989a) [12], Misevic (1989a,b) [5,13], Pfarr and Lamkey (1992b) [14]; among $\mu G'$, UBND, PTC and NI by Malvar *et al.*, (1997a,b) [15-16] and Revilla *et al.*, (1998) [17]; and among $\mu G'$, UBND, NI, PTC and PNGG by Ayarault *et al.* (1999) [18].

In general, $\mu G'$ was found to be best of all the estimators since it is the least biased estimator for identifying donors with frequency of favourable alleles not already present in the elite cross. The estimators UBND, NI, PTC and PNG_g were also found to be efficient next to $\mu G'$ as evident from their high *inter se* correlations. A breeding plan using these estimators is suggested in Fig 1. The proposed breeding plan

Table 1. Different estimates of favourable alleles, mean and GCA for grain yield per plot in eight potential donor lines, with hybrid LM-5 x LM-6 as the target cross

Inbred	$\mu G'$	UBND	NI	PTC	μa(B+G)	PNG_g	Mean grain yield (kg)	GCA
CM-131	0.60(4)	1.90(4)	0.30(3)	3.90(4)	0.40(2)	0.66(3)	2.54(3)	−0.14(5)
CM-211	0.62(3)	2.01(3)	0.25(4)	3.92(3)	0.44(1)	0.62(5)	2.15(4)	−0.16(7)
CM-111	0.50(7)	1.70(7)	0.21(6)	3.75(6)	0.31(4)	0.63(4)	1.96(7)	−0.20(8)
AML-102	0.68(1)	1.78(5)	0.38(1)	3.98(1)	0.34(3)	0.71(2)	2.70(1)	0.18(2)
AML-104	0.43(8)	1.75(6)	0.18(7)	3.72(7)	0.20(6)	0.58(7)	1.90(8)	−0.15(6)
AML-221	0.64(2)	2.07(1)	0.23(5)	3.94(5)	0.23(5)	0.61(6)	2.68(2)	0.05(4)
AML-224	0.54(6)	1.58(8)	0.35(2)	3.84(2)	−0.05(8)	0.73(1)	2.14(5)	0.20(1)
AML-226	0.58(5)	2.04(2)	0.15(8)	3.82(3)	−0.02(7)	0.54(8)	2.08(6)	0.17(3)

Numbers in parenthesis indicate the rank of the donors according to various estimators

Table 2. Rank correlations between $\mu G'$ and other estimators of favourable alleles for grain yield

Hybrid to be improved	Rank correlation coefficients between $\mu G'$						
	UBND	NI	PTC	μa(B+G)	PNG_g	Mean grain yield	GCA
LM-5 × LM-6	0.60	0.55	0.95**	0.50	0.21	0.95**	0.33
AML-221 × AML-226	0.78*	0.57	0.88**	0.71*	0.81**	0.07	0.71
AML-221 × AML-224	0.74*	0.76*	0.93**	0.97**	0.83**	–0.14	0.70*
AML-102 × AML-221	0.93**	0.83**	1.00**	0.90**	0.95**	–0.28	0.95**
LM-6 × AML-224	0.93**	0.97**	1.00**	0.78*	0.93**	0.70*	0.52

*,** = Significant at P = 0.05 and P = 0.01, respectively

using various estimators has taken the prime targeted single cross hybrid LM-5 × LM-6 as an indicator. The same scheme can be used in identifying donor inbreds to improve any target cross. However, the methods for improvement would vary according to the values of various estimators obtained for the donor inbred lines.

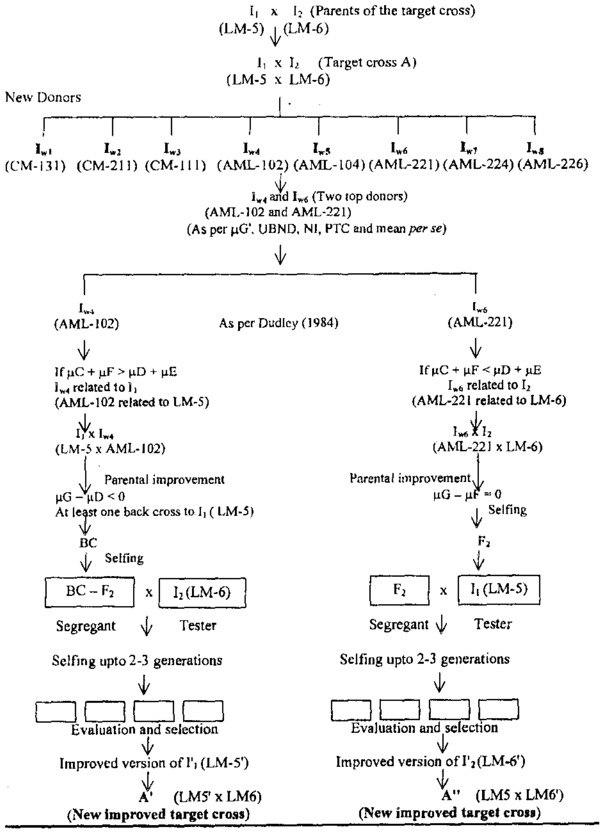

Fig. 1. Suggested breeding plan for utilization of selected donor lines to improve target cross yield

References

1. **Dudley J. W.** 1984. A method of identifying lines for use in improving parents of a single cross. Crop Sci., **24**: 355-357.
2. **Dudley J. W.** 1987. Modification of methods for identifying inbred lines useful for improving parents of elite single crosses. Crop Sci., **27**: 944-947.
3. **Gerloff J. E. and Smith O. S.** 1988. Choice of method for identifying Germplasm with superior alleles. I. Theoretical results. Theor. Appl. Genet., **76**: 209-216.
4. **Gerloff J. E. and Smith O. S.** 1988b. Choice of method for identifying germplasm with superior alleles. II. Computer simulation results. Theor. Appl. Genet., **76**: 217-227.
5. **Misevic D.** 1989a. Identification of inbred lines as a source of new alleles for improvement of elite maize single crosses. Crop Sci., **29**: 1120-1125.
6. **Zanoni U. and Dudley J. W.** 1989. Test cross evaluation of F2 populations from maize inbreds selected for unique favourable alleles. Crop Sci., **29**: 589595.
7. **Bernardo R.** 1990. An alternative statistic for identifying lines useful for improving parents of an elite single cross. Theor. Appl. Genet., **80**: 105-109.
8. **Hohls T., Clarke G. P. Y., Shanahan P. E. and Grevers H. O.** 1995. An unbiased estimator for identifying lines useful for the improvement of elite single crosses based on combining ability model. Heredity, **75**: 155-163.
9. **Sprague G. F. and Eberhart S. A.** 1977. Corn breeding. *In*: Corn and corn improvement. 2nd ed. Pp 305-363.
10. **Metz G.** 1994. Probability of net gain of favourable alleles for improving an elite single cross. Crop Sci., **34**: 668-672.
11. **Snedecor G. W. and Cochran W. G.** 1989. Statistical methods. 8th ed. Iowa state university press. Ames. IA.
12. **Zanoni U. and Dudley J. W.** 1989a. Comparison of different methods of identifying inbreds useful for incorporating elite maize hybrids. Crop Sci.. **29**: 577-582.
13. **Misevic D.** 1989b. Evaluation of three statistics used to identify maize inbred lines with new favourable alleles not present in elite single cross. Theor. Appl. Genet., **77**: 402-408.
14. **Pfarr D. G. and Lamkey K. R.** 1992. Comparison of methods for identifying populations for genetic improvement of maize hybrids. Crop Sci., **32**: 670-677.
15. **Malvar R. A., Revilla P., Cartea M. E. and Ordas A.** 1997a. Field corn inbreds to improve sweet corn hybrids for early vigor and adaptation to European conditions. Maydica, **42**: 247-255.
16. **Malvar R. A., Revilla P., Cartea M. E. and Ordas A.** 1997b. Identification of field corn inbreds adapted to Europe to improve agronomic performance of sweet corn hybrids. Crop Sci., **37**: 1134-1141.
17. **Revilla P., Malvar R. A., Cartea M. E. and Ordas A.** 1998. Identifying open pollinated populations of field corn as sources of cold tolerance for improving sweet corn. Euphytica, **101**: 239-247
18. **Ayarault S., Gouesnard B., Panouille A. and Boyat A.** 1999. Evaluation of late inbred lines in order to improve early single maize crosses by the bi-additive model and predictive genetic models. Maydica, **44**: 183-194.