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# Comparison of various statistics for identification of maize inbreds with favourable alleles useful for the improvement of single cross hybrid in maize (*Zea mays* L.)

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## Abstract

**Theory and methods for identifying inbred lines ($P_W$) where favourable dominant alleles are not present in an elite single cross hybrid ($P_1 \times P_2$) have recently been developed and gaining popularity in modern maize breeding programmes. In the present study, five methods are used to estimate the number of favourable alleles present in an inbred but not present in an elite hybrid namely estimator of Dudley ($\mu$ G′), upper bound estimates (UBND), predicted three way cross (PTC), net improvement statistic (NI) and unbiased estimator based on combining ability model ($\mu$a[B + G]) and were applied to a maize 10 × 10 diallel cross data. Besides these estimates, general combining ability estimates and mean *per se* value of the donor inbreds were also used for comparison studies. Results revealed that, though each and every method has its own conceptual and computational advantages as well as limitations, $\mu$ G′, NI, PTC and UBND, have higher *inter se* correlations. Hence, it is indicated that any one of these methods can successfully select the donor with the highest favourable alleles for the improvement of single cross hybrid. In general, no association was found between mean *per se* and all other estimates for all the three characters under consideration. Similarly, GCA and $\mu$a (B + G) failed to exhibit closer association in grain yield per plant and ear length.**

**Key words:** Maize, single cross, favourable alleles, $\mu$ *G′*, UBND, PTC, NI

## Introduction

Elite single cross hybrid ($P_1 \times P_2$) do not necessarily contain all the favourable alleles contributing the quantitative trait of interest. In breeding programmes aimed at improving the performance of single cross hybrids of corn (*Zea mays* L.), the choice of inbreds with the highest frequency of favourable alleles at loci for which both $P_1$ or $P_2$ carry unfavourable alleles is very much needed. Recent developments in the quantitative genetic theory, first developed by Dudley [1-2] and further modifications by himself as well as several other workers [3-12], have led to rethinking among the maize breeders regarding their relative importance and research emphasis that should be given to identify suitable donors with highest frequency of favourable alleles for inbred development in single cross hybrid breeding. Though, all these estimates which were intended for choice of donors with favourable alleles are based upon varied conceptual and computational advantages as well as limitations. Hence the present study has been undertaken to compare the different statistics aimed for identification of favourable alleles.

## Materials and methods

The material consisted of ten second cycle inbred lines of maize *viz.*, IPA34, IPA21, TCA21, FSA17, IP A3, IPA22, SC7, IPA29, IPA8 and CM117 of which two inbred lines (IPA34 and IPA21) are parents of a superior performing cross (Hence forth this cross IPA34 × IPA21 would be referred as "Target cross"). All these ten inbred lines possessed that possessed wide variation were mated in a diallel fashion with out considering the reciprocals. These ten parents and forty five $F_1$ hybrids thus developed were grown in separate but adjacent yield trials using randomized complete block design with three replications. The same experiment was carried out during *kharif* 1995 and 1996 seasons at the Division of Genetics, Indian Agricultural Research Institute, New Delhi and Haryana Agricultural University Regional Research Station, Uchani, Karnal (Haryana), thus making a total of four environments. Breeding nursery was grown at winter nursery, Maize Research Station, Amberpet, Hyderabad, during Rabi 1994 and 1995.

At each environment, experimental plot consisted of two rows of 5m length each with a row to row distance of 75cm and plant to plant distance of 25cm. Planting and harvesting was done by hand at each location. Though data were recorded on 11 important

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characters, three important characters *viz.*, grain yield per plant (g), earlength (cm) and eardiameter (cm) were considered for the comparison of different statistics for identification of favourable alleles. An analysis of variance was performed for all these traits in each environment separately and then combined over environments was performed after testing of homogeneity of error variances for both inbreds as well as hybrids. Estimates of favourable alleles present in the donor inbred, but lacking in the hybrid to be improved ($\mu G'$) were calculated using the procedure given by Dudley [2]. Similarly the other estimates used were upper bound estimate, UBND [4], predicted three way cross PTC [10], Net improvement NI [3] and $\mu$a (B + G) [5]. Besides these estimates, general combining ability [13] and mean *per se* value of the donor inbreds were used for comparison studies. Further, ranking of the inbreds was done method wise separately and rank correlation coefficients between all these estimates were calculated [14].

## Results and discussion

Estimates based on five different methods of identifying potential donor inbreds, namely $\mu G'$, UBND, PTC, NI and $\mu$ a (B + G) along with *gca* and mean *per se* have been presented (Table 1) for all the eight possible donor inbreds with their rankings to identify best donor for the improvement of the target cross (IPA34 × IPA21) for grain yield per plant, ear length and ear diameter.

For grain yield per plant the two methods, PTC and NI, generally showed similar ranking in as many as five of the eight donor inbreds. In the methods $\mu G'$ and UBND, IPA3 ranked first followed by FSA17. Similarly, in methods PTC and NI, the donor inbreds IPA22 and IPA3 recorded first and second ranks, respectively. However, though IPA29 ranked first in both $\mu$a (B + G) and mean *per se*, the second rank was shown by IPA8 in $\mu$a (B + G) and IPA3 in mean *per se* respectively. It is encouraging to observe that the donor inbred IPA3 was ranked first by three methods namely, $\mu G'$, UBND and *gca*, whereas the same was ranked second by PTC, NI and mean *per se*. Hence IPA3 could be considered as the best donor for the improvement of IPA34 × IPA21 via grain yield per plant. Similar situation as encountered in case of grain yield per plant could be seen for ear length also. IPA3 was ranked top by two of the seven methods namely, $\mu G'$ and UBND and CM117 was ranked first by three methods namely, PTC, NI and $\mu$a (B + G) and second by rest of the four methods. Thus, CM117 qualified for identification as the most promising donor followed by IPA3.

For ear diameter the donor inbred IPA8 could be identified as the most promising as it was ranked first by five of the seven methods, while it was ranked second by the methods NI and $\mu$a (B + G). Another donor, FSA17, could be identified as the second best source of favourable alleles as it was ranked first by $\mu$a (B + G) and second by the other three important methods namely, $\mu G'$, UBND and PTC. On the other hand, the donor SC7 was ranked the last (poorest) by five of the seven methods and last but one by two methods.

The rank correlations among these statistics for all the three characters are presented separately in Table 2, which reveals that there is no consistency in association of one with the other. However, four methods namely $\mu G'$, PTC, UBND and NI generally showed significant *inter se* correlations, indicating similar efficiency in identifying the donors with favourable alleles. Zanoni and Dudley [11], Misevic [8], Bernardof [3] and Hohls *et al.*, [5] also arrived at the same conclusion. In contrast, as in Hohls *et al.*, [5] findings, in the present study $\mu$a (B + G) is not correlated with any of the other estimate for grain yield per plant. In general, no association was found between mean per se and all other estimates for all the four characters under consideration. Similarly, *gca* and $\mu$a (B + G) failed to exhibit closer association in grain yield per plant and ear length. However, in general, both these estimates were significantly associated with $\mu G'$, PTC and UBND in ear diameter. No reports have been found for these characters.

Though each and every method has its own conceptual and computational advantages as well as limitations, from the present findings it is well understood that $\mu G'$, NI, PTC and UBND in general, have higher *inter se* correlations. So any one of these can successfully select the donor with the highest favourable alleles. Though NI, PTC and UBND are easy to compute over $\mu G'$, they have several limitations. For instance, the UBND procedure could seriously overestimate the potential usefulness of a line if there is a larger number of favourable alleles in both classes C and E. Similarly, the PTC may over estimate the number of class G loci [11] and a criticism of NI is that it may be confounded with the relatedness of Iw to I1 or I2. In contrast, the number of progenies to be grown are more and computational procedures of Dudley's [2] estimates ($\mu B'$, .... $\mu G'$) are cumbersome. However, these parameters provide additional information on relative relationship among lines, thus aiding in selection of either the genetically diverse donors to maximize heterosis in the new crosses or the genetic affinity of donors with the constituent parents to maintain improvement. Moreover, if information on $\mu B'$ is not important, then the Iw lines do not need to be grown, so that one can drastically reduce the progenies to be

**Table 1.** Different estimates of favourable alleles, mean and *gca* for grain yield per plant in donor lines, when the cross IPA 34 × IPA21 was designated as the hybrid to be improved

| Inbred | μ G ′ | UBND | PTC | NI | μa (B + C) | Mean | *gca* |
|---|---|---|---|---|---|---|---|
| **Yield per plant (gm)** | | | | | | | |
| TCA21 | 7.67(6) | 27.02(5) | 102.58(8) | 1.83(8) | 2.47(6) | 70.16(7) | –3.01(6) |
| FSA17 | 11.29(2) | 34.26(2) | 107.60(3) | 5.45(3) | 4.55(4) | 74.18(5) | –0.08(5) |
| IPA3 | 11.92(1) | 36.03(1) | 111.31(2) | 6.33(2) | 4.48(5) | 79.27(2) | 3.71(1) |
| IPA22 | 10.80(3) | 28.25(4) | 111.71(1) | 7.48(1) | 5.24(3) | 74.05(6) | 3.41(2) |
| SC7 | 6.61(8) | 21.98(8) | 103.38(7) | 2.22(6) | –2.02(8) | 74.41(4) | 2.27(3) |
| IPA29 | 8.83(4) | 29.35(3) | 103.51(6) | 2.99(5) | 6.37(1) | 79.95(1) | –5.98(8) |
| IPA8 | 6.88(7) | 23.10(7) | 103.93(5) | 2.21(7) | 6.07(2) | 60.74(8) | –5.26(7) |
| CM117 | 7.84(5) | 24.17(6) | 105.85(4) | 3.60(4) | 0.81(7) | 74.51(3) | 1.91(4) |
| **Ear length (cm)** | | | | | | | |
| TCA21 | 0.82(6) | 2.11(6) | 15.15(5) | 0.59(6) | 0.72(2) | 12.92(6) | –0.42(7) |
| FSA17 | 0.83(5) | 2.12(5) | 15.12(7) | 0.60(5) | 0.47(5) | 12.81(7) | –0.20(5) |
| IPA3 | 1.25(1) | 2.96(1) | 16.04(3) | 1.02(2) | 0.69(3) | 13.14(4) | 0.51(3) |
| IPA22 | 0.81(7) | 2.08(7) | 15.38(4) | 0.57(7) | 0.39(6) | 12.99(5) | 0.14(4) |
| SC7 | 1.13(3) | 2.66(3) | 16.06(2) | 0.93(3) | 0.33(7) | 13.77(3) | 0.89(1) |
| IPA29 | 1.08(4) | 2.48(4) | 15.13(6) | 0.91(4) | 0.65(4) | 14.50(1) | –0.35(6) |
| IPA8 | 0.25(8) | 0.66(8) | 14.29(8) | 0.16(8) | 0.27(8) | 12.08(8) | –0.82(8) |
| CM117 | 1.22(2) | 2.75(2) | 16.24(1) | 1.06(1) | 0.85(1) | 14.17(2) | 0.55(2) |
| **Ear diameter (cm)** | | | | | | | |
| TCA21 | 0.16(3) | 0.70(3) | 3.97(4) | –0.03(4) | –0.06(5) | 3.34(7) | 0.00(4) |
| FSA17 | 0.20(2) | 0.77(2) | 4.11(2) | 0.02(3) | 0.05(1) | 3.38(4) | 0.03(3) |
| IPA3 | 0.14(5) | 0.66(4) | 3.94(5) | –0.05(5) | –0.07(6) | 3.43(2) | –0.03(6) |
| IPA22 | 0.15(4) | 0.56(6) | 4.04(3) | 0.04(1) | –0.03(4) | 3.40(3) | 0.04(2) |
| SC7 | 0.07(8) | 0.49(8) | 3.84(8) | –0.12(8) | –0.11(7) | 3.07(8) | –0.09(7) |
| IPA29 | 0.13(6) | 0.65(5) | 3.92(6) | –0.06(6) | 0.01(3) | 3.37(5) | –0.12(8) |
| IPA8 | 0.21(1) | 0.79(1) | 4.14(1) | 0.03(2) | 0.03(2) | 3.51(1) | 0.08(1) |
| CM117 | 0.09(7) | 0.51(7) | 3.89(7) | –0.08(7) | –0.14(8) | 3.35(6) | –0.01(5) |

The numbers in brackets indicate the rank of the donors according to the various estimators. μ G ′ = Estimator of Dudley (1987); UBND = Minimum upper bound estimator proposed by Gerloff and Smith (1988); PTC = Predicted three-way cross (Sprague and Eberhart, 1977); NI = Net improvement statistic (Bernardo, 1990); μa (B + G) = Unbiased estimator on the basis of combining ability model (Hohls *et al.*, 1995); Mean = Mean *per se*; *gca* = General combining ability (Griffing, 1956)

**Table 2.** Rank correlations between different estimates of favourable alleles, mean and *gca* for yield per plant, ear length and ear diameter

| Estimator | Trait | μ G ′ | UBND | PTC | NI | μa (B + G) | Mean | *gca* |
|---|---|---|---|---|---|---|---|---|
| μ G ′ | Yield/plant | - | 0.95** | 0.76** | 0.81* | 0.31 | 0.40 | 0.38 |
| | Ear length | - | 1.00** | 0.71* | 0.98** | 0.55 | 0.69 | 0.26 |
| | Ear diameter | - | 0.93** | 0.98** | 0.86** | 0.79* | 0.62 | 0.81** |
| UBND | Yield/plant | | | 0.55 | 0.62 | 0.38 | 0.43 | 0.19 |
| | Ear length | | | 0.71* | 0.98** | 0.55 | 0.69 | 0.26 |
| | Ear diameter | | | 0.86** | 0.64 | 0.76* | 0.60 | 0.57 |
| PTC | Yield/plant | | | | 0.93** | 0.26 | 0.12 | 0.60 |
| | Ear length | | | | 0.76* | 0.45 | 0.64 | 0.45 |
| | Ear diameter | | | | 0.93** | 0.81* | 0.71* | 0.86** |
| NI | Yield/plant | | | | | 0.14 | 0.38 | 0.67 |
| | Ear length | | | | | 0.60 | 0.74* | 0.33 |
| | Ear diameter | | | | | 0.69 | 0.69 | 0.86** |
| μa (B + G) | Yield/plant | | | | | | –0.05 | –0.05 |
| | Ear length | | | | | | 0.43 | –0.26 |
| | Ear diameter | | | | | | 0.52 | 0.48 |
| Mean | Yield/plant | | | | | | | 0.17 |
| | Ear length | | | | | | | 0.10 |
| | Ear diameter | | | | | | | 0.55 |
| *gca* | Yield/plant | | | | | | | - |
| | Ear length | | | | | | | - |
| | Ear diameter | | | | | | | - |

*,**Significant at 1% and 5%, respectively.

evaluated. The mean *per se* and *gca* of the donors completely failed to give a clear picture of whether the donors, with reference to a particular target cross have favourable alleles or not to enhance the said target cross.

One parameter, $\mu a$ (B + G), though is based on combining ability effects, is purported to be free of the bias resulting from one of the most important restriction of complete dominance i.e. a = 1 [5]. This fact is, however, not borne by the results of the present study since $\mu a$ (B + G) has failed to rank the donor lines in harmony with other methods and also showed poor or no association with them. Ideally $\mu a$ (B + G) should have accounted for the situation and compensated in such a way so as to give true rankings. However, such results are expected as different sets of parents and crosses will give different values of $\mu a$ (B + G) even in the case of non-uniformity with dominance. In conclusion perusal of the present results indicate that $\mu G'$, NI, PTC and UBND have similarities in identifying donors with favourable alleles for improvement of single cross hybrid.

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