



Identification of favourable alleles in inbred parents for the improvement of single cross hybrid in maize (*Zea mays* L.)

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Ever since the recognition of heterosis and its commercial exploitation, development of hybrid cultivars has become indispensable in most of the crop species. Despite, plant breeders choose parents based on *per se* performance, combining ability and genetic divergence studies etc., selection based on identification of favourable alleles [1 to 3] in inbred parents for the improvement of single cross hybrids is gaining more importance. The present investigation has been, therefore undertaken to identify favourable alleles in maize inbred lines for the improvement of an elite hybrid (IPA34 × IPA21).

A set of ten inbred lines, of which two are the parents of the elite hybrid (IPA34 × IPA21) and eight are the second cycle inbred lines, were considered for this study. All the inbred lines *viz.*, IPA34, IPA21, TCA21, FSA17, IPA3, IPA22, SC7, IPA29, IPA8 and CM117 were crossed among themselves in a diallel fashion. These ten inbred lines along with the forty five hybrids generated through 10 × 10 diallel mating design were grown in separate but adjacent plots using randomized block design with three replications at Indian Agricultural Research Institute, New Delhi and Regional Agricultural Research Station, Uchani, Karnal for two years (Kharif, 95 and Kharif, 96) consecutively, thus making total four environments. 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.

Yield (g/plant) data were recorded by averaging five individual plants data for each entry in each replication at all the four locations and used for calculating different parameters of the model. Though all 45 crosses and their parents were evaluated a target cross (IPA34 × IPA21) which has been *a priori* projected to be improved was considered based on its proven performance in the previous yield trials conducted

over several years in the coordinated maize project and presumed for further scope of improvement by any means. It is to be seen that, whether any such alleles could be identified in this cross for giving further improvement. The identification of favourable alleles for grain yield/plant present in the donor line (from now onwards designated as $\mu G'$) but not in the hybrid to be improved was carried out by using Dudley [2] model. As mentioned earlier, since there are 10 lines in total in the experiment, there will be 8 donor inbred lines for each and every selected cross. Besides $\mu G'$, other parameters of the model $\mu B'$, $\mu C'$, $\mu D'$, $\mu E'$ and $\mu F'$ were also calculated.

The estimates of $\mu G'$ in the eight donor lines for the cross IPA34 × IPA21 for grain yield per plant was reported (Table 1) for individual environments as well as combined analysis separately. Considering the overall data, it may be inferred that estimates of $\mu G'$ in various donor inbreds greatly differed in different environments for the same trait. This may be attributed to the differential environment effects on the same set of genes governing the expression of the same trait. The various parameters to represent the different classes and the relationship of the donor inbreds of the cross concerned are presented in Table 2. It could be concluded from this table that IPA3 and FSA17 were the two top donor inbreds possessing high levels of positive favourable alleles not present in the constituents of the hybrid. There are other two inbreds, namely IPA22 and CM117 also possessing high frequency of positive alleles, thus qualifying as efficient donors for increasing the cross performance. It is interesting to note that the donor IPA22, though ranked third in magnitude of $\mu G'$ values after FSA17 and IPA3, gave enhanced yield (116.80g) when crossed with IPA34 comparative to the crosses, IPA34 × FSA17 (102.45g) and IPA34 × IPA3 (108.11g). It is because, though

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Table 1. Estimates of $\mu G'$ in the donor inbred lines for grain yield per plant at different environments and combined over environments, when the cross IPA34 \times IPA21 was designated as the hybrid to be improved

Inbred	$\mu G'$				
	Del. 95	Del. 96	Kar. 95	Kar. 96	Combined
Grain yield per plant					
TCA21	6.06 ^{bd}	4.01b	4.87 ^c	18.77 ^{*c}	7.67 ^{*b}
FSA17	10.78 ^{bd}	4.12 ^c	-2.07 ^c	31.46 ^{*a}	11.29 ^{*c}
IPA3	8.19 ^{bd}	14.62 ^{*c}	2.47 ^b	25.21 ^{*a}	11.92 ^{*c}
IPA22	N	14.71 ^{*a}	7.93 ^{*b}	15.74 ^{*b}	10.80 ^{*b}
SC7	1.78 ^c	9.60 ^{*b}	3.99 ^b	12.99 ^{*b}	6.61 ^{*b}
IPA29	2.45 ^c	5.77 ^a	5.29 ^c	21.82 ^{*a}	8.83 ^{*c}
IPA8	5.93 ^{bd}	10.27 ^{*c}	1.03 ^b	12.86 ^{*b}	6.88 ^{*b}
CM117	2.33 ^b	10.27 ^{*c}	1.19 ^b	18.96 ^{*b}	7.84 ^{*b}
S.E. a	2.53	2.49	2.73	2.27	2.51
S.E. b	2.53	2.49	2.73	2.27	2.51
S.E. c	3.17	3.12	3.38	2.84	3.13
S.E. d	3.17	3.12	3.38	2.84	3.13

a = q_{j0} , q_{k1} , b = q_{j1} , q_{k0} , c = q_{j0} , q_{j1} and d = q_{k0} , q_{k1}
 *Larger than $2 \times$ S.E.; N= $\mu G'$ values could not be obtained

Table 2. Estimates of $\mu B'$, ..., $\mu G'$ for grain yield per plant in the eight donor inbred lines when IPA34 \times IPA21@ is the hybrid to be improved

Donors	Class of loci					$\mu G'$	$\mu C' + \mu F'$	$\mu D' + \mu E'$	Genetic affinity with	Mean <i>per se</i> of IPA34 \times donor (g)	Mean <i>per se</i> of IPA21 \times donor (g)
	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$						
TCA21 ^b	8.91*	5.84*	5.84*	13.66*	8.76*	7.67*	14.61*	19.50*	IPA21	99.66	105.50
FSA17 ^c	8.29*	5.84*	5.84*	11.43*	10.99*	11.29*	16.83*	17.28*	IPA21	102.45	112.74
IPA3 ^c	8.58*	5.84*	5.84*	13.63*	8.79*	11.92*	14.63*	19.48*	IPA21	108.11	114.11
IPA22 ^b	13.02*	3.33	8.36*	19.10*	3.33	10.80*	6.66	27.46*	IPA21	116.80	106.73
SC7 ^b	8.64*	4.39	7.30*	18.04*	4.39	6.61*	8.77*	25.34*	IPA21	106.29	100.46
IPA29 ^c	3.77	5.84*	5.84*	12.25*	10.17*	8.83*	16.01	18.10*	IPA21	99.18	107.83
IPA8 ^b	15.75*	4.67	7.02*	17.75*	4.67	6.88*	9.34*	24.77*	IPA21	101.85	101.58
CM117 ^b	9.83*	4.25	7.44*	18.18*	4.25	7.84*	8.49*	25.62*	IPA21	106.27	102.65

@ mean of the cross IPA34 \times IPA21 is 101.85; *larger than $2 \times$ S.E.; b = q_{j1} , q_{k0} ; c = q_{j0} , q_{j1}

FSA17 and IPA3 had higher $\mu G'$ values, they also possessed higher $\mu F'$ (class where P_1 (IPA34) \times Pw (FSA17 or IPA3) have unfavourable alleles and P_2 (IPA21) has favourable alleles) compared to IPA22, which had non-significant $\mu F'$ value. Hence, when P_2 (IPA21) is replaced by Pw (FSA17 or IPA3), the significant $\mu G'$ values were nullified by significant $\mu F'$ values, which led to the lowering of mean *per se* values. On the contrary, opposite consequences were observed when P_2 (IPA21) is crossed with FSA17, IPA3 and IPA22, in which $\mu D'$ (class in which P_2 (IPA21) and Pw (FSA17 or IPA3 or IPA22) have unfavourable alleles and P_1 (IPA34) has favourable alleles) is higher in IPA22 (8.36) than FSA17 (5.84), resulting into the higher mean *per se* values of the crosses IPA3 \times IPA21 (114.11g) and FSA17 \times IPA21 (112.74g) compared to IPA22 \times IPA21 (106.73g). Hence, it may

be suggested that enhancement in performance in the cross combination (IPA34 \times IPA21) may be obtained by replacing IPA21 with IPA22. Likewise, the other constituent inbred IPA34 can be replaced by donors IPA3 or FSA17. While choosing, the option of replacing one of the parent based on this model one should be cautious of not sacrificing any of the positive quality of the original hybrid.

Based on the present results, it has been clearly observed that, if the improvement of this cross is sought *via* parental improvement, the donors IPA3, FSA17 and IPA22 can be used for recycling. Since these three have genetic affinity with IPA21, it may be surmised that enhancement of IPA21 by them will not cause any canceling effect which usually emanate from wide diversity of alleles coming together causing disequilibrium in the degree of association of dominant genes acting in opposite directions. Thus, this study has clearly confirmed the usefulness of this model in single cross hybrid improvement programmes. As mentioned earlier, the parameters ($\mu B'$ to $\mu G'$) of this model are helpful

for a breeder not only in precisely choosing the donors but also in estimating the degree of loss or gain, when a donor is exchanged/selected for recycling with either of the parent, which is novel and not available in other conventional methods for selection of parents.

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