



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

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### **ABSTRACT**

*The present investigation was aimed to identify lines with favourable alleles ( $\mu G'$ ) in the recycled inbred lines for the improvement of an elite single cross BML 6  $\times$  BML 7, which had the high mean yield per se value of the 45 crosses obtained from 10  $\times$  10 diallel and tested in five environments. 100- kernel weight, ear length and number of kernels per row which showed positive correlation with yield were also considered for this purpose. The results indicated that, the estimates of  $\mu G'$  were able to detect differences among the donor inbreds in the relative number of loci with new favourable alleles for grain yield, 100-kernel weight, ear length and number of kernels per row not present in the elite hybrid BML 6  $\times$  BML 7. The estimates of  $\mu G'$  in various donor inbreds varied in different environments for the same trait. Considering the parameters ( $\mu C + \mu F$ ) and ( $\mu D + \mu E$ ), it was found that the BML 7 can be utilized for the improvement through pedigree breeding by crossing to CM 131 or BML 10. These lines possessed favourable alleles for yield contributing characters viz., 100-kernel weight, ear length and number of kernels per row.*

**Keywords:** Maize, single cross hybrids, donor inbreds, favourable alleles.

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### **INTRODUCTION**

Maize breeding research in India, since its inception during late 1950's has passed through several varied breeding cultivar strategies, such as synthetics, composites, double cross hybrids, top cross hybrids. Though for the last few years, double cross hybrids have shown superiority over composites practically utilization of maximum heterosis is possible through single cross hybrids [6]. Hence the focus, of late, started to development of single cross hybrids for which production of commercially viable inbreds are of in great importance. The production of improved base populations which are heterotic to each other [7] when subjected to inbreeding, led to the development of inbred lines having high *per se* performance. The present set of second cycle inbred lines yielding more than 3 tones/ha may be considered as commercially viable to sustain single cross hybrids in the country [8]. To further enhance the productivity of superior single cross hybrids, the improvement of the constituent parental inbreds through recycling using backcross or pedigree method by identifying suitable donors with favourable alleles, not already present in either of the parents, could be considered most efficient methodology [2-5]. The present investigation was, therefore, initiated from a set of newly developed inbred lines with the objective of identifying favourable alleles to improve the selected elite single cross hybrids using Dudley [3] model.

### **Materials and methods**

The material consisted of ten second cycle inbred lines of maize (CM 119, CM 120, CM 131, CM 133, CM 210, CM 211, BML 6, BML 7, BML 13 and BML 10). All these ten inbred lines were genetically diverge with respect to different traits. Material for the present study consist of ten parents and 45 F<sub>1</sub> crosses (excluding reciprocals) were grown in randomized complete block design with three replications. Each entry was accommodated in one row plot of 4 meter length. Plant to plant distance of 20 cm and row to row distance of 75 cm were maintained. Ten inbred lines of maize were crossed in a half diallel during *kharif*, 2009 and *kharif*, 2010 at S.V Agricultural college farm, Tirupati, A.P. The entire forty five cross combinations were evaluated during *rabi* 2009, *summer* 2010, *kharif* 2010, *rabi* 2010 -11 and *rice fallow* 2010-11 in a Randomized Block Design (RBD) with three replications. The crop was raised as per the

recommended cultural practices. Though data were recorded on 14 important characters, keeping in mind the practical difficulty of simultaneous improvement of several characters, four important characters *viz.*, grain yield per plant, 100-kernel weight, ear length and number of kernels per row were considered for the identification of favourable alleles. An analysis of variance was performed for each environment separately and then combined over environments after testing of homogeneity of error variances for both inbreds as well as hybrids. For the identification of favourable alleles only the high yielding hybrid *i.e.* BML 6 × BML 7 was considered based on its proven performance assessed in the present trials conducted for five seasons/situations and presumed to represent the highest level of performance. Hence, it is to be seen that, whether any such favourable alleles could be identified for this cross for giving further improvement by any means. The identification of favourable alleles 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 [3] model. Of the 10 lines 8 will be donor inbred lines for the selected cross BML 6 × BML 7.

## Results and Discussion

The estimates of  $\mu G'$  in the donor inbred lines, when the hybrid to be improved is BML 6 × BML 7, are presented in Table 1. For grain yield per plant, in combined analysis as well as in individual environments, all the eight inbred lines had significant positive  $\mu G'$  estimates except CM 210 in *kharif* 2010 and *rabi* 2010-11 and BML 13 in *kharif* 2010 and *rice fallow* 2010-11. In combined analysis, BML 10 had shown the highest  $\mu G'$  estimate followed by CM 131 and CM 119. However, BML 13 showed the lowest  $\mu G'$  estimate among all donors. In *rabi* 2009-10, the donor inbred line CM 210 showed highest  $\mu G'$  estimate. Similarly BML 10 in *summer* 2010; CM 211 in *kharif* 2010; CM 131 in *rabi* 2010-11 and CM 119 in *rice fallow* 2010-11 showed the highest estimates in the respective environments.

For 100- kernel weight, seven inbreds namely CM 119, CM 120, CM 131, CM 133, CM 211, BML 13 and BML 10 showed significant positive  $\mu G'$  estimates in combined analysis, of which CM 133 gave the highest  $\mu G'$  estimate followed by CM 211 and CM 131. The donor CM 210 recorded the lowest  $\mu G'$  estimate in combined analysis. Considering the individual environments, all the eight inbreds except CM 210 in *rabi* 2009-10; CM 120, CM 131, CM 133, CM 211 and BML 10 in *summer* 2010; CM 131,

**Table 1. Estimates of  $\mu G'$  in the donor inbred lines for important quantitative traits at different environments and combined over environments, when the hybrid BML 6 × BML 7 (target cross) was designated as the hybrid to be improved**

Inbred	$\mu G'$					
	RA 09-10	SU 10	KH 10	RA10-11	RF 10-11	Combined
<b>Grain yield per plant</b>						
CM 119	21.745 <sup>a</sup>	20.222 <sup>a</sup>	19.015 <sup>b</sup>	21.413 <sup>b</sup>	22.132 <sup>b</sup>	21.270 <sup>b</sup>
CM 120	7.368 <sup>a</sup>	9.017 <sup>b</sup>	11.405 <sup>b</sup>	11.110 <sup>a</sup>	16.477 <sup>b</sup>	11.317 <sup>b</sup>
CM 131	25.360 <sup>a</sup>	18.163 <sup>b</sup>	20.888 <sup>b</sup>	23.920 <sup>b</sup>	20.253 <sup>b</sup>	21.918 <sup>b</sup>
CM 133	15.185 <sup>a</sup>	17.353 <sup>a</sup>	14.782 <sup>a</sup>	14.470 <sup>a</sup>	15.230 <sup>a</sup>	15.403 <sup>a</sup>
CM 210	25.462 <sup>c</sup>	8.398 <sup>a</sup>	4.985 <sup>a</sup>	4.325 <sup>a</sup>	7.650 <sup>a</sup>	7.490 <sup>a</sup>
CM 211	13.980 <sup>a</sup>	16.130 <sup>a</sup>	23.228 <sup>b</sup>	17.465 <sup>a</sup>	17.085 <sup>a</sup>	17.438 <sup>a</sup>
BML 13	9.595 <sup>b</sup>	11.855 <sup>b</sup>	2.975 <sup>a</sup>	6.795 <sup>b</sup>	4.420 <sup>b</sup>	7.265 <sup>b</sup>
BML 10	23.342 <sup>a</sup>	20.765 <sup>a</sup>	21.967 <sup>b</sup>	23.003 <sup>b</sup>	21.570 <sup>b</sup>	22.495 <sup>b</sup>
SE a	3.111	2.559	2.716	3.040	2.869	2.866
SE b	3.111	2.559	2.716	3.040	2.869	2.866
SE c	3.905	-	-	-	-	-
SE d	3.905	-	-	-	-	-
<b>100 - kernel weight</b>						
CM 119	1.523 <sup>a</sup>	0.520 <sup>a</sup>	0.735 <sup>a</sup>	1.155 <sup>a</sup>	0.742 <sup>a</sup>	1.935 <sup>a</sup>
CM 120	2.355 <sup>c</sup>	1.372 <sup>b</sup>	N	1.952 <sup>c</sup>	1.453 <sup>a</sup>	1.320 <sup>c</sup>
CM 131	1.825 <sup>a</sup>	1.512 <sup>b</sup>	2.375 <sup>c</sup>	3.105 <sup>b</sup>	1.710 <sup>b</sup>	2.067 <sup>b</sup>
CM 133	2.610 <sup>c</sup>	2.047 <sup>c</sup>	2.965 <sup>c</sup>	3.522 <sup>c</sup>	1.612 <sup>c</sup>	2.550 <sup>c</sup>
CM 210	0.590 <sup>b</sup>	0.997 <sup>c</sup>	-0.430 <sup>c</sup>	1.920 <sup>b</sup>	1.707 <sup>c</sup>	0.840 <sup>c</sup>
CM 211	2.005 <sup>c</sup>	1.932 <sup>c</sup>	1.845 <sup>b</sup>	2.987 <sup>c</sup>	2.392 <sup>c</sup>	2.220 <sup>c</sup>
BML 13	1.370 <sup>b</sup>	N	-0.760 <sup>b</sup>	2.323 <sup>b</sup>	1.353 <sup>a</sup>	1.110 <sup>b</sup>

BML 10	2.080 <sup>b</sup>	1.375 <sup>b</sup>	1.068 <sup>b</sup>	2.397 <sup>c</sup>	2.322 <sup>c</sup>	1.088 <sup>a</sup>
SE a	0.558	0.474	0.477	0.498	0.525	0.508
SE b	0.558	0.474	0.477	0.498	0.525	0.508
SE c	0.671	0.557	0.572	0.587	0.646	0.609
SE d	0.671	0.557	0.572	0.587	0.646	0.609

Contd...

Table 1. Contd...

Inbred	$\mu G'$					
	RA 09-10	SU 10	KH 10	RA10-11	RF10-11	Combined
<b>Ear Length</b>						
CM 119	0.812 <sup>a</sup>	0.810 <sup>c</sup>	0.712 <sup>b</sup>	1.243 <sup>a</sup>	1.188 <sup>b</sup>	0.945 <sup>c</sup>
CM 120	-0.250 <sup>b</sup>	-0.075 <sup>c</sup>	0.377 <sup>b</sup>	1.285 <sup>b</sup>	0.863 <sup>b</sup>	0.438 <sup>b</sup>
CM 131	0.990 <sup>c</sup>	0.980 <sup>b</sup>	1.547 <sup>a</sup>	1.655 <sup>c</sup>	1.370 <sup>b</sup>	1.295 <sup>b</sup>
CM 133	0.995 <sup>a</sup>	1.030 <sup>a</sup>	0.827 <sup>a</sup>	2.075 <sup>c</sup>	1.050 <sup>a</sup>	1.035 <sup>a</sup>
CM 210	0.477 <sup>a</sup>	0.640 <sup>c</sup>	0.115 <sup>a</sup>	-0.337 <sup>a</sup>	0.065 <sup>a</sup>	0.197 <sup>a</sup>
CM 211	0.420 <sup>a</sup>	1.165 <sup>c</sup>	0.637 <sup>a</sup>	1.423 <sup>a</sup>	1.605 <sup>a</sup>	0.905 <sup>a</sup>
BML 13	0.630 <sup>a</sup>	0.665 <sup>a</sup>	0.455 <sup>a</sup>	0.887 <sup>b</sup>	0.918 <sup>b</sup>	0.716 <sup>c</sup>
BML 10	1.195 <sup>b</sup>	1.012 <sup>b</sup>	1.098 <sup>b</sup>	1.185 <sup>b</sup>	1.055 <sup>b</sup>	1.107 <sup>b</sup>
SE a	0.283	0.274	0.275	0.313	0.281	0.286
SE b	0.283	0.274	0.275	0.313	0.281	0.286
SE c	0.354	0.345	-	0.385	-	0.356
SE d	0.354	0.345	-	0.385	-	0.356
<b>Number of kernels per row</b>						
CM 119	3.980 <sup>a</sup>	4.383 <sup>a</sup>	4.083 <sup>a</sup>	4.700 <sup>a</sup>	4.150 <sup>b</sup>	4.260 <sup>a</sup>
CM 120	2.723 <sup>b</sup>	2.460 <sup>b</sup>	2.770 <sup>b</sup>	3.115 <sup>a</sup>	3.562 <sup>a</sup>	3.065 <sup>b</sup>
CM 131	5.418 <sup>a</sup>	5.617 <sup>b</sup>	4.805 <sup>a</sup>	5.983 <sup>b</sup>	4.640 <sup>b</sup>	5.057 <sup>a</sup>
CM 133	4.808 <sup>a</sup>	4.137 <sup>a</sup>	4.115 <sup>a</sup>	4.750 <sup>a</sup>	3.985 <sup>a</sup>	4.360 <sup>a</sup>
CM 210	3.273 <sup>b</sup>	2.530 <sup>a</sup>	2.850 <sup>b</sup>	0.200 <sup>a</sup>	2.097 <sup>a</sup>	2.083 <sup>a</sup>
CM 211	3.018 <sup>a</sup>	3.970 <sup>a</sup>	2.568 <sup>a</sup>	3.650 <sup>a</sup>	3.590 <sup>a</sup>	3.360 <sup>a</sup>
BML 13	2.705 <sup>b</sup>	1.522 <sup>a</sup>	2.587 <sup>b</sup>	3.050 <sup>b</sup>	2.905 <sup>b</sup>	2.652 <sup>b</sup>
BML 10	4.853 <sup>b</sup>	5.205 <sup>b</sup>	4.203 <sup>b</sup>	5.541 <sup>a</sup>	2.773 <sup>a</sup>	4.170 <sup>a</sup>
SE a	0.450	0.421	0.593	0.617	0.617	0.547
SE b	0.450	0.421	0.593	0.617	0.617	0.547
SE c	-	-	-	-	-	-
SE d	-	-	-	-	-	-

RA 09-10 = Rabi 2009-10; SU 10= Summer 2010; KH 10= Kharif 2010; RA 10-11=Rabi 2010-11;  
RF 10-11= Rice fallow 2010-11.

\* Larger than 2 x SE; N =  $\mu G'$  values could not be obtained

a =  $q_{j0}$ ,  $q_{kl}$

b =  $q_{j1}$ ,  $q_{k0}$

c =  $q_{j0}$ ,  $q_{j1}$

d =  $q_{k0}$ ,  $q_{k1}$

**Table 2. Estimates of  $\mu B'$ .....  $\mu G'$  for grain yield per plant in eight donor inbred lines when BML 6  $\times$  BML 7 @ is the hybrid to be improved**

Class of loci											
Donors	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean <i>per se</i> of BML 6 $\times$ donor	Mean <i>per se</i> of BML7 $\times$ donor
CM 119	25.085*	11.255*	14.075*	13.080*	11.255*	21.270*	22.510*	27.155*	BML 7	140.090	134.450
CM 120	22.052*	12.332*	12.997*	12.003*	12.332*	11.317*	24.665*	25.000*	BML 7	118.030	116.700
CM 131	31.983*	11.382*	13.948*	12.953*	11.382*	21.918*	22.765*	26.900*	BML 7	141.130	136.000
CM 133	30.013*	21.492*	3.837	3.837	20.497*	15.403*	41.990*	7.675*	BML 6	109.870	143.190
CM 210	23.185*	19.705*	5.625	5.625	18.710*	7.490*	38.415*	11.250*	BML 6	97.620	123.790
CM 211	22.403*	19.172*	6.158*	6.158*	18.177*	17.438*	37.350*	12.325*	BML 6	118.580	142.620
BML 13	18.910*	10.405*	14.925*	13.930*	10.405*	7.265*	20.810*	28.855*	BML 7	113.780	104.740
BML 10	31.710*	12.190*	13.140*	12.145*	12.190*	22.495*	24.380*	25.285*	BML 7	140.670	138.770

@ Mean *per se* of the cross BML 6  $\times$  BML 7 is: 120.060

\* Larger than 2  $\times$  S.E.

a=  $q_{jo}$ ,  $q_{ki}$ ;

b=  $q_{j1}$ ,  $q_{ko}$ ;

c=  $q_{jo}$ ,  $q_{j1}$ ;

d=  $q_{ko}$ ,  $q_{k1}$

CM 133, CM 211 and BML 10 in *kharif* 2010; all eight donor inbreds in *rabi* 2010-11 and all the eight inbreds except CM 119 in *rice fallow* 2010-11 gave significant positive  $\mu G'$  estimates. It is interesting to note that in *summer* 2010 and *kharif* 2010,  $\mu G'$  estimates could not be obtained for the donor BML 13 and CM 120, respectively. The reasons may be due to the failure of the assumptions of complete dominance or epistasis [4].

For ear length, in combined analysis, six donors CM 119, CM 131, CM 133, CM 211, BML 13 and BML 10 showed significant positive  $\mu G'$  estimates, of which CM 131 gave the highest followed by CM 133, while CM 210 gave the lowest  $\mu G'$  value. Similarly, the donors CM 119, CM 131, CM 133, BML 13 and BML 10 in *rabi* 2009-10; CM 119, CM 131, CM 133, CM 211, BML 13 and BML 10 in *summer* 2010; CM 119, CM 131, CM 133, CM 211 and BML 10 in *rabi* 2010-11 and all the eight donor inbreds except CM 210 in both *rabi* 2010-11 and *rice fallow* 2010-11 had recorded significant positive  $\mu G'$  estimates. For number of kernels per row, all donors gave significant positive  $\mu G'$  estimates in combined analysis as well as in individual environments except CM 210 in *rabi* 2010-11. In combined analysis, the donor inbred CM 131 had exhibited the highest  $\mu G'$  value followed by CM 133 and CM 119, while CM 210 gave the lowest  $\mu G'$  value.

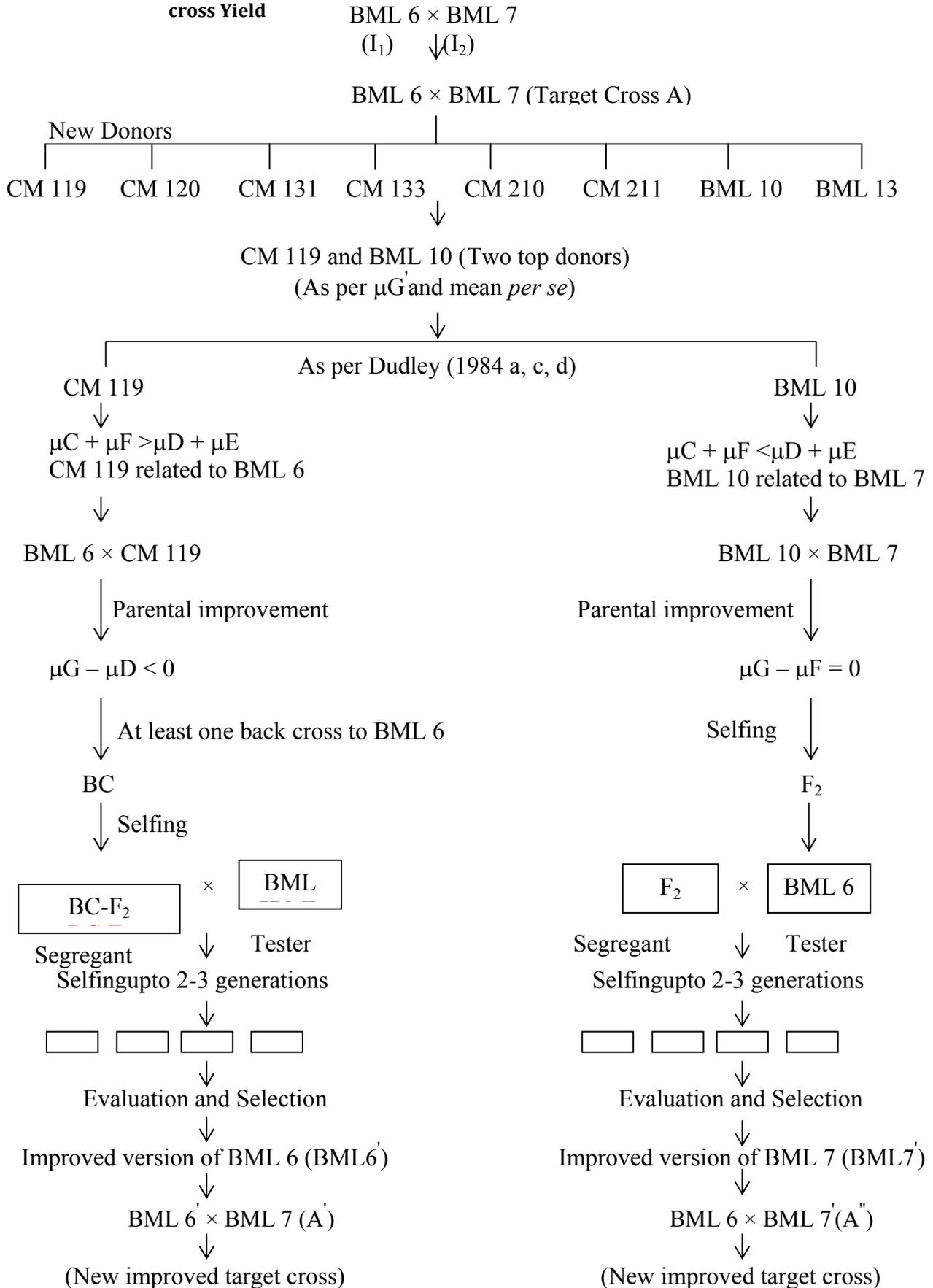
It is interesting to note that for some of the donors  $\mu G'$  values could not be obtained (indicated as 'N' in Table 1). The reasons, probably, due to failure of the assumptions of complete dominance or epistasis [3]. It is also observed that estimates of  $\mu G'$  in various donor inbreds greatly differed in different environments for the same trait. This may be attributed to differential environmental effects on the same sets of genes governing the expression of the same trait. However, considering the overall data, it may be inferred that BML 10 or CM 131 showed the highest significant positive favourable alleles for all the four characters in combined analysis there by indicating the existence of favourable alleles for further improvement of BML 6  $\times$  BML 7.

Apart from suggesting the donors for simultaneous improvement for all these characters, the characterization of donors with respect of favourable alleles and its interaction with the other classes of loci and genetic similarity estimates specific to grain yield per plant was also considered, since grain yield is the major trait for which genetic enhancement is mostly needed. The cross BML 6  $\times$  BML 7, which had the high mean yield was deliberately chosen with the premise that, this cross is generally supposed to have already accumulated the highest frequency of favourable alleles and the model should fail to identify for the improvement of this cross. However, surprisingly eight out of eight donors gave significant positive  $\mu G'$  values.

Critical study of mean *per se* values of the crosses and different parameters of the model taken into consideration together (Table 2) revealed that the findings were beyond expectations. For example, the donor inbred BML 10, though showed the highest significant  $\mu G'$  estimate (22.49) among the donors, expectedly should have given higher mean values in its cross combinations with the constituents (BML 6 and BML 7) of the original superior cross. However, such was not the case, which could be attributed to

higher estimates of  $\mu G'$  (class in which BML 6 and BML 10 have unfavourable alleles and BML 7 and BML 10 has favourable alleles). It is, therefore, obvious that these higher  $\mu F'$

**Fig. 1** : Suggested Breeding Plan for Utilization of Selected Donor lines to Improve Target cross Yield



and  $\mu G'$  values must have cancelled the effect of favourable alleles ( $\mu G'$ ) present in BML 10 and led to the lower mean *per se* values in the crosses (BML 6  $\times$  BML 10 and BML 7  $\times$  BML 10). The possibility of such findings was also expected by several workers [1-3]. Hence, no donor could be suggested for direct replacement of any parent in the superior cross. However, the donors BML 10, CM 131 and CM 119 may be suggested for the improvement of parental inbreds, as these three donors had higher  $\mu G'$  values compared to the rest.

In conclusion, considering the parameters ( $\mu C' + \mu F'$ ) and ( $\mu D' + \mu E'$ ), it was found that the parent BML 7 can be utilized for the improvement through pedigree selection by crossing to BML 10 or CM 131. If one among these two is to be considered, greater importance should be given to CM 131 since it has shown highest significant positive favourable alleles for the other contributing characters. A comprehensive breeding plan (Fig.1) may be suggested for practical utilization in the improvement programme of the elite hybrid BML 6  $\times$  BML 7. The present results also substantiate the usefulness of the  $\mu G'$  estimates besides assessing the other biometrical parameters. Similarly, several workers were also reported by Nagesh Kumar *et al* [9]; Reddy *et al* [10]; Rodriguez *et al* [11] and Secanski Mile *et al* [12].

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