

Identification of Favourable Alleles in Donor Inbreds for Improvement of Single Cross Hybrid of Maize (*Zea mays* L.)

M. Paramesh^{1*}, K.H.P. Reddy¹, D.M. Reddy¹, V. Rajarajeswari² and B.V. Bhaskara Reddy³

¹Department of Genetics & Plant Breeding, S.V. Agricultural College, Tirupati- 517502

²Department of Crop Physiology, S.V. Agricultural College, Tirupati- 517502

³Department of Plant Pathology, RARS, Tirupati- 517502

*Corresponding Author E-mail: parameshm026@gmail.com

Received: 2.07.2018 | Revised: 30.07.2018 | Accepted: 11.08.2018

ABSTRACT

Identification of new sources of favourable alleles for improvement of elite single cross hybrid ($P_1 \times P_2$) is one of the major goals in maize breeding programmes. The present investigation was carried out to identify the donor inbreds which have the greatest relative values of favourable alleles ($\mu G'$) for the improvement the elite single cross maize hybrid DHM 117 (BML 6 \times BML 7). The estimates of $\mu G'$ values revealed that the donor inbreds BML 15 and BML 2 could be used as source of favourable alleles for improving elite hybrid with respect to yield and yield components. This improvement might be possible by transferring favourable alleles from BML 15 and BML 2 to BML 6 through back crossing as they had high genetic affinity with BML 6.

Key words: Maize, Favourable Alleles, Single cross hybrid.

INTRODUCTION

The main objective in maize breeding programmes is to produce high yielding hybrids than those hybrids already identified as top yielders. This can be achieved by improving or recycling one or both the inbred lines in a single cross. The inbreds are usually derived from the cross between lines coming from the same heterotic or from different heterotic groups. The elite lines are improved for combining ability in terms of yield and yield component traits. Identifying potential donors of favourable alleles to the existing elite ones is important to a breeder. To ensure

higher probability of obtaining useful inbreds, the ability of the germplasm sources in improving the inbred parents of hybrids should be determined prior to line improvement. Improving single crosses basically involves crossing the parental inbreds (parents of the single cross) with donor inbreds, with or without backcrossing, and extracting new inbreds from the crosses. Dudley^{3,4} presented a method for the identification of lines useful in improving the parents of a single cross based on $\mu G'$, which is the estimate of favourable alleles present in the donor inbred but not present in the recipient hybrid.

Cite this article: Paramesh, M., Reddy, K. H. P., Reddy, D. M., Rajarajeswari, V. and Bhaskara Reddy, B. V., Identification of Favourable Alleles in Donor Inbreds for Improvement of Single Cross Hybrid of Maize (*Zea mays* L.), *Int. J. Pure App. Biosci.* 6(5): 521-526 (2018). doi: <http://dx.doi.org/10.18782/2320-7051.6990>

Assuming complete dominance, constant genotypic value for all loci controlling the trait and no epistasis, this model works for any three homozygous lines (two parents of single cross - I_1 and I_2 and donor line - I_w). The present experiment was carried out to identify the donor inbreds with highest frequency of favourable alleles ($\mu G'$) for the improvement the elite single cross maize hybrid DHM 117. DHM 117 is a single cross hybrid developed by crossing BML 6 and BML 7 maize inbred lines. It was developed and released by Acharya N.G. Ranga Agricultural University (ANGRAU) during 2010 in Andhra Pradesh state. The main features of this hybrid were uniform plant height, stay green at harvest stage and flint grain type. This hybrid was moderately tolerant to Maydis leaf blight (MLB), Turicum leaf blight (TLB) and Banded leaf and sheath blight (BLSB). The average kernel yield of this hybrid is 75 q/ha.

MATERIAL AND METHODS

The experimental material for this study comprised of eleven inbreds *viz.*, BML 51, BML 5, CM 105, BML 2, BML 6, BML 7, BML 15, BML 14, CM 118, CM 119 and CML 124 of which two inbred lines (BML 6 and BML 7) are parents of a superior performing hybrid DHM 117. Hence this cross BML 6 \times BML 7 would be referred as target cross. All these eleven inbred lines were mated in a diallel fashion without considering the reciprocals. These eleven parents and fifty five F_1 hybrids thus developed were grown in separate but adjacent yield trials using randomized block design (RBD) with three replications during *rabi*, 2015-16 at Sri Venkateswara Agricultural College Farm, Tirupati, Andhra Pradesh. The plot size for each entry was single row of five meter length, with a spacing of 75 cm and 20 cm between row to row and plant to plant, respectively. The crop was raised as per the recommended cultural practices. Data were collected on kernel yield per plant, 100 kernel weight, ear length and number of kernels per ear row. Statistical analysis was carried out as per methodology suggested by Dudley⁴.

Relative relationship of estimates

With μ constant, estimates of $\mu B'$, $\mu C'$,..... $\mu G'$ are estimates of relative numbers of loci in each class. A positive estimate of $\mu G'$ indicates that I_w (donor inbred) contains favourable alleles at loci where both parents I_1 and I_2 contain unfavourable alleles. Likewise, positive estimates of $\mu D'$ (class where I_2 and I_w had unfavourable alleles and I_1 had favourable alleles) and $\mu F'$ (class where I_1 and I_w had unfavourable alleles and I_2 had favourable alleles) indicate that I_1 and I_2 respectively, contain favourable alleles at loci where the other two lines have unfavourable alleles. The term $\mu B'$ estimates the relative number of loci where both I_1 and I_2 have plus alleles and I_w does not, $\mu C'$ estimates the relative number of loci where I_1 and I_w have plus alleles and I_2 does not; while μE estimates the relative number of loci where I_2 and I_w have plus alleles and I_1 does not. The equation $\mu C+F'$ represents the total relative number of loci for which I_1 and I_w have the same (either + or -) alleles, while $\mu D+E'$ reflects the total relative number of loci for which I_2 and I_w have the same alleles. Thus these expressions show the relative relationship of I_1 or I_2 with I_w . In order to maintain the heterotic pattern in $I_1 \times I_2$ those I_w lines with $\mu C+F' > \mu D+E'$ (most closely related to I_1) would be crossed with I_1 and those with $\mu D+E' > \mu C+F'$ (most closely related to I_2) would be crossed with I_2 ⁴.

Evaluation of parentage of donor (I_w) with elite hybrid parents (I_1 and I_2) can be performed by using the following formulas $[(I_2 \times I_w) - (I_1 \times I_w) + (I_1 - I_2)/2]$. Positive value points to the parentage between I_1 and I_w , while negative value points to the parentage between I_2 and I_w . Depending on which parent is being improved, I_1 or I_2 , the founding initial population for selection is determined by comparing values $\mu D'$ or $\mu F'$ with value $\mu G'$. If parent I_1 is to be improved, there are three possibilities:

1. $\mu D' = \mu G'$; the probability that the new line will have more loci with favourable alleles in class D and G than either I_1 or I_w is maximum. Then the approach will be hybrid self-fertilization ($I_1 \times I_w$).

2. $\mu D' > \mu G'$; back crossing of hybrids ($I_1 \times I_w$) with parent I_1 is recommended.
3. $\mu G' > \mu D'$; back crossing of hybrids ($I_1 \times I_w$) with donor I_w is recommended.

If parent I_2 is to be improved, there are three possibilities:

1. $\mu F' = \mu G'$; the probability that the new line will have more loci with favourable alleles in class D and G than either I_2 or I_w is maximum. Then the approach will be hybrid self-fertilization ($I_2 \times I_w$).
2. $\mu F' > \mu G'$; back crossing of hybrids ($I_2 \times I_w$) with parent I_2 is recommended.
3. $\mu G' > \mu F'$; back crossing of hybrids ($I_2 \times I_w$) with donor I_w is recommended.

The standard error (SE) of the estimators for $\mu B'$ to $\mu G'$ were calculated as the square root of the variance of the linear function associated with each estimator ignoring covariance. All estimates were considered different from zero, if they exceeded twice their standard error.

RESULTS AND DISCUSSION

The estimates of $\mu G'$ for the target hybrid DHM 117 (BML 6 \times BML 7) for four quantitative traits are presented in Table 1. For kernel yield per plant, three inbreds *viz.*, BML 15, BML 2 and BML 51 were identified as potential sources of favourable alleles as they exhibited significant positive $\mu G'$ estimates. For 100 kernel weight, the inbred BML 14 recorded highest positive significant $\mu G'$ estimate followed by CML 124 and BML 51. Hence, they were referred as potential sources of favourable alleles for 100 kernel weight. In case of ear length, four inbreds *viz.*, BML 2, CM 119, BML 15 and BML 14 exhibited significant positive $\mu G'$ estimates and denoted as donors for improvement of this trait. While for the trait number of kernels per ear row, four inbreds *viz.*, CML 124, BML 15, BML 2 and CM 119 were identified as potential sources of favourable alleles as they exhibited significant positive $\mu G'$ estimates. Similarly several workers^{16,2,8,5,7,11,6,14,10,17,12,13,9,15} have identified favourable alleles in donor inbred lines for improvement of elite single cross hybrids in maize using $\mu G'$ estimates.

Further characterization of various donor inbreds and their genetic similarity estimates (Table 2) have to be analyzed critically along with the other estimates ($\mu B'$ to $\mu G'$) to initiate the improvement programme for this target hybrid. The improvement of this hybrid is sought *via* parental improvement and the inbreds *viz.*, BML 15, BML 2 and BML 51 can be used as donors for recycling as they showed high $\mu G'$ values compared with other donors. Considering the parameters ($\mu C+F'$) and ($\mu D+E'$), the donor inbreds BML 15 and BML 2 have genetic affinity with BML 6 and it may be surmised that enhancement of BML 6 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. These two donors (BML 15 and BML 2) are also superior in showing significant frequency of favourable alleles each for two traits *viz.*, ear length and number of kernels per ear row and hence, these inbreds could be considered as the best donors for recycling of the parent BML 6. While, the donor BML 51 had genetic affinity with BML 7 and it is also served as donor for 100 kernel weight hence, it could be used in the recycling of BML 7.

As a further step the most efficient procedure for the introduction of the favourable alleles must be decided upon. The essence of the problem is to decide whether the development of new inbred strains should be initiated in the F_1 or in a later backcross generation. Bailey¹ has mathematically shown that during the selfing process the probability of isolating a new line with more favourable alleles than either of the parents is maximal if, for the loci at which the parents differ, each parent has an equal number of loci with favourable alleles. If the parents do not have an equal number of loci with favourable alleles, then a backcross to the line with the greatest number of positive alleles is suggested.

Therefore, in order to maximize the probability of isolating a new line to improve parent P_1 in the cross $P_1 \times P_2$ (BML 6 \times BML

7), the relative number of loci in class G should be equal to those in class D. For the donor BML 15, $\mu G' > \mu D'$ so one generation of backcrossing to the P_w line [(BML 6 \times BML 15) \times BML 15] could be recommended before selection is commenced. Alternatively, for the donors BML 2 and BML 51, $\mu D' > \mu G'$ and backcrossing to BML 6 could be recommended before selection is initiated [(BML 6 \times BML 2) \times BML 6 and (BML 6 \times BML 51) \times BML 6].

In order to maximize the probability of isolating a new line to improve parent P_2 in the cross $P_1 \times P_2$ (BML 6 \times BML 7), the relative number of loci in class G should be equal to those in class F. For all the three donors BML 15, BML 2 and BML 51, $\mu F' > \mu G'$, so one generation of backcrossing to the P_2 line is recommended before selection is commenced [(BML 7 \times BML 15) \times BML 7, (BML 7 \times BML 2) \times BML 7 and (BML 7 \times BML 51) \times BML 7].

However, when P_1 (BML 6) is replaced by P_w (BML 15 or BML 2 or BML 51) it was noticed that the cross BML 7 \times BML 15 gave enhanced yield (131.54 g) compared with other crosses BML 7 \times BML 2 (118.70 g) and BML 7 \times BML 51 (99.53 g). It

is because BML 15 had higher $\mu G'$ values along with low $\mu D'$ values. Hence, it may be suggested that enhancement in performance of the hybrid (BML 6 \times BML 7) might be obtained by replacing BML 6 with BML 15. Direct replacement for the parent BML 7 could not be rewarding because $\mu F' > \mu G'$ for all the donors. 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.

By and large, perusal of the results obtained with respect to the target hybrid DHM 117 (BML 6 \times BML 7) divulged that the donors *viz.*, BML 15, BML 2 and BML 51 gave the highest significant positive $\mu G'$ estimates indicating their worth in transferring favourable alleles in the target hybrid for kernel yield per plant along with some yield components. Hence, it was concluded that the top two donors BML 15 and BML 2 could be suggested for enhancement of the target hybrid DHM 117 (BML 6 \times BML 7). A comprehensive breeding plan (Fig. 1) has been suggested for practical utilization in the improvement programme of the target hybrid DHM 117.

Table 1: Estimates of $\mu G'$ in the donor inbreds for four quantitative traits when DHM 117 (BML 6 \times BML 7) was designated as the hybrid to be improved

S. No.	Inbred	Kernel yield per plant	100 kernel weight	Ear length	Number of kernels/ear row
1	BML 51	3.71 ^{*b}	2.09 ^{*b}	0.63 ^a	-0.42 ^b
2	BML 5	-11.76 ^{*a}	-1.16 ^{*a}	-0.57 ^b	-1.37 ^{*b}
3	CM 105	1.53 ^b	0.27 ^b	-0.11 ^b	0.97 ^b
4	BML 2	4.14 ^{*a}	-0.98 ^a	1.50 ^{*c}	1.45 ^{*a}
5	BML 15	18.10 ^{*c}	0.29 ^a	1.01 ^{*c}	1.53 ^{*a}
6	BML 14	-0.88 ^a	4.17 ^{*c}	0.88 ^{*c}	-0.45 ^a
7	CM 118	-1.22 ^a	0.60 ^b	-0.68 ^{*a}	-0.60 ^a
8	CM 119	-0.92 ^a	-0.14 ^a	1.36 ^{*c}	1.14 ^{*a}
9	CML 124	1.94 ^a	2.11 ^{*a}	0.07 ^a	2.02 ^{*a}
	SE a	1.60	0.56	0.32	0.50
	SE b	1.60	0.56	0.32	0.50
	SE c	2.06	0.70	0.40	-
	SE d	2.06	0.70	0.40	-

* Larger than 2 x SE; 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 kernel yield per plant in nine donor inbred lines when DHM 117 (BML 6 \times BML 7) is the hybrid to be improved

Donors	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean of BML 6 \times donor (g)	Mean of BML 7 \times donor (g)
BML 51	6.62*	12.61*	15.85*	13.93*	12.61*	3.71*	25.23*	29.78*	BML 7	106.00	99.53
BML 5	-0.15	15.43*	13.03*	13.03*	13.52*	-11.76*	28.95*	26.06*	BML 6	73.25	74.22
CM 105	9.39*	10.26*	18.21*	16.29*	10.26*	1.53	20.51*	34.50*	BML 7	106.35	90.45
BML 2	-5.36*	21.77*	6.69*	6.69*	19.86*	4.14*	41.63*	13.38*	BML 6	92.36	118.70
BML 15	-0.74	14.23*	14.23*	-14.40*	40.94*	18.10*	55.17*	-0.17	BML 6	78.12	131.54
BML 14	-5.64*	26.27*	2.20	2.20	24.35*	-0.88	50.62*	4.39	BML 6	73.34	117.65
CM 118	22.88*	24.30*	4.17*	4.17*	22.38*	-1.22	46.68*	8.33*	BML 6	76.60	113.03
CM 119	17.99*	26.80*	1.67	1.67	24.88*	-0.92	51.68*	3.33	BML 6	72.20	118.63
CML 124	15.71*	18.40*	10.06*	10.06*	16.49*	1.94	34.89*	20.12*	BML 6	94.71	107.56

Mean of BML 6 \times BML 7 is 123.80 g *Larger than 2 x S.E.; a = q_{j_0} , q_{k_1} ; b = q_{j_1} , q_{k_0} ; c = q_{j_0} , q_{j_1} ; d = q_{k_0} , q_{k_1}

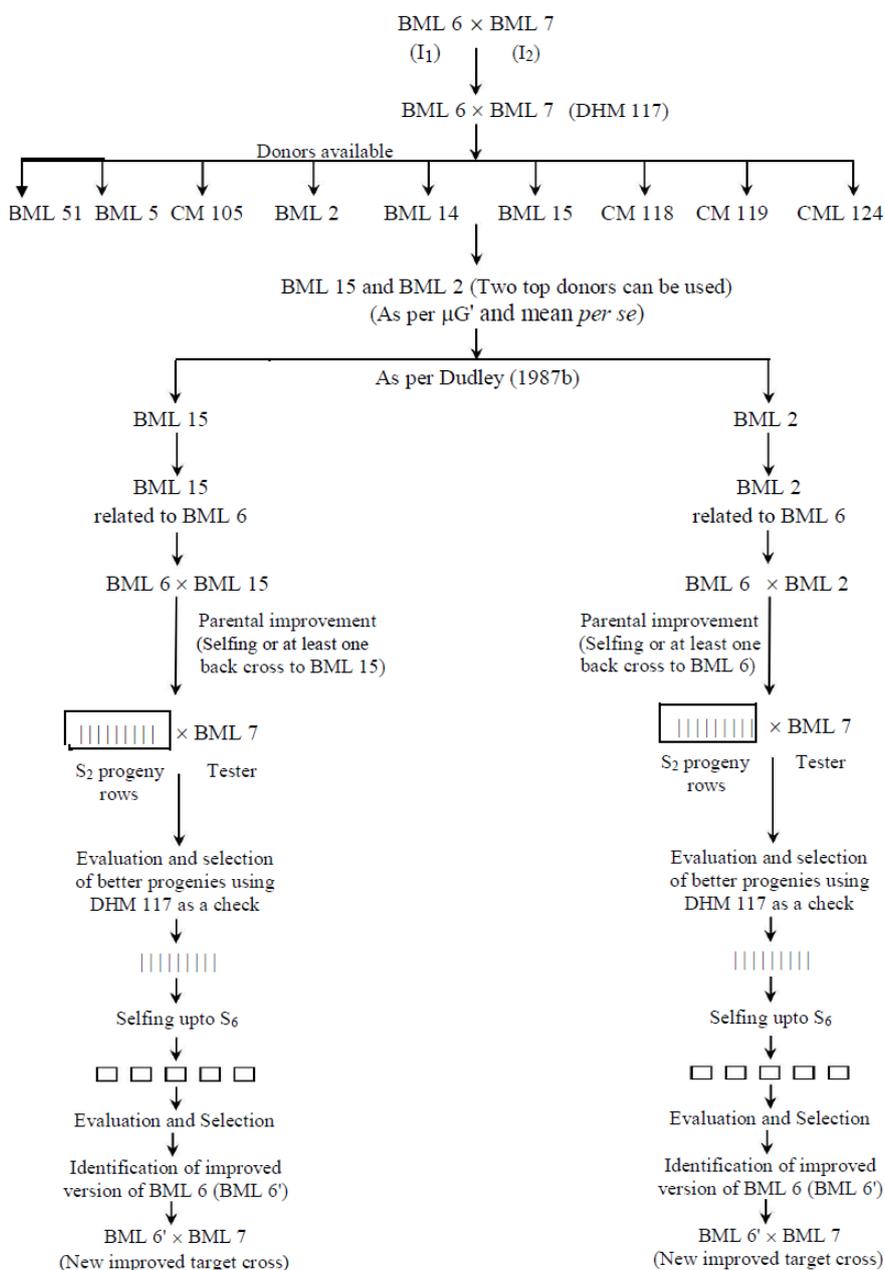


Fig. 1: Suggested breeding plan for utilization of selected donor lines to improve target hybrid DHM 117 (BML 6 \times BML 7)

REFERENCES

1. Bailey, T. B., Selection limits in self fertilizing populations following the cross of homozygous lines. *Proceedings of the International Conference on Quantitative Genetics*, Iowa State University Press, pp. 399-412 (1977).
2. Bernardo, R., An alternative statistic for identifying lines useful for improving parents of an elite single cross. *Theoretical and Applied Genetics*. **80**: 105-109 (1990).
3. Dudley, J. W., A method of identifying lines for use in improving parents of a single cross. *Crop Science*. **24**: 355-357 (1984).
4. Dudley, J. W., Modification of methods for identifying inbred lines useful for improving parents of elite single crosses. *Crop Science*. **27**: 944-947 (1987).
5. Dudley, J. W., Lamkey, K. R. and Geadelmann, T. L., Evaluation of populations for their potential to improve three maize hybrids. *Crop Science*. **36**: 1553-1559 (1996).
6. Kraja, A. and Dudley, J. W., Identification of tropical and temperature maize population having favourable alleles for yield and other phenotypic traits. *Crop Science*. **40**: 941-947 (2000).
7. Malvar, R. A., Cartea, M. E., Revilla, P. and Ordas, A., Identification of field corn inbreds adapted to Europe to improve agronomic performance of sweet corn hybrids. *Crop Science*. **37**: 1137-1141 (1997).
8. Metz, G., Probability of net gain of favourable alleles for improving an elite single cross. *Crop Science*. **34**: 668-672 (1994).
9. Naik, V. S., Genetic studies for improvement of single cross hybrids of maize (*Zea mays* L.) through identification of elite inbreds with favourable alleles for yield and yield components. *Ph.D. Thesis*, Acharya, N. G., Ranga Agricultural University, Guntur (2012).
10. Reddy, D. M., Ahuja, V. P. and Mukherjee, B. K., Identification of favourable alleles in inbred parents for the improvement of single cross hybrid in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding*. **63(3)**: 253-254 (2003).
11. Revilla, P., Malvar, R. A., Cartea, M. E. and Ordas, A., Identifying open pollinated populations of field corn as source of cold tolerance for improving sweet corn. *Euphytica*. **101**: 239-247 (1998).
12. Rodriguez, V. M., Malvar, R. A., Butron, A., Ordas and Revilla, P., Maize population as sources of favourable alleles to improve cold-tolerant hybrids. *Crop Science*. **47**: 1779-1786 (2007).
13. Secanski, M., Todorovic, G., Momirovic, G. S., Zivanovic, T. and Babic, M., Inbred lines of different cycles of selection as donors of favourable alleles for the improvement of F₁ maize hybrids. *Genetika*. **42(2)**: 339-348 (2010).
14. Trifunovic, S., Husic, I., Rosulj, M. and Stojsin, R., Evaluation of US and Yugoslavian Maize population as sources of favourable alleles. *Crop Science*. **41**: 302-308 (2001).
15. Yong, H., Li, H., Li, X., Zhang, X., Tie, S., Meng, Z., Zhang, D., Weng, J., Hao, Z., Ci, X., Li, X. and Zhang, S., Breeding potential of exotic maize populations to improve an elite Chinese hybrid. *Agronomy Journal*. **105(6)**: 1555-1564 (2013).
16. Zanoni, U. and Dudley, J. W., Comparison of different methods of identifying inbreds useful for improving elite maize hybrids. *Crop Science*. **29**: 577-582 (1989a).
17. Zivanovic, T., Vuckovic, S., Prodanovic, S. and Todorovic, G., Evaluation of inbred lines as sources of new alleles for improving elite maize hybrid. *Cereal Research Communications*. **34(2-3)**: 941-948 (2006).