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**N Sabitha**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

**D Mohan Reddy**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

**M Hemanth Kumar**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

**D Lokanadha Reddy**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

**B Ravindra Reddy**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

**Corresponding Author:**  
**N Sabitha**  
Acharya NG Ranga Agricultural  
University, SV Agriculture  
College, Tirupati, Andhra  
Pradesh, India

## Identification of favourable alleles for genetic improvement of selected single cross hybrid of maize (*Zea mays* L.)

**N Sabitha, D Mohan Reddy, M Hemanth Kumar, D Lokanadha Reddy and B Ravindra Reddy**

### Abstract

Identification of favourable alleles in the inbred lines ( $\mu G'$ ) not present in either of the parents given by Dudley is considered one of the most efficient method to enhance the productivity of superior single cross hybrids. The present investigation was conducted to identify favourable alleles ( $\mu G'$ ) among eight inbred lines for improvement of an elite single cross Heypool  $\times$  PDM 1474, which recorded the highest yield performance among the 45 hybrids that were generated through  $10 \times 10$  half diallel mating design and evaluated over three different seasons viz., *rabi*, *summer* and *kharij*. The results indicated that most of the donors showed significant positive  $\mu G'$  estimates for more than two characters studied in all seasons and pooled over seasons indicating the presence of favourable alleles. The donor inbred lines viz., DFTY and BML 2 were identified as the best donor inbred lines based on  $\mu G'$  estimates for yield and yield components for improvement of yield in the selected superior single cross hybrid Heypool  $\times$  PDM 1474. The  $\mu G'$  estimates for the same donor inbred lines greatly varied for the same character across seasons for the selected superior hybrid which could be attributable to the differential effect of environmental factors on the same set of genes governing expression of the same character in different seasons. Considering the genetic similarities and other parameters ( $\mu B'$  to  $\mu G'$ ) of the model suitable breeding strategy was suggested either to bring improvement in the performance of the superior hybrid Heypool  $\times$  PDM 1474 or to develop new hybrid using the best donor lines by improving any one of the parental lines of the selected hybrid.

**Keywords:** Favourable alleles, maize, Dudley's method, genetic enhancement in yield

### Introduction

Genetic improvement of the promising hybrids through identification of suitable donor inbred lines possessing favourable alleles not present in either of the parents and introgression of the favourable alleles adopting appropriate breeding methods is considered to be the most efficient method to enhance the productivity of superior single cross hybrids. Dudley (1984) [4] developed a methodology for identification of unique favourable alleles in the inbred lines for improving the constituent parents of desirable single cross hybrids of maize. Later on a modified method was also developed by Dudley (1987a and 1987b) [5, 6] for identification of donor lines possessing favourable alleles for use in improvement of parents of elite single cross hybrids through breeding programmes by crossing donor line to one of the parents of an elite  $F_1$  ( $I_1 \times I_2$ ) hybrid and or selfing the hybrid to recover a line superior to  $I_1$  or  $I_2$ . The modified method removes the assumptions that frequency of favourable alleles in the donor line is equal for all classes of loci except those for which the  $F_1$  lacks favourable alleles. The estimates determine which of the parental inbreds should be improved by crossing to donor inbred lines ( $P_w$ ) and whether to self directly in  $F_1$  or to backcross prior to selfing. Several researchers viz., Gerloff and Smith, 1988 [9]; Miseric, 1989 [13]; Zaoni and Dudley, 1989 [21]; Bernardo, 1990 [3]; Hohls *et al.*, 1995 [10]; Malvar *et al.*, 2004 [11]; Dudley *et al.*, 2004 [8] and Rodriguez *et al.*, 2007 [18] have also supported that single cross hybrid improvement could be possible by selecting donors possessing significant favourable alleles. The present study was carried out in maize with an objective of identification of donor lines with high frequency of favourable alleles for kernel yield and important contributing characters and to utilize them as source of donor lines for bringing genetic improvement in the kernel yield of selected superior single cross hybrid.

## Material and Methods

Ten diverse inbreds *viz.*, BML 2, BML 6, BML 7, BML 15, DFTY, Heypool, PDM 1416, PDM 1428, PDM 1452 and PDM 1472 were crossed in all possible combinations in a diallel fashion excluding reciprocals to obtain 45 single cross hybrids during *rabi* 2015-16 at the A.R.S Perumallapalle Farm, Tirupati. All the 45 hybrids were grown in three seasons *viz.*, *rabi*, 2016-17, *summer*, 2016-17 and *kharif*, 2017 in a Randomized Block Design with three replications. Each genotype was raised in a single row of 5.0 meter length adopting 75×20 cm during *kharif* and 60×20 cm during *rabi* and *summer* seasons. A fertilizer dose of 120:80: and 60 during *kharif* and 100:80:60 kg N, P and K was applied as per the recommendations for southern zone of A.P. All the recommended package of practices was followed in raising a healthy crop. Data were recorded on randomly selected five sample plants for cob length, number of kernels per row, 100 kernel weight and kernel yield per plant (g). Analysis of variance was carried out for all the characters studied separately for all the three seasons *viz.*, *Rabi*, 2016-17, *Summer*, 2016-17 and *Kharif*, 2017 following the procedures of (Panse and Sukhatme, 1978) [14]. Pooled data analysis of variance for the data over three seasons was also carried out after testing for the homogeneity of error variances by using Bartlett's test of homogeneity (Bartlett, 1937) [2]. The means of cob length, number of kernels per row, 100 kernel weight and kernel yield per plant were analysed following standard procedures. The least significant differences (LSD) were used to separate these means at 5% level of significance. Out of 45 hybrids from 10×10 diallel, only one hybrid *viz.*, Heypool × PDM 1474 which ranked 1<sup>st</sup> for high *per se* performance over seasons for kernel yield was considered in the present study for the identification of unique favourable alleles in the hybrid. Dudley's (1987b) [6] model was followed in the identification of favourable alleles (Designated as  $\mu G'$ ) present in donor inbred line but not in the hybrid to be improved using software SPIF-4 developed by Reddy, 1998.

## Results and Discussion

The estimates of  $\mu G'$  for the eight possible donor lines out of 10 inbred lines studied were determined for four important quantitative characters *viz.*, kernel yield per plant, cob length, number of kernels per row and 100 kernel weight (g) in individual seasons and pooled over seasons and were presented separately for the selected superior hybrid Heypool × PDM 1474 in Table 1. The positive estimates of  $\mu G'$  indicates that  $I_w$  (donor inbred) possesses favourable alleles at loci where both parents  $I_1$  and  $I_2$  contain unfavourable alleles. Inbred lines with higher and significant positive  $\mu G'$  estimates were considered as good source of favourable alleles. The estimates of  $\mu G'$  for same the donor inbred line greatly varied

over seasons in the present study for the same character. For example in the present study  $\mu G'$  estimates for BML 2 varied from 9.10 (*Kharif*, 2017) to 13.58 (*Rabi*, 2016-17) for kernel yield per plant. Similar observations were recorded for all other donor lines and yield components also. This may be attributable to the differential effect of environmental factors on the same set of genes governing the expression of the same character in different seasons. Almost all the donors showed significant positive  $\mu G'$  estimates for the characters studied over seasons indicating the presence of favourable alleles for the further improvement of the superior hybrid. Similar results in maize were reported by Bernardo (1990) [3]; Dudley *et al.* (1996) [7]; Malvar (1997) [12]; Ayrault *et al.* (1999) [1]; Reddy *et al.* (2005) [16]; Saida Naik *et al.* (2017) [19]; Pamesh *et al.* (2018) [15] and Suryanarayana *et al.* (2018) [20]. The detailed results on the estimates of  $\mu G'$  for kernel yield and major yield components were presented hereunder in respect of the selected superior hybrid Heypool × PDM 1474.

### Kernel yield per plant (g)

All the eight inbred lines registered significant positive  $\mu G'$  estimates pooled over seasons, *rabi*, *summer* and *kharif* seasons for kernel yield per plant. Among the eight inbred lines, DFTY (13.12) followed by BML 2 (11.75), BML 15 (11.30) and PDM 1452 (9.58) registered higher significant and positive  $\mu G'$  estimates in pooled data analysis over seasons for kernel yield indicating the presence of higher frequency of favourable alleles. Inbred lines *viz.*, BML 15 followed by DFTY and BML 2 in *rabi* and DFTY followed by PDM 1452, BML 7 and BML 15 in *kharif* displayed higher and significant positive  $\mu G'$  estimates. The inbred lines which recorded higher significant and positive  $\mu G'$  estimates in *summer* were BML 2 followed by BML 6, DFTY and BML 15. Among the inbreds PDM 1416 and BML 7 recorded the lowest  $\mu G'$  estimates for kernel yield in pooled over seasons. Based on the overall estimates of  $\mu G'$  in pooled and individual seasons, inbred lines *viz.*, DFTY, BML 2 and BML 15 were found to be the best donor lines with highest frequency favourable alleles for kernel yield (Table1).

### Cob Length (cm)

For cob length all the inbred lines showed significant and positive  $\mu G'$  estimates. Among the inbred lines DFTY (1.51) followed by BML 2 (1.28) and BML 6 (1.25) recorded consistently higher significant and positive  $\mu G'$  estimates in the pooled analysis over seasons and also in all the three seasons (Table 1). Estimates of  $\mu G'$  for PDM 1416 were low in all three seasons and pooled over seasons. The inbreds DFTY, BML 2 and BML 6 could be identified as the best donor sources of favourable alleles for cob length based on the higher positive and significant  $\mu G'$  estimates.

**Table 1:** Estimates of  $\mu G'$  in the donor inbred lines for kernel yield and important yield contributing characters in different seasons and over seasons for selected superior hybrid: Heypool × PDM 1474

Inbred (s)	$\mu G'$							
	Kernel yield per plant (g)				Cob length (cm)			
	<i>Rabi</i>	<i>Summer</i>	<i>Kharif</i>	Pooled	<i>Rabi</i>	<i>Summer</i>	<i>Kharif</i>	Pooled
BML 2	13.58 <sup>*b</sup>	9.54 <sup>*a</sup>	9.10 <sup>*a</sup>	11.75 <sup>*b</sup>	1.75 <sup>*b</sup>	1.22 <sup>*a</sup>	1.17 <sup>*a</sup>	1.28 <sup>*a</sup>
BML 6	10.00 <sup>*a</sup>	8.65 <sup>*a</sup>	9.68 <sup>*a</sup>	9.40 <sup>*a</sup>	1.36 <sup>*a</sup>	1.33 <sup>*a</sup>	1.05 <sup>*a</sup>	1.25 <sup>*a</sup>
BML 7	8.90 <sup>*b</sup>	1.91 <sup>a</sup>	12.84 <sup>*b</sup>	6.27 <sup>b</sup>	1.05 <sup>*b</sup>	1.24 <sup>*a</sup>	0.70 <sup>*b</sup>	1.08 <sup>*b</sup>
BML 15	16.69 <sup>*b</sup>	7.47 <sup>*a</sup>	12.14 <sup>*a</sup>	11.30 <sup>*a</sup>	1.40 <sup>*a</sup>	1.00 <sup>*a</sup>	0.84 <sup>*a</sup>	1.08 <sup>*a</sup>
DFTY	15.12 <sup>*b</sup>	8.53 <sup>*b</sup>	13.60 <sup>*a</sup>	13.12 <sup>*b</sup>	1.86 <sup>*b</sup>	1.17 <sup>*b</sup>	1.51 <sup>*b</sup>	1.51 <sup>*b</sup>
PDM 1416	6.90 <sup>*a</sup>	0.03 <sup>a</sup>	8.44 <sup>*a</sup>	5.12 <sup>b</sup>	0.98 <sup>*b</sup>	0.95 <sup>*b</sup>	0.60 <sup>*b</sup>	0.84 <sup>*b</sup>
PDM 1428	6.490 <sup>*a</sup>	4.52 <sup>*b</sup>	6.62 <sup>*a</sup>	5.57 <sup>a</sup>	1.44 <sup>*b</sup>	1.05 <sup>*b</sup>	0.51 <sup>*a</sup>	1.05 <sup>*b</sup>
PDM 1452	12.34 <sup>*a</sup>	5.13 <sup>*a</sup>	13.37 <sup>*b</sup>	9.58 <sup>*a</sup>	1.09 <sup>*a</sup>	1.02 <sup>*b</sup>	1.47 <sup>*b</sup>	1.06 <sup>*a</sup>

SE a	1.76	1.94	1.77	3.17	0.19	0.24	0.16	0.35
SE b	1.76	1.94	1.77	3.17	0.19	0.24	0.16	0.35
SE c	-	-	-	-	-	-	-	-
SE d	-	-	-	-	-	-	-	-
	<b>Number of kernels per row</b>				<b>100 kernel weight (g)</b>			
BML 2	3.66 <sup>*b</sup>	2.83 <sup>*b</sup>	2.67 <sup>*a</sup>	2.78 <sup>*a</sup>	3.39 <sup>*b</sup>	2.48 <sup>*b</sup>	1.62 <sup>*a</sup>	1.93 <sup>*a</sup>
BML 6	3.58 <sup>*a</sup>	2.41 <sup>*a</sup>	3.58 <sup>*a</sup>	3.19 <sup>*a</sup>	1.66 <sup>*a</sup>	1.42 <sup>*a</sup>	1.42 <sup>*a</sup>	1.51 <sup>*a</sup>
BML 7	3.25 <sup>*b</sup>	N	N	3.05 <sup>*b</sup>	2.51 <sup>*b</sup>	0.41 <sup>a</sup>	2.29 <sup>*b</sup>	2.00 <sup>*b</sup>
BML 15	3.92 <sup>*a</sup>	2.50 <sup>*a</sup>	3.41 <sup>*a</sup>	3.28 <sup>*a</sup>	2.65 <sup>*a</sup>	1.33 <sup>*a</sup>	1.61 <sup>*a</sup>	1.87 <sup>*a</sup>
DFTY	4.33 <sup>*b</sup>	3.41 <sup>*b</sup>	4.25 <sup>*b</sup>	4.00 <sup>*b</sup>	3.51 <sup>*b</sup>	1.26 <sup>*b</sup>	2.85 <sup>*b</sup>	2.54 <sup>*b</sup>
PDM 1416	3.41 <sup>*a</sup>	2.00 <sup>*b</sup>	2.75 <sup>*b</sup>	2.86 <sup>*b</sup>	2.68 <sup>*b</sup>	1.65 <sup>*b</sup>	2.41 <sup>*b</sup>	2.25 <sup>*b</sup>
PDM 1428	2.66 <sup>*b</sup>	N	2.00 <sup>*b</sup>	2.25 <sup>*b</sup>	2.85 <sup>*b</sup>	1.13 <sup>*a</sup>	2.62 <sup>*b</sup>	2.46 <sup>*b</sup>
PDM 1452	3.50 <sup>*a</sup>	2.33 <sup>*a</sup>	3.33 <sup>*a</sup>	3.05 <sup>*a</sup>	2.46 <sup>*a</sup>	1.82 <sup>*a</sup>	2.20 <sup>*a</sup>	2.16 <sup>*a</sup>
SE a	0.49	0.44	0.44	0.79	0.19	0.30	0.18	0.40
SE b	0.49	0.44	0.44	0.79	0.19	0.60	0.18	0.40
SE c								
SE d								

\*Larger than 2 × S.E; N = μG' values could not obtained

a = qj0; qk1; b = qj1, qk0; c = qj0, qj1; d = qk0, qk1

**Number of kernels per row**

All the eight possible donor lines identified for the hybrid Heypool × PDM 1474 registered significant and positive μG' estimates for number of kernels per row. Among the inbred lines DFTY (4.00) followed by BML 15 (3.28) and BML 6 (3.19) recorded higher positive and significant μG' estimates over seasons. The donor lines DFTY followed by BML 15, BML 2 and BML 6 in *rabi*; DFTY followed by BML 2, BML 15 and BML 6 in *summer* and DFTY followed by BML 6, BML 15 and PDM 1452 in *kharif* recorded the higher μG' estimates. A slight change in the ranking of donor inbred lines for μG' estimates observed in *rabi*, *summer* and *kharif* may be due to differential response of inbred lines to seasonal conditions. The μG' estimates for BML 7 in *summer* and *kharif* and PDM 1428 in *summer* could not be estimated. This may be due to the failure of assumptions of complete dominance or epistasis (Dudley, 1988). Overall, DFTY, BML 15 and BML 6 were identified as the best donor sources with higher frequency of favourable alleles for number of kernels per row character (Table 1).

**100 Kernel weight**

In the pooled analysis over seasons, all the inbred lines registered positive and significant μG' estimates for 100 kernel weight (Table 1). Among the inbred lines DFTY (2.54) followed by PDM 1428 (2.46) and PDM 1416 (2.25) recorded higher significant and positive μG' estimates for 100 kernel weight. In *rabi*, DFTY, BML 2, PDM 1428 and PDM 1416; in *summer* BML 2, PDM 1452 and PDM 1416 and in *kharif*, DFTY followed by PDM 1428 and PDM 1416 recorded the higher significant and positive μG' estimates for 100 kernel weight. Among the eight donors BML 6 recorded the lowest significant and positive μG' estimates for this character in the pooled over seasons. The inbred donor lines *viz.*, DFTY, PDM 1428 and PDM 1416 were found to be the best donor sources with high frequency of favourable alleles for 100 kernel weight.

It could be noted that the donor inbred lines DFTY recorded higher positive and significant μG' estimates for all the four characters *viz.*, kernel yield, cob length, number of kernels per row and 100 kernel weight, while BML 2 registered higher significant and positive μG' estimates for kernel yield and cob length among the eight inbreds. Hence, DFTY and BML 2 were considered as the best donor lines with higher frequency of favourable alleles for the genetic improvement of yield in superior hybrid Heypool × PDM 1474.

**Breeding plan for yield improvement**

To initiate improvement programme for kernel yield in the hybrid Heypool × PDM 1474, characterization of donor inbreds and their genetic similarity estimates (Table 2) are to be studied critically along with all other estimates (μB' to μG') of the model. For the hybrid Heypool × PDM 1474 kernel yield is only considered for genetic enhancement as simultaneous improvement for all the traits at a time is complex and requires different selection strategies. The genetic descent of the donor inbreds to one of the parents of the selected superior hybrid Heypool × PDM 1474 was evaluated according to the estimates of μC' + μF' and μD' + μE'. The estimates of μC' + μF' > μD' + μE' indicating that all the donors have genetic affinity with (P<sub>1</sub>) Heypool except DFTY and could be utilized for the improvement of parent Heypool while μD' + μE' > μC' + μF' revealing that the donor DFTY had genetic affinity with (P<sub>2</sub>) PDM 1474. For enhancing the performance of the selected superior hybrid Heypool × PDM 1474 through parental improvement DFTY and BML 2 could be considered as the best donor for recycling of the parent Heypool, while DFTY could be used in the recycling of PDM 1474 as these donors had higher μG' estimates. However, no inbred was found suitable for direct replacement with any of the constituents of the hybrid Heypool × PDM 1474. The reasons could be attributed to nullifying effect of higher μF' and μD' values on the favorable alleles μG' contributed by the donors.

**Table 2:** Estimates of μB',..... μG' for kernel yield plant<sup>-1</sup> (g) in eight donor inbred lines for the selected superior single cross hybrid: Heypool × PDM 1474

Donors	Class of loci										
	μB'	μC'	μD'	μE'	μF'	μG'	μC+F'	μD+E'	Genetic affinity with	Mean per se of Heypool × donor	Mean per se of PDM 1474 × donor
BML 2	14.25	16.60	17.73	13.88	16.60	11.75	33.20	31.61	Heypool	129.48	127.23
BML 6	14.48	22.15	12.18	12.18	18.31	9.40	40.46	24.35	Heypool	121.57	133.63

BML 7	10.92	19.64	14.69	14.69	15.79	6.27	34.43	29.38	Heypool	120.15	122.36
BML 15	15.87	22.05	12.28	12.28	18.20	11.29	40.25	24.56	Heypool	125.17	137.01
DFTY	9.96	14.18	20.14	16.30	14.18	13.12	28.37	36.44	PDM 1474	137.06	125.14
PDM 1416	12.59	21.17	13.16	13.16	17.32	5.12	38.49	26.32	Heypool	114.79	123.12
PDM 1428	12.83	20.11	14.22	14.22	16.27	5.57	36.38	28.43	Heypool	117.79	121.89
PDM 1452	13.04	19.29	15.04	15.04	15.44	9.58	34.73	30.08	Heypool	127.47	128.28

\*Larger than  $2 \times SE$ ;  $N = \mu G'$  values could not obtained;  $a = q_{j0}, q_{ki}$ ;  $b = q_{ji}, q_{ko}$ ;  $c = q_{j0}, q_{ji}$ ;  $d = q_{k0}, q_{ki}$

Mean kernel yield in selected superior single cross hybrid: Heypool  $\times$  PDM 1474 = 139.19 g.

The superior hybrid Heypool  $\times$  PDM 1474 showed the highest *per se* performance for kernel yield (139.19 g) out of 45 hybrids and this hybrid is generally supposed to have already accumulated the highest frequency of favourable alleles and the model should fail to identify any favourable alleles for the improvement of this hybrid. However, the inbred lines DFTY and BML 2 were found as the top donors since these inbred lines recorded higher  $\mu G'$  values compared with other donors. Critical study of mean performance of hybrids and different parameters of the model indicated the results obtained were not beyond expectations. For example, the donor inbred line DFTY registered the highest and significant  $\mu G'$  estimates (13.12) among the donors and expectedly should have given higher mean performance in its hybrids with the constituents of the original superior hybrid (Heypool  $\times$  PDM 1474). However, such was not the case, which could be attributed to higher estimates of  $\mu F'$  [class in which Heypool ( $P_1$ ) and donor DFTY have unfavourable alleles and PDM 1474 ( $P_2$ ) had favourable alleles] and  $\mu D'$  [class in which PDM 1474 ( $P_2$ ) and donor BML 2 had unfavourable alleles and Heypool ( $P_1$ ) had favorable alleles. It is obvious that these higher  $\mu D'$  and  $\mu F'$  values must have cancelled the effect of favourable alleles ( $\mu G'$ ) present in the donor DFTY and resulted in lowering the mean performance in the hybrid. Similar results were also reported by Bernardo (1990) [3]. Further, the values of  $\mu D'$  and  $\mu F'$  were significantly higher than the values of  $\mu G'$  estimates for the identified donors DFTY and BML 2 indicating that number of unfavourable and recessive alleles for kernel yield observed in the donors were significantly higher than the number of favourable alleles and dominant alleles. In order to avoid the introduction of unfavourable alleles, backcrossing of  $F_1$  hybrids (Heypool  $\times$  DFTY and PDM 1474  $\times$  DFTY) with Heypool and PDM1474, respectively is suggested before making selections. As  $\mu D'$  and  $\mu F'$  are greater than  $\mu G'$  estimates for all the donors, no donor inbred could be recommended for direct replacement of any parent in hybrid and hence backcross programme for the improvement of the parents with the top two donor inbreds (DFTY and BML 2) is suggested. For the improvement of the parent Heypool backcrosses *viz.*, (Heypool  $\times$  DFTY)  $\times$  Heypool and (Heypool  $\times$  BML 2)  $\times$  Heypool and for the improvement of the parent PDM 1474 back crosses *viz.*, (PDM 1474  $\times$  DFTY)  $\times$  PDM 1474 and (PDM 1474  $\times$  BML 2)  $\times$  PDM 1474 could be recommended which in turn contributes to the increased performance of the hybrid Heypool  $\times$  PDM 1474.

## Conclusions

The estimates of  $\mu G'$  for four favourable economic characters in respect of the superior hybrid Heypool  $\times$  PDM 1474 clearly helped in the identification of the best donor sources *viz.*, DFTY and BML 2 possessing higher frequency of favourable alleles. All these donor inbreds registered higher positive and significant  $\mu G'$  estimates for more than two character indicating their worth in transferring favourable alleles from the donor inbred lines to the parental lines of the selected

superior hybrid. Genetic enhancement in the superior hybrid Heypool  $\times$  PDM 1474 for kernel yield might be expected by recycling of the parents Heypool and PDM 1474 with BML 2 and DFTY through the backcrosses *viz.*, (Heypool  $\times$  BML 2)  $\times$  Heypool; (PDM 1474  $\times$  BML 2)  $\times$  PDM 1474; (Heypool  $\times$  DFTY)  $\times$  DFTY and (PDM 1474  $\times$  DFTY)  $\times$  PDM 1474 for introgression of favourable alleles from the donor inbred lines to the parental lines of the selected superior hybrid.

## References

1. Ayrault S, Gouesnard B, Panouille A, Boyat A. Evaluation of late inbred lines in order to improve early single maize crosses by the bi-additive model and predictive genetic models. *Maydica* 1999;44(3):183-194.
2. Bartlett MS. Some examples of statistical methods of research in agriculture and applied biology. *Supplement to Journal of Royal Statistical Society* 1937;4:137-170.
3. Bernardo R. An alternative statistic for identifying lines useful for improving parents of an elite single cross. *Theoretical and Applied Genetics* 1990;80:105-109.
4. Dudley JW. A method of identifying lines for using improving parents of single cross. *Crop Science* 1984;24:355-357.
5. Dudley JW. Modification of methods for identifying populations to be used for improving parents of elite single crosses. *Crop Science* 1987a;27:940-943.
6. Dudley JW. Modification of methods for identifying inbred lines useful for improving parents of elite single crosses. *Crop Science* 1987b;27:944-947.
7. Dudley JW, Lamkey KR, Geadelmann TL. Evaluations of populations for their potential to improve three maize hybrids. *Crop Science* 1996;36:1553-1559.
8. Dudley JW, Lamkey KR, Geadelmann TL. Verification of predictions from the estimators of favourable alleles to improve yield of sweet corn hybrids. *Maydica* 2004;49(1):49-55.
9. Gerloff JE, Smith OS. Choice of method for identifying germplasm with superior alleles. I. Theoretical results. *Theoretical and Applied Genetics* 1988;76:209-216.
10. Hohls T, Clarke GPY, Shanahan PE, Grevers HO. An unbiased estimator for identifying lines useful for the improvement of elite single crosses based on combining ability model. *Heredity* 1995;75:155-163.
11. Malvar RA, Cartea ME, Revilla P, Soengas P, Ordas A. Verification of predictions from estimators of favorable alleles to improve yield of sweet corn hybrids. *Maydica* 2004;49:49-55.
12. Malvar RA, Revilla P, Cartea ME, Ordas A. Field corn inbred to improve sweet corn hybrids for early vigour and adaptation to European conditions. *Maydica* 1997;42(3):247-255.
13. Misericvic D. Evaluation of three test statistics used to identify maize inbred lines with new favourable alleles not present in elite single cross. *Theoretical and Applied Genetics* 1989;77:402-408.
14. Panse VG, Sukhatme PV. *Statistical Methods for*

- Agricultural Workers. ICAR Publications, New Delhi 1978,68-75p.
15. Paramesh M, Reddy KHP, Reddy DM, Rajarajeswari V, Bhaskar Reddy BV. Identification of favourable alleles in donor inbreds for the improvement of single cross hybrids of Maize (*Zea mays* L). International Journal of Pure and Applied Bioscience 2018;6(5):521-526.
  16. Reddy DM, Ahuja VP, Mukherjee BK. 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.). Indian Journal of Genetics and Plant Breeding 2005;65(4):253-256.
  17. Reddy DM. SPIF-4- Statistical package for identification of favourable alleles (Unplished) 1998.
  18. Rodriguez VM, Malvar RA, Butron A, Ordas, Revilla P. Maize population as sources of favourable alleles to improve cold-tolerant hybrids. Crop Science 2007;47:1779-1786.
  19. Saida Naik V, Mohan Reddy D, Hariprasad Reddy K. Identification of favourable alleles in recycled inbred lines for the improvement of elite single cross hybrids in maize (*Zea mays* L.). Bulletin of Environmental, Pharmacology and Life Sciences 2017;6(1):179-184.
  20. Suryanarayana L, Reddi Sekhar M, Ratna Babu D, Ramana AV. Identification of donor lines containing favourable alleles for improveing target maize hybrid (BML 6 × BML 7). The Pharma Innovation 2018;7(7):512-514
  21. Zaroni U, Dudley JW. Test cross evaluation of F<sub>2</sub> populations from maize inbreds selected for unique favourable alleles. Crop Science 1989;29:589-595.