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# Breeding Value of Quality Protein Maize Inbreds

**A. Thanga Hemavathy [a++*], S. Kavitha [a++], Kavithamani Duraisamy [a++], M. Sakila [a++], V. Vijaya Geetha [a++] and V. Dhanushkodi [a++]**

[a] *Department of Genetics and Plant Breeding, ADAC and RI, Trichy, Tamil Nadu, India.*

***Authors' contributions***

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## ABSTRACT

The cultivar with high and positive breeding value can be used as a good parent for breeding of traits in hybridization programs because they can better transfer the desirable characteristics to the progeny in each case. To obtain the breeding value present investigation was carried out in maize with 33 inbreds of maize and seven inbreds of QPM lines to assess the breeding value of maize progenies for the better selection. The progeny values ranged from 62.04 (UMI 48 x CO 1) to 126.26 (CML 145 x CO 1). The breeding value ranged from 0.17 (UMI 48 x CO 1) to 0.39 (CML 145 x CO 1). CML 145 x CO 1 had high breeding value (0.39) with high progeny mean. UMI 48 x CO 1 had low breeding value (-0.17) with low progeny mean (90.80). The parent CML 145 was the superior most both for *perse mean* ($P_{38}$=126.26) as well as for its hybrid progeny mean ($C_2$= 168).

*Keywords: Top cross; QPM lines; breeding value; perse mean.*

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[++] *Associate Professor (PBG);*
**Corresponding author: E-mail: hemavathytnau@gmail.com;*

## 1. INTRODUCTION

Choice of parents for developing base population is crucial in breeding of cultivars, because it largely predetermines the outcome of subsequent selection processes and affects the optimum allocation of resources in breeding programmes .The top cross design was proposed by Davis [1] and Jenkins and Brunson [2] and is widely used for the selection of better hybrid combinations based on their breeding value. Breeding value (A) is the main parameter of initial screening through top cross analysis as it represents the *gca* effects. The analysis of overall pattern of top cross facilitates the selection of parents with higher yielder [3] these high yielding parents which facilitates the increased production area [4]. Although the choice of parents is without doubt of large importance in a breeding programme [5]; the planning and implementation of specific crosses can be considered as being at least as important. Genetic resources in each country are valuable assets for sustainable development. An accurate knowledge of genetic behavior and identification of genomic loci associated with important economic traits will help breeders to run efficiently their breeding programs [6-8]. The cultivar with high and positive breeding value can be used as a good parent for breeding of traits in hybridization programs because they can better transfer the desirable characteristics to the progeny in each case [9]. Current study was taken by using 40 top crosses derived from a 33 university maize inbred lines with seven quality protein maize lines for the selection of better hybrid combinations based on their breeding value, it is a simplest method of elimination of considerable number of undesirable lines in the beginning of a breeding programme.

## 2. MATERIALS AND METHODS

Seeds of thirty three maize inbred lines and seven QPM inbred lines (Table 2) were obtained from Maize Breeding unit, Department of millets, Centre or Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU) and CIMMYT, Mexico. Totally 40 parents are top crossed with standard parent CO 1 to evaluate the yield potential efficiency by Davis [1] method. The forty lines with one tester were raised in crossing block at Agricultural College & Research Institute, Madurai during March 2004. The genotypes were raised in ridges of five meter length spaced at 60 x 25 cm. Each of forty lines was crossed with CO 1 individually in a top cross model [1] to obtain 40 cross combinations. Using a single wide-based tester CO 1 as a pollen parent and the 40 test inbred as seed/female parents, single crosses are hand-made. The crosses can economically be made by detasseling only the inbred stocks in an isolated crossing block. The tester variety is not detasselled so as to provide pollen flow. These 40 top crosses (c=40) and the 40 parental inbreds (p=40) were raised in RBD repeated thrice (r= 3 and g = c + p = 80).

### 2.1 Breeding value

$$A_i = A'_I \; SD\,(A'_I) = \overline{c_i} - \overline{c} \; / \; SD\,(A'_I)$$

$$\text{Variance } A'_I = \sum_{i}^{p} A'^{2}_I \; / \; (p-1)$$

$$SD\,(A'_I) = VA \sqrt{Var\, A_i'}$$

### 2.2 Parent- Offspring Correlation ($r_{op}$)

$$r_{op} = \frac{COV(OP)}{\sqrt{Var\,(P) \times Var\,(O)}}$$

$$COV\,(OP) = \left[ \sum_{i}^{p} T_{gi} \times T_{gi+p} \,/r \right] - (T_p \times T_c / pr)$$

**Table 1. Anova for top cross**

| | Sources of variation | Df | SS | MSS |
|---|---|---|---|---|
| **(i)** | Replication ( r) | r-1 | rSS | rMS |
| **(ii)** | Entries (g) | g-1 | gSS | gMS |
| **(iii)** | Parents (p) | p-1 | pSS | pMS |
| **(iv)** | Topcrosses (c ) | c-1 | cSS | cMS |
| **(v)** | p (Vs) c | 1 | pcSS | pcMS |
| **(vii)** | Error | (g-1) (r-1) | eSS | eMS |
| **(vi)** | Total | (gr-1) | TSS | |

### 2.3 Parent-Offspring Regression ($b_{op}$)

$$b_{op} = \frac{COV\ (OP)}{p^{SS}}$$

### 2.4 Regression of a on Phenotypic Value ($b_{AP}$)

$$b_{op} = \frac{COV\ (AP)}{Var\ (P)}$$

$$SE\ (b_{AP}) = \left[ var\ (P) - \frac{CoV\ (AP)^2}{Var\ (A)} / (p-2)\ var\ (A) \right]^{5}$$

## 3. RESULTS AND DISCUSSION

The source populations for genotypes development were 33 university maize lines with seven quality protein maize lines. The pollen parent was a hybrid developed between (UMI 101x UMI 130) x (UMI 90 x UMI 285). Totally 40 top crosses are taken for study from the single tester CO 1, to select the crosses have the high yielding potential.

### 3.1 Variance and Other Statistics

Analyses of variance of the data in top cross analysis of 40 crosses were evaluated on replication mean basis for the important character seed yield per plant was presented in Table 3. The analysis revealed highly significant differences for 40 crosses. Significant difference among top crosses indicated that the parents and their crosses were quite distinct from each other in respect of seed yield per plant. Mean value, breeding value and single plant yield of genotypes and their crosses were presented in Table 4.

The progeny mean ranged from 62.04 (UMI 48 x CO 1) to 126.26 (CML 145 x CO 1). The breeding value ranged from 0.17 (UMI 48 x CO 1) to 0.39 (CML 145 x CO 1). Among the top crosses CML 145 x CO 1 had high breeding value (0.39) with high progeny mean. UMI 48 x CO 1 had low breeding value (-0.17) with low progeny mean (90.80).

Significance (P<0.01) of single degree of comparison variance (parents (VS) crosses) indicates substantial difference between the parental inbreds as a group and their hybrid progenies (top crosses) as another group (C= 5827.39 > P= 4270.89) (Table 4). This follows that average heterosis is significantly high. Differences among parents and among top crosses were also significantly high for grain yield. Thus, the parent CML 145 was the superior most both for *perse mean* ($P_{38}$=126.26) as well as for its hybrid progeny mean ($C_2$= 168) (Table 4).

In the present study, the high yielding crosses are selected from the 40 top crosses based on the breeding value of individuals. The substantial difference was noticed between the parent inbreds and crosses, by comparing the mean value of both. This follows that average heterosis is significantly high. The breeding value seems to be the important component to determine the trait [10]. Based on the breeding value and the progeny mean the crosses viz., UMI 9 x CO 1, UMI 21 x CO 1, UMI 29 x CO 1, UMI 57 x CO 1, UMI 42 x CO 1, UMI 70 x CO 1, UMI 113 x CO 1, UMI 189 x CO 1, UMI 426 x CO 1, UMI 427 x CO 1, UMI 524 x CO 1, UMI 841 x CO 1,CML 141 x CO 1, CML 142 x CO 1, CML 143 x CO 1, CML 145 x CO 1, CML 144 x CO 1, CML 146 x CO 1, CML 147 x CO 1 are the higher yielder. Owing to high $BA_p$ (=16.56 ±1.26) which is analogous to heritability the parental-potential is seemingly quite authentic and reliable.

Breeding value (A) is the main parameter of initial screening through top cross analysis as it represents the *gca* (general combining ability) effects of individual test inbred, larger the breeding value greater the *gca* effects. On this basis, the order of breeding value of parental genotype are CML 145 > CML 144 > UMI 426 > UMI 524 >UMI 841 >UMI 189 > UMI 70 > UMI 29 >UMI 42 >UMI427 >CML 142 >CML 141 >CML 146 > UMI 9 > CML 147 > CML 143 > UMI 21 > UMI 57 > UMI 113. Their corresponding means ($P_i$) also follow the same trend (Table 4). Therefore, operation of additive gene action is a clean indication in this set of test inbreds. However, some of the genotypes like UMI 10, UMI 17, UMI 27, UMI 35, UMI 37, UMI 48, UMI 51, UMI 61, UMI 64, UMI 76, UMI 79, UMI 86, UMI 118, UMI 131, UMI 128, UMI 226, UMI 285, UMI 420, UMI 620, UMI 814, UMI 889 manifested negative A, hence undesirable for further exploitation. Thus top cross analysis is the simplest method of elimination of considerable number of undesirable lines in the beginning of a breeding programme.

**Table 2. List of genotypes and their parentage**

| Accession No. | Parentage | Source |
|---|---|---|
| UMI 9 | MS-9 | MBS, Coimbatore |
| UMI 10 | MS-10 | MBS, Coimbatore |
| UMI 17 | CM-202 | MBS, Coimbatore |
| UMI 21 | CM 420 | MBS, Coimbatore |
| UMI 27 | CM 105 x CM 104 C | MBS, Coimbatore |
| UMI 29 | CM 500 x CM 201 | MBS, Coimbatore |
| UMI 35 | THl DMR-5x Taiwan comp.DeF$_2$x (CM 202x CM 111) | MBS, Coimbatore |
| UMI 37 | P.DMR-5 x Cuprico F$_3$ x (CCM 202x CM 111) | MBS, Coimbatore |
| UMI 42 | P.DMR-5 x Taiwan comp. MSC$_1$ F$_4$ x (CM 202 x CM 111) | MBS, Coimbatore |
| UMI 48 | PHIL DMR-2 | MBS, Coimbatore |
| UMI 51 | PHIL DMR-5 | MBS, Coimbatore |
| UMI 57 | Taiwan DMR-3 | MBS, Coimbatore |
| UMI 61 | Taiwan DMR-13 | MBS, Coimbatore |
| UMI 64 | Bagor Comp. – 10 | MBS, Coimbatore |
| UMI 70 | Puerto Gurad-2 | MBS, Coimbatore |
| UMI 76 | Chain cross | MBS, Coimbatore |
| UMI 79 | Pioneer-102 | MBS, Coimbatore |
| UMI 86 | Amber | MBS, Coimbatore |
| UMI 113 | YUZP-SC-48 A (UMI 113/A white kernels) | MBS, Coimbatore |
| UMI 118 | YUZP-206 | MBS, Coimbatore |
| UMI 128 | PKT-1 | MBS, Coimbatore |
| UMI 131 | PKT-4 | MBS, Coimbatore |
| UMI 189 | 2407 | MBS, Coimbatore |
| UMI 226 | South African Tall x Akbar comp. | MBS, Coimbatore |
| UMI 266 | Malan local (Rajasthan Udaipur) | MBS, Coimbatore |
| UMI 285 | Suwan-1 (Indonesia composite) | MBS, Coimbatore |
| UMI 420 | (UMI29) x (UMI 51) | MBS, Coimbatore |
| UMI 426 | (UMI 47) x (UMI 134) | MBS, Coimbatore |
| UMI 427 | (UMI 25) x (UMI 51) | MBS, Coimbatore |
| UMI 524 | 96123 (Sarhael x Suwan 1) x (Suwan 1) | MBS, Coimbatore |
| UMI 620 | (Sakathi x CM 111) x F$_4$ | MBS, Coimbatore |
| UMI 814 | Diara EVF –10 | MBS, Coimbatore |
| UMI 841 | LODANA 8929 MEX/2441 | MBS, Coimbatore |
| UMI 889 | Plot No 1332 | MBS, Coimbatore |
| CML 141 | Pob 62C 5HC 24-5-3-2-1-B-B-2-B-B-# | CIMMYT, Mexico |
| CML 142 | Pob 62 C 5HC 93-5-6-1-3-B-B-B-7-B-B-# | CIMMYT, Mexico |
| CML 143 | Pob 62C 6HC 88-1-1-B-B-B-10-B-B-# | CIMMYT, Mexico |
| CML 144 | Pob 62 C 5 HC 182-2-1-2-B-B-B-3-1-#-# | CIMMYT, Mexico |
| CML 145 | Pob63cOHC181-3-2-14#-2B-B-B-B-#-# | CIMMYT, Mexico |
| CML 146 | AC 8563 MH 35-3-1-B-2-1-B-B-1-B-B-# | CIMMYT, Mexico |
| CML 147 | Pob63c2HC53-1-1-B-B-B-9-B-B-# | CIMMYT, Mexico |

**Table 3. Anova for single plant yield in corn**

| Sources of variation | Df | SS | MSS |
|---|---|---|---|
| Replication | 2 | 9.82 | 4.91 |
| Entries | 139 | 150748.76 | 3865.35** |
| Parents (P) | 39 | 38236.58 | 980.425** |
| Topcrosses ( c) | 39 | 20763.23 | 532.39** |
| P (*vs*) C | 1 | 91748.94 | 91748.94** |
| Error | 158 | 35.7783 | 30.54 |

**Table 4. Breeding value for yield and allied parameters**

| | Parents | $A_i$ | $P_i$ | $C_i$ (inbred x CO 1) | $R_{OP}$ | $B_{OP}$ | $B_{AP}$ |
|---|---|---|---|---|---|---|---|
| 1 | UMI 9 | 0.31 | 66.24 | 128.38 | 49.01* | 36.12 | 16.56 ± 1.26 |
| 2 | UMI 10 | -0.21 | 79.93 | 119.28 | | | |
| 3 | UMI 17 | -0.24 | 70.29 | 117.20 | | | |
| 4 | UMI 21 | 0.29 | 96.90 | 138.00 | | | |
| 5 | UMI 27 | -0.28 | 90.80 | 141.78 | | | |
| 6 | UMI 29 | 0.32 | 116.00 | 128.00 | | | |
| 7 | UMI 35 | -0.24 | 119.27 | 158.12 | | | |
| 8 | UMI 37 | -0.25 | 92.26 | 156.23 | | | |
| 9 | UMI 42 | 0.32 | 124.50 | 127.00 | | | |
| 10 | UMI 48 | -0.17 | 62.04 | 108.28 | | | |
| 11 | UMI 51 | -0.29 | 120.72 | 139.00 | | | |
| 12 | UMI 57 | 0.29 | 151.53 | 140.41 | | | |
| 13 | UMI 61 | -.022 | 105.75 | 116.12 | | | |
| 14 | UMI 64 | -0.26 | 127.59 | 150.00 | | | |
| 15 | UMI 70 | 0.33 | 87.12 | 132.00 | | | |
| 16 | UMI 76 | -0.24 | 118.89 | 121.52 | | | |
| 17 | UMI 79 | -0.27 | 120.12 | 147.87 | | | |
| 18 | UMI 86 | -0.22 | 98.86 | 128.12 | | | |
| 19 | UMI 113 | 0.27 | 91.08 | 146.36 | | | |
| 20 | UMI 118 | -0.24 | 98.12 | 158.12 | | | |
| 21 | UMI 128 | 0.31 | 121.02 | 132.56 | | | |
| 22 | UMI 131 | -0.32 | 123.20 | 128.02 | | | |
| 23 | UMI189 | 0.34 | 119.00 | 138.23 | | | |
| 24 | UMI226 | -0.22 | 112.11 | 116.23 | | | |
| 25 | UMI285 | -0.25 | 121.00 | 135.26 | | | |
| 26 | UMI420 | -0.24 | 111.00 | 129.00 | | | |
| 27 | UMI426 | 0.38 | 115.00 | 165.12 | | | |
| 28 | UMI427 | 0.32 | 117.00 | 141.23 | | | |
| 29 | UMI524 | 0.37 | 88.00 | 144.89 | | | |
| 30 | UMI620 | -0.24 | 111.04 | 158.15 | | | |
| 31 | UMI814 | -0.23 | 119.79 | 163.23 | | | |
| 32 | UMI841 | 0.35 | 106.52 | 142.50 | | | |
| 33 | UMI 889 | -0.29 | 97.78 | 139.00 | | | |
| 34 | CML 141 | 0.31 | 107.98 | 153.26 | | | |
| 35 | CML 142 | 0.32 | 114.21 | 128.61 | | | |
| 36 | CML 143 | 0.30 | 95.81 | 135.03 | | | |
| 37 | CML 144 | 0.38 | 118.97 | 144.23 | | | |
| 38 | CML 145 | 0.39 | 126.26 | 168.00 | | | |
| 39 | CML 146 | 0.31 | 115.25 | 167.23 | | | |
| 40 | CML 147 | 0.30 | 98.02 | 142.18 | | | |
| | | | 4270.89 | 5827.39 | | | |

*$A_i$- Breeding value*
*$\overline{P_i}$ – Parental mean*
*$\overline{C_i}$ – Crosses mean*
*$R_{op}$ – Parent offspring correlation*
*$B_{op}$ – Parent offspring regression*
*$B_{AP}$ – Regression of A on phenotypic value*
** Significant at 5% Level*

## 4. CONCLUSION

Genetic resources in each country are valuable assets for sustainable development. An accurate knowledge of genetic behavior and identification of genomic loci associated with important economic traits will help breeders to run efficiently their breeding programs. The cultivar with high and positive breeding value can be used as a good parent for breeding of

traits in hybridization programs because they can better transfer the desirable characteristics to the progeny in each case [9]. Breeding value (A) is the main parameter of initial screening through top cross analysis as it represents the *gca* (general combining ability) effects of individual test inbred, larger the breeding value greater the *gca* effects. Based on the breeding value and the progeny mean the crosses viz., UMI 9 x CO 1, UMI 21 x CO 1, UMI 29 x CO 1, UMI 57 x CO 1, UMI 42 x CO 1 may be forwarded for explotation of Hybrid vigour.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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