

Original Research Article

Breeding value of Quality Protein Maize inbreds

Abstract

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 hybrid 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 ($C_2=168$).

(Key words: Top cross, QPM lines, Breeding value, *perse mean*)

Introduction

Choice of parents for developing base population is crucial in breeding of cultivars, because it largely predetermines the outcome of subsequent selection steps and affects the optimum allocation of resources in breeding programmes. The top cross design was proposed by Davis (1927) and Jenkins and Brunson (1932) 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 (Smith, 1999) these high yielding parents which facilitates the increased production area (Ghodratollahfathi, 2005). 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.

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Materials and Methods

Seeds of thirty three maize inbred lines and seven Quality Protein maize lines (Table1) 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 (1927) 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 (Davis, 1927) 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.

Comment [nk2]: These are lines or inbred lines

Comment [nk3]: Check this two lines, these are look like similar to some extant

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).

a) 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	

b) Breeding value

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

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

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

c) Parent- offspring correlation (r_{op})

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

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

d) Parent-offspring regression (b_{op})

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

e) Regression of A on phenotypic value (b_{AP})

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

$$SE (b_{AP}) = \left[\frac{CoV (AP)^2}{Var (A)} \right]^{1/2} / (p-2) \left[\frac{5}{Var (A)} \right]^{1/2}$$

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.

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Comment [nk5R4]: Information about pollen parent in method and material is different

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 2. 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 3.

Comment [nk6]: Single plant seed yield
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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 3). 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 *per se mean* ($\bar{P}_{38} = 126.26$) as well as for its hybrid progeny mean ($\bar{C}_2 = 168$) (Table 3).

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 (Goodman, 2000). 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 $BA_p (= 16.56 \pm 1.26)$ 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 > UMI 427 > 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 3). 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.

Table1. 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	THI 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 2: 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

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Table 3 . Breeding value and allied parameters

Comment [nk8]: Breeding value for which trait is calculated

	Parents	A _i	P _i	$\overline{C_i}$	R _{OP}	B _{OP}	B _{AP}
				(inbred x CO 1)			
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	-0.22	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	UMI889	-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
	i		4270.89	5827.39

ng 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.

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