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Selection of Tester for Evaluation of Inbred Lines in Hybrid Maize (*Zea mays* L.)

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Abstract

An experiment was conducted with 72 hybrids of maize made in line × tester design along with four testers and 18 parents evaluated in randomized block design with three replications during *rabi* of 2003-2004. Ten quantitative characters viz. days to 50% tassel, days to 50% silk, plant height, ear height, days to maturity, ear length, ear diameter, number of kernel row per ear, number of kernels per row and grain yield at 15% moisture (q/ha) were used to estimate the correlation coefficient of gca with top cross progenies and genotypic coefficient of variation among test cross progenies. Result revealed that the tester MSIDRS$_6$ ⊗ had maximum correlation followed by CM 400# for grain yield along with ear height, ear length, kernels per row coupled with high genotypic coefficient of variation among test cross progenies suggested narrow genetic base tester of diverse origin should be taken into account for discriminating the inbred lines for their general combining ability.

Key words : Tester selection, Inbred lines, Hybrid maize (*Zea mays* L.).

The proper selection of tester is important to get maximum information on the lines under evaluation. Plant breeders are confronted with the problem of choice of tester parents for knowing the general combining ability of inbred lines. Highly conflicting result on the use of testers for judging the combining ability of inbred lines has been reported. Hence the relative efficiency of maize has been worked out using line × tester approach (1).

Methods

Eighteen diverse inbred lines viz. P502-C$_2$-24-S$_6$⊗, CML-345#, CML32-⊗, P-501-C$_2$-280-215-S$_6$⊗, P 501-C$_2$-53-1-2 S$_6$⊗, M$_9$⊗ –S$_6$-2-2#, CM 601-S$_6$-2-2#, AB (W)-S$_6$-3-2#, Pop. (49)-C$_4$-S$_7$⊗, SPESINIFTICOELS-S$_6$⊗, CML-78#, 89 G 32/DMR, STEW-S$_6$⊗, SIDS-8445-S$_7$ ⊗, Varieded VS-L-S$_6$⊗, Tuxpeno Sequia C$_6$-S$_6$-⊗, AB (w)-4-1-S$_6$⊗, Pop. 412 EISEWGPO S$_6$⊗ and Jogia-S$_6$⊗, were planted during *kharif* of 2003 in line × tester mating design. Resulting a complete set of experimental material comprising 18 lines, 4 testers and 72 F$_1$s with two check hybrids were evaluated in randomized block design with three replications during *rabi* of 2004-05. Each entry was planted in two-row plot of 5 m length with spacing of 75 × 25 cm. Observations were recorded on randomly taken ten competitive plants from each entry in each replication for the days to tassel (50%), days to silk (50%), plant height (cm), days to maturity, ear length (cm), ear girth (cm), kernel rows per ear, number of kernels per rows, grain yield at 15% moisture (q/ha). To have proper choice of tester correlation were computed for general combing ability of lines with performance of crosses involving individual diverse origin of testers. Genotypic coefficient of variation in the top cross progenies were also estimated adopting standard procedures.

Results and Discussion

The analysis of variance for combining ability revealed that difference among treatments was highly significant for all the characters, indicating inherent genetic differences among treatments for all the characters (Table 1). Partitioning of variance was due to treatments into parents, crosses and all the characters. The crosses also showed highly significant differences for all the traits. Correlation coefficients of gca with top progenies are presented in Table 2 which revealed that the tester MS$_1$DR S$_6$⊗ had maximum correlation (0.83) followed by tester CM 400# (0.68)

Table 1. Analysis of variance for line × testers mating design in maize (mean sum of squares). *Significant at 5% level, **Significant at 1% level.

Source of variation	df	Days to 50% tassel	Days to 50% silk	Plant height (cm)	Ear height (cm)	Dats to maturity
Replication	2	65.11	9.48	57.35	30.16	20.90
Treatments	93	78.95**	34.46**	1457.12**	991.67**	20.15**
Parents	21	25.48	29.45**	1336.34**	1100.00**	25.33**
Parents vs Crosses	1	813.65*	1020.44**	65768.59**	25457.23**	231.26**
Crosses	71	84.41**	22.05**	587.05**	615.04	15.64**
Lines	17	162.30*	50.35**	831.87**	928.84**	21.14**
Testers	3	58.00*	36.81**	1976.94**	4591.69**	122.07**
Lines × Testers	51	60.00**	11.75**	423.68**	276.52**	7.55**
Error	186	41.91	6.41	138.52	93.74	4.39

Table 1. Continued.

Sourice of variation	df	Ear length (cm)	Ear diameter (cm)	Kernel rows per ear	Kernel per row	Yield (q/ha)
Replication	2	0.01	0.01	0.76	1.43	13.17
Treatments	93	6.52**	0.53**	5.18**	57.06**	960.36**
Parents	21	9.87**	0.53**	12.06**	78.18**	371.79**
Parents vs Crosses	1	122.26**	19.55**	28.48**	1845.01**	60798.49**
Crosses	71	3.91**	0.26**	2.82**	25.63**	285.73**
Lines	17	8.45**	0.40**	4.06**	45.75**	559.57**
Testers	3	12.26*	0.23*	11.33*	94.81**	36.00*
Lines × Testers	51	1.90**	0.22*	1.90**	14.86**	209.15**
Error	186	0.58	0.02	0.59	4.48	12.77

for grain yield indicated that the narrow genetic base tester was better in discriminating the inbred lines for their general combining ability for ear height, days to maturity, ear length, kernels per row. Usually several

Table 2. Correlation coefficient (r) between gca of lines and performance of top cross of different males and the degree of determination (r^2) in percent. *Significant at 5% level, **Significant at 1% level.

Characters		CM400#	CM300#	MS1DR-S6⊗	PKMS-49-S6⊗
Days to 50% Tassel	r	0.16	0.33	0.36	0.43
	r^2	2.60	10.94	13.12	19.78
Days to 50% silk	r	0.67**	0.86**	0.85**	0.80**
	r^2	44.34	73.20	71.74	63.74
Plant height (cm)	r	0.20	0.67**	0.66**	0.76**
	r^2	3.99	44.99	44.39	58.47
Ear height (cm)	r	0.60**	0.52*	0.61**	0.33
	r^2	36.21	27.29	43.70	10.77
Days to maturity	r	0.45	0.44	0.81**	0.88**
	r^2	20.57	19.35	79.31	77.54
Ear length (cm)	r	0.45	0.73**	0.83**	-0.08
	r^2	20.49	54.62	68.90	0.70
Kernel rows per ear	r	0.34	-0.01	0.13	0.38
	r^2	12.13	0.01	1.90	14.58
Kernel per row	r	0.65**	0.73**	0.77**	0.68**
	r^2	43.46	53.47	60.66	46.37
Ear diameter (cm)	r	0.54*	0.61**	0.11	0.39
	r^2	29.65	37.29	1.31	15.33
Grain yield (q/ha)	r	0.68**	0.49*	0.83**	0.53*
	r^2	47.36	24.97	69.13	29.07

Table 3. Eastimates of genotypic coefficient of variation of cross progenies.

Characters	CM400#	CM300#	MS1DR-S6 ⊗	PKMS-49-S6 ⊗
Days to 50% tassel	2.80	2.85	2.77	2.83
Days to 50% silk	2.38	2.43	2.37	2.42
Plant height (cm)	11.37	10.92	12.32	11.21
Ear height (cm)	18.34	19.25	26.31	30.41
Days to maturity	1.37	1.41	1.40	1.34
Ear length (cm)	10.84	9.31	11.24	11.13
Kernel rows per ear	7.31	6.54	6.37	8.21
Kernel per row	14.60	11.98	17.35	17.32
Ear diameter (cm)	11.02	9.36	10.02	12.20
Grain yield (q/ha)	24.68	23.21	33.40	26.14

alternatives in the selection of tester have been considered such as broad vs narrow genetic base, high vs. low gene frequency, general vs specific combining ability, high vs low gene frequency, general vs specific combining ability, high vs low yield, several vs one tester. Sprague and Tatum (2) concluded that inbred × variety cross measured general combining ability, whereas single cross combination determined best specific combinations. Green (3) tested Nulls hypothesis and suggested the use of a homozygous recessive tester for lodging resistance. Rawlings and Thompson (4) defined a good tester as one that classifies correctly relative performance of the lines and discriminates efficiently among the lines under test. Charcosset et al. (5) observed that a tester F251 an early French flint line with poor *per se* value gave a better prediction than the other testers F252 and F230 for single cross hybrids. Nirala and Jha (6) suggested the broad base testers were better discriminator for green fodder and dry matter but narrow based tester were better for grain yield.

Based on the result the narrow genetic base tester $MS_1DR\ S_6\otimes$ was found to be a good tester for grain yield. Besides grain yield it had maximum correlation coefficient for ear height, day to maturity, ear length, kernels per row coupled with high genotypic coefficient of variation amongst test cross progenies, suggested narrow genetic base inbred tester of diverse origin should be taken into account for evaluation of inbred in hybrid maize breeding program.

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