

# Top Cross Analysis of Maize (*Zea mays* L) Inbred Lines for Some Agronomic Traits in Central Rift Valley of Ethiopia

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**Abstract:** Drought stress tolerant maize breeding program of Melkassa Agricultural Research Center (MARC) which is experimental farm of Ethiopian Institute of Agricultural Research (EIAR) in collaboration with CIMMYT has developed a large number of drought stress tolerant and/or early maturing elite maize inbred lines. The effort is aimed at identifying better combining inbred lines for the development of hybrids for drought stressed areas of the country as no hybrid maize variety has been released for this target area so far. To initiate effective hybrid breeding program, information on the combining ability of inbred lines is an essential and critical factor. In the current study, therefore, an attempt was made to generate information on 24 elite maize inbred lines crossed to two testers in line x tester mating fashion and evaluated the GCA and SCA of the inbred lines and the test cross performance of the hybrids for traits like date of emergence, anthesis to silking interval, days to maturity, number of kernels per row, number of rows per ear, stand count after thinning and biological yield. The genotypes were planted in 6x9 alpha lattice design replicated twice. Analysis of variance indicated significant mean squares due to genotypes for days to maturity, biomass yield, number of ears per plant and number of kernels per row which could be utilized for future evaluation for possible release or used in maize breeding activities. Highly significant differences were noticed among the crosses for biomass yield, number of kernels per row, number of ears per plant, number of rows per ear, indicating that the presence of numerous variations among each other for these traits. Similarly, mean squares due to SCA were highly significant for biomass yield, and number of kernels per row, and number of rows per ear.

**Keywords:** inbred lines, GCA, SCA, inbred lines, agronomic traits

## 1. Introduction

To establish a sound basis for any breeding program, aimed at achieving higher maize production, breeders must have information on the nature of combining ability of parents, their behavior and performance in hybrid combination (Chawla and Gupta, 1984). Furthermore, such information also shows the type of gene action involved in controlling quantitative characters, thereby assisting breeders in selecting suitable parent materials (Hallauer and Miranda, 1988). Combining ability studies are also useful for classifying parental materials into distinct heterotic groups (Sprague and Tatum, 1942).

Although combining ability studies on maize inbred lines has been made in highlands (Twumasi *et al.*, 2001; Teshale, 2001 and Gudeta, 2007) and mid altitudes (Legesse *et al.*, 2009; Mossisa *et al.*, 2009) of high potential maize growing areas of Ethiopia, little efforts have been done on low lands of the country on the performance of maize inbred lines. In the current study, therefore, an attempt was made to generate information on 24 elite maize inbred lines crossed to two testers of known heterotic groups in line x tester mating fashion and evaluated with the objectives to evaluate the test cross performance and to estimate the GCA and SCA of the inbred lines for grain yield and yield related traits.

## 2. Materials and Methods

The experiment was carried out at MARC in 2010 main cropping season. A total of fifty two entries including 48 test crosses produced by crossing twenty four elite inbred lines with two testers (CML312/CML442, tester A and CML202/CML395, tester B) and four standard checks

(BH540, BHQPY-545, Melkassa-2, Melkassa-6Q) were used for the study. The experiment was planted at MARC in 6x9 alpha-lattice design (Patterson and Williams, 1976) with two replications. Each plot comprised of 4 rows of 5.1 m long with the spacing of 0.75 m between rows and 0.30 m between plants. Other cultural practices like weeding and pest management has been done manually throughout the entire growing season as required.

Data were collected on date of emergence, stand count after thinning, anthesis to silking interval, days to maturity, biomass yield, and number of ears per plant, number of kernel rows per ear and number of kernels per row.

**Table 1:** Descriptions of the lines, testers and checks used in Melkassa in 2010

Line Code	Pedigree	Stock ID
L1	CML505-B	M22-1
L2	CML509-B	M22-2
L3	CML507-B	M22-3
L4	ZEWAc1F2-300-2-2-B-1-B*4-1-B-B	M22-4
L5	ZEWAc1F2-134-4-1-B-1-B*4-1-B-B	M22-5
L6	ZEWAc1F2-254-2-1-B-1-BB-1-B-B	M22-6
L7	ZEWBc1F2-216-2-2-B-2-B*4-1-B-B	M22-7
L8	MAS[MSR/312]-117-2-2-1-B*3-B	M22-8
L9	CML442-BB-B	M22-9
L10	CML444-BB-B	M22-10
L11	CML443-BB-B	M22-11
L12	CML395-BB-B	M22-12
L13	CML488-BB-B	M22-13
L14	CML489-BB-B	M22-14
L15	CML440-B	M22-15
L16	CML445-B	M22-16
L17	[CML444/CML395//ZM521B-66-4-1-1-1-BB]-3-3-1-1-B-B	M22-17

Volume 3 Issue 11, November 2014

[www.ijsr.net](http://www.ijsr.net)

L18	[CML312/CML444/[DTP2WC4H255-1-2-2-BB/LATA-F2-138-1-3-1-B]-1-3-2-3-B]-2-1-2-BB-B-B	M22-18
L19	[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-1-B*4-B	M22-19
L20	[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-3-B*4-B	M22-20
L21	Pool15QPMFS57-B-5-B-#-B-B-B-B-B	M22-21
L22	Pool15QPMFS440-B-4-B-#-B-B-B-B-B	M22-22
L23	Pool15QPMFS309-B-1-B-B-B-B-B	M22-23
L24	Pool15QPMFS51-B-8-B-B-B-B-B	M22-24
<b>Testers</b>		
T1	CML312/CML442	Tester A
T2	CML202/CML395	Tester B
<b>Checks</b>		
BH-540	SC-22 x 124b-(113)	Medium maturing normal maize hybrid
Melkassa-2	ZM-521	Drought tolerant normal maize OPV
Melkassa-6Q	Pool15 C7 QPM	Drought tolerant QPM OPV
BHQPY-545	CML161 x CML165	Medium maturing QPM hybrid

**2.1. Statistical Analysis**

The data collected for all yield and yield-related traits were analysed using PROC MIXED procedure in SAS (SAS, 2004). In the analysis, entries were used as fixed factor while replications and incomplete blocks within replication

**Table 2:** Mean squares due to genotypes and errors for grain yield and yield related traits of maize test crosses evaluated at Melkassa in 2010.

Sources of variation	Df	Mean squares				
		EPP (No)	NKR (No)	BY (t/ha)	DM (days)	KRE (No)
Replication (R)	1	0.001ns	1.40ns	6.45ns	15.64*	1.64*
Incomplete block (blk/R)	16	0.025ns	9.54ns	2.22ns	7.97*	0.45ns
Genotype (G)	51	0.017**	27.52**	10.35**	4.79**	0.83**
Cross (C)	47	0.0168**	26.06**	10.81**	4.08ns	0.88**
Check (Ch)	3	0.017 ns	36.40 ns	6.39 ns	11.83 ns	0.34 ns
Check vs Cross ( Ch vs C)	1	0.025 ns	69.73 ns	0.73 ns	17.33 ns	0.18 ns
Error(E)	51	0.005	4.085	1.63	1.78	0.19

\*and \*\* = Significant and highly significant, respectively ns= non significant, DM = days to maturity, KRE= number of kernel rows per ear, BY = biomass yield, EPP= number of ears per plant, NKR=number of kernels per row

**3.2. Combining Ability Analysis**

Line GCA mean squares were highly significant for biomass yield, number of kernels per row, number of rows per ear and number of ears per plant (Table 3). For tester GCA, number of kernels per row showed highly significant differences. The non significant difference tester mean square observed for most the traits suggest that the testers used for the current study had comparable potential for the studied traits. In line with the results of this study, Legesse *et al.* (2009) found significant mean squares due to GCA of lines. Mosa (2010) found highly significant mean square due

were considered as random factors. Entry means adjusted for block effects as analyzed according to lattice design (Cochran and Cox, 1957) were used to perform combining ability analysis. Further analysis was done according to the line x tester analysis to partition the mean square due to crosses into lines, tester and line by tester effects (Dabholkar, 1999, Singh and Chaudary, 1985) using SAS computer program (SAS, 2004) for traits that showed significant differences among crosses.

**3. Results and Discussion**

**3.1 Mean Square Performance**

Analysis of variance showed that mean squares were highly significant for traits such as number of kernel rows per ear, number of ears per plant, number of kernels per row and biomass yield. But non-significant differences were obtained for anthesis-silking interval, date of emergence, stand count after thinning and ear diameter (Table 2). Due to this fact, further genetic analysis and discussions were not done for these traits with non significant genotype mean squares. In line to these findings, significant mean square due to genotypes for grain yield and yield related traits in maize were also reported by previous investigators (Bayisa, 2004; Gudeta, 2007; Akbar, *et al.*, 2009; Rahman *et al.*, 2010; Shams, 2010). Mean squares due to crosses were highly significant for days to maturity, biomass yield, number of kernels per row, number of rows per ear and number of ears per plant. This indicates that the crosses were sufficiently different from each other for these traits and hence, selection is possible to identify the most desirable crosses. The differences among the checks were not significant for all the traits studied. The current finding is in line with the findings of Legesse *et al.* (2009) and Mosa (2010).

to top crosses entries, checks, line GCA and non-significant mean square due to check vs crosses for most traits he studied.

Analysis of variance for SCA also showed highly significant differences for biomass yield, number of ears per plant, number of kernels per row and number of rows per ear (Table 3). In conformity to this result, several findings have been reported by earlier investigators (Ahmad and Saleem, 2003; Bayisa *et al.*, 2008). This indicates importance of non additive gene action in controlling the traits under consideration.

**Table 3:** Mean squares for grain yield and yield related traits in 48 test crosses evaluated at Melkassa in 2010

Sources of variation	Df	EPP (No)	NKR (No)	BY (t/ha)	DM (days)	KRE (No)
Line (GCAf)	23	0.0252**	24.91**	12.59**	4.88ns	1.32**
Tester (GCAM)	1	0.00075ns	28.83**	1.32ns	0.33 ns	0.25 ns
Line x Tester (SCAfm)	23	0.0091 **	27.08**	9.43**	3.43ns	0.46**
Error (E)	47	0.0057	4.49	1.75	1.89	0.12

\*and \*\* = Significant and highly significant, respectively, DM = days to maturity, KRE= number of kernel rows per ear and BY = biomass yield, EPP= number of ears per plant, NKR=number of kernels per row.

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