

COMBINING ABILITY AND HETEROTIC GROUPING OF HIGHLAND TRANSITION MAIZE INBRED LINES

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ABSTRACT - The objectives of the present study were to examine combining ability of highland transition maize inbred lines for grain yield and other desirable traits, to determine heterotic groups of germplasm of the inbred lines and to identify promising hybrid crosses. Twenty-six inbred lines were factorially mated (Design II) with six testers and the resulting F₁s along with two checks and the parents were evaluated in separate trials at five locations namely: Ambo, Awassa, Bako, Holeta and Kulumsa, all in Ethiopia during 2002. General combining ability (GCA) and specific combining ability (SCA) effects were calculated using line x tester analysis. GCA mean squares due to lines and, testers were highly significant ($P < 0.01$) for all the traits. Similarly SCA mean squares for most traits except for days to physiological maturity and for northern leaf blight (NLB, caused by *Exserohilum turcicum*) were found highly significant ($P < 0.001$). The ratio of GCA/SCA mean square further exhibited the preponderance of additive gene effects in the inheritance of all traits. Estimates of GCA effects indicated that three inbred lines showed good combiners for grain yield. For days to silking four, for grey leaf spot (GLS caused by *Cercospora zea-maydis* Tehon), three, and for NLB one inbred lines revealed significantly negative GCA effects. These inbred lines can be a good source of variability for the improvement of the traits in the breeding program. Significantly different SCA effects were revealed for crosses involving most traits. A number of single crosses out-yielded the hybrid checks (BH660 and BH 540) and also revealed desirable plant height performances. Moreover, two best contrasting heterotic group (Pool 9A-MHM x 142-1-e) composed of 13 and 10 inbred lines, respectively, have been determine to initiate heterotic source germplasm. This heterotic group may have wide applicability in the east African highland maize breeding programs, as well.

KEY WORDS: Combining ability; Heterotic groupings; Inbred lines; Testers; *Zea mays* L.

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INTRODUCTION

Information about combining ability of experimental breeding materials is imperative to a breeding program aiming to develop high yielding hybrids and composite varieties. Such information can show the type of gene action involved in controlling quantitative characters, thereby assisting breeders in selecting suitable parent materials (HALLAUER and MIRANDA, 1988). Significant values for general combining ability (GCA) and specific combining ability (SCA) may be interpreted as indicating the performance of additive and non-additive gene action, respectively (SPRAGUE and TATUM, 1942). GCA enabled breeders to exploit the existing variability in the breeding materials, to identify individual genotypes conferring desirable attributes and to distinguish relatedness among genotypes (VACARO *et al.*, 2002; MELANIA and CARENA, 2005). While SCA is serving to determine heterotic patterns among populations or inbred lines, to identify promising single crosses and to assign inbred lines into heterotic groups (VASAL *et al.*, 1992; HEDE *et al.*, 1999; PARENTONI *et al.*, 2001; REVILLA *et al.*, 2002).

Combining ability studies aiming to identify inbred lines with good GCA and SCA effects rely on the availability of genetic diversity among groups of genotypes involved in a breeding program. HAN *et al.* (1991) studied combining ability effects of inbred lines derived from CIMMYT populations and germplasm pools. They observed significantly positive SCA effects for crosses of inter-population inbred lines and concluded that inbred lines derived from different populations are more likely to show superior yielding performances. ZEHUI *et al.* (2000) studied inbred lines derived from different populations and found significant GCA effects for a number of yield related and morphological traits. KADLUBIEC *et al.* (2001) using flint and dent types of maize

inbred lines reported a higher proportion of GCA effects than SCA effects for yield and various other agronomic traits. Studies conducted on the inheritance of GLS in maize revealed the importance of both additive and non-additive type gene action (GEVERS *et al.*, 1994; MENKIR and AYODELE, 2005), while some others found GLS under control of additive gene action (DONAHUE *et al.*, 1991).

Maize is grown over a diverse range of environments in sub-Saharan African countries starting from lowlands, midaltitude to highland ecologies (BYERLEE and EICHER, 1997). In Ethiopia, highland maize production is estimated to cover around 20% of the total land allotted to maize production and 30% of small-scale farmers in the area depend on it for their livings. However, breeding efforts to develop high yielding improved maize varieties for highland areas (altitude = 1700-2400 m) has been recently launched. Most of the varieties grown in the region are low yielding local cultivars with susceptibility to various leaf diseases such as NLB, GLS and common rust, and are very tall in plant and ear height that result into root and stalk lodging, and also are late in physiological maturity. Enhancement of maize production and productivity can be achieved by identifying elite parent materials which can be used to develop high yielding varieties and by forming broad based source population serving the breeding program. The objectives of this study were to: 1) estimate combining ability effects of highland transition maize inbred lines for grain yield, days to flowering, days to physical maturity, GLS and NLB, 2) determine heterotic groups of germplasm of the inbred lines, and 3) identify promising hybrid crosses which may go into production, swiftly.

MATERIALS AND METHODS

Genetic materials

The study materials involved 26 maize inbred lines derived from three different populations, 1) Kitala Synthetic II × N3-type lines, 2) Ecuador-573 × SC-type lines, and 3) Pool9A × IITA's mid-altitude streak resistant population by the CIMMYT regional program in Zimbabwe. They were introduced to Ethiopia and selected for tolerance to common foliar diseases [NLB, common rust (*Puccinia sorghii*); and GLS], vigour and general adaptation to the highland regions (TWUMASI-AFRIYIE, 2001). The inbred lines were crossed with six local testers: three populations (Kitala Syn. II, Ecuador 573, and Kuleni) and three inbred line testers (142-1-e, F7215, Pool9A-MHM) in a factorial mating design (Design II) that resulted in 156 F₁ progenies. Kitala Syn. II and Ecuador 573 are well known heterotic populations in Kenyan highland maize ecologies (DARRAH, 1986). Kuleni is an improved version of

Pool9A, a population developed by CIMMYT for tropical highland transition maize agro-ecologies (LOTHROP, 1989). The pedigree and genetic background of the inbred lines and the testers is given in Table 1.

Field evaluation

The 156 F₁ crosses along with two hybrid checks (BH540, BH660) and their parents were evaluated in separate trials across wide range of environments representing mid-altitude and highland of Ethiopia namely: Ambo, Awassa, Bako, Holeta and Kulumsa in 2002. Awassa and Bako lie in the mid-altitudes between 1,650 m and 1,700 m, above sea level and receive 1,250 and 1,110 mm annual rainfall, respectively. Ambo, Kulumsa and Holeta are found in the highland ranging from 2,200 m to 2,400 m above sea level. The average annual rainfall at Ambo, Holeta and Kulumsa are 1,115, 1,250, and 830 mm, respectively. The experimental design was alpha-0, 1-lattice (PATTERSON and WILLIAMS, 1976) with two replications at each location. The trials of the parents were grown directly adjacent to the F₁ progenies. The experimental unit consisted of a single five-meter long row plot with 75 cm spacing in between rows. Planting was done using two seeds per hill and 25 cm apart between hills. Thinning was performed at the three to five leaf stages to attain a final plant density of 53,000 plants ha⁻¹. All other management practices such as fertilization, weeding and harvesting were performed according to the recommendations for each location.

Data for all parameters were recorded on a per plot basis at each testing location. Grain yield (Mg ha⁻¹) was computed from unshelled cobs by taking 0.8 shelling percent and adjusting it to 12.5% moisture. Time to silking was recorded as number of days from planting to 50% extruded silks. Time to physiological maturity was recorded as number of days from planting to when 50% of the plants showed black layers on the tip of the kernel. Plant height (cm) was taken from soil surface to the point where tassel branching begin emerging. GLS and NLB data were assessed as visual scoring of the disease symptoms in scale of 1 (no infestation) to 5 (severely infested).

Statistical analyses

Analyses of variance were conducted for all the traits measured, using individual plot data for each environment separately. Prior to combined data analysis across locations Bartlett's test for grain yield was conducted to test homogeneity of variance (GOMEZ and GOMEZ, 1984), considering grain yield as the primary factor of interest. Based on the test result, data from four locations excluding Kulumsa were analyzed for all traits combined using agro-base software package (AGROBASE, 2001).

Line x tester analyses of variance was performed to estimate general combining ability (GCA) and specific combining ability (SCA), assuming the following statistical model (SINGH and CHAUNDHARY, 1996):

$$Y_{hijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + R_h + \epsilon_{hijk}$$

where

Y_{hijk} = the observation of the k-th full-sib progeny in a plot in h-replication of the i-th paternal parent and the j-th maternal parent; μ = the general mean; α_i = the effect of the i-th male parent; β_j = the effect of j-th female parent; $(\alpha\beta)_{ij}$ = the interaction of paternal and maternal genotypes; R_h = the effect of h-th replication and ϵ_{hijk} = the environment effect and remainder of the genetic effect between full sibs on the same plot.

TABLE 1 - Identification and pedigrees of highland adapted maize inbred lines (1-26) and their testers (26-32) evaluated across five locations in Ethiopia in 2002.

No.	Genotypes	Pedigree	Parents	Source
1	AMBOON6-1	KIT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 6-1	Kitale Syn II	CIMMYT
2	AMBOON6-4	KIT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 14-1	Kitale Syn II	CIMMYT
3	AMBOON6-8	KIT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 7-3	Kitale Syn II	CIMMYT
4	AMBOON6-9	KIT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 11-1	Kitale Syn II	CIMMYT
5	AMBOON6-14	KT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 11-2	Kitale Syn II	CIMMYT
6	AMBOON6-15	KIT/SNSYN ((N3) TUXC1F1# # # (GLS=1) 14-2	Kitale Syn II	CIMMYT
7	AMBOON6-20	SRSYN95 ((KIT/N3) TUXF1# # # (GLS=1) 6-1	Kitale Syn II	CIMMYT
8	AMBOON6-21	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=1.5) 16-1	Ecuador 573	CIMMYT
9	AMBOON6-22	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=2.0)-3-1	Ecuador 573	CIMMYT
10	AMBOON6-23	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=2.0)-8-2	Ecuador 573	CIMMYT
11	AMBOON6-25	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=2.5)-24-2	Ecuador 573	CIMMYT
12	AMBOON6-26	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=2.5)-42-3	Ecuador 573	CIMMYT
13	AMBOON6-27	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=3.0)-23-1	Ecuador 573	CIMMYT
14	AMBOON6-29	ECU/SNSYN (SC/ETO) C1 F1# # # (GLS=3.5)-41-1	Ecuador 573	CIMMYT
15	AMBOON6-37	SRSYN95 ((ECU/SC/ETO) F1# # # (GLS=3)-21-1	Ecuador 573	CIMMYT
16	AMBOON6-38	SRSYN95 ((ECU/SC/ETO) F1# # # (GLS=3.5)-40-1	Ecuador 573	CIMMYT
17	AMBOON6-39	SRSYN95 ((ECU/SC/ETO) F1# # # (GLS=3.5)-4-2	Ecuador 573	CIMMYT
18	AMBOON6-40	SRSYN95 ((ECU/SC/ETO) F1# # # (GLS=3.5)-39.1	Ecuador 573	CIMMYT
19	AMBOON6-41	POOL9AC-7-SR (BC2) FS-1-1-3-1	Pool9A	CIMMYT
20	AMBOON6-42	POOL9AC-7-SR (BC2) FS-1-4-2-3	Pool9A	CIMMYT
21	AMBOON6-44	POOL9AC-7-SR (BC2) FS-4-3-SR-1-1	Pool9A	CIMMYT
22	AMBOON6-47	POOL9AC-7-SR (BC2) FS-50-1-2-3	Pool9A	CIMMYT
23	AMBOON6-49	POOL9AC-7-SR (BC2) FS-89-2SR-1-1	Pool9A	CIMMYT
24	AMBOON6-54	POOL9AC-7-SR (BC2) FS-170-2-1-3	Pool9A	CIMMYT
25	AMBOON6-59	POOL9AC-7-SR (BC2) FS-232-4-1-3	Pool9A	CIMMYT
26	AMBOON6-60	POOL9AC-7-SR (BC2) FS-48-1-1-3	Pool9A	CIMMYT
27	Kitale Syn. II (Pop. tester)	Tuxpe o derived germplasm	Pool9A	Kenya
28	EUCADOR-573 (Pop. Tester)	Montana race	Pool9A	Ecuador
29	KULENI (Pop. tester)	Pool 9A		CIMMYT
30	142 -1-e (line tester)	Unknown (Derived from Ecuador 573)		Ethiopia
31	F7215 (line tester)	Unknown (Derived from Kitale Syn. II)		Ethiopia
32	POOL9A-MHM (line tester)	Unknown (Derived from Pool 9A)		Ethiopia

In the analyses, environment was considered random and genotype as fixed effect. Mean square of variance was determined for lines and testers and their interaction effects. GCA effects for each parents (inbred line/ tester) was estimated as the mean of all crosses involving that parent (inbred line/ tester) minus the overall mean, and SCA was estimated as mean of a cross minus mean of all inbred line crosses involving that line, mean of all tester crosses involving that tester and the over all mean. The F-test for main effects such as entries and its partitions were tested against their respective interactions with environment, and the interaction with environment terms were tested against the pooled error. Significance of GCA and SCA effects were performed computing the standard error for lines, testers and crosses and then tested against t- test by taking the degree of freedom of pooled error mean square. Heterosis (%) for grain yield was calculated over the mid-parent values.

Heterotic groupings

Grain yield GCA effects of all the six testers were estimated to identify a pair of testers with significantly contrasting GCA to assign the inbred lines and to initiate heterotic groups. Furthermore, three putative heterotic groups were also initiated among the rest of the testers which were not identified on the bases of their GCA values. In all cases, the inbred lines based on the SCA values computed from their crossing performance with the testers were assigned toward any one or both of the heterotic tester groups. An inbred line which possessed negative SCA with any one of a heterotic tester was grouped with the tester with which it revealed negative effects. Another inbred line revealing positive SCA with both testers was assigned towards both groups and, the one which revealed negative SCA with the two testers was discarded (VASAL *et al.*, 1992; PARENTONI *et al.*, 2001).

After assigning the inbred lines, the SCA values of all the

four heterotic groups were determined separately by adding the values of all the crosses brought together to initiate a heterotic group and then compared in pair using t-test statistics (PARENTONI *et al.*, 2001). Similarly grain yield mid-parent heterosis was computed for all crosses with respect to each tester and then the average value determined and compared likewise in order to verify the appropriateness of the testers (ORDAS, 1991) which have been identified based on contrasting GCA effects and to which assigning of the inbred lines have been suggested to initiate the heterotic group bases on SCA.

RESULTS AND DISCUSSION

Analysis of variance

Mean grain yield for crosses ranged from 7.5 Mg ha⁻¹ at Bako to 8.1 Mg ha⁻¹ at Holeta. Significantly

different mean values for grain yield, days to silking, days to maturity GLS and NLB were found across locations. Genotypes on the average revealed high grain yield at Holeta condition, which exhibited the latest flowering and days to physiological maturity. On the other hand, the lowest mean for GLS and the highest for NLB scores were recorded at Ambo. GLS incidence appears to be most prevalent in the intermediate elevated locations (Awassa and Bako), (Table 2) sites with high temperature, high relative humidity and abundant rainfall, which constitute ideal conditions for GLS disease development (DE-NAZARENO *et al.*, 1993). Similar result was reported by DAGNE *et al.* (2001) in a survey conducted to assess prevalence and severity of GLS incidence in Ethiopia.

TABLE 2 - Location means of crosses for grain yield, days to silk, maturity, gray leaf spot and northern leaf blight disease scores.

Location	Grain yield (Mg ha ⁻¹)	Silking (-days-)	Plant height (-mts-)	Maturity (-days-)	GLS (—score-(1-5) ^b —)	NLB
Ambo	7.4	89.3	2.9	166.0	1.1	2.5
Awasa	7.8	72.9	1.9	140.2	2.2	1.5
Bako	7.5	73.6	2.7	144.0	2.1	1.9
Holeta	8.1	106.8	2.3	194.1	-	1.6
Mean	7.7	85.6	2.4	166.0	1.8	1.9
S.E	0.20	0.83	0.02	0.33	0.06	0.04

^b 1 = tolerance, and 5 = susceptibility.

TABLE 3 - Combined analysis of variance of bigland maize inbred line crosses for grain yield, days to silking, days to maturity, plant height, GLS and NLB disease incidence.

Source	DF	Mean Squares					
		Grain yield (Mg ha ⁻¹)	Silking (-days)	Maturity (-days)	Plant height (-mts-)	GLS (Score)	NLB (Score)
Sites (S)	3	36.868	79903.146**	191201.799**	64.868**	130.609**	63.428**
Rep/S	4	12.946	216.015	34.651	0.150	1.042	0.476
Entry (E)	155	8.744**	37.155**	60.772**	0.183**	0.337**	0.223**
E x S	465	3.575**	9.177*	40.614**	0.046	0.156**	0.154
GCA (L)	25	15.095**	84.018**	86.175**	0.369**	0.528**	0.259*
GCA (T)	5	116.799**	380.248**	616.292**	2.542**	3.312**	1.669**
SCA (L x T)	125	3.152**	14.059**	33.471	0.052**	0.180**	0.158
GCA (L x S)	75	7.622**	11.112*	53.451**	0.049	0.180**	0.154
GCA (T x S)	15	22.403**	38.486**	136.273**	0.038	0.782**	0.231
SCA x S	375	2.156	7.618	34.220	0.046	0.127	0.162
Error	620	1.893	7.509	29.741	0.042	0.123	0.131
C.V %		17.87	3.20	3.39	8.38	19.48	19.47

** , * Significant at 0.01 and 0.05 probability levels, respectively.

L, and T represent, Lines and Testers with their corresponding GCA.

Mean squares for location effects on days to silking, days to physiological maturity, plant height, GLS and NLB were highly significant ($P < 0.01$). Significant variances due to crosses were observed across locations for all traits. Similarly, mean squares due to crosses \times locations for all traits, except plant height and NLB revealed significant ($P < 0.05$) to highly significance ($P < 0.01$) variations. The non-significant genotype \times location effects observed especially for NLB is in agreement with the findings of ASSEFA *et al.* (1994).

GCA mean squares due to lines and testers for all characters were highly significant. Similarly, highly significant variation was found due to SCA for grain yield, days to silking, plant height, and GLS (Table 3). It indicated preponderance of significant variability existing in breeding material attributable to genotype additive and non-additive effects except non-significant mean square due to SCA for days to physiological maturity and for NLB across testing locations. The GCA/SCA variance ratio further exhibited the predominance of additive gene effects in the inheritance of all traits. Several researchers also have indicated additive effects in the inheritance of different agronomic traits in maize (ZEHUI *et al.*, 2000; VACARO *et al.*, 2002; BAYISA *et al.*, 2008). Mean squares due to GCA \times locations for lines and testers were highly significant for all characters, except for plant height and NLB. In contrast, non-significant SCA \times location effects were found for all the study traits.

General combining ability effects

General combining ability estimates for grain yield, days to silking, maturity, plant height, GLS and NLB for each parental line with the respective standard errors are given in Table 4. GCA effects for grain yield ranged between -1.31 Mg ha^{-1} to 0.90 Mg ha^{-1} . Most of the inbred lines related to Kitale Syn.II and a few of the Ecuador 573 related lines revealed positive GCA effect for grain yield. Nevertheless, lines 2, 7 and 19 were found most attractive general combiners. These inbred lines can be desirable parents for hybrids as well as for inclusion in breeding program, since they may contribute favorable alleles in the synthesis of new varieties. On the other hand parents 1, 7, 20, 24 and 25 for days to silking as well as parent 26 for plant height manifested significantly negative GCA values. Similarly, parents 3, 4, 10, and 24 for GLS as well as parent 26 for NLB are good general combiners suggesting the importance of these inbred lines in the improvement of the traits.

Desirable GCA effects were observed in the breeding material used for grain yield, days to physiological maturity, plant height, GLS and NLB (SCHECHERT *et al.*, 1996; MENKIR and AYODELE, 2005; BAYISA *et al.*, 2008). Among the tester parents, the highest GCA values for grain yield was revealed by 142-1-e, (Fig. 1) an inbred line tester of EC-573 origin.

Specific combining ability effects

Among the 26 inbred lines crossed with population testers, nine with Kitale Syn.II, 10 with Ecuador 573, 12 with Kuleni (Pool9A), and among line testers 13 with 142-1-e, 15 with F 7215, 12 with Pool9A-MHM yielded positive SCA effects for grain yield (data not shown). Inbred lines derived from Pool 9A parent showed similar affinity to both Kitale Syn. II and Ecuador 573 testers parents and gave significantly positive SCA effects for grain yield. This suggests that lines derived from Pool9A may exhibit good heterotic response when crossed with any one of the population testers. However, a line related to the Kitale Syn.II manifested the highest positive SCA (1.5 Mg ha^{-1}) (Table 5) effects when crossed with 142-1-e, the inbred line tester. Similarly, several lines related to Kitale Syn.II revealed significantly positive SCA effects when crossed with Ecuador 573 and 142-1-e testers. This phenomenon is evident, because Kitale Syn.II and Ecuador 573 are well known heterotic pairs under eastern African conditions revealing positive heterosis in most circumstances (DARRAH, 1986).

For days to silking, SCA effects manifested by most of the crosses were noted to be less desirable in terms of their importance for earliness. SCA effects revealed by the earliest hybrid cross for days to silking showed only six-day differences as compared to the latest hybrid (Table 5). In contrast, SCA effects for plant height were in a desirable direction. A number of high yielding hybrids crosses revealed significantly desirable plant height performances as compared to the hybrid check BH660 (Fig. 1). BAYISA *et al.* (2008) using inbred lines of transition highland material found out hybrid crosses which revealed significantly attractive SCA for plant height. For GLS several crosses manifested significantly negative SCA effects, implying the importance of non-additive gene action to be in the desirable direction for the improvement of the genotypes against GLS incidence. In the same manner the highly significant GCA effects revealed by a number of inbred lines in the study may also indicate the importance of additive type of gene action for GLS

TABLE 4 - General combining ability effects of grain yield, days to silking plant height, maturity, gray leaf spot and northern leaf blight diseases scores based on combined data analysis.

General combining ability effects						
Lines	Grain yield (Mg ha ⁻¹)	Silking (—days—)	Maturity	Plant height (—mts—)	GLS (—Scores—)	NLB
1	0.05	-1.88**	-0.55	-0.14*	-0.05	-0.01
2	0.88**	0.39	1.03	0.07	0.23**	-0.07
3	0.20	-0.86	-0.72	-0.03	-0.12*	0.09
4	0.31	-0.67	-0.33	0.02	-0.15*	-0.07
5	0.28	0.79	0.65	0.10*	-0.09	-0.02
6	0.76*	-0.55	-0.16	0.05	0.19*	0.00
7	0.90**	-2.24**	-0.80	-0.03	0.09	0.07
8	-0.91**	1.41*	0.90	-0.04	-0.03	-0.09
9	-1.31**	1.64**	-0.53	-0.08	0.19*	0.15*
10	-0.81**	1.27*	1.65	-0.05	-0.13*	-0.08
11	0.29	-1.03	-1.74	0.00	0.08	-0.02
12	0.35	1.27*	2.49*	0.03	0.02	0.01
13	0.11	-1.07	-0.10	-0.10*	-0.02	0.01
14	-0.37	0.29	0.43	-0.02	-0.03	-0.08
15	-0.37	1.29*	-0.01	0.13*	0.19*	0.06
16	-0.01	1.91**	0.40	0.01	0.01	0.00
17	0.55*	2.95**	3.53**	0.01	0.11	-0.08
18	0.16	0.47	-2.20*	0.03	0.12	0.02
19	0.87**	-0.84	0.30	0.26**	0.05	-0.04
20	-0.16	-1.57**	-0.78	0.10*	-0.02	-0.11
21	-0.55*	0.54	0.36	-0.06	-0.09	0.09
22	-0.27	0.22	0.22	-0.08	-0.13	-0.12
23	0.00	0.16	-0.03	0.03	-0.02	0.03
24	-0.23	-1.32*	0.47	-0.14*	-0.20*	0.02
25	-0.49	-1.36*	-2.12	-0.01	-0.01	0.12
26	-0.23	-0.23	-1.24	-0.35**	-0.08	-0.19**
S.E	0.20	0.40	0.79	0.25	0.05	0.05

* and ** = refers to significant to highly significant difference from zero.

TABLE 5 - Minimum and maximum specific combining ability effects for grain yield days to silking, plant height and GLS disease incidence for hybrid crosses determined based on combined data analysis.

Parameters		Minimum	Maximum	Standard error	Range
Grain yield	(Mg ha ⁻¹)	-1.61	1.54	0.45	31.2
Days to silking	(days)	-2.96	2.95	0.09	5.91
Plant height	(mts)	-0.21	0.18	0.03	0.39
Gray leaf spot	(scores)	-0.35	0.48	0.01	0.83

inheritance. This finding is in agreements with the findings of several researchers who reported the role of additive and non-additive type gene action in the inheritance of GLS (GEVERS *et al.*, 1994; MENKIR and AYODELE, 2005).

In general, significant SCA variation detected in the analysis of variance for most traits is a good indication of non-additive gene effects predominance. Among the tester parents, the highest overall crossing performance for grain yield was observed by

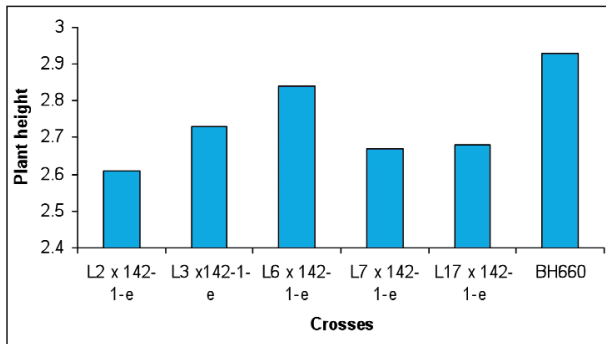


FIGURE 1 - Plant height performances of high yielding crosses and a hybrid check (BH660).

142-1-e. Lines that were crossed with unrelated testers yielded desirable SCA effects, in most circumstances. Consequently, several single cross combinations were identified possessing far better yields than the hybrids checks (Table 6) and manifesting high SCA effects across locations. This is in line with the findings of several authors who estimated combining ability effects of inbred lines derived from different germplasm origins (HAN *et al.*, 1991; VASAL *et al.*, 1992; ROSA *et al.*, 2000; VACARO *et al.*, 2002).

Formation of heterotic groups

Among the tester parents highly significant grain yield GCA effects were determined for the two testers, 142-1-e and Pool9A-MHM. The GCA values of these testers were exceptionally divergent (Fig. 1) indicating presence of relatively enormous genetic variation between them. On the bases of this assumption, Pool9A-MHM and 142-1-e were suggested to be most contrasting candidate testers for as-

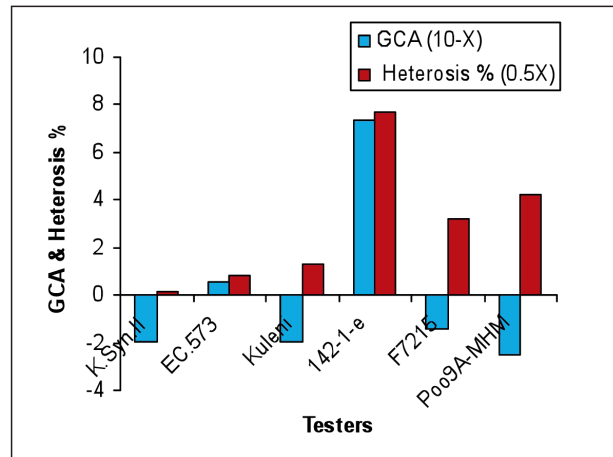


FIGURE 2. Grain yields GCA (Mg/ha¹) and Mid-Parent heterosis (%) of population and line testers.

signing the inbred lines into heterotic groups, each group involving 13 and 10 inbred lines, respectively (Table 7). A further confirmation of the resultant testers was also positively signified the appropriateness of their divergence mainly by determining the average SCA values of the four pairs of putative testers including the candidates and comparing values of each heterotic pair, in a pair wise fashion. In this case, highly significant difference was shown for inbred lines assigned towards Pool9A-MHM × 142-1-e group. Kitale Syn.II × Ecuador 573, despite their importance as heterotic markers (DARRAH, 1986), the inbred lines assigned towards these testers failed to reveal significantly higher overall SCA values. High SCA value indicates the significance of non-additive gene action and thus it is generally manifested between crosses of two geneti-

TABLE 6 - Location mean of Grain yield (Mg ha⁻¹) performance of promising single cross hybrids evaluated at for sites in Ethiopia in 2002.

Crosses	Locations					% Check
	Ambo	Awassa	Bako	Holeta	Across	
2 x142-1-e	12.1	9.2	10.2	9.9	10.3	121
6x142-1-e	10.4	9.6	8.6	13.2	10.4	122
7 x142-1-e	12.2	9.4	13.0	11.6	11.6	136
18x142-1-e	9.1	9.7	8.2	12.0	9.8	115
19 x142-1-e	10.3	8.4	9.2	13.0	10.2	120
23 x142-1-e	9.4	8.0	9.6	11.2	9.7	114
26 x142-1	9.1	8.6	9.4	9.4	9.6	107
BH 660 (Check)	8.0	8.5	9.3	8.2	8.5	100
S.E ^a	0.8	0.8	1.0	1.1	1.0	

TABLE 7 - Identification and number of lines clustered together under each contrasting tester group.

No.	Kitale x Ecuador		Kuleni x Ecuador		F7215 x 142-1-e		Pool9A-MHM x 142-1-e	
Heterotic groups								
	Lines in a tester group *		Lines in a tester group		Lines in a tester group		Lines in a tester group	
1	3	1	3	1	1	1	1	2
2	4	3	4	2	2	5	2	5
3	5	8	5	5	3	6	3	9
4	7	9	7	8	4	11	4	10
5	11	10	9	10	6	14	6	13
6	15	12	11	12	7	15	7	16
7	17	14	15	13	9	18	9	18
8	18	15	18	14	10	20	11	21
9	19	16	19	17	17	22	17	22
10	20	17	20	19	18	24	18	26
11	24	22	24	21	19	25	19	
12		23		23	21	26	23	
13				24	23		26	
14				25	26			

* = the identification and the pedigree of the lines indicated in Table 1.

cally divergent inbred lines mainly due to the preponderance of dominance gene effects. PARENTONI *et al.* (2001) in a study to identify appropriate heterotic group among others initiated based on SCA in tropical maize germplasm, compared the overall SCA values of the groups in a similar manner.

In the same line, estimates of average mid parent heterosis determined for all crosses with respect to each tester asserted significantly higher percent heterosis for 142-1-e and Pool9A-MHM (Fig. 2). Several authors applied degree of heterosis to determine genetic distance among genotypes for assigning germplasm into heterotic groups. Heterotic response in most cases is a function of non-additive gene action and degree of genetic distance (HALLAUER and MIRANDA, 1988), expressed in the performance of the crosses through estimates SCA effects and degree of heterosis (ORDAS, 1991; VASAL *et al.*, 1992; PARENTONI *et al.*, 2001; SANTOS *et al.*, 2002; BAYESA *et al.*, 2008).

CONCLUSION

Results of our investigations indicated inbred lines with desirable GCA combiners for grain yield,

days to silking, plant height, GLS and NLB, hence suggesting presence of valuable genetic material that could be successively used for further breeding work. The promising single cross combinations identified for grain yield could be recommended for commercial production shortly after evaluation of these crosses across locations. The study also identified two contrasting heterotic groups, inbred lines grouped with, "Pool9A-MHM x 142-1-e" which were verified to be the best combinations to initiate source germplasm. The inbred lines in each group will be recombined and further improved using appropriate breeding schemes to enhance the level of heterosis. For broadening the genetic base of the group, some more germplasm will be tested and continuously infused into either group. These heterotic groups may have wide applicability in the eastern African highland maize growing regions as well.

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