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Research Article

Evaluation of Diallel Crosses of Highland Adapted QPM Maize Hybrids under Optimum and Low Nitrogen Conditions

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Abstract: Eight inbred lines collected from Ambo Agricular Research Center Highland maize sub-program and were evaluated under optimum and Low Nitrogen condition at Ambo and Haramaya University in 2018. Breeding programs have created inbred lines of maize introduced from CIMMYT; they were tested locally for their heterosis. The objective of this study was to generate information regarding the combining ability effect of selected highland adapted maize inbred lines and their crosses for further breeding and cultivar development in view of this limitation. P6 was the lines that exhibited positive and hence good combiner for gain yield in all locations and environmental condition and crosses found to be good yield potential in this study were (P1xP2), (P2xP7) and (P4xP6).

Keywords: Diallel, QPM, Breeding program, CIMMYT.

INTRODUCTION

Maize (*Zea mays* ssp. *mays* L) has key importance in assuring the world food security and a high yielding cereal crop as well [1]. In Ethiopia, maize crop has been considered as one of the most important food security assurance and expansion of its agricultural production. According to the Central Statistic Agency report of 2018, maize is an important staple crop, ranking first among cereals in total grain production (27.43%) and second in area coverage (16.79%). However, the national average yield of maize (3.9t ha$^{-1)}$ is still low [2] compared to the world average.

In Ethiopia QPM development program was launched in 1994 with the evaluation of open pollinated varieties (OPVs) and pools introduced from CIMMYT [3]. Higher content of lysine and tryptophan have been successfully increased in maize through conventional breeding.

The Ambo highland breeding program is one of the three maize breeding programs under National Maize Research Program of the Ethiopian Institute of Agricultural Research. Yearly, the breeding program handles several numbers of QPM and non QPM crosses generated at different stages of the breeding pipeline with the aim of identifying, superior genotypes for the target agroecolgy. This is because improved commercial maize varieties suited to highland areas of Ethiopia have been fewer and consequently access to maize seed has also been limited. Evaluation of the genetic potential or performances of maize genotypes within the breeding, pipeline will help identifying genotypes with good traits of interest for future use in breeding and cultivar development.

For target environment mating design such as diallel play an important role in the selection o and advancement of breeding materials. Hayman [4] and Griffing [5] proposed the concept of diallel cross as the recombination of genetic variability available in the program, performing crosses among all lineages. The diallel scheme of analysis allows estimating useful genetic information to select parental lines and verify the combining ability effect, which are described as general and specific. The objective of this study was, therefore, to generate information regarding the combining ability effect of selected highland adapted maize inbred lines and their crosses for further breeding and cultivar development in view of this limitation.

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Material and Method

Study Location

The study was conducted at Ambo (optimum and Low-N conditions), Agricultural Research Center and Haramaya University in the main cropping season of 2019. The locations represent highland, sub-humid maize growing environments of Ethiopia [6].

Experimental Materials

Eight QPM inbred lines were selected depending on their performance and diverse pedigree back grounds (Table 1). The experiment was composed of 28 F1 crosses formed using half diallel mating design at Ambo during the main cropping season of 2019 and Two (2) commercial hybrid checks: check-1 (Kolba) and check-2(Jibat).

Table-1: List of highland QPM inbred lines selected and used for diallel cross formation

S/N	Lines Code	Pedigree	Source
1	L1	[ECU/SNSYN[SC/ETO]]c1F1-##(GLS=1)-34-3-1-2/CML144(BC2)-34-8-2-2-1-1-#-1-B-#-#-B	AHMBP
2	L2	[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#/CML144(BC2)-10-11-2-4-1-2-#-#-B	AHMBP
3	L3	[POOL9Ac7-SR(BC2)]FS68-1-1-2-1-1/CML144(BC2)-33-10-2-4-1-2-#-1-B-#-B	AHMBP
4	L4	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB)F2)-B-B-9-1-B-#	AHMBP
5	L5	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB)F2)-B-B-35-2-B-#	AHMBP
6	L6	(CML197/(CML197/[(CLQRCWQ50/CML312SR)-2-2-1-BB/CML197]-BB)F2)-B-B-44-2-B-#	AHMBP
7	L7	(CML197/(CML197/(CLQRCWQ50/CML312SR)-2-2-1-BBB)F2)-B-B-18-2-B-#	AHMBP
8	L8	(CML395/(CML395/CML511)F2)-B-B-37-1-B-#	AHMBP

*AHMBP = Ambo Highland Maize Breeding Program

Experimental Design and Cultural Practices

In each location alpha lattice experimental design (5x6) were used with two replications. Each plot consisted a single row of 5.25m long. The spacing was 75 cm between rows and 25 cm between plants. Planting was done in the rainy season of 2019 after reliable moisture level of soil attained to ensure good germination and seedling development using two seeds per hill and thinned out to one plant after 35 days of planting.

Data Collection

The data were recorded by field scorer and taken mostly from twenty- one maize plants for each plot. Traits such as Grain yield, days to anthesis, days to silking, Plant height, ear height, root and stalk lodging, husk cover, ear rot, disease (TLB and Rust), plant aspect, ear aspect, days to maturity, Ear per plant, number of ear and number of plant were recorded for the study.

Days to 50% silking and 50% anthesis were calculated as number of days from sowing until 50% of plants in each row showing tassel and silks. Anthesis-silking interval (ASI; days) computed as the difference between days to 50% anthesis and silking. Plant height (PH; cm) was measured as the distance from the soil surface to the top of tassel. Ear height (EH; cm) was measured as the distance from the soil surface to the main ear bearing node. Plant aspect was recorded by observing overall phenotypic appearance of the plant in a plot by using 1 to 5 scoring scale; where 1 = excellent and 5 = poor. Ear aspect was recorded by observing overall phenotypic appearance of the ears in a plot at harvesting time by using 1 to 5 scoring scale; where 1 = excellent and 5 = poor. Kernel modification data measured by using 1 to 5 scoring scale of opaque's of the kernel. 1=excellent and 5= choky type.

Data Analysis

ANOVA for individual was conducted using PROC GLM procedure of SAS, version 9.0 [7] to determine the differences among the genotypes.

Further genetic analysis were done for traits that showed statistically significant different among genotypes. F1 diallel crosses were subjected to combining ability analysis using modification of the DIALLEL-SAS program [8].

Results and Discussion

Analysis of Variance (ANOVA)

Individual location analysis of variances were made on grain yield and yield related traits such as days to anthesis, days to silking, plant and ear height, ear per plant, bad husk cover, ear rot, ear aspect, plant aspect, ear texture, anthesis silking interval, root lodge, (Rust) diseases, stalk lodge and *E.turcicum* leaf blight (TLB) for each location.

Result in table 2 indicated that mean squares due to entries (genotypes) revealed significant highly ($p<0.01$) difference for grain yield and other related traits at Ambo (optimum and low-N condition) and Haramaya as well, indicating that there is variability between materials evaluated. As the study result showed that significant differences were observed among F1 hybrids for all traits in line with the report of Mohamed Ali, 2020 [16].

Results in Table 2 indicate that mean squares of genotypes and most character in all location and environmental condition were significantly different. Under managed low N stress F1 hybrids were significant for most traits. This finding is similar with the report of Susan *et al*., [9].

Table-2: Mean squares due to genotypes for grain yield and related traits at three locations under optimum and low –N conditions in 2019

Means Squares						
Ambo (Opt.)			Ambo (Low-N)	Haramaya (Opt)		
Genotypes	Error	Genotypes	Error	Genotype	Error	
Traits	DF= 29	DF=18	DF=29	DF=18	DF=29	DF=18
GY	4.30**	0.80**	0.82**	0.43*	9.20**	1.43**
AD	26.41**	8.21**	21.60**	3.41*	84.5^{NS}	97.6^{NS}
ASI	18.23*	6.04 *	26.1*	10.1**	0.38^{NS}	0.29^{NS}
EPP	0.8**	0.02**	0.11^{NS}	0.08^{NS}	0.08**	0.02**
HC	396.4**	122.4**	5.91^{NS}	7.02^{NS}	1830.6*	670.4
EA	0.3**	0.04**	0.28**	0.1**	0.34**	0.1**
PA	0.4**	0.51**	0.41**	0.2*	0.3**	0.1**
TXT	0.29^{NS}	0.21*	0.42**	012**	----	----
CV	18.7		41.9		15.9	
GY mean	4.8		1.5		7.5	

** = highly significant at ($p<0.01$), * = significant at ($p<0.05$), GY = grain yield, AD = number of days to anthesis, ASI=anthesis - silking interval, EPP = number of ears per plant, HC=husk cover, EA= ear aspect, PA= plant aspect, TXT = seed texture (Modification) Opt.=optimum condition, Low –N = low nitrogen condition

Combining ability analysis

Analysis of variances for combining ability revealed that variances for general combining ability (GCA) and specific combining ability (SCA) were significant for some traits while non-significant for most traits under the three environmental conditions and its similar with the finding of [10].

Traits like ear rot were revealed significant variation for GCA at Haramaya site. At Ambo (optimum condition) traits that showed significant variation for GCA were days to tasseling and plant aspect, whereas at Ambo (Low N condition) husk cover and ear aspect were revealed significant for GCA.

Table-3: Diallel analysis of variance for yield and yield related traits of highland maize hybrids grown at Ambo (optimum and Low -N) and Haramaya

Source	Df	Mean squares							
		DA	DS	ASI	HC	PA	Kmod	EA	(Yield (t ha-1)
Ambo (opt)									
Crosses	27	21.4	1.4	11.8	110.3	0.28	0.3*	0.31*	3.3
GCA	7	35.3*	2.1*	12.6	150.8	0.3*	0.2	0.1	0.8
SCA	20	22.4	1.5	12.1	96.9*	0.4	0.3*	0.2	4.5
Error	22	13.1	25.2	16.11	106.3	0.2	0.2	0.2	2.9
Ambo (Low N)							SEN		
Crosses	27	1.1	15	0.6	0.2	0.3*	0.3*	0.22	0.6
GCA	20	1.2	18.4	0.8	0.3*	0.2	2.0	0.3*	0.9
SCA	7	0.9	13.8	0.5	0.2	0.3*	3.3	0.23	0.6
Error	22	15.0	15	27.7	0.3	0.29	2.7	0.19	0.5
Haramaya							ER		
Crosses	27	68.8	69.5	0.31*	187.5*	0.19	172.1*	0.29*	2.5
GCA	7	130.2	127.1	0.16	162.3	0.18	216.3*	0.19	0.8
SCA	20	80.1	83.2	0.4	195.7**	0.2	156.6	0.28*	3.1
Error	22	190.1	184.9	0.4	699.4	0.19	83.5	0.14	3.2

*Significant at $P < 0.05$. ** Significant at $P < 0.01$. GCA, general combining ability; SCA, specific combining ability; DT, days to tasseling; DS, days to silking; ASI, anthesis silking interval; PA, plant aspect; Kmod,kernel modification; EA, ear aspect; HC, husk cover and GY, grain yield, SEN , senesces , ER , ear rot

General Combining Ability (GCA) Effects

Estimates of general combining ability effects are presented in Table (4). Some inbred parents showed positive and significant GCA effects for some traits at Ambo (optimum and Low- N conditions) site. Parents with significantly desirable GCA effects were considered as high combiners, Low or poor combiners had significant but negative (undesirable) GCA effect fpr grain yield [11]. At Ambo (opt.) the good general combiners for major yield determining characters were P2, P4, P5, P6 and P7, while at Low-N condition P1 and P8 were good combiner or had good *per se* performance. At Haramaya inbred lines such as P3 and P6 showed positive gca effect for gain yield thought not significant. Lines with Positive gca estimate have genes that contribute to the increment of yield and the GCA effects represent the additive nature of gene action and a good general combiner parent is characterized by its better breeding value when crossed with other parentsas stated in the in the report of Kumar *et al*., [12].

Table-4: Estimates for general combining ability effects of inbred parents

Ambo (opt)

Parents	**DA**	**DS**	**ASI**	**PA**	**Kmod**	**HC**	**EA**	**GY**
SE(gi)	0.69	0.9	0.7	0.08	0.07	1.9	0.09	0.32
Ambo(Low N)								
Parents	DA	DS	ASI	PA	SEN	HC	EA	GY
P1	-0.75	-2.23	1.48	-0.10	0.00	-0.16	0.06	0.32*
P2	-1.00	-2.81*	1.81	0.10	-0.33	-0.16	0.10	0.01
P3	0.50	1.69	-1.19	-0.23*	-0.42	0.79	0.23*	-0.38*
P4	-0.92	0.10	-1.02	0.02	-0.17	-0.60	-0.06	0.14
P5	-1.25	-2.73*	1.48	0.01	0.50	-0.60	0.10	-0.36*
P6	1.58*	2.77*	-1.19	0.06	0.58	-0.04	-0.15	0.02
P7	2.00*	2.02	-0.02	-0.06	0.00	0.79	-0.16	-0.08
P8	-0.17	1.19	-1.35	0.06	-0.17	-0.04	-0.23*	0.35*
SE(gi)	0.74	1.17	1.00	0.10	0.31	0.47	0.08	0.14

Ambo (Low N)

Parents	DA	DS	ASI	PA	SEN	HC	EA	GY
P1	-0.75	-2.23	1.48	-0.10	0.00	-0.16	0.06	0.32*
P2	-1.00	-2.81*	1.81	0.10	-0.33	-0.16	0.10	0.01
P3	0.50	1.69	-1.19	-0.23*	-0.42	0.79	0.23*	-0.38*
P4	-0.92	0.10	-1.02	0.02	-0.17	-0.60	-0.06	0.14
P5	-1.25	-2.73*	1.48	0.01	0.50	-0.60	0.10	-0.36*
P6	1.58*	2.77*	-1.19	0.06	0.58	-0.04	-0.15	0.02
P7	2.00*	2.02	-0.02	-0.06	0.00	0.79	-0.16	-0.08
P8	-0.17	1.19	-1.35	0.06	-0.17	-0.04	-0.23*	0.35*
SE(gi)	0.74	1.17	1.00	0.10	0.31	0.47	0.08	0.14

Haramaya (Opt)

Parent	**DA**	**DS**	**ASI**	**PA**	**ER**	**HC**	**EA**	**Gy**
P1	0.35	0.38	-0.02	-0.17	-6.55*	-14.29*	-0.10	-0.16
P2	-2.31	-2.21	-0.10	0.08	-4.56*	-11.49*	-0.19*	-0.15
P3	2.02	1.96	0.06	0.13	-1.17	1.25	0.06	0.58
P4	1.44	1.46	-0.02	0.08	2.46	12.24*	0.10	-0.31
P5	2.60	2.71	-0.10	0.00	0.19	11.99*	0.06	-0.09
P6	-5.65*	-5.71*	0.06	0.08	7.20*	14.27*	0.19*	0.08
P7	-2.73	-2.63	-0.10	0.00	1.58	-4.10	-0.10	0.01
P8	4.27	4.04	0.23	-0.21*	0.84	-9.87	-0.02	0.04
SE(gi)	2.63	2.59	0.12	0.08	1.74	5.04	0.07	0.34

Specific Combining Ability (SCA) Effects

Results of the SCA effects of the crosses for yield and different yield related characters are presented in Table 5. Positive SCA effect for grain yield was observed in 14 crosses but significant positive effects were observed on three crosses for gain yield as well. For traits such as days to silking and plant aspect, the cross (P1xP7) showed significant negative SCA effect, but positive and significant effect for the trait kernel modification from the same crosses at this location.

At Ambo Low-N condition, 12 F1 crosses revealed positive SCA effect for grain yield, of these crosses (P1xP3) and (P3xP8) showed significant positive SCA effect for gain yield. From (P2xP5) positive and significant SCA effect observed for the traits Senesces but significant negative effect for days to anthesis. At Haramaya 12 crosses revealed positive SCA effect for gain yield thought not significant .The cross of (P3 x P) and (P5 x P6) exhibited significant SCA effect for traits husk cover, ear rot and ear aspect indicating tolerant to open tip and rotting. This finding is in line with the report of in line with the report of Francis *et al*., [13]. At all testing and environments crosses that exhibited positive SCA effect for gain yield indicating the prevalence of non-additive gene effects for the inheritance of these traits as the report of Motiar *et al.,* [14]. Significant SCA effects indicated that the crosses performed better or poorer than what would be expected based on GCA effects of the respective parent as the report of Bitew *et al*., [15].

Table-5: Estimates of specific combining ability (SCA) effects on yield and its components in diallel cross of maize

Ambo (opt)

Crosses	*DA*	*DS*	*ASI*	*PA*	*Kmod*	*HC*	*EA*	*GY*
P1xP2	1.40	0.26	1.14	0.71**	-0.54*	-4.84	0.35	-2.06*
P1xP3	1.32	1.76	-0.44	0.01	-0.12	-1.00	-0.40	0.66
P1xP4	2.82	5.10	-2.27	0.34	0.05	1.71	0.05	-0.29
P1xP5	5.15*	7.51*	-2.36	0.38	-0.29	-0.59	0.43	0.22
P1xP6	-3.26	-2.90	-0.36	-0.37	0.21	5.59	-0.20	1.00
P1xP7	-2.85	-6.74*	3.89	-0.54*	0.84**	-4.63	-0.07	-0.35
P1xP8	-4.60	-4.99	0.39	-0.54*	-0.16	3.77	-0.15	0.83
P2xP3	-0.35	-1.57	1.23	-0.24	0.55*	-4.79	0.01	-0.19
P2xP4	-2.35	-6.74*	4.39*	-0.41	0.46	-2.84	-0.03	0.52
P2xP5	-1.01	0.18	-1.19	0.13	-0.37	-7.04	0.10	-1.53
P2xP6	-1.93	1.26	-3.19	-0.37	-0.37	8.15	-0.03	2.15*
P2xP7	-0.01	2.93	-2.94	-0.04	0.01	11.58*	-0.15	0.11
P2xP8	4.24*	3.68	0.56	0.21	0.26	-0.22	-0.24	1.01
P3xP4	-3.43	-5.74	2.31	-0.37	0.13	-0.74	-0.03	-0.27
P3xP5	0.90	2.68	-1.77	0.42	-0.20	6.81	0.35	-1.27
P3xP6	3.49	2.26	1.23	0.42	-0.45*	-6.86	0.22	-1.74
P3xP7	-4.10*	-0.57	-3.52	-0.24	0.17	4.52	-0.15	2.68*
P3xP8	2.15	1.18	0.98	0.01	-0.08	2.07	0.01	0.14
P4xP5	0.40	0.01	0.39	0.01	-0.29	-4.04	-0.20	-0.22
P4xP6	-2.51	-0.90	-1.61	-0.24	0.21**	11.25*	-0.07	1.31
P4xP7	5.40*	6.76*	-1.36	0.59*	-0.41	-6.87*	0.55	-1.80
P4xP8	-0.35	1.51	-1.86	0.09	-0.16	1.53	-0.28*	0.76
P5xP6	1.32	-0.99	2.31	-0.20	0.38**	-5.55	-0.20	-0.28
P5xP7	-2.76	-6.32*	3.56	-0.37	0.01	10.68*	-0.32	2.09*
P5xP8	-4.01*	-3.07	-0.94	-0.37	0.76	-0.27	-0.15	1.00
P6xP7	2.32	1.76	0.56	0.38	0.01	-10.49*	-0.20	-0.71
P6xP8	0.57	-0.49	1.06	0.38	0.01	-2.09	0.47	-1.72
P7xP8	1.99	2.18	-0.19	0.21	-0.62	-4.80	0.35	-2.01*
SE(ij)	2.16	2.99	2.39	0.27	0.23	6.16	0.29	1.02

Ambo (Low N)

Crosses	*DA*	*DS*	*ASI*	*PA*	*SEN*	*HC*	*EA*	*GY*
P1xP2	-2.75	-0.51	-2.24	-0.41	-0.88	2.45	-0.54*	0.99*
P1xP3	5.25*	2.99	2.26	0.84*	2.20*	-1.15	0.33	-1.18**
P1xP4	0.67	3.57	-2.90	-0.33	-1.05	0.24	-0.38	0.44
P1xP5	1.00	-4.10	5.10	0.17	0.29	0.24	0.46	-0.41
P1xP6	-0.33	-0.60	0.26	0.34	0.70	-0.32	0.46	-0.22
P1xP7	0.75	2.15	-1.40	-0.37	-0.21	-1.15	-0.13	-0.19
P1xP8	-4.58	-3.51	-1.07	-0.24	-1.05	-0.32	-0.21	0.57
P2xP3	0.50	-0.93	1.43	0.13	0.54	-1.15	0.04	-0.37
P2xP4	0.92	1.15	-0.24	0.21	0.29	0.24	0.08	-0.46
P2xP5	-2.25	-7.51*	5.26	0.21	2.12*	0.24	0.17	-0.16
P2xP6	1.42	1.99	-0.57	0.13	-0.46	-0.32	-0.08	-0.21
P2xP7	2.00	2.74	-0.74	0.17	-0.88	-1.15	0.58*	0.35
P2xP8	0.17	3.07	-2.90	-0.45	-0.71	-0.32	-0.25	-0.15
P3xP4	-0.58	-2.35	1.76	-0.04	-0.63	-0.71	-0.04	0.03
P3xP5	2.75	5.49	-2.74	-0.04	0.70	-0.71	-0.21	0.25
P3xP6	-3.08*	-0.01	-3.07	-0.62*	-1.38	-1.27	0.04	0.57

P3xP7	-3.50	-3.76	0.26	-0.08	-0.80	6.25*	-0.04	0.77*
P3xP8	-1.33	-1.43	0.10	-0.20	-0.63	-1.27	-0.13	-0.07
P4xP5	-0.33	2.07	-2.40	0.05	-0.55	0.68	0.08	0.35
P4xP6	-1.67	-1.43	-0.24	-0.29	-0.63	0.13	-0.17	0.46
P4xP7	-2.08	-5.18	3.10	0.26	1.45	-0.71	-0.25	-0.41
P4xP8	3.08	2.15	0.93	0.13	1.12	0.13	0.67*	-0.41
P5xP6	1.67	1.90	-0.24	-0.29	-1.30	0.13	-0.08	-0.13
P5xP7	-1.75	2.15	-3.90	-0.49	-1.71*	-0.71	-0.42	0.11
P5xP8	-1.08	-0.01	-1.07	0.38	0.45	0.13	0.00	-0.01
P6xP7	1.42	0.15	1.26	0.42	2.20*	-1.27	0.08	-0.57
P6xP8	0.58	-2.01	2.60	0.30	0.87	2.92*	-0.25	0.11
P7xP8	3.17	1.74	1.43	0.09	-0.05	-1.27	0.17	-0.05
SE(ij)	2.30	3.66	3.14	0.32	0.97	1.49	0.26	0.43

Haramaya(opt)

Crosses	***DA***	***DS***	***ASI***	***PA***	***HC***	***ER***	***EA***	***GY***
P1xP2	-0.02	0.23	-0.25	-0.27	6.79	26.3	0.20	1.13
P1xP3	-3.36	-3.44	0.08	0.43	1.21	-3.11	0.20	-1.08
P1xP4	-3.27	-3.44	0.17	-0.02	6.13	10.3	0.41*	-0.08
P1xP5	-3.94	-4.19	0.25	-0.44	-2.31	-17.7	-0.30	1.11
P1xP6	3.81	4.23	-0.42	0.23	-9.32	-26.1	-0.17	-1.40
P1xP7	1.89	1.64	0.25	-0.19	0.46	5.3	-0.38	1.15
P1xP8	4.89	4.98	-0.08	0.27	-2.96	5.11	0.04	-0.82
P2xP3	8.81	9.14	-0.33	-0.07	-0.28	-12.9	-0.46*	0.86
P2xP4	8.89	9.14	-0.25	-0.27	-6.57	-20.3	-0.51	0.33
P2xP5	3.23	3.39	-0.17	0.31	1.35	10.01	0.04	-1.10
P2xP6	-15.02*	-15.7*	0.67	0.23	-1.91*	-28.9	0.41*	1.10
P2xP7	-6.44	-6.77	0.33	-0.19	0.32*	30.64	-0.05	1.14
P2xP8	0.56	0.56	0.00*	0.27	0.30	-4.8	0.37	-1.26
P3xP4	-2.94	-2.52	-0.42	0.43	-0.25	50.6	0.24	-1.20
P3xP5	-4.11	-3.77	-0.33	0.02	-2.93	4.71	0.04	-0.65
P3xP6	3.14	3.14	0.00	-0.57*	-9.69*	-29.9*	-0.59*	0.64
P3xP7	1.73	1.56	0.17	0.27	15.53	8.2**	0.45	-0.05
P3xP8	-3.27	-4.11	0.83*	-0.52*	-3.58	-17.53	0.12	1.48
P4xP5	-7.52	-7.77	0.25	0.06	-6.07*	-47.23	-0.26	-0.73
P4xP6	4.23	3.64	0.58	-0.02	15.9*	44.2*	0.37	0.43
P4xP7	4.81	5.06	-0.25	0.06	-5.35*	-30.9	-0.09	-0.42
P4xP8	-4.19	-4.11	-0.08	-0.23	-3.82	-6.72	-0.17	1.67
P5xP6	7.56	7.39	0.17	0.06	14.49	66.4**	0.41*	1.36
P5xP7	4.64	4.31	0.33	0.14	-0.08	-9.04	0.45*	-1.23
P5xP8	0.14	0.64	-0.50	-0.15	-4.45	-7.11	-0.38	1.25
P6xP7	-6.11	-5.27	-0.83*	-0.19	-17.4*	-30.4**	-0.42*	0.90
P6xP8	2.39	2.56	-0.17	0.27	7.94	4.76	-0.01	-0.83
P7xP8	-0.52	-0.52	0.00	0.10	6.57	26.27	0.04	-1.49
SE(ij)	8.24	8.12	0.38	0.26	5.46	15.80	0.22	1.07

Table-6: Mean square due to combined analyses of genetic variance for grain yield and agronomic traits of maize

Source	**df**	**Yield**	**KPE**	**EL**	**ED**	**HC**	**ER**
ENV	2	134.02**	0.09	4.66	2.54**	14.06	57.26**
REP (ENV)	6	5.64	13.88*	3.68	0.57**	17.96	64.02*
Crosses	65	5.52	32.64**	16.22**	0.2**	204.91**	197.12**
Crosses*Env	130	5.63	9.95*	6.22*	0.12*	73.55**	69.53**
GCA	11	9.81*	22.38**	10.31**	0.27**	157.96**	114.73**
SCA	54	4.65	34.74**	17.42**	0.18**	214.48**	213.90**
GCA * ENV	22	8.31*	1.72	2.67	0.17**	9.07	20.30*
SCA * ENV	108	5.42	1.36	2.07	0.09	4.41	7.61
Error	528	5.26	6.29	4.2	0.1	33.32	33.74
Mean		7.34	31.25	14.66	4.49	9.48	9.11
CV		18.63	8.03		7.20	45.88	43.69

CONCLUSION

In conclusion, inbred lines such as P2, P4, P5, P6 and P7 had positive but non-significant GCA effect for grain yield at Ambo optimum condition. P2, P4 and P6 were significant positive GCA effect while, P1 and P8 showed significant positive GCA for gain yield at Ambo low N condition. At Haramaya P3, P6. P7 and P8 had positive but insignificant GCA effect for gain yield. Therefore, P6 was the lines that exhibited positive and hence good combiner for gain yield in all locations and environmental condition. For SCA effects the crosses of those line were selected for further breeding purpose. Positive SCA effects observed from cross such as (P2xP4), (P2xP6), (P2xP7), (P3xP8), (P4xP) 8 and (P5xP8) both at Ambo (opt.) and Haramya. At Ambo (optimum and Low –N) condition cross that revealed positive SCA effects were (P1xP8), (P2xP7), (P3xP7), (P4xP6) and (P5xP7). In the same pattern the cross that exhibited positive SCA effect in both Ambo low-N and Haramaya were (P1xP2), (P2xP7) and (P4xP6).The overall study indicated cross that showed positive SCA effects in all testing and environment are (P2xP7) and (P4x P6). Therefore those crosses with per se performance could be more rewarding in a hybrid breeding program in the future career.

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