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RESEARCH ARTICLE

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COMBINING ABILITY ANALYSIS FOR GRAIN YIELD AND YIELD RELATED TRAITS IN QUALITY PROTEIN MAIZE (ZEA MAYS L.)

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ABSTRACT

Maize is a major cereal crop for human nutrition in Ethiopia. For communities that rely heavily on maize as the staple, development of maize cultivars with enhanced quality protein can be one means to fight protein malnutrition. Development of single cross hybrids significantly boosted up the grain yield potential of maize. Estimation of combining ability is main step in the development and evaluation of hybrids. Thus this study was conducted to estimate general combining ability (GCA) of parents and specific combining ability (SCA) of the crosses of quality protein maize (QPM).The crosses were made during 2016 by 6x6 half diallel mating design which produced 15 F1 single crosses. These single crosses along with three checks were evaluated in two replications of the alpha lattice design at Bako and Arsi Negelle during the 2017 main cropping season for their grain yield (GY) and related agronomic traits. Significant mean squares due to general combining ability (GCA) were observed for plant height, ears per plant, thousand kernel weight, ear length, ear diameter, kernel rows per ear and grain yield in across location results; indicating the importance of additive gene action in the inheritance of these traits. Inbred lines L3, L4 & L6 had high positive GCA effects for grain yield. Furthermore, the finding of this study indicates the possibility of developing high yielding QPM varieties for the mid-altitude agro-ecology of Ethiopia from the QPM inbred lines included in this study.

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INTRODUCTION

Maize (*Zea mays* L.) is the third most important cereal crop of the world, having a diversity of uses. It is the most versatile crop that is being grown in more than 169 countries across the globe, covering nearly 240 million hectares of land (FAOStat, 2010). In Ethiopia maize is one the most important strategic crop ranking second following teff in area coverage and first in total production with about 8.4 million tonne harvest per annum (CSA, 2018). However, similar to other cereals, maize is known to be of poor protein nutritional quality, due to lysine and tryptophan deficiency (Twumasi-Afriyie *et al*, 2012). Hence, protein malnutrition is common among children whose diet is dominated by maize and other cereals. The discovery of the biochemical effects of mutant allele o2 (Mertz *et al*, 1964) opened an opportunity for improving the quality of maize endosperm protein. This mutant alters amino acid profile and composition of maize endosperm protein and results in two-fold increase in the levels of lysine and tryptophan compared to what is observed in the non-QPM genotypes (Villegas *et al*, 1992). Combining ability analysis is one of the powerful tools in identifying the better combiners which may be hybridized to select better crosses for direct use or further breeding work (Lavanya and Chandramohan, 2003).Combining ability of inbred lines gives information about genetic nature of quantitative traits and also helpful for selection of most appropriate parents to be used for heterosis breeding. Breeding value of a line based on mean performance is regarded as general combining ability (GCA). Predominance of GCA is conducive for enhancement of selection efficiency in segregating populations (Bocanski *et al.,*2009). Specific combining ability is cumulative performance of any two lines in their specific hybrid combination. Variance due to GCA is an indicator for extent of additive gene action whereas; variance due to specific combing ability (SCA) shows the extent of non-additive gene action.

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Selection of appropriate breeding program for maximum genetic improvement is based on relative values of GCA and SCA (Hayman, 1954; Griffing, 1956).Thus this study was conducted with the aim to estimate the GCA ofQPM inbred lines and the SCA of their crosses.

MATERIALS AND METHODS

Description of the Experimental Sites: The experiment was conducted at two locations in the mid-altitude sub-humid agro-ecology of Ethiopia namely Bako and Arsi-Negelle.

Experimental Materials: A total of 18entries composed of 15 single crosses formed by crossing six QPM inbred lines in a half-diallel mating design in 2016 and three standard checks (BH546, BH547 and BHQP548) were studied. The QPM inbred lines were developed by Bako National Maize Research Center (BNMRC) of Ethiopia (Table 2).

Experimental Design and Field Management: The experimental design was alpha lattice design (Patterson and Williams, 1976) with 6 plots per an incomplete block and 3 incomplete blocks with in the replication. Each entry was planted in a one row 5.1 m long plot with spacing's of 0.75 m and 0.30 m between rows and plants respectively. The experiment were hand planted with two seeds per hill, which were later thinned to one plant to get the recommended planting density for the testing sites, 44,444 plants per hectare. Planting was conducted on the onset of the main rainy season after an adequate soil moisture level was reached to ensure good germination and seedling development. Other agronomic practices were carried out as per the required for the testing sites.

Data Collection: Data on grain yield and other traits were collected on a plot and sampled plants/ears bases. Data collected on a plot basis include days to 50% anthesis, days to 50% silking, anthesis to silking interval, biomass yield, harvest index, actual moisture content, field weight (kg/plot) while data recorded on sampled plants basis were ear height (cm), plant height (cm), thousand kernel weight (gm), ear length (cm) and ear diameter (cm) . Grain yield per hectare was calculated based on field weight per plot, moisture content adjusted to 12.5%, 80% constant shelling percent, and t/ha adjustment factor.

Data Analysis: Data were subjected to analyses of variance using the PROC GLM procedure in SAS software version 9.0 (SAS, 2002). In the analysis, genotypes were used as a fixed factor while replications, incomplete blocks within replication, and locations were considered as random factors. This was specified using the RANDOM statement in the PROC GLM model of SAS. Before conducting the combined analysis, the homogeneity of error variance of the two locations was determined. Combined ANOVA was performed only for traits where the error variances were homogenous. For traits that showed significant genotype by location interaction, the correlation among the genotypes and the locations mean for each trait were checked to determine whether there is a change of ranks among the genotypes across the location. Furthermore, Griffing (1956) method IV diallel analysis for combining ability was executed for traits that exhibited significant differences among crosses.

The mathematical model for combining ability analysis of combined analysis is:

$$Yijk= \mu + lk+ gi+ gj+ sij+ (lg)ik+ (lg)jk+ (ls)ijk+ eijk$$

Where Yijk is the mean over replications and blocks within replications of the single cross (i x j) in the kth environment; is the overall mean; lk is the k th environment effect; gi, gj and sij are general and specific combining ability effects (Griffing, 1956); (lg)ik and (lg)jk are GCA effects of i and j parents and their interaction with environment respectively; (ls)ijk is SCA interaction with environment; eijk is the error term.

RESULT AND DISCUSSION

Combining Ability Analysis: The combined analysis of variance showed significant mean squares due to hybrids for plant height, ears per plant, thousand kernels weight, ear length, ear diameter, number of kernel rows per ear and grain yield (Table 3).

Mean squares due to GCA were significant for plant height, ears per plant, thousand kernel weight, ear length, ear diameter, number of kernel rows per ear and for grain yield. GCA x Location interaction was significant for days to silking, anthesissilking interval and ear length, while SCA x Location interaction was significant for days to anthesis, days to silking, plant height, anthesissilking interval, harvest index and biomass yield. The Hybrid x Location interaction was significant for all these traits. In line with this study (Wolde *et al*., 2017) reported significant GCA mean squares due to lines for grain yield, days to silking and plant height and significant SCA mean squares for grain yield and plant height; significant GCA x location for grain yield in across location analysis. Similarly, (Tilahun *et al*., 2017) reported on the combined analysis significant GCA and SCA for grain yield, days to silking, anthesissilking interval, plant height, plant aspect and ear aspect and only significant GCA for ear per plant, das to anthesis and ear height. This same trial revealed significant mean square of GCA × location interaction for days to anthesis, plant aspect and ear aspect and non-significant SCA × location interaction for grain yield, days to anthesis, days to silking, plant height, anthesissilking interval and ear per plant. In a combined analysis, (Hossein*et al*., 2014) reported significant mean squares due to SCA and GCA for days to silking, plant and ear height, ear length, thousand kernel weight, number of rows per ear and kernel yield maize.

In line with the current study, (Legesse *et al*., 2009) reported highly significant GCA and SCA mean squares due to lines and testers for grain yield, days to silking and plant height. Mean square due to GCA x location were significant for grain yield and days to silking. Bayisa*et al*. (2008) found significant mean squares due to GCA and SCA for several studied traits in a line by tester analysis conducted across locations.

General Combining Ability Effectsof inbred lines: Across location genetic analysis of variance showed that 3 (L3, L4 & L6) of the inbred lines expressed positive and significant GCA effect which means significantly good combiners for an increase grain yield. On the other hand, L1, L2 and L5 expressed significantly negative GCA effects (Table 4). The result of the current study agreed with(Tilahun *et al*., 2017, Wolde *et al*., 2017, Alamerew and Warsi, 2015, Legesse *et al*., 2009, Asefa *et al*., 2008) who reported significant positive and

Table 1. Description of the study area

Sites	Altitude (m.a.s.l)	Latitude N	Longitude E	Temperature (^{0}C)		Rain fall (mm)	Soil type
				Min	Max		
Bako	1650	9^{0}6'	37^{0}09'	13.3	28.0	1244	Nitosols
Arsi-Negelle	1960	7° 20’	38^{o}9’	9	26	886	Vertisol

Table 2. List of lines used in the diallel cross

No.	Code	Pedigree
1	L1	ZM621A-10-1-1-1-2-B*10-B-B-B
2	L2	[MSRXG9]C1F2-205-1(OSU23i)-5-3-X-X-1-BBB-1-BB-1-BB-B-B-B
3	L3	MAS[206/312]-23-2-1-1-B*5-B-B
4	L4	BK02-Z-311-28(F2)-B-1 X CML-144(F2)-15-2-1-1-1
5	L5	[[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4/CML511]-1-B-1-BBB-1-B-B-B-B
6	L6	(CML-142 X 144-7-b(F2) x 144-7-b(F2) x 144-7-b)-B-20-1-1-2-1-1

Table 3. Mean square of combined analysis of GCA and SCA for grain yield and different traits in diallel crosses in 2017 cropping season

Source of variation	Df	grain yield	Days to anthesis	Days to silking	Plant height	Anthesissilking interval	ear per plant
Hybrids	S	7.25**	36.54 ^{NS}	31.56 ^{NS}	1448.03***	6.67 ^{NS}	0.16**
GCA	5	18.20*	58.17 ^{NS}	52.22 ^{NS}	3433.84**	4.30 ^{NS}	0.34**
SCA	9	1.16 ^{NS}	24.39 ^{NS}	20.08 ^{NS}	344.80 ^{NS}	7.99 ^{NS}	0.07 ^{NS}
Location	1	30.37 ^{NS}	968.02 ^{NS}	1550.42***	76469.40*	99.00*	0.06 ^{NS}
Hybrids x location	14	1.87 ^{NS}	22.34***	20.20***	199.79**	3.24*	0.03 ^{NS}
GCA x location	5	2. 21 ^{NS}	10.67 ^{NS}	11.37*	141.18 ^{NS}	3.80*	0.03 ^{NS}
SCA x location	9	1.68 ^{NS}	28.82***	25.11***	232.36**	2.93*	0.04 ^{NS}
Error	28	0.93	5.28	4.16	66.66	1.19	0.03
% contribution of GCA		94	70	72	91	35	83
% contribution of SCA		6	30	28	9	65	17

Source of variation	Df	thousand kernel weight	Ear length	Ear diameter	Kernel row per ear	Harvest index	Biomass yield
Hybrids	14	10002.32***	8.97**	0.14***	3.87***	145.35 ^{NS}	28.49 ^{NS}
GCA	5	26701.70**	23.87*	0.32**	9.69***	83.68 ^{NS}	50.92 ^{NS}
SCA	9	724.88 ^{NS}	0.68 ^{NS}	0.03 ^{NS}	0.64 ^{NS}	179.61 ^{NS}	16.03 ^{NS}
Location	1	11878.38 ^{NS}	49.84*	1.38*	44.06**	5283.24 ^{NS}	1456.11*
Hybrids x location	14	845.20 ^{NS}	2.40*	0.02 ^{NS}	0.27 ^{NS}	140.62*	14.01**
GCA x location	5	1632.22 ^{NS}	3.44*	0.02 ^{NS}	0.28 ^{NS}	126.47 ^{NS}	7.52 ^{NS}
SCA x location	9	407.96 ^{NS}	1.83 ^{NS}	0.03 ^{NS}	0.26 ^{NS}	148.47*	17.61**
Error	28	496.07	1.05	0.02	0.35	58.62	4.74
% contribution of GCA		97	97	91	94	32	76
% contribution of SCA		3	3	9	6	68	24

Table 4. Across location GCA estimates of grain yield and yield related traits

Line	Grain yield	Plant Height	Ear Per Plant	Thousand kernel Weight	Ear Length	Ear Diameter	Kernel Row Per Ear
1	-1.09***	-7.10***	-0.21***	-14.46**	-0.65**	0.23***	1.16***
2	-0.51*	-2.92	-0.13**	35.54***	1.09***	-0.11**	-0.53***
3	1.19***	0.46	0.15***	-4.82	-0.43	0.03	0.01
4	0.99***	4.90*	0.14**	18.74***	0.07	0.07*	-0.29*
5	-1.21***	-19.79***	-0.01	-71.45***	-1.73***	-0.15***	0.61***
6	0.63**	24.46***	0.04	36.74***	1.64***	-0.08*	-0.97***
SE	0.22	1.86	0.04	5.08	0.23	0.03	0.13

***= Significant at P<0.001 level of probability, ** significant at P<0.01, * = Significant at P<0.05 Level of probability.

negative GCA effects for grain yield in pooled analysis of combining ability. For plant height, three inbred lines expressed negative GCA effects out of which L1 & L5 showed significant for the reduction of plant height while L4 and L6 expressed positive and significant GCA effects for an increase of plant height (Table 4). The result of this study is in conformity with the findings of (Wolde *et al*., 2017, Alamerew and Warsi, 2015, Gudeta Napir, 2015). Inbred lines L3 and L4 were significantly better combiners for an increasing of number of ears per plant while L1 and L2 were significantly least combiners for this trait (table 4). Positive and significant GCA effects for umber of ears per plant indicate prolificacy which is desirable in increasing maize productivity where as negative and significant GCA effects for this trait indicate non-prolificacy which is undesirable. Similarly, (Tilahun *et al*., 2017) found both negative and positive GCA effect for number of ear per plant. For thousand kernel weight, L2, L4 and L6 showed positive and highly significant GCA effect for an increase of thousand-kernel weight while L1 and L5 showed negative and significant GCA effect for reduced thousand kernel weight (table 4). In line with the current findings (Gebre, 2017, Tilahun *et al*., 2017) and (Gurmu, 2007) reported significant positive and negative GCA effects for thousand kernel weight in maize. Three inbred lines showed positive GCA effect out of which L2 & L6 were significantly better combiners for increasing ear length while L1 & L5 showed negative and significant GCA effect for reduced ear length (table 4). The present result agreed with (Alamerew and Warsi, 2015, Asefa *et al*., 2008).Three of six inbred lines showed positive GCA effect out of which L1 & L4 were significantly better combiners for increased ear diameter. On the other hand, L2, L5 & L6 expressed negative and significant GCA effect (table 4). This result was in agreement with (Gebre, 2017); (Alamerew and Warsi, 2015, Tajwar and Chakraborty, 2013, Gurmu, 2007) and who reported both positive and negative GCA effects for ear diameter in maize. For number of kernel rows per ear, two of the inbred lines L1 & L5 expressed positive and significant GCA effect which means significantly good combiners for an increased kernel row per ear. On the other hand, L2, L4 and L6 expressed significantly negative GCA effects (table 4). The result in this study agreed with the finding of (Gebre, 2017) who reported both negative and positive GCA effect for this trait.

SUMMARY AND CONCLUSION

Analysis of variance showed significant mean squares due to hybrids for grain yield and most of yield related traits. Mean square values of GCA variances for most of the traits were higher than SCA variances indicated as there was predominance of additive gene action. Inbred lines L3, L4 & L6 were good combiners to enhance grain yield across location. Inbred lines L2, L4 & L6, for thousand kernel weight, L2 & L6 for ear length, L1 &L4 for ear diameter and L1 & L5 for number of kernel row per ear were best combiners for increasing these traits. Generally, inbred lines with good GCA have been identified for the traits studied. This indicates the possibility of developing desirable hybrids and synthetic varieties through crossing and or recombination of inbred lines with desirable traits of interest for mid-altitude agro-ecology of Ethiopia.

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