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General and Specific Combining Ability of Quality Protein Maize (*Zea mays* L.) Inbred Lines for Major Foliar Diseases, Grain Yield and Other Agronomic Traits Evaluated at Mid-altitude Agroecology of Ethiopia

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ABSTRACT: Despite the fact that maize is a crucial cereal crop for food security, several foliar diseases are the main threats and limitations maize production in Ethiopia, resulting in low yields, particularly quality protein maize (QPM). Accordingly, national maize research program of Ethiopia has released QPM maize varieties adapted to the mid-altitude, low moisture stress and highland agro-ecologies of the country. Nonetheless, the market share of these varieties is generally small due to these reason and other features that have limited their adoption by farmers. General and specific combining ability analysis is one of the powerful instruments in identifying the best combiners that may be used in crosses to accumulate biotic resistance and productive alleles. A line x tester analysis involving 36 crosses generated by crossing 9 selected maize inbred lines with 4 testers were evaluated for different desirable agronomic traits during 2019/2020 main season at Bako and Jimma. The purpose of the experiment were to determine the GCA and SCA combining ability of QPM inbred lines, adapted to mid altitude agroecology of Ethiopia for grain yield and major foliar diseases. The crosses were evaluated in alpha lattice design replicated 3 times. For analysis of days to silking interval, days to maturity, turcicum leaf blight, grey leaf spot, common rust disease severity index, and grain yield were recorded. Analyses of variances showed significant mean squares due to crosses for almost all the traits studied. GCA mean squares due to lines and testers were significant ($P<0.05$ or $P<0.01$) for most studied traits. SCA mean squares were also significant for most attributes and major foliar maize diseases across locations. The comparative importance of GCA and SCA variances observed in the current study for most studied traits. Inbred lines L1, L2, L5 and L8 exhibited negative and highly significant GCA effects for husk cover. From this conduct it can be decided that better performing hybrids, inbred lines with desirable GCA and cross combinations with desirable SCA effects for grain yield, major foliar maize diseases and other traits were successfully identified.

Keywords: Combining ability, GCA, GCA effect, line by testers, major foliar diseases, Quality protein maize, SCA and SCA effect.

RESEARCH PAPER

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INTRODUCTION

Maize is a very significant cereal crop that is grown in a variety of environmental condition and has a variety of uses for human and animal nutrition. It is a major source of food for a large portion of the world's population, as well as livestock and poultry feed (Prasanna, 2012). It contributes roughly 15% of total caloric intake and the preponderance of protein, vitamin, and mineral consumption in the diets of most African families. Furthermore, in bountiful countries without protein supplements, it is routinely fed to babies as young as 2–3 months old until they are weaned at the age of 15–24 months, as well as to pre-school children (3–5 years old) (Badu-Apraku *et al*. 2015). It also provides 40 to 75 percent of total the main element of livestock and poultry feed (Badu- Apraku *et al*. 2011). It is one of Ethiopia's most important cereal crops for achieving food security. Along with other main cereal crops including tef, wheat, and sorghum, it subsidizes the biggest share of production and consumption (CSA, 2018). It is primarily produced and consumed by the small-scale farmers that comprise about 80% of the population (Dawit *et al*., 2008). It plays a key role in Ethiopian diets, particularly in rural areas, and has progressively spread into metropolitan areas. This is mostly demonstrated by green maize cobs being sold at roadside stands across the country as a hunger-relieving snack from May to August each year (Twumasi *et al*., 2012).

Despite the importance of maize, a cereal crop for food security, several biotic and abiotic stresses are the main threats and limit maize production in Sub-Saharan Africa, resulting in low yields. Accordingly, to date, in spite the importance of maize as a principal

food security crop, its average yield in Africa (2t/ha) is still low as compared to the world average (5.6 t/ ha) (FAO, 2019). Among biotic stresses, maize production in Ethiopia is constantly threatened by the potential outbreak of major foliar diseases such as Turcicum leaf blight (TLB), Gray leaf spot (GLS) and Common leaf rust (CLR) (Deressa *et al*.,2018). Northern corn leaf blight (TLB) disease of maize caused by *Exserohilum turcicum Pass Leonard & Suggs* is the most common biotic factor in Ethiopia, causing yield losses of up to 100% on vulnerable maize varieties (Wende *et al*. 2013). Also, Mosisa *et al*., (2012) reported turcicum leaf blight (TLB), caused by the fungus Exserohilum turcicum is one of the widespread and economically very important diseases of maize production in Ethiopia. Infection occurs during both off-season and peak season, but is more severe during peak season in constantly humid areas. According to Tewabech *et al*. (2012), leaf blight of northern maize (E. *turcicum*) was reported to cause the highest kernel yield loss of 16.4 and 50% of 1000 kernels on susceptible genotypes. And according to this reported, the other foliar diseases, notably gray dot (*Cercospora zeaemaydis Tehon & Daniels*) and common rust (*Puccinia sorghi Schr*.) are also the most important infectious diseases of maize in the country. The incidence of disease ranges from 95-100% in areas with constant humidity and high humidity and yield loss can be as high as 70%. Thus, biotic and abiotic restrictions continue to limit maize production and productivity throughout Ethiopia's maize-growing regions (Abate *et al*., 2017).

TLB is thus one of the most common maize diseases in Ethiopia, with a wide distribution and significant economic impact. During the wet rainy seasons, the disease is prevalent from lowland humid to highland humid agro-ecologies (Keno *et al*.2018). Grey leaf spots (GLS), caused by C. *zeae-maydis*, is a common foliar disease of maize in many parts of the world. In the early 2000s, a major epidemic occurred, resulting in significant maize grain yield losses (Tilahun et al., 2012). Currently, the disease is one of the most serious hazards to maize production in Ethiopia, with yield losses of up to 29.1%. (Wegary *et al*.,2004; Keno et al.2018). In favorable settings, these diseases are known to cause large yield losses, especially when these two or more diseases impact maize (Keno *et al*.2018). The Maize Streak Virus causes Maize Streak Disease (MSV). In Sub-Saharan Africa, it is a significant viral maize disease (Karavina, 2014). This disease was previously solely known in Gambella, according to Keno *et al*.2018 (the western low land sub-humid plains bordering South Sudan). According to this report, the disease has become increasingly important in Ethiopia's mid-altitude agroecology in recent years, posing a serious threat to the country's maize production. Moreover, the majority of commercial types are now under study. Common leaf rust (CLR), caused by Puccinia sorghi Schwein, is another severe maize disease in Ethiopia, according to Keno et al. (2018). It is widely spread throughout the country's key maize growing regions. It is particularly severe in the country's southern mid-altitude and highland sub-humid maize-growing agro-ecologies. The first quality protein maize hybrid variety registered in Ethiopia, "BHQP542," was short-lived in commercial production and seed systems due to this disease, as this report shown.

In general, Ethiopia's national maize research program has published QPM maize varieties that are adapted to the country's mid-altitude, low-moisture-stress, and highland agro-ecologies. However, due to various characteristics that have hampered their adoption by farmers, such as high susceptibility to CLR (e.g., BH542), especially when planted in rust hot spots; susceptibility to TLB (AMH760Q); and low seed production of BHY545; the market share of these cultivars is generally minimal (Adefris *et al.,* 2015). As a result, high yielding and biotic stress tolerant maize inbred lines are required, particularly significant foliar, resistant quality protein maize inbred lines. Thereby, improvement of host resistance to these diseases can provide an important component of integrated disease management, which is the most effective and practical method of managing maize diseases (Deressa *et al.,*2018).

Maize is an important cereal crop and is stale food for millions of people round the globe. For any breeding programme to be successful, selection of genotypes for crossing is the basic and important step and knowledge on general and specific combining ability is useful for generation of hybrids which are resistant to foliar diseases. According to Tilahun *et al*.(2017), research on the benefits of combining abilities for newly produced QPM inbred lines on grain yield, agronomic attributes, and disease resistance has been restricted in Ethiopia. As a result, there is currently a lack of information on the general and specific combining ability of newly introduced and improved quality protein maize inbred lines to employ for constructing biotic stress tolerant hybrids for Ethiopia's mid-altitude agroecology.

Genotype information on general and specific combining ability of quality protein maize inbred lines is provided by line x tester analysis. So far, general and specific combining ability analysis has proven to be one of the most effective tools in the identification process. Legesse *et al*. (2009) proposed that the information on general and specific combining ability may be utilized to assist in the selection of elite inbred lines in attempt to decide the sort of gene action that governs grey leaf spot resistance. Inbred lines' general and specific combining ability defines their potential utility in the development of crosses or synthetic varieties with improved yield, quality traits, and biotic resistance, particularly TLB, GLS, CLR, PLS, and MSV or maize foliar diseases stress resistant. To date, the goal of this

research has been to assess the general and specific combining ability for major foliar diseases of newly introduced inbred lines of quality protein maize from IITA and CIMMYT.

MATERIALS AND METHODS

Descriptions of experimental sites

The experiment was conducted at Bako National Maize Research Center (BNMRC) and Jimma Agricultural Research Center (JARC) during 2019 cropping season. BNMRC is in East Wollega zone of the Oromia National Regional State, Western Ethiopia. BNMRC lies between 9°06' North Latitude and 37°09' East Longitude in the sub-humid agro-ecology, at an altitude of 1650 meters above sea level. The mean minimum and maximum temperatures of the location are 19.7°C and 22.7°C, respectively. The long-term annual rain fall of the site is 1245 mm per year and relative humidity of 63.55%. The soil type at BNMRC is characterized by reddish brown in color and clay and loam in texture (nitisols) with pH of 6.0 and 5.9 (Girma *et al*., 2015). JARC is in Jimma zone, Oromia National Regional State, South Western of Ethiopia. The center is located between 7°40'37'N and 36°49'47'E and at an altitude of 1753 m.a.s.l. The average maximum and minimum temperatures are 11.9 and 26.2°C, respectively. It receives an average annual rainfall of 1532 mm. The long-term annual rain fall of the site is 1572 mm per year with RH of 67%. The soil type at JARC is characterized by reddish brown/ nitisols with pH of 5.20 (Lemi *et al.,* 2018).

Experimental materials

The experiment consisted of 36 F_1 hybrids and 13 parental lines. The 36 F1 hybrids were generated by using line by tester cross formation in 2018/2019 cropping season at Bako National Maize Research Center from 13 parental lines (9 females and 4 males) introduced from CIMMYT and IITA for QPM germplasm development.

Experimental design and field management

At the main cropping season of 2018, the hybrid (36F1) and four commercial checks with total of 40 entries were planted by laid out in 5x8 alpha lattice experimental design with 3 replications. Each entry was planted in one row per plot of 5m long with spacing of 0.75 m between rows and 0.25 m between plants within a row. Two seeds were planted per hill to ensure uniform and enough stand and then thinning at the 3 to 5 leaf stages to attain a final plant density of 53333 plants per hectare as EIAR recommendations. Planting was conducted on the onset of the main rainy season once adequate soil moisture level was reached in order to ensure good germination and seedling development. Pre-emergence herbicide. NPS and urea fertilizers were applied at the rate of 150 kg/ha and 250 kg/ha, respectively.

DATA COLLECTED

Data on grain yield, major foliar diseases and other important agronomic traits were collected on a plot and sampled plants bases. Five plants were selected randomly in each plot and were labeled. These plants were measured individually and the mean value was recorded for the plot. The severity of major diseases such as grey leaf spot (GLS), TLB and common leaf rust (CLR) was recorded on the whole plot using a 1 to 5 scale where 1=no symptoms, 2=moderate lesion below leaves subtending the ear, 3=heavy lesion development on and below the leaf subtending the ear with a few lesions above it, 4=severe lesion development on all but uppermost leaves may have few lesions and 5=all leaves dead. The other agronomic traits such as PLS= phaeosphaeria leaf spot, MSV=maize streak virus, SL=stock lodging, RL=root lodging, ER=ear rot, HC=husk cover and grain yield was determined as weight of the total shelled grain after adjusting grain moisture to 12.5% and then converted to ton per hectare.

STATISTICAL ANALYSIS

Analysis of variance (ANOVA)

Analyses of variance (ANOVA) were computed for grain yield and other agronomic traits for individual location. Prior to combined data analysis across locations, Bartlett's test for grain yield and related traits were conducted to test homogeneity of error variances (Gomez and Gomez, 1984). As a result, combined analysis over the 2 locations was carried out for these traits by using PROC GLM and PROC MIXED in SAS (SAS, 2014). Further, analyses were performed according to the line x tester analyses to partition the mean square due to crosses into lines, tester, and line by tester effects (Singh and Chaudhary, 1985) using SAS program for the traits with significant differences among crosses. The combining abilities were investigated GCA and SCA effects were estimated according to the formula given in the following section.

Combining ability analysis

Line x tester analysis was done for traits that showed statistically significant differences among crosses in each environment and across environments using the adjusted means based on the method described by Kempthorne (1957). General combining ability (GCA) and specific combining ability (SCA) effects for grain yield and other agronomic traits were calculated using line x tester model.

$$\mathbf{Y_{ijk} = \mu + r_k + g_i + g_j + S_{ij} + e_{ijk}}\text{.....equation}\mathbf{(1)}$$

Where, Y_{ijk} = the value of a character measured on cross of line i by tester j in kth replication μ = Population means, r_k = Effect of kth replication, g_i = General combining ability (GCA) effects of ith line, g_j = General combining ability (GCA) effect of the jth

tester, S_{ij} = Specific combining ability (SCA) of i^{th} line and jth testers such that Sij equal to Sji, and e_{ijk} = Experimental error for ijkth observation. General and specific combining abilities of lines were computed for characters that showed significant differences among crosses following line by tester (LxT) analysis as suggested by Singh and Chaudhary (1985). The main effects due to females and males were considered as GCA effects while, male x female interaction effects were represented as the SCA. Then the combining ability mean squares were calculated based on cross means of each genotype from each location, error mean squares calculated for crosses above were used to test the significance of GCA and SCA interactions with location (Singh and Chaudhary, 1985).

Estimation of GCA effects

This was computed based on formula recommended by Singh and Chaudary (1985) as follows:

a) Lines: $g_i = \frac{X_i..}{tr} - \frac{X...}{ltr}$ ……equation(2)

b) Testers: $g_j = \frac{X._j.}{lr} - \frac{X...}{ltr}$ ……equation(3)

Where, gi= GCA effect for i^{th} line, g_j= GCA effect for j^{th} tester, $X._j.$= sum of the j^{th} tester, $X._i..$= Sum of the i^{th} line, X… = grand sum, l= number of lines, t= number of testers and r = number of replications.

$$\sum g_i = \sum g_j = 0$$ ……equation(4)

Estimation of SCA effects

SCA effects was calculated as a deviation of each cross mean from all hybrids mean adjusted for corresponding GCA effects of parents. They were computed as follows as given by Singh and Chaudary (1985).

$$S_{ij} = \frac{X_{ij}.}{r} - \frac{X_i..}{tr} - \frac{X._j.}{lr} + \frac{X...}{ltr}$$ ……equation(5)

Where, S_{ij}= SCA effect of the ij^{th} crosses, $X_{ij.}$= i x j cross sum, $X_{i..}$=i^{th} line sum, $X_{.j.}$=j^{th} tester sum, l= number of lines, t= number of testers and r= number of replications

Standard errors for combining ability effects were calculated as follow:

1. Standard error for general combining ability effects

a) Line: SE (GCA for line) = $\sqrt{\text{Mse}(l-1)/\text{ltr}}$……..equation(6)

b) Tester: SE (GCA of tester) = $\sqrt{\text{Mse}(t-1)/\text{ltr}}$…….equation(7)

2. Standard error for specific combining ability effects

SE (SCA effects) = $\sqrt{\text{Mse}(l-r)(t-r)/\text{ltr}}$…….equation(8)

3. Standard error of the difference between combining ability effects

a) Standard error of the differences between general combining ability effects

SE (g_i-g_j) line = $\sqrt{2\text{Mse}/\text{rt}}$.....equation(9)

SE (g_i-g_j) tester = $\sqrt{2\text{Mse}/\text{rl}}$.....equation(10)

b) Standard error of the differences between specific combining ability effects

SE (S_{ji}-S_{kl}) = $\sqrt{2\text{Mse}/r}$ .....equation(11)

The significance of GCA and SCA effects were estimated by dividing the corresponding SCA and GCA values by their respective standard error and comparing the obtained t value with tabular t-value at error degree of freedom**.** The values of GCA(males), GCA(females) and SCA effects were evaluated based on the procedure as recommended by Singh and Chaudhary (1977).The significance of general and specific combining ability effects was tested using the formula of Cox and Frey (1984).

(a) General Combining ability effect:

t=$\frac{GCA}{SE\ gca(male)}$where, S.E (GCA male) = $\frac{(mse)1/2}{r*f}$……equation(12)

t= $\frac{GCA}{SE\ gca(females)}$ where, S.E (GCA female) =$\frac{(mse)1/2}{r*m}$ ……equation(13)

Where:- Mse = error mean square, r = number of replications, f = number of females, m = number of males, S.E = standard error

(b) Similarly, significance of SCA effect:

t=$\frac{\boldsymbol{SCA}}{\boldsymbol{SE\ sca(line*tester)}}$ where, S.E (SCA) =$\frac{(mse)1/2}{r}$……equation(14)

Where: Mse= error mean square and r = number of replications

4. Proportional contribution of line, tester, and line by tester estimations

The proportion contribution of lines, tester, and line x tester to the sum square of crosses were assessed with the ratio between sum of squares of each component and the cross sum of squares according to given by (Singh and Chaudhry, 1985) as the following formulas:-

Contribution of lines=$\frac{Sum\ square\ of\ line}{Sum\ square\ of\ Cross} x100$……..equation(15

Contribution of tester=$\frac{Sum\ square\ of\ tester}{Sum\ square\ of\ Cross}$x100……..equation(16)

Contributions of line by tester=$\frac{\text{Sum square of Line x Testers}}{Sum\ square\ of\ crosses}x100$……equation(17)

RESULT AND DISCUSSION

Combined analysis of variance showed significant differences among the two locations for all the studied traits. The result also showed highly significant (P>0.01) mean squares due to genotypes for all traits studied. It showed highly significant (P ≤ 0.01) and significant (P ≤ 0.05) mean squares due to GCA and SCA for all traits((Table-1). This indicated that significant variance exists among the genotypes with respect to GCA and SCA combining ability and thus both additive and non-additive gene actions were vital for the expression of the traits. Nedi *et al*.(2018) observed the mean square due to GCA showed highly significant difference (P ≤ 0.01) for grey leaf spot, turcicum leaf blight and common rust, whereas SCA revealed non-significant difference. It showed the resistant genes controlled by additive types of gene action for Grey leaf spot, turcicum leaf blight, and common rust diseases in this study. Cumulative gene action plays an important role in developing grey leaf spot, turcicum leaf blight and common rust tolerant variety.

The interaction between locations and GCA of lines were highly significant (p<0.01) and significant (P< 0.05) for ASI, EPO, PA, HC, SL, and RL while GCA of testers were highly significant (p<0.01) and significant (P< 0.05) for GY, CLR, TLB, PA, EA, HC and RL, indicating that the performances of the testers and lines were not consistent across locations for these traits and there is adequate genetic variability among the testers to consent good advancement from selection for improvements of the traits. On the other hand, significant differences were observed in SCA (LxT)*Loc only for GY and ASI (Table-1).The significance of the interaction of GCA of parents with the locations and SCA of the crosses with the locations showed that the GCA effects of the parents and SCA of the crosses over the test locations were vary. Similar results were reported significant GCAL, GCAT and SCA_{LxT} for GY, PA, and EA by Tulu *et al*. (2021) and Zeleke *et al*.(2020) suggested significant for GCA and SCA for GY and ASI. Akinwale et al.(2021) also observed significant different due to GCA and SCA for GY, ASI EA, PA and ER. The significance of both GCA and SCA mean squares for all of the conducted for major foliar diseases and other agronomic traits shows the role of additive and non-additive gene action in the inheritance of the traits. Meseka et al.(2020) reported significant GCA and SCA of inbred lines for GY, PA, EA, CLR, MSV and TLB and Eisele *et al*.(2020) also observed significant mean square due to GCA and SCA for GY and GLS of inbred lines in diallel analysis. Thereby the significance of both GCA and SCA mean squares for most of the traits indicates the role of additive and non-additive gene action in the inheritance of the characters.

Table-1: Analysis of variance for combining ability combined across the two locations and proportional contribution of GCA and SCA in hybrids evaluated in 2019.

Source of Variations	DF	GY	ASI	DM	GLS	CLR	EPO	TLB	PA	EA	ER	HC	PLS	SL	RL	MSV
Locations(L)	1	823.68**	23.34**	580.2*	20.47**	26.04**	0.11**	10.44**	31.12**	6.33**	260.04*	49.11**	1.04*	262.24**	133.79**	7.4**
Rep(Site)	4	5.65*	3.29*	885.8**	0.37**	0.53**	0.006*	0.39**	0.49	1.96**	4.14*	13.78**	0.670	1.01	10.16**	0.05
Lines	8	3.23**	13.3*	455.9*	1.11**	1.63*	0.02**	0.22*	2.08**	3.05**	3.23*	9.83**	0.88*	3.96*	5.40**	2.8*
Testers	3	26.08**	0.41*	614.13*	1.49**	2.33*	0.016*	0.29*	2.83**	1.25*	10.82*	6.98*	4.6*	20.16*	7.22**	8.54*
Lines*Testers	24	2.58**	28.74**	465.5*	0.47**	0.18*	0.018*	0.154*	0.40*	0.63*	46.12*	2.97*	3.99*	3.41*	2.38**	0.11*
Lines*L	8	30.15	3.34*	77.38	0.059	0.081	0.006*	0.201	1.52**	0.051	0.52	10.42*	0.14	21.45**	4.15**	0.36
Testers*L	3	2.65*	0.212	152.60	0.10	0.29*	0.003	0.51**	0.91**	1.21**	2.604	6.96**	0.197	2.14	1.99*	0.285
Lines*Tester*L	24	2.51*	0.879	97.42	0.12	0.17	0.0017	0.08	0.26	0.52*	1.141	2.31	0.106	2.54	1.07	0.17
Error	140	1.096	1.053	147.43	0.083	0.113	0.002	0.078	0.23	0.31	1.42	1.62	0.144	1.68	0.94	0.282
Line GCA (%)		13.4	16.2	35.8	26.9	18.2	59.4	27.3	28.3	47.5	38.6	48.9	19.4	42.2	39.5	31.1
Testers GCA (%)		50.5	19.4	10.2	18.5	45.7	17.5	33.5	47.9	11.9	7.1	15.3	14.5	16.8	11.7	10.8
GCA %(T+L)		63.9	44.7	54.0	45.4	63.9	76.9	60.8	76.2	59.4	45.7	64.2	33.9	59	51.2	41.9
LxT SCA (%)		36	55.3	35.8	54.5	36.1	23.1	39.2	23.8	40.6	54.3	35.8	66.1	41	48.8	58.1
GCA/SCA		1.8	1	1	0.8	1.8	3.3	1.6	3.2	1.5	0.8	1.8	0.5	1.4	1	1

*=Significance level at 0.05, **=Significance level at 0.01 no asterisk of */**=non-significance at 0.05 and 0.01 levels, GCA=general combining ability SCA=specific combining ability, Df=degree of freedom, GY=grain yield, ASI=anthesis silking interval, DM= days to maturity, EPO= ear position, TLB= turcicum leaf blight, GLS=gray leaf spot, PA=plant aspect, EA=ear aspect, EPO=ear position, ER= ear rot, HC=husk cover, PLS= phaeosphaeria leaf spot, SL=stock lodging, RL= root lodging, MSV=maize strike virus.

General combining ability effect estimates

The estimated general combining ability of inbred lines across locations is presented in Table-2. Among the 12 inbred lines, only L3 had significantly positive GCA effects for GY. Similarly, among the four testers T1 and T2 showed highly significant positive GCA effects for this trait. Therefore, the inbred line and the testers with positive and significant GCA effects are good combiner for improving GY. On other hand, L6, L9, T3 and T4 were showed significantly negative GCA effects for GY, indicating, that these inbred lines and testers were not good combiner within this group of inbred lines and may not be exploited for GY advancement. Matched with the current study, several authors reported either positive or negative significant GCA effects of inbred lines for GY in other group of inbred lines (Tolera *et al.,* 2017; Dufera *et al.,* 2018; Tesfaye *et al*., 2019; Tulu *et al*., 2021).

For ASI, all lines and testers showed negative and positive non-significant GCA effects. Regarding to EPO or ear displacement L1, L2, L3, L8 and L9 showed positive and highly significant GCA effect, while only L4 for line and T1and T3 for testers showed negative and significant GCA effects indicating desirable combiners for this traits and these lines contribute favorable allele to improve desirable characters such as uniform, clean, non-lodge and disease free; therefore, it could be encouraged to the next stage of evaluation in agreement with yielding ability. Among the inbred lines, only L4 and L5, L6 and L8 were with significantly positive GCA effects for EA and PA respectively. On other hand T1 and T3 showed negative and highly significant mean GCA effects for EA, indicating that the testers with positive and significant GCA effects are poor combiner for improving EA and the inbred lines and testers with negative GCA effects for both traits were good combiners in improving these traits.

Concerning disease reactions, the GCA effects estimate of parental lines for GLS, all lines and testers respond positive and negative non-significant. Regarding to TLB L4 and L9 for lines and T3 and T4 showed positive and significant GCA effects, while only L6 for lines and for testers T1 and T2 showed negative and significant GCA effects. Regarding to common leaf rust L9 showed positive and significant GCA effect which indicates to undesirable direction there is increased susceptibility of crosses they involved. Parental lines L1, L2, L5 and L8 exhibited negative and highly significant GCA effects for husk cover, which indicates desirable for protection from bird attack, rain, ear rot and other yield loss factors. while L4, L7 and L9 showed positive and highly significant GCA effects for husk cover, which indicates poor general combining ability of the lines for the trait under study since it contributed to open husks. L6 showed negative and significant GCA effect for PLS, whereas L4 and L8 revealed positive and significant GCA effect for PLS. On the other hand, L3 and L8 showed positive and significant GCA effect for MSV, while L5 and L6 revealed negative and significant GCA effect for MSV. In general, parental lines that showed positive and significant GCA effects for major foliar maize diseases reactions indicates contribute disease susceptible alleles in the synthesis of new hybrid varieties; whereas parental lines showed negative and significant GCA effects for major foliar maize diseases reactions indicates those have the potential for tolerance to these major foliar maize diseases. Positive and significant GCA effects for stock lodging were observed for parental lines L4 and L6 which are undesirable as these crosses showed increased stalk lodging; whereas L8 showed negative and significant GCA effect indicating that these crosses were good general combinations for reduced stalk lodging. Parental lines L7 and L8 exhibited negative and significant GCA effects for root lodging, indicating that these lines were good GCA for resistance to root lodging; whereas L4 and L6 showed positive and significant for root lodging percent which are undesirable as these lines showed higher root lodged percent. On the other hand, L2, L4 and L6 showed negative and highly significant GCA effect for ear rot, while L5, L8 and L9 revealed positive and highly significant GCA effect for ear rot. Negative or low GCA effects indicate that the ears were not damaged by ear rots. The reduction of ear rots infections is also important because it results in the reduction of mycotoxins in the grain making it safer for consumption. Finally, the result is in line with several researchers report. Accordingly, the result of this finding agrees with Worku *et al*. (2008), Legesse *et al*. (2009), Girma *et al*. (2015), Tolera *et al*.(2017), Tulu *et al*.(2018), Woldu *et al*.(2020), Dufera *et al*.(2021) they were found positive and negative significant GCA effect for the same traits.

Specific combining ability effect estimates

Specific combining ability effects for grain yield and yield related traits for combined across locations is presented in Table-3. For grain yield, the crosses; L2xT4, L3xT3, L3xT4, L4xT4, L5xT2, L7xT2, L9xT1 and L9xT4 showed positive significant SCA effects which indicates that these were best combinations with favorable SCA estimates for grain yield. The crosses, L1xT4, L3xT1, L5xT3, L6xT1, L7xT4, L8xT4, L9xT2 and L9xT3 displayed negative significant SCA effects which indicates that these were poor combinations with unfavorable SCA estimates for grain yield. With respect to ear position the crosses L1×T3, L1×T4, L2×T1, L2×T2, L3×T1, L4×T1, L4xT3, L5xT2, L5xT4, L6xT2, L6xT4, L7xT4, L8xT3, L9xT3 and L9×L4 showed negative and highly significant SCA effects for ear displacement towards the desirable direction of shortness, which indicated that this crosses were good specific combiner for ear position. As a result, these short-statured ear displacement crosses plants are desirable to reduce stem

lodging problems in maize and for ease of mechanized operations also very vital trait. Regarding to days to maturity the crosses, L1×T2, L4×T1, L4×T2, L5×T3, L7×T4, L8×T2, L8×L6, L4×T3, and L9×T3 showed negative and highly significant SCA effects for days to maturity, which are considered desirable as those were observed to be associated with earliness; Hence, earliness is a desirable character as it is useful in multiple cropping system and increases water and land use efficiency. Quite the reverse the cross L2×T3, L5×T2, L8×T1, L8×T4, and L9×T2 showed positive and highly significant SCA effect for days to maturity which indicates undesirable direction of lateness.

Concerning to GLS, the crosses L1xT3, L2xT3, L5xT2, L8xT1 and L9xT4 displayed negative and significant SCA effects whereas the cross L1xT4, L2xT2, L4xT1, L5xT3 and L8xT2 showed positive and significant SCA effect. Regarding to turcicum leaf blight, the crosses L1xT3, L1xT4, L2xT4, L3xT1, L4xT1 and L6xT2 exhibited negative significant SCA effect. Hence such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing tolerant maize genotypes to Turcicum leaf blight; whereas L1xT1, L1xT2, L4xT4 and L6xT3 displayed positive and significant SCA effect which are undesirable as these crosses showed higher percent incidence in their crosses combinations. The crosses L2xT1, L2xT4, L7xT3, L8xT2 and L9xT4 revealed negative and significant SCA effects for PLS indicating that these crosses were good specific combinations for resistance to PLS. Hence such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing tolerant maize genotypes to PLS. On the other hand, crosses L5xT1, L7xT4, and L9xT3, revealed positive and significant SCA effects for MSV which are undesirable as these crosses showed higher percent incidence in their hybrid combinations. The crosses, L1xT1, L2xT1, L2xT3, L3xT1, L4xT1, L4xT2, L5xT2, L5xT3, L5xT4, L6xT1, L6xT2, L7xT2, L7xT4, L8xT2,L9xT2 and L9xT4 expressed negative and significant SCA effects for ear rot percent (ER) which indicating that these crosses were good specific combinations for resistance to ER. Hence, such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing ear rot free genotypes. Concerning husk cover, the crosses L1xT3, L1xT4, L2xT4, L3xT1, L3xT2, l3xT3, L4xT1, L4xT2, L4xT4, L5xT2, L5xT4, L6xT3, L7xT1, L7xT3, L8xT3, and L9xT4 expressed negative and significant SCA effects for HC indicating that these crosses were good specific combinations for resistance to husk cover. On the other hand, crosses L1xT1, L2xT2, L3xT4, L4xT3, L5xT1, L7xT4, L8xT1, L9xT1, L9xT2, and L9xT3 revealed positive and significant SCA effects for husk cover which are undesirable as these crosses showed higher opened husk in their hybrid combinations. These results were comparable with the finding of (Tolera *et al.*, 2017; Dufera *et al*., 2018; Tesfaye *et al*., 2019; Woldu *et al*.(2020) and Tulu *et al*., 2021) with corresponding to the traits.

Table-2: Estimates of general combining ability (GCA) effects of lines and tester for grain yield and other agronomic traits combined across locations evaluated in 2019.

Crosses	GY	ASI	DM	EPO	PA	EA	GLS	TLB	CLR	ER	HC	SL	RL	PLS	MSV
L1	0.23	0.10	0.08	0.01**	0.01	-0.36**	0.02	0.09	-0.18	-0.03	-0.7**	-0.10	0.11	-0.09	-0.01
L2	-0.15	0.07	0.68	0.03**	-0.39**	-0.11	-0.15	-0.08	0.07	-0.24*	-0.26*	-0.13	-0.26**	0.06	-0.08
L3	0.6*	-0.20	0.31	0.02**	-0.17*	0.16	-0.06	-0.13	0.16	0.08	0.14	-0.13	-0.03	0.07	0.14*
L4	-0.07	0.14	-1.6	-0.01**	-0.21**	0.34**	0.09	0.19*	-0.09	-0.3**	0.8**	0.4**	0.28**	0.11*	-0.14*
L5	0.5	-0.29	-1.52	-0.03	0.18*	-0.10	-0.05	0.00	0.13	0.3**	-0.44*	0.04	0.08	-0.03	-0.14*
L6	-0.62*	0.13	0.03	-0.04	0.34**	0.24	0.06	-0.17*	-0.14	-0.3**	-0.4**	0.4**	0.28**	-0.19**	0.03
L7	-0.4	0.29	-0.4	-0.02	-0.08	0.05	-0.04	-0.02	0.00	-0.2	0.8**	0.08	-0.08	-0.05	0.09
L8	0.46	-0.12	2.94*	0.01**	0.01*	-0.45**	-0.02	-0.06	-0.16	0.5**	-0.43*	-0.5**	-0.25**	0.12*	0.11*
L9	-0.59*	-0.12	-0.52	0.03**	0.30	0.24	0.15	0.18*	0.21*	0.19*	0.5**	-0.04	-0.13	-0.01	0.01
SE(lines)	**0.28**	**0.28**	**3.30**	**0.01**	**0.13**	**0.15**	**0.08**	**0.08**	**0.11**	**0.09**	**0.10**	**0.07**	**0.08**	**0.10**	**0.14**
SEd(lines)	**0.22**	**0.22**	**0.74**	**0.05**	**0.15**	**0.16**	**0.12**	**0.11**	**0.14**	**0.17**	**0.19**	**0.13**	**0.14**	**0.13**	**0.16**
T1	0.60**	0.17	1.03	-0.01**	-0.30**	-0.14**	-0.08	-0.10*	-0.2**	-0.06	-0.5**	0.10	0.06	-0.09*	0.08*
T2	0.6**	0.15	-0.14	0.01**	-0.06	0.18**	-0.04	-0.13**	0.12*	0.28**	-0.11	0.10	-0.16**	-0.03	-0.1**
T3	-0.9**	-0.16	-0.16	-0.02**	0.29**	-0.12*	0.08	0.11*	0.38*	-0.14	0.4**	-0.3**	-0.01	0.06	0.03
T4	-0.3*	-0.16	-0.73	0.01**	0.08	0.07	0.04	0.12**	-0.3**	-0.08*	0.24	0.10*	0.11*	0.06	-0.01
SE(Tester)	**0.17**	**0.17**	**2.02**	**0.01**	**0.08**	**0.09**	**0.05**	**0.05**	**0.06**	**0.06**	**0.06**	**0.04**	**0.05**	**0.06**	**0.09**
SEd(Tester)	**0.17**	**0.17**	**0.58**	**0.04**	**0.12**	**0.12**	**0.08**	**0.075**	**0.095**	**0.09**	**0.10**	**0.07**	**0.08**	**0.10**	**0.12**

SE(lines)=standard error of general combining ability effect for lines, SE(testers)= standard error of general combining ability effect for testers, SEd(lines)=Standard error of the difference of general combining ability effects of lines, SEd(testers)=Standard error of difference of general combining ability effects of testers.

Table-3: Estimates of specific combining abilities of Line x tester across locations for yield and yield related characters

Crosses	GY	ASI	EPO	DM	GLS	TLB	CLR	PA	EA	ER	PLS	HC	MSV
L1 xT1	0.32	0.06	0.01**	-0.2	0.098	0.18**	-0.02	0.07	0.00	-0.23**	0.14	0.48**	-0.06
L1xT2	0.23	-0.25	0.02**	-3.3*	-0.06	0.17*	0.21	0.08	0.10	0.36**	-0.09	0.05	0.12
L1xT3	-0.0012	-0.44	-0.01**	0.8	-0.26**	-0.25**	-0.10	-0.27*	-0.35*	-0.06	0.08	-0.44**	-0.01
L1xT4	-1.46**	0.40	-0.01**	2.6	0.21**	-0.17**	0.11	0.35**	0.38*	0.21*	-0.17	-0.19*	-0.06
L2xT1	-0.67**	0.10	-0.02**	-1.6	-0.11	0.052	0.03	0.39**	0.67**	-0.64**	-0.25*	0.08	0.17
L2xT2	-0.41	0.03	-0.02**	-1.5	0.15*	0.13	0.12	-0.02	-0.06	0.53**	0.15	0.23*	0.02
L2xT3	-0.37	0.60	0.03**	4.7**	-0.18*	0.002	-0.17*	-0.20	-0.10	-0.56**	0.11	0.00	-0.03
L2xT4	1.25**	-0.90*	0.03**	0.2	0.03	-0.17**	-0.22**	-0.08	-0.62**	-0.13	-0.14**	-0.42**	-0.07
L3xT1	-1.01**	0.20	-0.01**	-0.4	-0.11	-0.23**	-0.22**	-0.16	-0.18	-0.58**	0.04	-0.49**	0.04
L3xT2	0.14	0.21	0.00	-1.2	-0.06	-0.03	0.077	0.18	0.50	0.26**	-0.02	-0.09	-0.03
L3xT3	0.50*	-0.05	0.00	2.4	0.03	0.010	0.002	-0.30*	-0.11	0.01	-0.19	-0.32**	-0.08
L3xT4	0.73**	-0.14	0.03**	-2.9	0.03	0.19	-0.14	0.29*	0.03	0.44**	0.31	0.85**	0.13
L4xT1	-0.21	-0.14	-0.02**	-7**	0.16*	-0.47**	0.03	-0.03	0.30	-0.34**	-0.10	-0.29**	-0.01
L4xT2	-0.091	-0.29	0.00*	-6**	-0.21**	-0.02	0.24**	0.23	0.15	-0.18*	0.09	-0.55**	0.09
L4xT3	-0.43	0.03	-0.01**	3.5	0.09	-0.02	-0.17*	0.38**	0.04	0.41**	-0.16	1.63**	-0.05
L4xT4	0.53*	0.28	0.01**	4.6	-0.035	0.19**	0.13	-0.33**	-0.28	0.09	0.85	-0.45**	-0.01
L5xT1	0.17	0.12	0.01**	-2.4	-0.073	0.06	-0.11	-0.09	0.24	1.38**	-0.12	0.25**	0.21*
L5xT2	0.51*	-0.03	-0.01**	6.3**	-0.19**	-0.07	-0.06	-0.17	-0.08	-0.32**	-0.10	-0.18*	0.06
L5xT3	-0.69**	-0.21	0.02**	-6**	0.53**	0.09	0.28**	0.32*	0.06	-0.23**	0.07	0.17	-0.16
L5xT4	0.041	0.12	-0.01**	2.5	-0.02	-0.08	-0.11	-0.06	-0.22	-0.63**	0.15	-0.25**	-0.11
L6xT1	-0.57*	0.54	0.01**	2.1	-0.073	0.06	-0.01	-0.01	-0.26	-0.03	-0.21*	-0.12	-0.02
L6xT2	-0.31	-0.45	-0.01**	1.8	-0.023	-0.24**	-0.37**	-0.08	0.09	-0.19*	0.07	0.11	0.08
L6xT3	1.92**	-0.30	0.01**	-1.0	0.11	0.61**	0.36**	-0.10	-0.11	0.27	0.07	-0.78**	-0.13
L6xT4	-0.14	0.52	-0.01**	-2.9	-0.015	0.002	0.16	0.19	0.28	0.16	0.07	0.71**	-0.02
L7xT1	0.10	-0.42	0.00	2.4	0.03	0.08	0.52**	-0.26*	-0.07	0.27**	-0.66	-0.29**	-0.21*
L7xT2	1.27**	0.10	0.01**	3.7	0.081	-0.05	-0.27**	-0.08	0.13	-0.40**	0.26*	-0.05	0.02
L7xT3	-0.34	0.08	0.01**	3.2	-0.04	0.031	-0.26**	0.23	-0.31	0.35**	-0.24*	-0.54**	-0.11
L7xT4	-1.03**	0.25	-0.02**	-9**	-0.08	-0.06	0.015	0.11	0.22	-0.22**	0.01	0.88**	0.26*
L8xT1	0.41	-0.05	0.00	7.4**	-0.16*	0.04	-0.17*	0.08	-0.44**	0.02	-0.06	0.21*	0.15
L8xT2	0.38	-0.03	0.01**	-5.4*	0.23**	-0.01	-0.04	0.08	-0.39**	-0.32*	-0.37**	0.11	-0.17
L8xT3	0.13	0.29	-0.02**	-5.8*	-0.06	0.073	0.05	-0.18	0.24	-0.07	0.46**	-0.20*	0.11
L8xT4	-0.91**	-0.21	0.01**	3.7*	-0.02	-0.10	0.16	-0.06	0.39**	0.37**	-0.04	-0.12	-0.09
L9xT1	1.12**	-0.55	0.05**	-2.6	0.09	-0.023	0.14	-0.22	-0.09	0.48**	0.52**	0.30**	-0.25*
L9xT2	-0.97**	0.64	0.00	5.6*	0.06	0.094	-0.06	0.04	-0.24	-0.19*	-0.12	0.36**	-0.15
L9xT3	-0.80**	0.29	-0.04**	-4.7*	0.03	0.010	-0.05	0.36**	0.56**	-0.11	-0.04	0.55**	0.30*
L9xT4	0.67**	-0.38	-0.01**	1.7	-0.18**	-0.081	-0.084	-0.68**	-0.44**	-0.18*	-0.37**	-1.20**	0.09
SE(LxT)	**0.25**	**0.24**	**0.01**	**0.80**	**0.07**	**0.07**	**0.08**	**0.11**	**0.13**	**0.06**	**0.07**	**0.06**	**0.13**
SE(Sji-Skl)	**0.41**	**0.40**	**0.08**	**3.91**	**0.24**	**0.23**	**0.29**	**0.27**	**0.30**	**0.28**	**0.34**	**0.31**	**0.29**

GY=grain yield, ASI= anthesis silking interval, EPO= ear position, GLS=gray leaf spot, TLB=turcicum leaf blight, CLR=common leaf rusts, PA= plant aspect, EA= ear aspect, PLS= phaeosphaeria leaf spot, SL=stock lodging, RL= root lodging, MSV=maize strike virus, SE (LxT) =standard error of specific combining ability of lines by testers, SE (Sji-Skl) =standard error differences of specific combining ability effects of lines by testers.

Correlation analysis of major foliar diseases with grain yield and other traits

Pearson correlation analysis revealed grain yield (GY) is not significant and negatively correlated with EA, SL, GLS, TLB, HC, CLR, ER and MSV, but significant and negatively correlated with PA, RL, PLS and HC Table-4).This indicated that the traits progress had a negative effect on grain yield. However, positive associations were observed among other traits. Days to maturity and ear position showed significant and positive association with grain yields indicating, increments in these traits resulted in the exertion of days to maturity and ear positions.

Table-4: Phenotypic correlation analysis for major foliar disease reactions, grain yield and other agronomic traits in quality protein maize.

ASI	MD	EPO	PA	EA	SL	RL	GLS	TLB	CLR	PLS	MSV	ER	HC	GY
1.00	-0.05	0.02	-0.11	0.13	0.05	-0.05	0.03	-0.011	-0.05	-0.030	0.001	-0.004	0.05	0.05
	1.00	0.251*	-0.11	-0.25*	-0.005	-0.21*	-0.25*	-0.08	-0.41*	-0.21*	-0.03	0.11	-0.11	0.27**
		1.00	-0.15	-0.12	-0.12	-0.16	0.01	0.02	-0.14	0.05	-0.05	0.21*	-0.11	0.33**
			1.00	0.19*	0.15	0.16	0.21*	0.13	0.02	-0.004	0.07	-0.08	0.42**	-0.55**
				1.00	0.13	0.12	0.15	-0.07	0.21*	0.06	0.17	-0.16	0.36**	-0.11
					1**.00**	0.07	0.08	-0.05	-0.19*	0.03	-0.02	-0.012	0.010	-0.14
						1.00	0.20*	-0.06	-0.09	0.07	-0.05	-0.04	0.34**	-0.18*
							1.00	0.08	0.27*	0.21*	-0.05	0.06	0.11	-0.15
								1.00	0.17	0.11	-0.05	-0.07	0.21*	-0.07
									1.00	0.08	0.09	0.03	0.01	-0.05
										1.00	-0.01	-0.01	0.17	-0.03
											1.00	0.05	0.04	-0.07
												1.00	-0.05	0.16
													1.00	-0.36**
														1.00

** Correlation is significant at the 0.01 level, * Correlation is significant at the 0.05 level.

SUMMERY AND CONCLUSION

Analysis of variance showed that both additive and non-additive gene effects were most elaborate in the control of major foliar diseases and other traits. Though, the proportion of GCA sum of squares was higher than that of SCA for most of the major foliar diseases and other traits. Additive and non-additive gene actions are imperative in governing grain yield and major foliar quality protein maize. In this study the estimated GCA effect on grain yield only L3 exhibited positive and significant that it is reflected as anticipated good combiner; whereas L6 and L9 displayed negative significant GCA effects. For TLB L6 for lines and for testers T1 and T2 showed negative and significant GCA effects which indicates desirable lines and could be used in the development of resistant genotypes against TLB. Among the conducted parental lines L1, L2, L5 and L8 exhibited negative and highly significant GCA effects for husk cover. On the other hand, the MSV GCA effect was negative and significant for L4 and L5, showing that the genotypes examined had different reactions to the two disorders. Among the studied lines L8 showed negative and significant GCA effect for stalk lodging indicating that these crosses were good general combinations for reduced stalk lodging. Parental lines L7 and L8 exhibited negative and significant GCA effects for root lodging. The crosses L2xT4, L3xT3, L3xT4, L4xT4, L5xT2, L7xT2, L9xT1, and L9xT4 displayed positive significant SCA direct effect on grain yield. Regarding to major foliar maize diseases reactions, the crosses L1xT3, L2xT3, L5xT2, L8xT1 and L9xT4 displayed negative and significant SCA effects for GLS; while the crosses L1xT3, L1xT4, L2xT4, L3xT1, L4xT1 and L6xT2 exhibited negative significant SCA effect for turcicum leaf blight. The crosses L2xT1, L2xT4, L6xT1, L7xT3, L8xT2 and L9xT4 revealed negative and significant SCA effects for PLS.

The crosses, L1xT1, L2xT1, L2xT3, L3xT1, L4xT1, L4xT2, L5xT2, L5xT3, L5xT4, L6xT1, L6xT2, L7xT2, L7xT4, L8xT2, L9xT2 and L9xT4 expressed negative and significant SCA effects for ear rot percent (ER). In either hand Pearson correlation analysis revealed grain yield (GY) significant and negatively correlated with PA, RL, PLS and HC which indicates that the traits progress had a negative effect on grain yield were observed. Better performing hybrids, inbred lines with desirable GCA, and cross combinations with desirable SCA effects for grain production, main foliar maize diseases, and other traits were efficiently identified relying on the results of the study. In general, this finding provides fundamental information on breeding of quality protein maize (QPM) hybrid varieties with the desirable potential for grain yield, disease resistance and other traits in addition to the adaptability to mid-altitude environments of Ethiopia. However, further experiments are recommended to confirm the results obtained in this study based on the field tests conducted in multiple locations and cropping years.

Conflict of interests

The authors have not acknowledged any conflict of interests.

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