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RESEARCH ARTICLE

Estimates of Combining Ability and Association among Morpho-Agronomic Traits of Single Cross Maize (*Zea mays* L.) Hybrids

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ABSTRACT

Screening genotypes have a crucial role to increase the efficiency of selections in plant breeding program. Therefore, this study was emphasized to determine combining ability and the association between traits among themselves and yield. The experiment was conducted at Haramaya University Research Station (Raare) for two years (2018 and 2019) using 4x7 alpha-lattice design with three replications. Pooled analysis of variance revealed highly significant (p≤0.01) variations among crosses for grain yield and related traits. According to the result of combining ability analysis, parental line L3 was identified as a good general combiner for grain yield, ear diameter, 1000-kernel weight, and days to maturity. Similarly; L1, L2, and L8 proved as the best general combiner for number of kernels per row. Crosses L1×L6, L3×L5, L4×L6, L4×L8, and L5×L7 were found good specific combiners for 1000-kernel weight. Furthermore, the cross L5×L6 was the best specific combiner for ear diameter, whereas L4×L7 for both number of kernels per row and 1000-kernel weight. Likewise, the crosses L1×L5, L3×L8, L6×L7, and L7×L8 were identified as the best specific combiner towards earliness. Moreover, thousand kernel weight showed significant positive correlation with grain yield, conversely, days to anthesis, days to silking, ear aspect, and *Puccinia sorghi* exhibited significant negative correlation with grain yield at genotypic and phenotypic levels. Ear length, 1000-kernel weight, number of kernel rows per ear, and *Turcicum* leaf blight had positive direct effect on grain yield at genotypic and phenotypic level. In general, the result presented in the study might be useful for further breeding process to improve the productivity of maize.

Introduction

Maize (*Zea mays* L.) has a crucial role for human diet as well as animal nutrition, especially in developing countries. It is the most important and widely grown cereal crop in Ethiopia next to teff. Maize belongs to the grass family Poaceae and historically believed that the crop was originated from Mexico and introduced to Ethiopia around the late 17th century (Haffangel, 1961). Even if the introduction of maize to Ethiopia is a recent phenomenon, it dominates the total cereal production of the country and provides livelihood food security. Maize crop has a versatile use, wider genetic variability, high grain yield per unit area and can grow in a wide range of environments. Maize together with wheat and rice comprise a major component of the human diet, accounting for an estimated 42 percent of the World's food calories and 37 percent of protein intake [average 2016-18 (FAO, 2021)]. As a result, maize is considered the strategic crop to secure food self-sufficiency and the growing demand for maize has steadily increased in Ethiopia. Therefore, to address the growing demand of farmers, there is a need to improve the productivity of maize through breeding. Studies on genetic parameters and the correlation between yield and yield-related traits are pre-requisite to plan a meaningful breeding program and thereby enhance the productivity of the crop (Reddy & Jabeen, 2016).

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The foremost requirement in any hybrid breeding program is identification and selection of diverse parents that have good general and specific combining ability with other parents for yield and yield contributing traits (Fasahat et al., 2016). Indeed, diallel mating system is one of the suitable means to detect the performance of offspring, as well as the parents and progeny performance can be statistically separated into components relating to GCA and SCA (Murtadha et al., 2018). Combining ability analysis is the most powerful biometrical tool in identifying the better combiners and measure the relative capacity of the parental line to transmit genetic information to its offspring for the development of outstanding hybrids. The role of combining ability in maize breeding for selection of better parents as it discloses to the mode of inheritance for various plant traits and determines the nature and magnitude of gene action involved in the inheritance of the traits has been well documented (Gissa et al., 2007; Abdel-Moneam et al., 2009; Gouda et al., 2013; Mogesse et al., 2020).

In genetic breeding, plant selection can be conducted directly or indirectly by studying linear relationships among traits, such relationships can be determined by correlation coefficient and by complementary methods, such as path analysis. Therefore, understanding the interrelationship of quantitative characters with grain yield is crucial to determine the efficiency of selection and providing the basis for planning an effective breeding program. Correlation is the linear association between two variables (Gomez & Gomez, 1984) measured by correlation coefficient, which is required in plant breeding to quantify the degree of genetic and non-genetic association between two or more traits. Moreover, the coefficient of correlations aids in determining the level of relationship between two separate traits as well as the levels at which these traits are mutually variable (Johnson et al., 1955). A positive correlation coefficient indicates simultaneous relationship between dependent and independent traits in selection (Eleweanya et al., 2005). The low phenotypic correlation could arise due to the modifying effect of the environment on the association character at genetic level (Alake et al., 2008).

Information like association among traits and the relative contribution of each trait is required to determine selection criteria in plant breeding. Therefore, path coefficient analysis, which was proposed by Wright (1921) used to partition correlation coefficient into direct and indirect effects and provides information on the actual contribution of a trait to the yield. Furthermore, path coefficient analysis produces a clear picture of a set of independent variables on the dependent variable and provides realistic relationship of the characters, which helps in identifying traits that are useful as selection criteria to improve crop yield (Milligan et al., 1990; Chaudhary et al., 2017; Mogesse, 2021). Thus, correlation and path coefficient analysis are important tools to assist breeders in defining priority traits for selection, quantifying the level of

relationships between the traits, provide reliable and useful information on the nature, extent, and direction of selection (Mallikarjuna et al., 2011; Zeeshan et al., 2013; Nabila et al., 2017; Wedwessen & Wolde, 2020; Mogesse, 2021). Thus, to improve the production and productivity of maize as well as tackling newly emerging challenges, continuous maize research is required. As a result, widely adapted maize varieties that suit different cropping systems and farming conditions are required to enhance food self-sufficiency, cash generation, and poverty reduction in the country. Therefore, the research aimed to verify combining ability and association of morpho-agronomic traits to practice indirect selection for further breeding process.

Materials and Methods

Descriptions of Study Area

The study was undertaken at the research farm of Haramaya University (Raare), which is located at an altitude of 2020 meter above sea level, latitude 9º26' N and longitude 42º3' E. The area received an average annual rainfall 727 mm with minimum and maximum average temperatures of 8.99 ºC and 25.15 ºC, respectively during 2018/19 cropping season.

Experimental Design and Field Management

Eight maize inbred lines were obtained from Haramaya university maize research program, and crossed in a half-diallel mating design (Griffing's Method IV, Model I) during 2017 cropping season. The resulting twenty-eight single cross F_1 maize hybrids were evaluated in 2018 and 2019 cropping seasons using 4x7 alpha-lattice design in three replications. The experiment comprised two rows per plot with 5.1 m long and 0.75 m inter and 0.30 m intra row spacing. An alley left 1.5 m between blocks. During planting, two seeds per hole were planted to ensure enough stand and later thinned after two weeks of emergence (when seedlings were 3-4 leaf stage) to have a single healthy seedling per hole and to retain 44,444 plants stand ha^{-1}. Urea and NPS fertilizers were applied at the recommended rates. Moreover, all other necessary field management practices were carried out as per the recommendation of the study area and the crop.

Data Collection and Analysis

Field data on phenology, growth, grain yield and yield related traits, and disease reaction were recorded on plot and individual plant basis at the appropriate plant growth stages. Data related to days to anthesis (DA), days to silking (DS), days to maturity (DM), and grain yield (GY) were recorded on the plot basis, whereas, plant height (PH), ear height (EH) were recorded from five randomly selected plants, and number of kernel rows per ear (NKRE), number of kernels per row (NKR), ear length (EL), ear diameter (ED) and 1000-kernel weight from five randomly selected ears leaving border plants of each row. The average was taken as the mean value of the treatment. Grain yield was measured from entire ears of each experimental

unit. Moreover, grain yield was adjusted to 12.5% moisture content and converted yield per plot into ton per hectare.

Data obtained from field measurement were subjected to analysis of variance using the PROC MIXED procedure of SAS (2002) to test the level of significance resulting from 8x8 diallel cross. The traits, which showed significant difference were subjected to diallel analysis using AGD-R (Analysis of Genetic Designs in R). Significant genotypic variance of each trait was further partitioned to GCA, SCA, and experimental error. Diallel analysis of variance was conducted to estimate general combining ability (GCA) and specific combining ability (SCA) following Griffing's approach Model I, Method IV [n(n−1)/2], which only includes one set of crosses with neither reciprocals nor parents as suggested by Griffing (1956). The estimates of genotypic and phenotypic correlation were computed by the method described by Singh and Chaundry (1985).

Results and Discussion

Analysis of Variance

Analysis of variance revealed that there were significant differences among crosses for ear diameter, 1000-kernel weight, anthesis-silking interval, grain yield, days to maturity, number of kernels per row, and number of kernel rows per ear suggesting that the presence of variability among crosses. The traits which showed significant difference were subjected to genetic analysis of variance to determine GCA and SCA variance. The combined analysis of GCA exhibited highly significant difference for number of kernels per row implying

that additive gene action contributes to the expression of the trait, whereas the mean squares of SCA were also significant for thousand kernel weight indicating non-additive gene action contributes to the expression of the trait (Table 1). Several studies (Gissa et al., 2007; Abdel-Moneam et al., 2009; Gouda et al., 2013; Mogesse et al., 2020) showed that significant GCA and SCA effects. The SCA sums of squares were higher than GCA sums of squares for ear diameter, anthesis-silking interval, and number of kernels per row implying that non additive gene action is important for controlling the inheritance of these traits. The results were in parallel with the previous reports of Elmyhum (2013) and Sugiharto et al. (2018). On the other hand, GCA sums of squares were higher than SCA for number of kernel rows per ear, grain yield, number of days to maturity, and thousand kernel weight that implies additive gene action is important in controlling the inheritance of this trait. The results were comparable with the previous reports of Wende (2013) and Tessema et al. (2014). Significant year effects were observed for the traits of ear diameter, grain yield, anthesis-silking interval, and number of kernels per row. The mean squares of crosses × year interaction effect were also significant for all traits, except anthesis-silking interval. Similar results were reported by Bello and Olawuyi (2015) in their previous studies on gene action, heterosis, correlation, and regression estimates in developing hybrid cultivars in maize. Similarly, significant GCA × year interaction was observed for days to maturity, number of kernels row per ear, and 1000-kernel weight; while significant positive SCA × year interactions were found for all traits studied, except anthesis-silking interval and number of kernel rows per ear.

Table 1. Pooled analysis of variance, mean and CV for grain yield and yield component in single crosses F_1 maize hybrids evaluated at Haramaya, Ethiopia in 2018 and 2019.

Source of Variation	df	ED	ASI	DM	GY	NKR	NKRE	TKW
Year (Y)	1	1.880**	4.124**	34.118	105.695**	98.296**	1.030	303.843
Crosses (C)	27	0.247	0.366	71.116	6.957	20.946	2.107	4945.718
GCA	7	0.216	0.310	96.683	14.686	13.944**	5.742	6854.160
SCA	20	0.264	0.395	65.742	4.803	23.945	0.875	4761.619*
Crosses × Y	27	0.340**	0.196	67.868**	9.071*	20.396**	2.814**	3721.877**
GCA × Y	7	0.644	0.167	138.857*	12.916	4.450	8.313**	9649.455**
SCA × Y	20	0.327**	0.207	46.657**	8.446*	26.536**	0.899	2083.011**
Error	96	0.144	0.192	16.626	4.929	8.605	0.882	728.425
Grand Mean		4.593	3.274	164.786	8.870	38.929	12.651	364.235
Min		3.517	3.000	142.000	5.033	27.800	10.300	304.870
Max		5.250	3.667	170.667	10.883	43.567	15.867	416.170
CV (%)		6.513	10.572	0.696	21.736	5.204	3.107	8.855

GY: Grain yield (t ha⁻¹), NKRE: Number of kernels row per ear, DM: Days to maturity, ASI: Anthesis-silking interval, ED: Ear diameter, NKR: Number of kernel per rows, TKW: Thousand kernel weight, **Significant at p<0.01 level of probability, and *Significant at p<0.05 level of probability.

Estimates of GCA Effects

According to the result of GCA analysis in Table 2, significant differences were observed among lines for various traits. Significant positive GCA effect (0.635) for grain yield was observed in L3. Thus, L3 was proven as a good general combiner for yield and could be used extensively in hybrid breeding programme with view to increase the yield level. However, L1 and L5 proved as poor general combiner for grain yield. On the other hand, significant positive GCA effects for number of kernel rows per ear were observed in L1, L2, and L8 implying that they are good general combiners and might be selected for obtaining high yielding hybrids, while L3, L5, L6, and L7 exhibited significant negative GCA effect for number of kernel rows per ear, which may contribute undesirable trait for grain yield improvement. Significant positive GCA effects for 1000-kernel weight were obtained from L2 and L3; therefore, these lines could be considered as potential parents for genetic improvement of grain yield through 1000-kernel

weight. Conversely, parental lines L1 and L8 showed highly significant negative GCA effect for 1000-kernel weight implying that they are poor general combiners to improve grain yield through 1000-kernel weight. Positive and significant GCA effect for ear diameter was detected in parental lines L3 and L8 showing the tendency of the parents to enhance ear diameter and thereby improve grain yield. Significant negative GCA effect for days to maturity was observed in L2 and L7 depicting that these lines have genes for earliness, which also contributes desirable trait in improving maize maturity period. In contrary, L3 showed significant positive GCA effect for days to maturity, implying that the tendency of the parent to contribute delay in maturity to their progeny. Significant negative GCA effect for anthesis-silking interval was observed in L5 towards desirable direction, whereas L6 showed significant positive GCA effect for anthesis-silking interval. The results were in agreement with the earlier reports of Amiruzzaman et al. (2013), Hosana et al. (2015), Genet et al. (2017), and Gemechu et al. (2018).

Table 2. Estimates of general combining ability effects (GCA) for grain yield and yield related trait of maize inbred lines evaluated at Haramaya, Eastern Ethiopia.

Parent	ASI	DM	ED	NKR	NKRE	TKW	GY
L1	-0.097	-0.944	-0.073	0.672	0.255[*]	-26.341[**]	-0.918[*]
L2	0.014	-2.222[**]	-0.015	0.267	0.566[**]	10.959[**]	0.268
L3	-0.014	3.139[**]	0.099[*]	0.722	-0.270[*]	17.748[**]	0.635[*]
L4	0.042	0.444	-0.070	-0.681	0.035	0.731	0.199
L5	-0.153[*]	0.694	-0.042	0.561	-0.259[*]	4.251	-1.093[*]
L6	0.125[*]	-0.500	-0.051	-0.525	-0.273[*]	4.412	0.310
L7	-0.014	-1.306[*]	0.022	-0.289	-0.534[**]	1.070	0.418
L8	0.097	0.694	0.130[*]	-0.728	0.480[**]	-12.830[**]	0.182
SE (gi)	0.048	0.450	0.042	0.323	0.104	2.975	0.245

GY: Grain yield (t ha⁻¹), TKW: Thousand kernel weight, NKRE: Number of kernels row per ear, NKR: Number of kernels per rows, DM: Days to maturity, ASI: Anthesis-silking interval, ED: Ear diameter, [**]Significant at p<0.01 level of probability, and [*]Significant at p<0.05 level of probability.

Estimates of SCA Effects

The estimate of specific combining ability (SCA) effects of the crosses for grain yield and yield related traits are illustrated in Table 3. Among all crosses evaluated in this experiment, L1×L6, L3×L5, L4×L6, L4×L8, and L5×L7 possess significant desirable positive SCA effect for 1000-kernel weight, that implies these well combined hybrids might be used for obtaining higher 1000-kernel weight and thereby improve grain yield. Conversely, the crosses L1×L4, L1×L5, L2×L3, L4×L5, L6×L7, and L7×L8 exhibited significant negative SCA effect for thousand kernel weight, suggesting the tendency of the hybrid to decrease the trait. Significant positive SCA effects for number of kernels per row and 1000-kernel weight were observed in L4×L7, indicating the tendency of the hybrids to improve grain yield. Conversely, L3×L8, L4×L5, and L6×L7 exhibited significant negative SCA effect for number of kernels per row, implying that the tendency of poor hybrids

combinations to improve the trait. The results were comparable with the finding of Hassan et al. (2019).

Positive and significant SCA effects were observed in L5×L6 for ear diameter, implying that was the best specific combiner for higher ear diameter and might be used for obtaining high yielding hybrids. Conversely, L1×L5 and L6×L7 exhibited significant negative SCA effect for ear diameter. Significant negative SCA effects for days to maturity were observed in L1×L5, L3×L8, L6×L7, and L7×L8 towards earliness. Conversely, L1×L8, L3×L7, and L6×L8 had significant positive SCA effect for days to maturity towards lateness. Significant negative SCA effects for anthesis-silking interval were observed in L2×L4, L4×L6, and L7×L8. Conversely, L2×L6 and L4×L8 showed significant positive SCA effect for anthesis-silking interval.

Table 3. Estimates of specific combining ability (SCA) effects for yield and yield related trait of maize inbred lines evaluated in eastern Ethiopia.

Cross	ASI	DM	ED	NKR	NKRE	TKW	GY
L1×L2	-0.190	-2.286	-0.073	0.133	0.479	17.030	1.463
L1×L3	0.004	-1.813	-0.137	1.044	0.115	0.775	-0.704
L1×L4	-0.052	-0.119	0.066	-1.487	0.209	-38.992**	-1.784*
L1×L5	0.143	-3.702*	-0.278*	-2.095	-0.363	-29.912**	0.591
L1×L6	0.032	2.492	0.263	-0.242	0.184	25.327*	0.388
L1×L7	0.004	2.464	0.208	1.455	0.029	8.069	-0.187
L1×L8	0.060	2.964*	-0.050	1.194	-0.652	17.702	0.233
L2×L3	0.060	2.798	-0.145	-0.717	-0.096	-23.459*	0.477
L2×L4	-0.329*	-1.341	0.125	-1.448	-0.502	11.275	-0.687
L2×L5	0.032	-0.758	-0.187	0.644	-0.208	0.738	0.355
L2×L6	0.587**	-1.563	-0.012	0.663	-0.460	-10.456	-0.448
L2×L7	-0.107	2.075	0.066	0.527	0.201	11.886	-0.523
L2×L8	-0.052	1.075	0.225	0.199	0.587	-7.014	-0.637
L3×L4	0.198	-0.536	0.177	0.696	0.451	8.069	0.696
L3×L5	-0.107	1.381	0.150	0.555	-0.238	23.616*	1.005
L3×L6	-0.218	0.909	-0.042	-0.126	-0.091	-6.445	-0.915
L3×L7	0.087	3.214*	0.152	0.805	0.170	7.013	0.260
L3×L8	-0.024	-5.952**	-0.156	-2.256*	-0.310	-9.570	-0.820
L4×L5	0.004	-1.591	-0.198	-2.576*	-0.227	-53.634**	-1.059
L4×L6	-0.440**	1.437	-0.139	1.410	0.070	32.322**	1.055
L4×L7	0.198	0.909	0.072	2.924**	-0.069	19.680*	0.563
L4×L8	0.421*	1.242	-0.103	0.480	0.067	21.280*	1.216
L5×L6	-0.079	1.520	0.283*	1.769	0.631	16.919	-0.404
L5×L7	-0.107	2.825	0.111	1.433	0.142	36.828**	-0.612
L5×L8	0.115	0.325	0.119	0.271	0.262	5.444	0.124
L6×L7	0.282	-8.313**	-0.464**	-5.365**	-0.427	-56.650**	0.469
L6×L8	-0.163	3.520*	0.111	1.891	0.092	-1.017	-0.145
L7×L8	-0.357*	-3.175*	-0.145	-1.779	-0.046	-26.825**	0.030
SE (ij)	0.151	1.407	0.131	1.012	0.324	9.312	0.766

GY: Grain yield (t ha^{-1}), NKRE: Number of kernels row per ear, DM: Days to maturity, ASI: Anthesis-silking interval, ED: Ear diameter, NKR: Number of kernel per rows, TKW: Thousand kernel weight, **Significant at p<0.01 level of probability, and *Significant at p<0.05 level of probability.

Genotypic and Phenotypic Correlation

Grain yield is a complex quantitative trait, which is influenced by several component traits (Crosbie & Mock, 1981). The cumulative effects of such traits determine the yield. Therefore, to determine such relationships, correlation analyses were used, which enables to describe the direction and magnitude of relationship of targeted characters with attribute traits. The result obtained from correlation analysis showed that grain yield had significant positive genotypic correlation with 1000-kernel weight and ear diameter. This implies that 1000-kernel weight and ear diameter tend to enhance grain yield. Conversely, days to tasseling, days to silking, *Turciccum* leaf blight, plant aspect, ear aspect and *Puccinia sorghi* showed negative genotypic correlation with grain yield (Table 4).

Grain yield showed significant positive phenotypic correlation with 1000-kernel weight and anthesis-silking interval, whereas days to anthesis, days to silking, *Puccinia sorghi*, and ear aspect were exhibited significant negative

phenotypic correlation with grain yield. The results were in parallel with the report of Reddy and Jabeen (2016), who highlighted that significant positive correlation of grain yield with 1000-kernel weight and ear diameter. The traits, days to silking and days to anthesis were exhibited highly significant negative correlation with grain yield at genotypic and phenotypic levels, which indicated that breeding for earliness has the potential of increasing yield unlike selection for flowering. The results were comparable with the report of Mhoswa et al. (2016).

Thousand kernel weight exhibited significant positive correlation with ear length, ear diameter, plant height, ear height, days to maturity, and number of kernels per row and hence, selection for these traits will help in further improvement of the given trait. On the contrary, the trait like days to anthesis, days to silking, *Turciccum* leaf blight, plant aspect, ear aspect, and *Puccinia sorghi* were negatively correlated with 1000-kernel weight at phenotypic and genotypic level. Likewise, number of kernels per row showed significant positive

association with plant height, ear length, ear diameter, ear height, days to maturity, and 1000-kernel weight at genotypic and phenotypic level, which implies that the trait needs to be considered for indirect selection to improve the trait simultaneously. Conversely, days to anthesis, days to silking, *Puccinia sorghi*, plant aspect, and ear aspect were negatively correlated with number of kernels per row at genotypic and phenotypic level.

Ear diameter manifest significant positive association with plant height, days to maturity, ear height, ear length, number of kernels per row, number of kernel rows per ear, and 1000-kernel weight at genotypic and phenotypic level, indicating the possibility of simultaneous improvement of the trait, whereas days to anthesis, days to silking, plant aspect, and ear aspect were negatively correlated with ear diameter at genotypic and phenotypic level. The results were comparable with the report of Abenezer et al. (2020), who highlighted significant positive correlation of ear diameter with plant height, ear height, number of kernels per row, and 1000-kernel weight. Likewise, ear length exhibited significant positive correlation with ear height, plant height, days to maturity, ear diameter, number of kernels per row, and 1000-kernel weight at genotypic and phenotypic levels. Conversely, days to anthesis, days to silking, plant aspect, ear aspect, *Turciccum* leaf blight, and *Puccinia sorghi* were negatively correlated with ear length at phenotypic and genotypic level.

Days to maturity exhibited significant positive correlation with plant height, ear height, ear diameter, ear length, number of kernels per row, number of kernel rows per ear, and 1000-kernel weight at genotypic and phenotypic levels, implying that simultaneous selection of this trait might bring an improvement to grain yield at the expense of maturity period, while days to anthesis, days to silking, plant aspect, ear aspect, *Turciccum* leaf blight, and *Puccinia sorghi* were negatively correlated with days to maturity at genotypic and phenotypic level. Therefore, the positive and significant genotypic and phenotypic association of days to maturity with plant height and ear height tends to improve their height and maturity period simultaneously. The results were supported by the report of Mogesse (2021).

Number of kernel rows per ear, ear length, ear diameter, 1000-kernel weight, plant height, ear height, days to maturity showed positive and significantly inter correlated with each other. Accordingly, increasing ear diameters tends to increase the number of kernel rows per ear and consequently increases the grain yield. Likewise, increasing ear length tends to increase number of kernels per row, and thereby increase grain yield significantly. Therefore, selection for these traits will help in grain yield improvement.

Genotypic Path Coefficient Analysis

Genotypic path coefficient analysis was conducted to determine direct and indirect effects of secondary traits on grain yield (Table 5). According to the result of path coefficient analysis; days to anthesis, plant aspect, ear height, number of kernel rows per ear, 1000-kernel weight, ear length, *Turciccum* leaf blight, and days to maturity exhibited positive direct effects on grain yield, whereas days to silking, number of kernels per row, ear diameter, plant height, ear aspect, and *Puccinia sorghi* exhibited negative direct effects on grain yield at genotypic level. The results were comparable with earlier reports of Pandey et al. (2017) and Nabila et al. (2017).

The highest positive direct effect on grain yield was exhibited by *Turciccum* leaf blight followed by days to maturity, ear height, and days to anthesis at genotypic level. On the other hand, *Puccinia sorghi* had highest indirect effect on grain yield through days to anthesis followed by ear diameter through *Puccinia sorghi* and ear aspect, and days to silking through number of kernels per row.

Days to anthesis showed positive direct effect and significant negative association with grain yield at genotypic level. As a result, the direct effects are positive and the correlation coefficients are significantly negative, the indirect causal factors which are having positive effects *viz.,* ear diameter, plant aspect, plant height, *Turciccum* leaf blight, and number of kernels per row along with days to anthesis are to be considered simultaneously during selection.

The direct negative effect of ear diameter was more than compensated by its indirect effects hence resulting in positive correlation with grain yield, implying that grain yield can be improved through ear diameter indirectly. Positive indirect effects through days to silking, ear height, ear length, days to maturity, number of kernel rows per ear, ear aspect, and 1000-kernel weight are the possible causes of positive correlation between ear diameter and grain yield. Therefore, these characteristics should be taken into account if selection is made through ear diameter. Similar conclusion was also drawn by Mogesse (2021).

Number of kernel rows per ear, ear height, ear length, 1000-kernel weight, and days to maturity exhibited positive direct effects and also had positive association with grain yield. Therefore, number of kernel rows per ear, ear height, ear length, 1000-kernel weight, and days to maturity are important traits contributing to total grain yield and could be used as reliable indicators in indirect selection for grain yield as they have positive relationship to yield.

Table 4. Estimate of phenotypic (below diagonal) and genotypic (above diagonal) correlations for yield and yield related traits in maize.

Traits	DA	DS	ASI	PS	ET	PA	PH	EH	DM	EA	EL	ED
DA	**1.000**	0.993**	-0.277	0.871**	0.494**	0.775**	-0.800**	-0.787**	-0.667**	0.615**	-0.811**	-0.682
DS	0.982**	**1.000**	-0.151	0.771**	0.479**	0.712**	-0.784**	-0.780**	-0.592**	0.605**	-0.848**	-0.596
ASI	-0.178	-0.065	**1.000**	-0.691**	-0.147	-0.162	-0.031	-0.046	-0.136	-0.103	-0.128	0.052
PS	0.598**	0.572**	-0.359	**1.000**	0.695**	0.593**	-0.768**	-0.788**	-0.784**	0.371	-0.461*	-0.429
ET	0.309	0.299	-0.130	0.665**	**1.000**	0.435*	-0.643**	-0.761**	-0.571**	0.442*	-0.494**	-0.340
PA	0.598**	0.617**	-0.020	0.527**	0.415*	**1.000**	-0.781**	-0.999**	-0.820**	0.744**	-0.789**	-0.864
PH	-0.661**	-0.680**	0.019	-0.628**	-0.543**	-0.715**	**1.000**	0.922**	0.695**	-0.424*	0.804**	0.464
EH	-0.641**	-0.657**	0.023	-0.578**	-0.556**	-0.798**	0.861**	**1.000**	0.677**	-0.680**	0.874**	0.664
DM	-0.582**	-0.605**	-0.115	-0.664**	-0.491**	-0.676**	0.697**	0.651**	**1.000**	-0.510**	0.586**	0.728
EA	0.515**	0.518**	-0.001	0.353	0.354	0.690**	-0.395*	-0.604**	-0.552**	**1.000**	-0.770**	-0.833
EL	-0.731**	-0.751**	-0.092	-0.417*	-0.414*	-0.724**	0.755**	0.794**	0.667**	-0.698**	**1.000**	0.619
ED	-0.540**	-0.541**	0.044	-0.372	-0.292	-0.721**	0.456*	0.592**	0.656**	-0.757**	0.605**	**1.000**
NKR	-0.665**	-0.693**	-0.131	-0.381*	-0.212	-0.799**	0.671**	0.693**	0.619**	-0.639**	0.871**	0.645
NKRE	-0.109	-0.115	0.022	-0.294	-0.316	-0.401*	0.270	0.215	0.392*	-0.492**	0.141	0.597
TKW	-0.590**	-0.599**	-0.038	-0.340	-0.363	-0.592**	0.598**	0.731**	0.556**	-0.556**	0.836**	0.554
GY	-0.504**	-0.455*	0.455*	-0.429*	-0.263	-0.330	0.108	0.242	0.217	-0.463*	0.270	0.370

GY: Grain yield, DA: Days to anthesis, ASI: Anthesis-silking interval, ED: Ear diameter, EH: Ear height, EL: Ear length, NKR: Number of kernels per row, PH: Pla to silking, TKW: Thousand kernels weight, DM: Days to maturity, PA: Plant aspect, EA: Ear aspect, PS: *Puccinia sorghi*, ET: *Turcicum* leaf blight caused by *Exs* probability, and *Significant at p<0.05 level of probability.

Table 5. Partitioning genotypic in to direct (diagonal bold) and indirect (off diagonal) effects of different traitson grain yield of maize.

Traits	DA	DS	PS	ET	PA	PH	EH	DM	EA	EL	ED
DA	**0.441**	-0.362	-0.016	0.327	0.097	0.476	-0.563	-0.517	-0.719	-0.196	0.205
DS	0.417	**-0.386**	-0.330	0.284	0.089	0.447	-0.602	-0.259	-0.307	-0.205	0.054
PS	0.998	-0.609	**-0.314**	0.865	0.074	0.417	-0.566	-0.607	-0.433	-0.111	0.759
ET	0.701	-0.421	-0.508	**0.683**	0.054	0.186	-0.311	-0.242	-0.316	-0.119	0.601
PA	0.666	-0.212	-0.172	0.167	**0.125**	0.441	-0.621	-0.435	-0.368	-0.191	0.529
PH	-0.754	0.656	0.777	-0.724	-0.097	**-0.845**	0.832	0.538	0.495	0.195	-0.820
EH	-0.707	0.239	0.324	-0.041	-0.125	-0.702	**0.466**	0.124	0.238	0.115	-0.174
DM	-0.296	0.006	0.191	-0.532	-0.102	-0.283	0.345	**0.638**	0.354	0.142	-0.287
EA	0.118	-0.050	-0.858	0.185	0.093	0.782	-0.350	-0.395	**-0.168**	-0.186	0.472
EL	-0.789	0.472	0.066	-0.324	-0.099	-0.484	0.136	0.254	0.499	**0.242**	-0.095
ED	-0.345	0.018	0.993	-0.911	-0.108	-0.856	0.318	0.564	0.972	0.150	**-0.769**
NKR	-0.537	0.364	0.061	-0.772	-0.110	-0.373	0.399	0.269	0.611	0.215	-0.195
NKRE	-0.439	0.468	0.452	-0.232	-0.048	-0.509	0.33	0.129	0.426	0.052	-0.021
TKW	-0.283	0.112	0.646	-0.193	-0.091	-0.172	0.406	0.231	0.371	0.199	-0.091

DA: Days to anthesis, ASI: Anthesis-silking interval, ED: Ear diameter, EH: Ear height, EL: Ear length, NKR: Number of kernels per row, PH: Plant height, NKRE: Thousand kernels weight, DM: Days to maturity, PA: Plant aspect, EA: Ear aspect, PS: *Puccinia sorghi*, and ET: *Turcicum* leaf blight caused by *Exserohilum turci*

Phenotypic Path Coefficient Analysis

The phenotypic path coefficient analysis was done to determine direct and indirect effects of secondary traits on grain yield. The results of phenotypic direct and indirect effects of secondary traits on grain yield are illustrated in Table 6. According to phenotypic path coefficient analysis number of kernel rows per ear, ear length, days to silking, *Turciccum* leaf blight, and 1000-kernel weight exhibited positive direct effects on grain yield; whereas days to anthesis, days to maturity, number of kernel per row, ear diameter, ear aspect, plant aspect plant height, ear height, and *Puccinia sorghi* showed negative direct effect on grain yield at phenotypic level, implying that selection for high yield can be carried out indirectly through yield components. Among all the highest positive direct effect on grain yield was exhibited by 1000-kernel weight followed by days to silking and ear length at phenotypic level. The results were in line with the earlier report of Rafiq et al. (2010). On the other hand, plant height had highest indirect effect on grain yield through days to anthesis (0.911) followed by ear height

(0.883) through days to anthesis and plant aspect (0.836) through number of kernels per row. Therefore, these traits could be considered as the main components for selection in further breeding process to improve grain yield. A negative direct effect was observed in plant height, plant aspect, ear height, ear aspect, days to maturity, days to anthesis, ear diameter, number of kernels per row, and *Puccinia sorghi* on grain yield. The results were in accordance with the previous report of Mogesse (2021). Moreover, plant height, ear height, days to maturity, ear diameter, and number of kernels per row exhibited positive phenotypic correlations with grain yield. The trait, days to 50% silking exhibited positive direct effects and significant negative association with grain yield at phenotypic level. Since the direct effects are positive and the correlation coefficients are significantly negative, the indirect causal factors which are having positive effects *viz.*, plant height, ear height, days to maturity, and number of kernels per row along with days to 50% silking are to be considered simultaneously during selection.

Table 6. Partitioning phenotypic in to direct (diagonal bold) and indirect (off diagonal) effects of different traits on grain yield of maize.

Traits	DA	DS	PS	ET	PA	PH	EH	DM	EA	EL	ED	NKR	NKRE	TKW	rg
DA	**-0.473**	0.511	-0.359	0.050	-0.472	0.166	0.248	0.177	-0.185	-0.084	0.060	0.352	-0.014	-0.481	-0.504
DS	-0.368	**0.596**	-0.247	0.048	-0.487	0.171	0.182	0.144	-0.166	-0.086	0.060	0.203	-0.015	-0.488	-0.455
PS	-0.825	0.473	**-0.432**	0.107	-0.416	0.158	0.341	0.202	-0.114	-0.048	0.041	0.398	-0.038	-0.277	-0.429
ET	-0.426	0.247	-0.287	**0.161**	-0.328	0.136	0.329	0.149	-0.114	-0.048	0.032	0.222	-0.041	-0.296	-0.263
PA	-0.823	0.510	-0.228	0.067	**-0.790**	0.179	0.471	0.205	-0.222	-0.083	0.080	0.836	-0.051	-0.482	-0.330
PH	0.911	-0.562	0.271	-0.088	0.564	**-0.251**	-0.509	-0.212	0.127	0.087	-0.051	-0.702	0.035	0.487	0.108
EH	0.883	-0.543	0.250	-0.090	0.630	-0.216	**-0.591**	-0.198	0.194	0.091	-0.066	-0.726	0.028	0.596	0.242
DM	0.803	-0.500	0.287	-0.079	0.534	-0.175	-0.385	**-0.304**	0.177	0.077	-0.073	-0.648	0.050	0.453	0.217
EA	-0.710	0.428	-0.153	0.057	-0.545	0.099	0.357	0.168	**-0.321**	-0.080	0.084	0.669	-0.063	-0.454	-0.463
EL	0.807	-0.621	0.280	-0.067	0.571	-0.190	-0.469	-0.203	0.224	**0.215**	-0.067	-0.911	0.018	0.682	0.270
ED	0.744	-0.447	0.161	-0.047	0.569	-0.114	-0.350	-0.199	0.243	0.070	**-0.111**	-0.675	0.077	0.451	0.370
NKR	0.461	-0.573	0.164	-0.034	0.286	-0.168	-0.410	-0.188	0.205	0.100	-0.072	**-0.047**	0.021	0.354	0.100
NKRE	0.151	-0.095	0.127	-0.051	0.317	-0.068	-0.127	-0.119	0.158	0.016	-0.066	-0.170	**0.128**	-0.019	0.182
TKW	0.813	-0.495	0.147	-0.059	0.467	-0.150	-0.432	-0.169	0.179	0.096	-0.062	-0.712	-0.003	**0.815**	0.436

DA: Days to anthesis, ASI: Anthesis-silking interval, ED: Ear diameter, EH: Ear height, EL: Ear length, NKR: Number of kernels per row, PH: Plant height, NKRE: Number of kernel rows per ear, DS: Days to silking, TKW: Thousand kernels weight, DM: Days to maturity, PA: Plant aspect, EA: Ear aspect, PS: *Puccinia sorghi*, and ET: *Turcicum* leaf blight caused by *Exserohilum turcicum* (Pass.).

Conclusion

Information on combining ability of parent and relationship among traits are required to increase the efficiency of selection in plant breeding programs. Therefore, the research aimed to quantify combining ability and the relationships between grain yield and yield contributing traits. According to combining ability analysis of variance L2 and L7 were found the best general combiner towards earliness. Likewise, parental line L3 identified as good general combiner to improve grain yield, 1000-kernel weight, ear diameter, and lateness in maturity. Therefore, L3 might be used in hybrid breeding program to obtain high yielding hybrids. Similarly, L2 was proved as the

best general combiner for number of kernel row per ear and 1000-kernel weight. L1 and L8 were found good general combiner for number of kernel row per ear. Therefore, based on SCA effects, it might be concluded that L1, L2, L3, and L8 could be used for obtaining high yielding hybrids. On the other hand, crosses L1×L6, L4×L6, L4×L8, and L5×L7 exhibited significant positive SCA effects for 1000-kernel weight. Similarly, the cross L5×L6 was good specific combiner for ear diameter, while L4×L7 for both number of kernels per row and 1000-kernel weight. Moreover, the crosses L1×L5, L3×L8, L6×L7, and L7×L8 showed significant negative SCA effect for days to maturity that depicted the contribution of genes for

earliness. According to correlation and path coefficient analysis, grain yield exhibit significant positive correlation with anthesis-silking interval and 1000-kernel weight at genotypic and phenotypic level. However, ear aspect, days to tasseling, days to silking, and *Puccinia sorghi* showed negative and significant correlations with grain yield. On the other hand, number of kernel rows per ear, 1000-kernel weight, and ear length exhibited positive direct effect on grain yield at genotypic and phenotypic levels. Thus, these traits can be considered as the main components for selection in hybrid breeding program with a view to obtaining high yielding hybrids.

Conflict of Interest

The authors declare that they have no conflict of interest.

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