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Combining Ability of Indonesian Tropical Maize in Two Different Seasons

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ABSTRACT

Testing an inbred cross for hybrid development requires a proper test cross method. The diallel is one crossing method to find out the magnitude of inbred combining ability, both general general (GCA) and specific combining ability (SCA) and specific combining ability, that is useful in hybrid development. The objective of the study is to determine the GCA, SCA and heterosis of 6 inbred lines in two seasons. All the inbreds were crossed in diallel design and further evaluated for their combining ability and genetic ratio following the respective methods of Griffing and Baker. The results revealed that GCA, SCA and Reciprocal (REC.) were influenced by planting seasons for almost all yield and yield-related traits. Non-additive gene action was more important in controlling ear length, ear row number, shelled ear weight and yield. The best GCA for yield trait was detected on inbreds G2 and G5. The conclusion from the interpretation of both SCA and REC. is that the inbred crosses of G1 x G6, G2 x G5, G4 x G6, and G5 x G6 have the best yields followed by high heterosis values.

INTRODUCTION

Maize is a valuable commodity and crop in Indonesia. It is a food item and highly demanded for animal feed due to its carbohydrate and protein contents (Rouf Shah, Prasad, & Kumar, 2016). To support food and feed availabilities, cultivar development that has not only high productivity, yet highly adapted as well is considered important. One solution for this is the development of a hybrid variety with higher yields and broader environment adaptability (Kinfe et al., 2017). The first step to achieve these highly desirable characteristics of hybrid varieties is the development of promising inbred lines.

At a certain generation, inbred lines will become less vigorous, yet will become more vigorous due to inbreeding depression, leading to high uniformity in the F1 generation of the hybrid. According to Luckett & Halloran (2003), the advantage of maize hybrid variety is that the parents are homozygotes and usually stable each year. The F1 gathered from crossing is, thus relatively uniform with predictable performance. The advantage of hybrids is also linked to the heterosis phenomenonin which the performance of hybrid varieties exceeds from the average value of both parents. As such, testing for combining ability and heterosis is required to ensure the qualification of an inbred as a hybrid parent. The test cross is a useful and powerful instrument for this purpose. The most popular and frequently employed test cross method for hybrid development and evaluation of inbred lines is the complete diallel cross method. This method was proposed by Griffing (1956) and has been widely employed by many researchers to evaluate the potentials of inbred lines as hybrid parents under complex mating pairs. This method can demonstrate the inbred combining ability, as its general combining ability (GCA) and specific combining ability (SCA). This will allow accurate forecasts of the fates of inbred lines in the future (Fasahat, Rajabi, Rad, & Derera, 2016).

In the case of the hybrid variety, breeders might expect the presence of the specific combining ability as it becomes the main feature of non-additive gene action that results in high heterosis.

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GCA possesses a direct relationship with additive gene action, while SCA is related to the role of non-additive genes (particularly dominant ones) that are deviations from the additive model. Therefore, the size of the value in a certain analysis of variety often becomes a reflection and indicator of gene action that is directly relevant to the inheritance of a trait (Fasahat, Rajabi, Rad, & Derera, 2016; Tripathi, Shrestha, & Gurung, 2016). Nevertheless, the challenge of making decisions to select a promising inbred based on SCA is the proper environment. Sometimes, the proportion of SCA and GCA might change in different environment conditions. Thus, testing the combining ability in different environments will enrich insights for inbred selection based on SCA, which will allow the true SCA potential of the inbred to be properly recognized. The process of finding out the genetic effects of a line does not require testing in all environmental conditions, but can be done through testing of planting with different time gaps or planting in places with different elevations (Coelho et al., 2020; Murtadha, Ariyo, & Alghamdi, 2018).

Presently, researchers of PT. Golden Indonesia Seed have successfully developed potential inbred lines from crosses of tropical Indonesian maize varieties and created 6 promising candidates based on the yield trait. The performance of these inbred has not been evaluated and thus, it becomes necessary to conduct further research to find out the inbred potential. The objective of the study is to determine the pattern and effect of general combining ability (GCA) and specific combining ability (SCA) in different seasons.

MATERIALS AND METHODS

The research has two consecutive experiments. The first part of the research was to develop the hybrid crosses and the second part was for progeny evaluation. The activity of inbred crosses was conducted from February-June 2018, while the second part was conducted in the early wet season (November 2018-March 2019) and the middle of the wet season (January-May 2019). The utilized genetic materials in this research were developed from the Indonesian maize variety, comprised of the 6 inbreds of NB-10 (G1), NB-11 (G2), NB-12 (G3), YG-1 (G4), PG-1 (G5), and PP-2 (G6) and their 30 hybrid combinations (including reciprocal crosses). All the genetic materials were evaluated by the randomized block design (RBD) with two replications in a maize belt located in Malang Regency (± 600 masl), Indonesia.

The distance of the planting point was arranged in 70 cm x 20 cm, and each plot contained 100 plants. The observed characteristics included ear length (cm), ear diameter (cm), number of ears in a row, moisture content at harvest (%), weight of 100 seeds (g), shelled ear weight (g), shelling (%) and yield (t/ha). All the collected data were subjected to analysis of variance and combining ability analysis, following the model suggested by Owolade et al. (2006):

$$Y_{ijkl} = \mu+g_i+g_j+s_{ij}+r_{ij}+l_k+b(l)l_k+gl_{ik}+gl_{jk}+sl_{ijk}+rl_{ijk}+e_{ijkl} \ldots\ldots 1)$$

Where: Y_{ijkl} is the observation value in each unit, μ is the population mean value, g_i is the general combining ability (GCA) for parent *i*, g_j is the GCA for parent *j*, s_{ij} is the specific combining ability (SCA) effect for parent *i* and parent *j*, r_{ij} is the reciprocal (REC.) effect for parent *i* and parent *j*, l_k is the seasonal effect from season *k*, $b(l)_{lk}$ is the replication effect *l* within season *k*, gl_{ik} is the interaction effect of GCA x season of parent *i* on location *k*, gl_{jk} is the interaction effect of GCA x location of parent *j* on location *k*, sl_{ijk} is the interaction effect of SCA x location of parent *ij* on location *k*, rl_{ijk} is the interaction effect of SCA x location of parent *ji* on location *k*, and e_{ijkl} is the error.

To account for the type of genetic control of each characteristic, genetic ratio analysis (GRA) as suggested by Baker (1978) was utilized through the following equation:

$$GRA = 2MS_{GCA} / (MS_{GCA}+MS_{SCA}) \ldots\ldots 2)$$

If the value of calculated genetic ratio is > 1, the additive genetic control is more important. If the value of calculated genetic ratio is < 1, the non-additive genetic control is more important in controlling the observed main characteristics. Combined analysis to estimate GCA and SCA across seasons was carried out using AGD-R (Analysis of Genetic Designs with R for Windows) Software version 5.0 Version 13.0 developed by CIMMYT (2018).

RESULTS AND DISCUSSION

Combining Ability Analysis

The results of variance analysis of combining ability are presented in Table 1. The components of combining ability comprise of the GCA, SCA, REC. and the effects of their interactions toward the environment. The results indicated that GCA and SCA were significant for all observed parameters while, the effects of REC. were not significant in two parameters, i.e. ED and MC. Similarly, the interaction effect of GCA x E revealed 5 characteristics with significant effects, i.e. EL, TF, FEW, HSW, and SHL. The results of SCA x E were slightly different, in that significant variance was detected at EL, ED, ERN, FEW, SEW, SCA, and Yield. Significant effect of REC. x E was found only in EL, SEW, SHL, and Yield.

The interactions of the parts of combining ability x environment were not consistent for all studied characteristics. As an example, deviating results found for the ED, ERN, SEW, MC, and yield characteristics, showed significant variation based on only on GCA but showed opposite results when analyzed against the environment. Similar patterns were also observed on the characteristics of TF, HSW, and MC for SCA, and TF, ERN, and MC for REC. This finding demonstrated that there is a poptentially genetic instability for these characteristics and the proper environment for genetic analysis should be considered (Emami, Nemati, Azizi, & Mobli, 2018).

Interaction between genotype x environments has recently become the most popular and common concept to analyze the response of genotype toward various environments that finally produce a specific plant phenotype. This is not surprising, as this will become one of the strongest determinant factors for the breeder to find out the best genotype for variety development. This approach as the strategy in plant breeding had been employed by various researchers (Fan et al., 2016; Fan et al., 2018; Nyaligwa, Shimelis, Laing, & Mwadzingeni, 2017), and once the interaction was detected, the breeder can determine the favorable environment for breeding activity based on their objectives.

The GRA estimated from the mean value of combining ability is included in Table 1. The lowest GRA value was recorded for MC, whereas the highest GRA values were recorded for TF and SHL with values of 3.80 and 3.84 respectively. Based on the listed GRA, 4 characteristics, i.e. TF, FEW, HSW, and SHL, were found to have GRA values greater than 1, while the others had values less than 1. The genetic control of all studied traits in this research was based on Machikowa, Saetang, & Funpeng (2011) and Murtadha, Ariyo, & Alghamdi (2018) who regarded the genetic control as additive if the GRA is greater than 1 and non-additive if the GRA is less than 1. Therefore, the results from the analysis of all the studied characteristics show that they are predominantly controlled by additive and non-additive gene action. This finding implies that all the inbreds can be programmed for hybrid variety and can properly inherit traits to their progeny. Among all the studied characteristics, the GRA values for TF, FEW, HSW, and SHL indicated greater additive inheritance. Therefore, the consideration of hybrid vigor for hybrid development should be excluded from these characteristics and more focus on EL, ED, ERN, HSW, MC, SHL, and Yield (Emami, Nemati, Azizi, & Mobli, 2018). This finding from the data is rougly similar with the report of Kashif & Khaliq (2003).

General Combining Ability

The analysis of GCA in 6 inbreds is presented in Table 2. The best GCA effect indicates that the inheritance of positive traits is spread properly in all mating combinations. Based on the magnitude of GCA, the best GCA for EL was observed for Inbred 5 and 6, while the best GCA for ED, ERN, and MC was observed for Inbred 3 and 4. Inbred 2 accumulated desirable GCA only for TF, whereas the others had undesirable GCA. For FEW, only Inbred 3 had the best GCA, while for HSW, only Inbred G5 had the best GCA. For SHL, Inbred 1 and 3 are the best parents, whereas the best inbred GCA for Yield was Inbred G2 and G5.

As demonstrated by the GCA value, inbreds G2 and G5 tended to show considerable GCA for Yield. However, the positive GCA on Yield was not totally supported by other characteristics in the same direction, and in fact, some were in the opposite direction (Kanyamasoro, Karungi, ASEA, & Gibson, 2012). Similar results were also confirmed by Fan et al. (2016), Kumar & Bharathi (1970) and Murtadha, Ariyo, & Alghamdi (2018). The most relevant yield-related traits that had the same linear direction with the finding were observed only ERN and SEW for G2 and HSW for G5. The findings showed that yield improvement on the crosses that accompanied G2 and G5 were due to favorable complementation of alleles that additively improved the number of ears and ear size and ultimately increased genotype productivity (Sugiharto, Nugraha, Waluyo, & Ardiarini, 2018; Sugiharto, Nugraha, Waluyo, Ardiarini, & Azrai, 2018).

Table 1. Mean value and GRA of combined variance analysis based on Griffing 1

Source of Variation	EL	TF	ED	ERN	FEW	SEW	HSW	MC	SHL	Yield
GCA	10.10 **	2.68 **	0.59 **	20.68 **	7,939.23 **	1,592.95 **	54.8 **	7.12 **	143.55 **	4.42 **
SCA	14.91 **	0.93 **	0.12 **	2.97 **	5,604.95 **	3,228.99 **	60.75 **	4.47 *	52.12 **	20.11 **
REC.	2.61 **	0.76 *	0.05	3.96 **	883.06	1,217.38 **	15.63	5.17 **	19.98	2.02 **
GCA x E	2.48 *	1.67 **	0.04	1.76	5,472.97 **	751.15	50.09 *	0.06	83.4 **	0.92
SCA x E	3.10 **	0.44	0.07 *	3.26 **	2,961.24 **	1,143.20 **	17.26	0.16	21.74 *	1.72 **
REC. x E	2.76 **	0.53	0.05	1.06	1,346.63	1,469.01 **	26.24	0.19	40.48 **	2.28 **
Residual	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53
GRA	0.80	3.80	0.57	0.54	1.85	0.66	2.90	0.38	3.84	0.53

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling percentage (%)

Table 2. GCA effect of 6 inbreds in two growing seasons

Inbreds	EL	TF	ED	ERN	FEW	SEW	HSW	MC	SHL	Yield
G1	-0.31	2.35	-0.06	-0.87 **	-19.61 **	-2.28	1.25	-0.17	1.54 *	-0.15
G2	-0.58 **	-11.00 **	0.05	0.45 *	6.76	7.31 *	-1.09	0.52 *	0.62	0.38 **
G3	0.01	-1.01	0.13 **	0.54 *	12.10 *	0.79	-0.33	-0.23	1.21 *	0.11
G4	-0.20	4.89 **	0.08 *	0.73 **	4.52	-5.06	-0.68	-0.53 *	-1.81 *	-0.41 **
G5	0.50 *	0.11	-0.02	-0.45 *	8.67	5.98	1.43 *	0.31	0.99	0.27 *
G6	0.58 **	4.67 **	-0.17 **	-0.40 *	-12.44 *	-6.73 *	-0.59	0.11	-2.55 **	-0.19
SE	0.13	1.10	0.02	0.14	3.92	2.41	0.52	0.19	0.45	0.09

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling percentage (%)

Table 3. SCA and reciprocal effects of 15 hybrid cross combinations from 6 inbreds

Inbred Crosses	EL		TF		ED		ERN		FEW	
	SCA	REC	SCA	REC	SCA	REC	SCA	REC	SCA	REC
G1 x G2	0.99 **	-0.19	0.07	0.56 **	0.05	0.00	-0.07	-0.15	17.94	-0.24
G1 x G3	-3.34 **	0.25	0.55 *	-0.25	0.02	-0.02	0.05	-0.35	-22.12 *	10.92
G1 x G4	-0.31	-0.22	-0.05	0.24	0.01	-0.14 **	-0.10	-0.80 **	4.98	4.89
G1 x G5	1.08 **	-0.14	0.00	-0.27	-0.06	-0.04	-0.23	-0.04	5.13	9.20
G1 x G6	-2.82 **	0.21	-0.34	-0.36 *	0.10	0.06	0.60	0.11	31.43 **	10.66
G2 x G3	1.20 **	-1.04 **	0.09	-0.46 *	-0.02	0.08	0.14	1.66 **	-0.76	-1.05
G2 x G4	0.93 **	-0.10	0.66 **	-0.13	-0.12	-0.05	0.47	0.21	-3.88	3.76
G2 x G5	-3.92 **	-1.63 **	-0.36	0.01	0.09	0.01	-0.99 **	-0.80 **	12.40	-1.81
G2 x G6	0.16	0.23	-0.11	0.14	0.06	0.05	0.20	0.29	-6.74	0.19
G3 x G4	1.00 **	-0.15	-0.20	0.26	0.08	-0.01	0.49	0.30	24.65 *	-4.25
G3 x G5	0.49	0.56 *	-0.06	0.09	-0.04	0.10 *	-0.07	0.25	13.12	15.50 *
G3 x G6	-1.92 **	0.56 *	-0.33	-0.03	0.10	0.12 *	0.45	0.88 **	22.36 *	14.38 *
G4 x G5	0.07	-0.44	0.20	0.28	0.00	0.00	0.18	-0.05	-10.83	-12.67
G4 x G6	0.12	0.04	-0.05	0.36 *	0.15 *	0.05	0.29	0.06	25.13 *	2.81
G5 x G6	0.26	0.19	0.05	-0.49 **	0.06	0.18 **	-0.01	1.48 **	10.90	25.74 **
SE	0.42	0.19	0.26	0.12	0.08	0.03	0.43	0.19	12.38	5.54

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling percentage (%)

Table 4. SCA and reciprocal effects of 15 hybrid cross combinations from 6 inbreds (continue)

Inbred Crosses	SEW		HSW		MC		SHL		Yield	
	SCA	REC	SCA	REC	SCA	REC	SCA	REC	SCA	REC
G1 x G2	23.90 **	-9.67 *	4.20 **	-2.52 *	0.43	0.08	2.94 *	-0.54	1.08 **	-0.28
G1 x G3	-92.26 **	1.61	-0.28	-0.03	0.14	-0.71 *	-8.35 **	-1.11	0.50 *	0.10
G1 x G4	10.23	-11.47 *	-0.44	1.92 *	0.71	1.07 *	-1.04	-3.16 **	0.11	-0.49 *
G1 x G5	-3.58	-0.95	1.04	1.97 *	0.23	0.10	-0.38	-0.52	0.18	0.02
G1 x G6	-59.31 **	1.27	4.38 **	0.39	-1.37 **	-0.26	3.35 *	3.18 **	0.68 **	-0.36 *
G2 x G3	19.62 **	9.39 *	-1.72	1.33	0.59	-0.08	1.30	2.63 **	0.04	0.36 *
G2 x G4	27.31 **	-9.57 *	-0.58	-1.74	0.16	0.79 *	1.33	-0.72	0.61 *	-0.51 *
G2 x G5	-79.50 **	-23.73 **	-0.17	-1.87	-0.19	0.30	0.28	-0.52	1.84 **	-0.30
G2 x G6	4.09	-9.61 *	-0.77	-0.79	-0.43	0.23	-0.26	-0.67	0.35	-0.47 *
G3 x G4	4.93	-9.28 *	4.23 **	0.15	-1.14 *	-0.91 *	-1.84	-0.28	0.68 **	-0.25
G3 x G5	5.66	26.73 **	0.21	0.67	0.60	-0.76 *	0.06	-0.51	0.18	1.18 **
G3 x G6	-77.99 **	13.32 *	-2.26	1.25	0.48	1.13 **	1.34	1.60	0.83 **	0.71 **
G4 x G5	2.81	-13.32 *	-1.95	1.95 *	-0.66	-1.04 *	2.66 *	-1.64 *	0.29	-0.37 *
G4 x G6	20.41 **	-5.68	0.61	0.02	-0.37	-0.77 *	-1.41	1.31	1.16 **	-0.35 *
G5 x G6	13.80 *	-5.42	0.31	-0.74	0.86	-1.68 **	-1.13	0.32	0.62 **	-0.66 **
SE	7.63	3.41	1.65	0.74	0.61	0.27	1.42	0.63	0.29	0.13

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling percentage (%)

Specific Combining Ability and Reciprocal Effect

The SCA and reciprocal effects of 6 inbreds-crosses is displayed in Table 3 and Table 4. The SCA illustrates the performance of inbreds in specific mating crosses, while the reciprocal effect represents the relative performance of a reciprocal mating cross toward its direct cross. Based on the analysis, the crosses of G1 x G5 and G2 x G3 was found to possess the best SCA for EL, while the cross of G1 x G6 was the best for TF and ERN. For the characteristics of ED and FEW, inbred crosses G1 x G6 and G4 x G6 were found to be desirable as the best mating pairs. More varied SCA values were found for SEW and Yield, and the best inbred crosses for these characteristics were found on G2 x G4 and G2 x G5. For HSW and MC, the best mating pairs was observed on G1 x G6 and G3 x G4, whereas for SHL, only the G1 x G6 had the best SCA.

In the perspective of hybrids, the most considerable trait that should become the main consideration is yield. In this study, several inbred cross combinations were found to have the most desirable SCA, i.e. G1 x G2, G1 x G6, G2 x G5, G3 x G4, G3 x G6, G4 x G6 and G5 x G6. These have the indication that non-additive gene action highly contributed to the inheritance of the yield trait on these cross combinations (Bahari, Rafii, Saleh, & Latif, 2012). Therefore, a successful hybrid can be developed from these crosses by considering the mean value on yield and other yield-related traits (Sugiharto, Nugraha, Waluyo, Ardiarini, & Azrai, 2018). The analysis revealed that good SCA in yield tended to be linear with SCA of yield-related traits. This was identified in the selected inbred cross combinations, which also showed desirable SCA for FEW and SEW. Similar findings were reported by Choudhary, Marker, Battacharjee, & Ramnath (2018), El-Badawy (2013) and Rani, Nirala, & Acharya (2018). The genetic patterns of inbred crosses that showed good SCA were established. Based on the background of combining ability, it was found that inbred cross patterns of good GCA x Poor GCA and Poor GCA x Poor GCA resulted in additive x non-additive and non-additive x non-additive patterns, respectively. Uniquely, one considerable inbred cross combination with the additive x additive genetic pattern was also discovered. However, this type of genetic complementation usually resulted in a non-functional value for yield, compared to additive x non-additive or non-additive x non-additive allelic complementation. This finding is supported by the work of Katkar, Sridevi, Salimath, & Patil (2012).

Determining the best inbred crosses based on reciprocal effect might be different with the determination of inbred crosses with the best SCA. Based on reciprocal effect, the best inbred crosses tend to have inverse values toward SCA. In all inbred combination with reciprocal crossing, it was found that G1 x G4 had the best reciprocal effect for ED and ERN. For the characteristics of TF and ED, different inbred crosses were found as the best mating partners. The best mating partners with a good reciprocal effect were found to be G1 x G2 and G2 x G3 for TF, whereas for ED only G1 x G4 was as such. None of the available inbred crosses had a desirable reciprocal effect for FEW. For the characteristic of SEW, two crosses were found to have a considerable reciprocal effect, i.e. G2 x G5 and G4 x G5, while for G1 x G2 was observed for HSW. The cross of G1 x G4 seemed to have a consistent reciprocal effect for MC, SHL, and Yield. Other inbred crosses that could be considered regarding MC, SHL, and Yield were G3 x G6, G4 x G5, and G5 x G6 respectively.

REC. gives complementary information in addition to SCA regarding breeding activity. The combination of information from SCA and REC. will be more valuable in determining the best inbred cross for further variety development. If positive SCA values are desired, interpreting REC. simultaneously with SCA should be directed toward negative values since it compares itself with direct inbred cross. Therefore, with the negative value of REC., it can be interpreted that reciprocal crosses show better performance than direct crosses. In this research, several cross combinations with good SCA also had considerable REC., except for G1 x G2, G2 x G5, and G3 x G4. This finding demonstrated that there was no maternal effect control in inheriting a positive yield trait in these inbred crosses. Conversely, G1 x G6, G4 x G6, and G5 x G6 were found to be desirable reciprocal crosses, indicating that switching the mating pairs on crossing combinations can increase the chance of cytoplasm gene expression that supports nuclear gene effect to produce better performance (Bucheyeki, Tongoona, Derera, & Nchimbi-Msolla, 2017; Zhang, Fan, Yao, Piepho, & Kang, 2016).

Heterosis

The results of heterosis analysis are presented in Table 5 and Table 6. The best heterosis (MPH and HPH) for EL is positive, while TP is negative. Heterosis of ear diameter (ED) character shows a relatively positive value and combinatiion of pairs G5 x G3, G6 x G4 and G6 x G5 which have a significantly different SCA effect, also had significant variation on MPH (Bhusal & Lal, 2020). The same results were found in the research of Kamara, El-Degwy, & Koyama (2014). The positive values of MPH and HPH are significantly different, giving an explanation that there are dominant and over-dominant that contribute to desirabe F1 (Acquaah, 2012). A positive values for the heterosis indicated that the trait was under the control of the partial dominance genes of the early pure line, and a negative value for the heterosis which explains the control of the genes of over dominance of the higher pure line on the trait in these crosses (Abd-allah Ramadan, Mukhlif, & Abdulhamed, 2021).

Table 5. Heterosis of 15 hybrid combinations from 6 inbreds

Inbred Crosses	EL		TF		ED		ERN		FEW	
	MPH	HPH	MPH	HPH	MPH	HPH	MPH	HPH	MPH	HPH
G1 x G2	21.78 **	12.35 *	25.01	-23.63	3.44	0.05	-3.52	-11.71 *	80.05 **	70.5 **
G1 x G3	13.34 *	10.67	73.45 *	71.92 *	3.00	-1.33	0.78	-4.23	80.59 **	70.33 **
G1 x G4	19.86 **	11.24 *	66.09	-7.31	0.02	-3.22	-2.35	-7.54	90.64 **	84.05 **
G1 x G5	10.34 *	6.7	-13.61	-17.86	-0.01	-1.98	-6.37	-11.58 *	78.37 **	72.07 **
G1 x G6	10.52 *	4.92	-51.37	-58.05	11.51 **	4.66	10.19	6.91	104.74 **	90.44 **
G2 x G1	24.43 **	14.79 *	-20.89	-51.67	3.33	-0.05	-1.55	-9.91 *	95.58 **	85.21 **
G2 x G3	21.86 **	14.96 **	-18.42	-50	3.12	2.09	10.78	6.46	95.58 **	64.67 **
G2 x G4	35.14 **	34.25 **	368.76 **	257.14 *	-1.63	-1.67	7.11	3.30	93.39 **	77.16 **
G2 x G5	6.59 **	-4.64	-23.81	-54.29 *	3.01	1.61	-15.84 *	-18.62 **	96.74 **	92.99 **
G2 x G6	17.26 **	3.15	-13.86	-50 **	8.70 **	-1.09	7.08	-4.65	77.51 **	57.01 **
G3 x G1	10.12 *	7.54	59.86 *	58.45 *	3.69	-0.66	5.58	0.33	71.68 **	61.92 **
G3 x G2	36.46 **	28.72 **	78.95	9.68	-0.18	-1.17	-7.50	-11.11	61.33 **	60.63 **
G3 x G4	28.9 **	22.35 **	41.35	-20.97	4.13	3.06	12.93 *	12.50 *	89.85 **	73.24 **
G3 x G5	24.51 **	17.67 **	-1.52	-7.14	3.11	0.71	0.97	0.32	103.6 **	98.89 **
G3 x G6	17.08 **	8.67	-38.26	-47.13 *	11.97 **	0.97	18.52 *	9.45	117.71 **	91.85 **
G4 x G1	22.87 **	14.03 *	12.15	-37.41	6.11	2.67	8.57	2.80	99.66 **	92.76 **
G4 x G2	36.62 **	35.73 **	467.24 **	332.18 *	0.38	0.35	4.48	0.77	110.39 **	92.73 **
G4 x G3	30.99 **	24.34 **	-17.79	-54.03	4.60	3.52	9.03 *	8.62 *	107.61 **	89.45 **
G4 x G5	19.49 **	7.53	71.12	-5.48	1.65	0.30	1.59	1.32	81 **	68.79 **
G4 x G6	22.68 **	8.53	17.67	-36.21 *	11.55 **	1.53	12.59 *	3.61	118.26 **	109.98 **
G5 x G1	12.02 *	8.32	18.7	12.86	1.63	-0.37	-5.86	-11.09 *	77.4 **	71.13 **
G5 x G2	28.08 **	14.58	-26.19	-55.71 *	2.69	1.30	-5.90 *	-9.01 **	137.57 **	133.04 **
G5 x G3	17.5 **	11.05 **	-12.12	-17.14	-1.18	-3.47	-2.27	-2.89	47.59 **	44.17 **
G5 x G4	25.2 **	12.67	12.5	-37.86	1.72	0.38	2.20	-2.89	100.87 **	87.32 **
G5 x G6	12.22 *	10.09	-45.86	-51.15	11.56 **	2.78	11.73	2.57	104.5 **	83.99 **
G6 x G1	8.06 *	2.58	-12.73	-24.71	8.42 **	1.76	8.49	5.27	121.08 **	105.63 **
G6 x G2	14.36 **	0.6	-36.63	-63.22 **	6.47 **	-3.13	3.20	-8.11	96.38 **	73.7 **
G6 x G3	10.21 **	2.3	-35.57	-44.83 *	6.54 **	-3.93	6.17 *	-8.11	96.81 **	73.43 **
G6 x G4	22.2 **	8.1	-42.76	-68.97 *	9.26 **	-0.56	11.71 *	2.80	142.79 **	133.58 **
G6 x G5	10.05 *	7.96	4.46	-5.75	3.43 **	-4.71	-8.93	-16.40	117.29 **	95.5 **

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling percentage (%); MPH: Mid Parent Heterosis, HPH: high parent heterosis

Table 6. Heterosis of 15 hybrid combinations from 6 inbreds (continue)

Inbred Crosses	SEW				HSW				MC				SHL				Yield			
	MPH		HPH		MPH		HPH		MPH		HPH		MPH		HPH		MPH		HPH	
G1 x G2	98.72	**	95.98	**	23.96	**	17.09	*	3.23		1.41		10.09	**	3.49		101.38	**	94.06	**
G1 x G3	71.84	**	59.03	**	14.74		4.63		-0.66		-1.89		-4.20		-6.51		65.83	**	51.92	**
G1 x G4	74.53	**	61.47	**	24.90		18.12		4.52		3.12		-8.37		-11.58		62.47	**	46.34	**
G1 x G5	75.35	**	68.06	**	23.27		6.39		3.12		2.6		-1.17		-2.05		70.90	**	65.38	**
G1 x G6	127.23	**	96.92	**	37.73	**	30.71	**	-7.33	*	-9.9	**	11.82		4.10		96.47	**	68.56	**
G2 x G1	118.71	**	115.68	**	42.24	**	34.35	*	2.59		0.78		11.62	**	4.92		115.21	**	107.39	**
G2 x G3	77.43	**	62.11	**	0.59		-3.10		4.29		1.21		6.52		-2.13		79.23	**	58.77	**
G2 x G4	107.25	**	94.25	**	-3.07		-3.21		2.13		1.69		6.77		3.90		97.62	**	84.19	**
G2 x G5	109.55	**	98.17	**	-5.64		-14.29		3.05		1.73		6.74		-0.51		122.57	**	107.82	**
G2 x G6	99.36	**	74.85	**	0.19		-0.31		-1.21		-2.25		11.95	**	10.80	*	107.96	**	84.26	**
G3 x G1	68.82	**	56.23	**	14.94		4.81		4.86		3.56		-1.34		-3.72		61.43	**	47.88	**
G3 x G2	59.61	**	45.83	**	-8.15		-11.52		4.92		1.82		-0.70		-8.76		62.84	**	44.25	**
G3 x G4	87.96	**	61.98	**	17.84	*	13.37		-9.03		-11.35	*	-1.03		-6.71		71.94	**	43.30	**
G3 x G5	90.22	**	83.38	**	2.08		-3.97		2.31		0.55		-6.03		-7.48		86.08	**	75.81	**
G3 x G6	114.48	**	74.14	**	0.70		-3.47		5.76		1.59		0.28		-8.72	**	113.01	**	69.96	**
G4 x G1	99.8	**	84.85	**	10.98		4.96		-3.55		-4.85		0.33		-3.18		88.63	**	69.90	**
G4 x G2	128.66	**	114.32	**	8.84		8.69		-3.69		-4.11		8.87		5.94		126.07	**	110.71	**
G4 x G3	106.65	**	78.08	**	16.88	*	12.44		-2.06		-4.56	*	-0.28		-6.01		84.15	**	53.48	**
G4 x G5	74.64	**	55.39	**	2.04		-7.43		-7.28		-8.07		-3.26		-7.45		75.26	**	53.31	**
G4 x G6	129.46	**	113.65	**	9.34		8.94		-8.07		-9.42	*	4.81		0.97		129.54	**	117.31	**
G5 x G1	77.21	**	69.84	**	10.52		-4.62		2.38		1.88		0.21		-0.68		70.02	**	64.53	**
G5 x G2	156.43	**	142.5	**	5.89		-3.82		0.8		-0.49		8.20		0.86		137.26	**	121.53	**
G5 x G3	42.13	**	37.03	**	-1.90		-7.72		8.14		6.28		-4.71		-6.18		35.77	**	28.28	**
G5 x G4	102.6	**	80.27	**	-9.98		-18.33		0.57		-0.29		1.20		-3.18		94.37	**	70.03	**
G5 x G6	101.9	**	68.81	**	1.33		-8.38		-3.00		-5.23		0.28		-7.41		90.30	**	58.87	**
G6 x G1	124.25	**	94.33	**	34.90	**	28.03	**	-5.44	*	-8.06	**	2.75		-4.34		116.52	**	85.77	**
G6 x G2	122.34	**	95	**	5.65		5.12		-2.87		-3.88		13.99	**	12.82	*	135.68	**	108.82	**
G6 x G3	86.04	**	51.05	**	-7.57		-11.39		-2.75		-6.59		-4.17		-12.77	**	77.32	**	41.48	**
G6 x G4	144.08	**	127.26	**	9.18		8.78		-2.43		-3.86	*	0.92		-2.78		151.58	**	138.17	**
G6 x G5	114.01	**	78.93	**	5.93		-4.22		9.44		6.92		-0.62		-8.24		126.33	**	88.95	**

Remarks: * significant at P-0.05, ** significant at P-0.01; FEW: Fresh Ear Weight, HSW: Hundred Seed Weight, ED: Ear Diameter, ERN: Ear Row Number, EL: Ear Length, MC: Moisture Content, TF: Tip Filling, SEW: Shelled Ear Wight, SHL: Shelling Percentage (%); MPH: Mid Parent Heterosis, HPH: High Parent Heterosis

The crosses with positive MPH and HPH on ERN also have different values on ED and positive values for MPH. The cross G4 x G6 shows FEW value in GCA this was the only significantly different and followed by a combined heterosis value above 100%. Meanwhile, some crosses only show that the value of HPH in MC is influenced by the environment, such as G1 x G6, G3 x G4, G4 x G6 and G6 x G1. For the Shelling percentage character (SHL), the heterosis appearance was found only on G2 x G6 and the recipient which showed that the MPH and HPH results were significantly different. Positive value for mid parent heterosis is associated with dominant influence, while a positive value for best or high parent heterosis shows the over-dominant influence in the expression of a particular trait (Drinic et al., 2015). Yield characters, or result accumulation of all characters, there are several pairs with heterosis values above 100%, but only the cross G1 x G2, G1 x G6, G2 x G5, G4 x G6 and G5 x G6 have a significantly different combined SCA effect. The specific combining ability of maize yield characters is only an option which ultimately depends on the heterozygosity of the gene for manifestation (Mukherjee, 1995). If the SCA value is good and shows a good heterosis value, then the cross pairs can be used as candidates in the formation of hybrid varieties.

CONCLUSION

GCA, SCA, and REC. are influenced by planting seasons for almost all yield and yield-related traits. Determining the best season for genetic analysis became useful to find out the real representation of the genetic potential of each inbred line. The best GCA for the yield trait was found in G2 and G5, and these could be considered as test lines for further breeding programs in yield improvement. Based on SCA and REC. values, the inbred crosses of G1 x G6, G4 x G6, and G5 x G6 have the best yields followed by high heterosis values. Therefore, these inbred crosses can be utilized and considered as hybrid varieties and for further genetic studies.

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