





Tillering Potential, Yield, and Yield Components in Super-Sweet Maize: Gene Action, Combining Ability, and Heterosis Analysis (*Zea mays* L. var *saccharata*)

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ABSTRACT

The success of hybrid breeding programs across the world depends on an understanding of the impacts of gene activity, combining ability, and heterosis on desired characteristics. This project's major goals included the identification of better-inbred lines and hybrids based on combining prowess and heterosis effects in genotypes of super-sweet maize (*Zea mays* L. *Saccharata*) and the research of genetic factors and gene activity influencing agronomic attributes. In 2021, three inbred lines (as female parents) were crossed with three testers (as male parents) using the line-to-tester mating design. In a Randomized Complete Block Design (RCBD) with three replications in 2022, nine F1 hybrids with six parental lines were assessed for thirteen agronomic variables, including tillering potential (TP), conservable grain yield (CGY), and yield components. The findings showed that for all the attributes under study, the genotype-related mean squares and their distributions to parents crosses, and parents' crosses were significant ($P < 0.05$). Numerous agronomic characteristics, including TP, CGY, plant height, and tassel length, were considerably influenced by additive gene action, while others were influenced by non-additive gene action, according to the ratio of $2GCA / 2SCA$ and narrow-sense heritability (H_{ns2}). For CGY and TP characteristics, the *SSBas-1* and *SSChal-5* combination showed positive specific combining ability (SCA) benefits. Most hybrids also showed positive heterosis and SCA effects, which explained the heterosis in the hybrid's performance. The best general combiners for the majority of the analyzed traits were the parents *SBas-1* among the lines and *Chal-3* among the testers, which might be employed in further research to create high-yielding super-sweet corn hybrids.

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1. Introduction

A common staple food in both fresh and preserved forms, sweet corn (*Zea mays* L. var. *Saccharata*) ($2n=20$), a member of the Gramineae family, will generate 895,387 tons of frozen grains globally in 2020. (FAOSTAT, 2023). The primary way that sweet corn differs from field corn is in the gene(s) that control the synthesis of starch in the seed endosperm. In sweet corn, one or more simple recessive alleles increase the amount of water-soluble polysaccharides (sugars) and reduce the amount of starch (Dinges *et al.*, 2001). The three main varieties of sweet corn are standard (*su*), super-sweet (*sh2*), and sugar-enhanced (*se*), which vary

in seed vigor, sweetness, and storage quality. *Shrunken-2* sweet corn (super-sweet) is at least two to three times sweeter than regular or Sugar-enhanced varieties, and there is barely any sugar-to-starch conversion (Shahrokhi *et al.*, 2020).

Sweet and super sweet corn is mainly grown for the purpose of using its fruit (cob) and among the group of crops classified as vegetables, in terms of agricultural value for processing industries (canning and freezing), It is the second most resistant and has the fourth place for fresh consumption (Afsharmanesh, 2013).

Finding novel cultivars and choosing superior types is essential to boost domestic output, considering the

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potential of the area for increasing sweet corn agriculture and the few adapted super-sweet corn hybrids accessible to Iran's food-processing sectors. The type of gene activity of each yield-contributing trait is crucial in determining the best breeding strategy since sweet corn may be bred in a variety of ways to maximize its potential grain yield.

Researchers have been debating the amount of corn tillers per plant for decades, and in the past this has raised worries about resource allocation and production impacts. Almost all sweet corn types only yield one or two tillers, and the quantity depends on the climate, plant density, and hybrid genetics (Veenstra et al., 2021). The presence of tillers in the corn plant can lead to neutral, positive, and negative effects on grain yields (Sangoi et al., 2009; Hansey and de Leon, 2011; Sangoi et al., 2012; Frank et al., 2013).

In order to more effectively identify prospective inbred parents and choose superior crossings for upcoming breeding operations or direct usage, breeders combine ability determination with estimates of the amount of heterosis. A parent's capacity to pass on a desired trait to the offspring after mating is known as combining ability (Sprague and Tatum, 1942). The phenomenon known as heterosis occurs when a hybrid F1 child surpasses either the mean of the two parents (for example, mid-parent heterosis) or the best of the two parents (for example, better-parent heterosis). One of the best instances of using heterosis in crops to increase agricultural productivity is maize (Hochholdinger and Baldauf, 2018). In order to produce better hybrids, the parents must have a thorough awareness of their genetic makeup, be skilled at producing hybrids, and apply the right mating strategies (Fasahat et al., 2016; Awata et al., 2018).

L (line) × T (tester) mating design, proposed by Kempthorne (1957), reveals the general combining ability (GCA) of the lines and testers as well as the special combining ability (SCA) of each cross. GCA variation is influenced by additive and additive-by-

additive variances, whereas SCA variation is influenced by non-additive variances (Reif et al., 2007). Effective L T interactions explain why different testers score experimental lines differently and why the chosen tester must assess new germplasm lines (Khalil et al., 2010). Authors have documented the successful application of this mating strategy in sweet corn for a number of years (Kumari et al., 2008; Khan et al., 2020; Ravikesavan et al., 2020; Chavan et al., 2022).

The goal of the current study was to create better super-sweet corn hybrids by assessing the combining potential of parental inbred lines and estimating the heterosis impacts on TP, grain yield, and agronomic parameters in a line-by-tester approach.

2. Materials and methods

2.1. Quality of irrigation water

The results of the chemical analysis of Irrigation water are given in Table 1. Irrigation water salinity was 0.8 deci-siemens/meter.

Table 1. The results of chemical properties of used Irrigation water

pH	EC (dS/m)	Anions (mill equivalent per liter)				Cations (mill equivalent per liter)		
		CO ₃ ²⁻	HCO ₃ ⁻	Cl ⁻	SO ₄ ²⁻	Ca ²⁺	Mg ²⁺	Na ⁺
7.8	0.8	1.8	-	3.2	2.35	2.4	2.4	3

2.2. Physical and chemical characteristics of the soil of the test site

To determine the physical and chemical properties of the soil of the test site, composite samples were prepared from the depths of 0-20, 20-40, 40-60, and 80-60 cm from the soil of the test site, then some physical and chemical properties such as apparent specific gravity, moisture in Field capacity point (FC), moisture at permanent wilting point (PWP), soil texture, electric conductivity of saturated extract and pH were measured. The results of soil analysis are presented in Table 2.

Table 2. The results of physical and chemical properties of soil

Soil Depth (cm)	Saturated Hydraulic Conductivity(Mm/Hr)	pH	EC (Ds/M)	Volumetric Moisture Percentage In F.C	Volumetric Moisture Percentage In P.W.P	Apparent Density (G/Cm3)	Soil Texture	Sand (%)	Silt (%)	Clay (%)
0-20	13.29	8	1.74	27.99	12.20	1.41	Silty loam	28	58	14
20-40	10.04	8	1.78	27.90	12.70	1.51	Silty loam	24	54	22
40-60	7.66	8.1	1.78	26.94	13.30	1.45	loam	26	50	24
60-80	3.37	8.2	1.78	23.71	9.80	1.42	loam	36	46	18

2.3. Plant samples

The inbred lines for this study were isolated in S6 from the initial crop of foreign super-sweet hybrids, primarily from Europe. At the Agricultural Research, Education and Extension Organization (AREEO), in Mashhad, Iran, three parental lines (used as female lines) and three tester lines (used as male lines) were planted in May 2021 using a crossover in line tester mating scheme. Female plants have shoot sacks covering their ears before silk emerges. When 20% of the male plants began to discharge pollen, the pollen was gathered and bulked from the male plants. Nine hybrids (F1) were produced as a consequence, and their seeds were collected in August 2021.

2.4. Experimental design

At AREEO, Mashhad, Iran, in 2022, three replications of the randomized complete block design (RCBD) were used to seed the nine F1 hybrids, three parental inbred lines, and three tester lines. Table 3 contains a list of the lines, tests, crossings, and sources. In order to achieve a plant population density of 66,500 plants per hectare, two rows of a 2 1.5 m plot were planted between the border rows with a plant spacing of 75 20 cm. After careful thinning, one healthy seed was retained per hill. During the crop-growing phase, the advised cultural methods were used. Fertilizer application was conducted with 46 kg N ha⁻¹, 36 kg P₂O₅ ha⁻¹, and 60 kg K₂O ha⁻¹ as base rates. In addition, 23 kg N ha⁻¹ was applied four weeks after planting. The crop measurements for TP, ear length (EL cm), number of rows per ear (NRPE), number of kernels per row (NKPR), ear diameter (ED' mm), cob diameter (CD' mm), kernel depth (KD' mm), stem diameter (SD' mm), ear height (EH' cm), plant height (PH' cm), tassel length (TL' cm), and total leaves number (TLN) were recorded on ten randomly plants in each plot. For the end of the season, grain yield (CGY t/ha) was measured and expressed in tons per hectare (t/ha).

Using the Line Tester function of the "Agricolae" package (Mendiburu and Yaseen, 2020) in R software version 4.2.2, analysis of variance, combining ability, and genetic parameters were carried out for all analyzed traits after data collection. AGD-R was used to investigate mid-parent heterosis (MPH) and best-parent heterosis (BPH) (Rodríguez et al., 2015) utilizing R software and the "ggplot2" program, and then shown as a heatmap (Wickham, 2016). The

proportionate contribution of lines, testers, and their interactions to total variances was shown using the same program.

Table 3. List of super sweet maize genotypes

NO.	Lines	Sources
1	SBas-1	Europe
2	Shak-13	Europe
3	SPasn	Europe
Testers		
1	SChal-3	Europe
2	SChal-5	Europe
3	SChal-10	Europe
Crosses		
1	SBas-1× SChal-3	
2	SBas-1× SChal-5	
3	SBas-1× SChal-10	
4	Shak-13× SChal-3	
5	Shak-13× SChal-5	
6	Shak-13× SChal-10	
7	SPasn × SChal-3	
8	SPasn × SChal-5	
9	SPasn × SChal-10	

3. Results

3.1. Analysis of variance

The ANOVA findings showed that entry mean squares were highly significant (P<0.01) for all examined features, indicating the presence of a large range of genetic diversity among genotypes and the possibility of creating high-yielding sweet corn hybrids. The parents of the qualities under study also showed significant differences (P<0.05 and P<0.01), demonstrating adequate variation in the parental lines. Significant variances in the parent-cross interactions demonstrated a wide range of variability for all variables. For practically all investigated characteristics, with the exception of SD and TL, crosses were divided into lines, testers, and line tester effects. Their interaction was extremely significant, demonstrating that hybrids had different SCA impacts. For the TL and CGY traits, line mean squares regarded as GCA for females showing additive gene action were likewise significant. The TP trait demonstrated a significant difference in the mean squares of testers (male GCA effects signifying additive gene action) (P 0.05). In this instance, SCA had a major impact on how the qualities influenced by non-additive variation expressed themselves. Since the SCA and heterosis value are related, heterosis breeding for this characteristic may be successful. While the results across testers were significant only for TP, the variation among the lines was significant for TL and CGY.

3.2. Estimates of genetic components

The analysis of variance for the combining abilities showed a higher magnitude due to lines (σ^2 lines) than those of the testers (σ^2 testers) for NRPE, EL, ED, CD, KD, SD, PH, TL, and CGY traits (Table 4), which indicates the higher contribution of lines toward σ^2 GCA. Also, σ^2 testers were greater than those of lines for NKPR, EH, TLN, and TP, indicating a higher contribution of testers towards σ^2 GCA for these traits. Results revealed a higher estimation of σ^2 SCA compared to σ^2 GCA for almost all studied traits, except PH, TL, CGY, and TP. A lower than one value for σ^2 GCA/ σ^2 SCA ratio indicates a preponderance of non-additive gene action in the inheritance of these traits. When creating hybrids or varieties for yield components through heterosis breeding, certain features should be taken into account.

3.3. Broad/Narrow sense heritability

The broad (H_{bs}^2) and narrow (H_{ns}^2) sense heritability were calculated for all studied traits. The findings of H_{bs}^2 were rather high and varied from 81 to 99%, indicating a significant genetic impact (Va) in regulating the examined variables. In this circumstance, choosing may be useful. The H_{ns}^2 values for NKPR, EL, ED, CD, KD, SD, and TLN traits were lower than those of H_{bs}^2 , which indicates higher effects of non-additive genes in controlling these traits. High values of narrow-sense heritability for the characteristics PH, TL, CGY, and TP, however, suggested that additive genes played a substantial role in controlling these characters and that selection methods in advanced generations (F6 or F7) would be useful for assessing these traits.

Table 4. Estimates genetic parameters, GCA and SCA effects for 13 studied traits in super sweet maize genotypes

Source	Df	NRPE	NKPR	EL	ED	CD	KD	SD	EH	PH	TL	TLN	CGY	TP
Replications	2	0.13	2.48	1.13	0.03	1.55	0.4	9.86**	3.40	32.19	2.91	0.74	0.06	2.05
Genotypes	14	5.35**	82.79**	15.65**	62.3**	29.85**	3.64**	5.01**	163.9**	533.89**	41.16**	2.1**	61.23**	914.8**
Parents	5	5.81**	37.18**	12.88**	61.41**	33.78**	2.93**	3.60*	20.3**	64.42**	29.08**	1.15**	26.99**	523.2**
Parents × Crosses	1	16.43**	751**	110.8**	378.9**	196.06**	7.47**	28.17**	1528.4**	5710.44**	338.24**	13.9**	411.05**	26.3**
Crosses	8	3.68**	27.77**	5.47**	23.27**	6.62**	3.6**	3*	83.15**	180.24**	11.57**	1.22**	38.9**	1270**
Lines	2	10.32	16.82	9.22	37.31	9.8	3.91	3.78	24.66	283.09	27.4*	0.4	130.9*	1679
Testers	2	0.79	46.38	3.17	16.16	1.5	2.03	3.05	219.7	281.31	11.54	1.6	1.95	2730*
Lines × Testers	4	1.8*	23.95**	4.76**	19.82**	7.6**	4.25**	2.6	44.08**	78.27**	3.68	1.43**	11.38**	336**
Error	28	0.58	5.78	0.97	1.46	1.67	0.26	1.09	2.52	14.89	2.54	0.22	0.3	1.19
Estimate of Genetic Components														
σ^2 lines		0.95	-0.79	0.50	1.94	0.25	-0.04	0.14	-2.16	22.76	2.64	-0.11	13.28	149
σ^2 testers		-0.11	2.49	-0.18	-0.41	-0.68	-0.25	0.05	19.52	22.56	0.87	0.02	-1.05	266
σ^2 GCA		0.42	0.85	0.16	0.77	-0.02	-0.14	0.09	8.68	22.7	1.75	-0.05	6.11	207
σ^2 SCA		0.49	6.41	1.17	5.91	1.92	1.34	0.4	13.84	22.7	0.38	0.44	3.65	111
σ^2 GCA / σ^2 SCA		0.86	0.13	0.14	0.13	-0.11	-0.1	0.23	0.63	1.00	4.73	-0.11	1.67	1.86
σ^2 additive		0.84	1.70	0.32	1.54	-0.44	-0.28	0.18	17.36	45.32	3.51	-0.1	12.22	414
σ^2 dominance		0.49	6.41	1.17	5.91	1.92	1.34	0.4	13.84	22.7	0.38	0.44	3.65	111
H_{bs}^2		0.97	0.95	0.93	0.97	0.93	0.99	0.81	0.99	0.98	0.91	0.98	0.99	0.99
H_{ns}^2		0.45	0.11	0.11	0.11	0.00	0.00	0.15	0.38	0.49	0.75	0.00	0.62	0.65

**significant at level 1%, *significant at level 5%, NRPE: number of rows per ear, NKPR: number of kernels per row, EL: ear length, ED: ear diameter, CD: cob diameter, KD: kernel depth, SD: stem diameter, EH: ear height, PH: plant height, TL: tassel Length, TLN: Total leaf number, CGY: conservable grain yield, TP: tillering potential, H_{bs}^2 : Broad sense heritability, H_{ns}^2 : Narrow sense heritability.

3.4. Proportional contribution

The relationship between lines, tests, and how they interact is shown in Fig. 1. Values for lines in TL, NRPE, and CGY were much higher than those for interactions and tests, suggesting that female parents were the main source of variance in the entire model. The choice of tester parents for changing TP, PH, and EH should be given more weight than the choice of line parents because testers' contributions to these traits were larger than those of lines and interactions.

3.5. Heterosis

Heterosis is a result of F1 progenies doing better than their respective parents, as seen by this. It has also been applied to develop maize hybrids with enhanced traits. Fig. 2 displays the various levels of heterosis, including the best-parent heterosis (BPH) and mid-parent heterosis (MPH), for the attributes that were being studied.

The MPH in CGY trait generally ranged from 18-60.4 % in all combinations, except SCBasn-1 × SChal-

5(166.5%) and SCBasn-1× SChal-3(121%). The BPH also showed similar results and generally ranged from 0-33.9%, except those of the above-mentioned crosses (151.7% and 96.2%, respectively). The SPasn × SChal-5 combination showed the highest numbers for MPH in ear height (EH) and plant height (PH) traits (73.8% and 42.8%, respectively). Similar results were also observed for EH and PH traits in BPH for this combination (59.4% and 37.2%, respectively). The SPasn × Challenger-3 and SCBasn-1× SChal-10 combinations showed the lowest values of MPH and BPH (30%) for EH. SCBasn-1× Challenger-3 combination also showed the lowest values of MPH and BPH for the PH trait (15.8% and 10.5%, respectively).

The lowest values of MPH (-9.2%) and BPH (-12.5%) for kernel depth (KD) were recorded for the SPasn × SChal-5 combination, where Shak-13 × SChal-5 showed the highest values for MPH and BPH (36.1% and 26.6%, respectively). For the number of kernels per row (NKPR) trait, Shak-13 × SChal-5 showed the lowest values both in MPH (7.2%) and BPH (3.9%), where the SPasn × SChal-10 combination showed the highest values (49.4% for MPH and 35.8% for BPH). Values for the number of rows per ear (NRPE) trait ranged from -1% to 17.3% for MPH and

-10.5% to 13.4% for BPH, where the lowest and highest values belonged to SSBasin-1× SChal-5 and SPasn × SChal-10, respectively. The SPasn × SChal-5 combination showed the highest values of MPH for both ear length (EL) (41.3%) and total leaves number (TLN) (22.7%). Similar outcomes for the EL and TLN characteristics in BPH were also seen (29.9% and 14.2%, respectively).

The MPH and BPH for cob diameter (CD) ranged from 5.7-22.5% and -6.6% to 18.8%, respectively. The lowest MPH and BPH for ear diameter (ED) were found in the SPasn × SChal-5 combination (1.9% and -5.3%, respectively), where SPasn × SChal-10 cross showed the highest values for CD in MPH (21.7%) and BPH (17.2). The Shak-13 × Challenger-3 combination showed the highest values of MPH and BPH for stem diameter (SD) (19.5%), whereas SCBasn-1× SChal-10 showed the lowest values (2.6%) for MPH and SPasn × SChal-10 with -3.2% in BPH.

The SPasn × Challenger-3 cross showed the lowest MPH and BPH for the tillering potential (TP) trait (87%), indicating this hybrid can be used in further breeding programs to improve this trait, whereas Shak-13 × SChal-10 showed the highest numbers for MPH and BPH (102%) (Fig. 2).

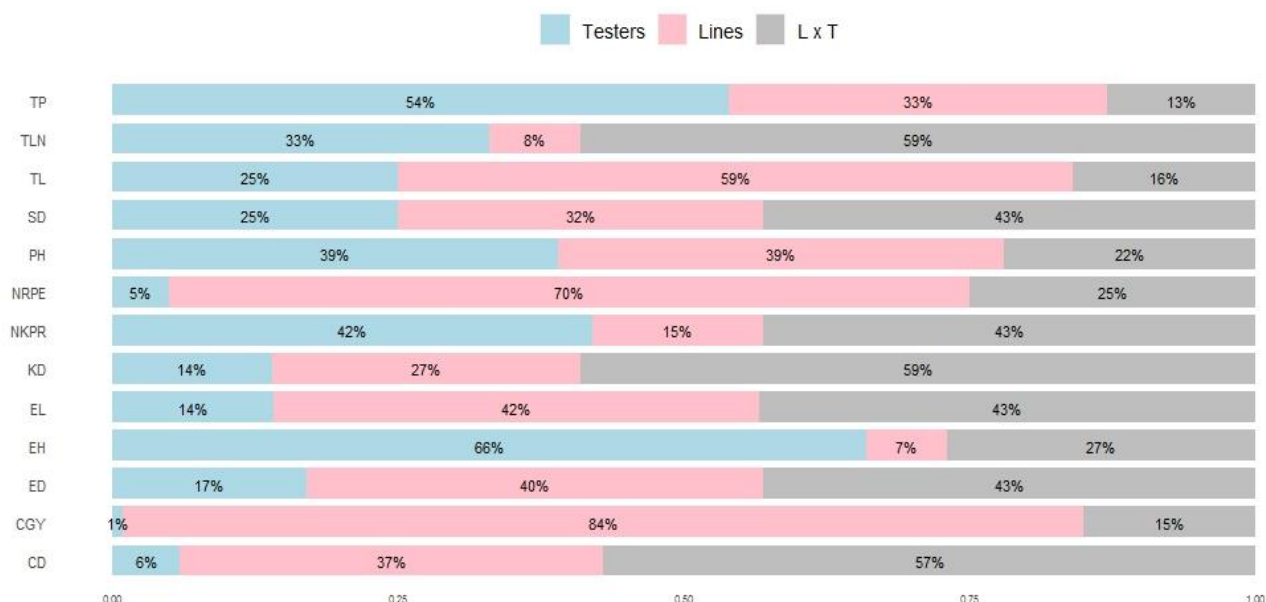


Figure 1. Proportional contribution of 13 agronomic traits in super sweet maize genotypes

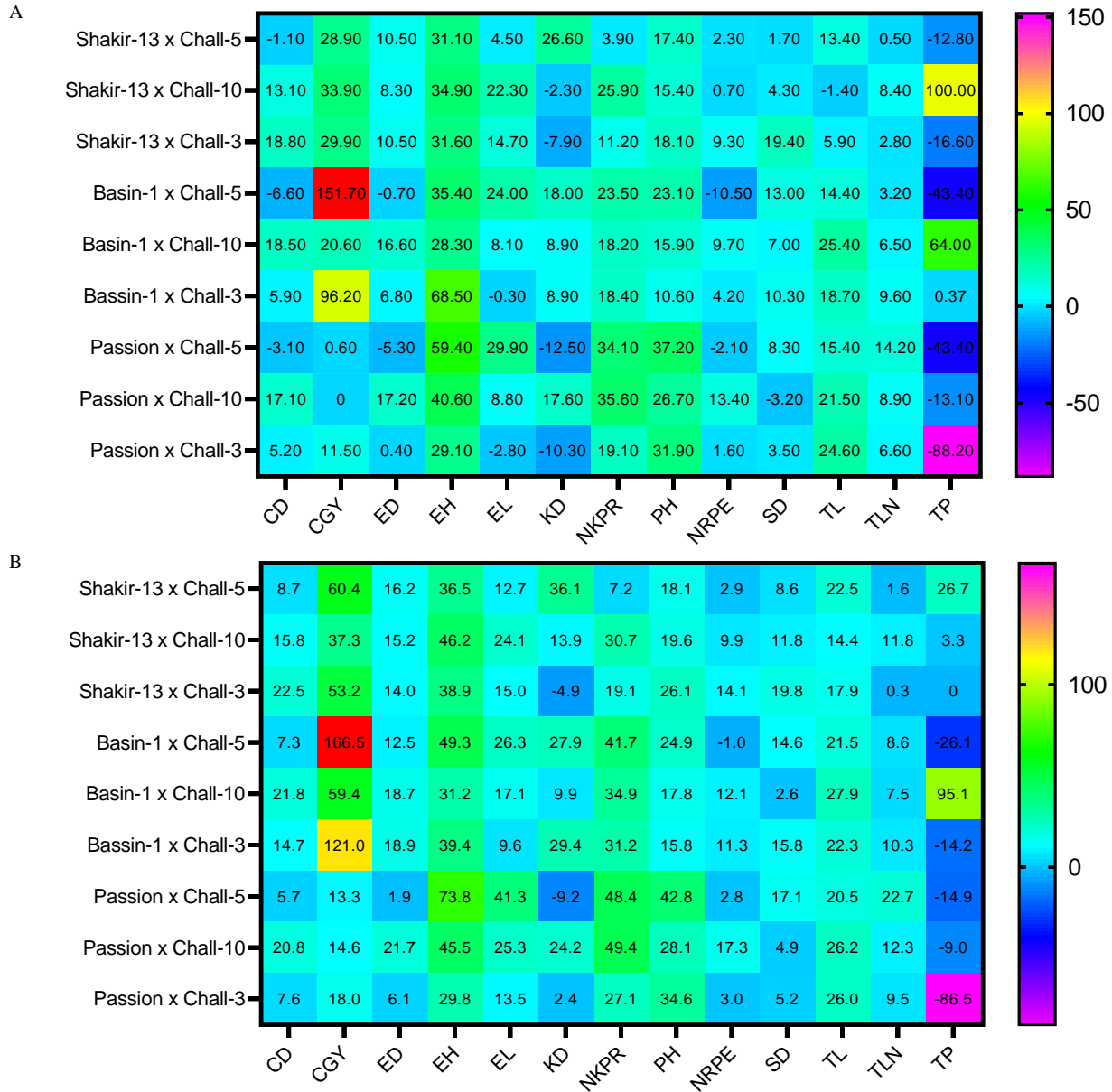


Figure 2. Heterosis heatmap for several agronomic characteristics in super sweet maize from each cross combination. MPH (mid-parent heterosis) and BPH (best-parent heterosis) (Chall=Challenger)

3.6. Estimates of General / Specific combining ability

Especially for heterosis breeding, choosing parents with high general combining ability (GCA) is a crucial component of any successful breeding operation. Table 5 displays the impacts of GCA and SCA. Generally speaking, GCA is linked to additive gene activity in the transmission of characteristics. According to the findings of the GCA research, the line SCBasn-1 is the greatest general combiner for utilizing more favorable alleles for CGY and SD characteristics. Additionally, in order to create dwarf hybrids, shorter plant and ear height must evolve. This is due to the detrimental impacts of GCA on PH, EH, and TL characteristics. Additionally, KNPR and TLN features appeared to be

enhanced by the SPasn line. However, it was shown to be a poor general combiner in creating dwarf plants and developing the characteristics ED, SD, KD, TP, and CGY (though with the greatest positive values for EH and PH).

Due to its low readings for EH and PH, Challenger-3 was regarded as one of the study's testers with the most promise for genetically enhancing grain production through RNPE, ED, and KD, as well as for producing dwarf hybrids. However, it revealed that EL, KNPE, TLN, and CGY had the lowest GCA effects.

Among the nine cross combinations, high SCA effects were recorded by three crosses (Shak-13 × Schal-3, Shak-13 × Schal-10, SPasn × Schal-5) for

EL, KNPR, and SD characters. The Shak-13 × SChal-5 cross showed SCA effects with negative values for ear and plant height traits, whereas the Shak-13 × SChal-10 combination recorded the highest positive amount of SCA effect for tassel length character. In maize, negative values of plant height and ear height are expected for the dwarf plant type. The SPasn × SChal-10 cross exhibited the highest positive SCA effects for RNPE, ED, and TLN traits. Regarding cob diameter, the SCA effects were high and positive in Shak-13 × Challenger-3 cross and suitable for obtaining high-

yielding hybrids. Crosses Shak-13 × SChallenger-5 and SPasn × SChal-5 were the best and poor specific combiners for kernel depth character, respectively (Table 5).

Positive and negative effects of SCA are estimated for TP character, where the negative values of this trait are expected for lower tillers number per plant. SCBasn-1 × SChal-5 combination (average × good general combiner) recorded the highest negative values for SCA, followed by SPasn × Challenger-3 (good × average general combiner).

Table 5. Estimates of combinations of SCA and GCA impacts on yield and component characteristics in genotypes of super-sweet maize.

NO.		EL	RNPE	KNPR	ED	CD	SD	EH	PH	TL	KD	CGY	TLN	TP
Line														
1	SSBasn-1-1	-0.68	-1.01	-1.34	-0.91	-1.02	0.59	-1.85	-4.93	-1.31	0.05	2.58	-0.22	0.32
2	Shak-13	1.16	1.12	-0.04	2.33	1.06	0.09	0.51	-1.17	1.98	0.63	1.79	0.02	13.50
3	SPasn	-0.48	-0.11	1.39	-1.41	-0.05	-0.69	1.33	6.10	-0.67	-0.68	-4.30	0.20	-13.80
	<i>S.E. (GCA)</i>	<i>0.33</i>	<i>0.25</i>	<i>0.80</i>	<i>0.40</i>	<i>0.43</i>	<i>0.34</i>	<i>0.52</i>	<i>1.29</i>	<i>0.53</i>	<i>0.17</i>	<i>0.18</i>	<i>0.15</i>	<i>0.36</i>
	<i>S.E. (gi - gj)</i>	<i>0.46</i>	<i>0.36</i>	<i>1.13</i>	<i>0.56</i>	<i>0.61</i>	<i>0.49</i>	<i>0.74</i>	<i>1.82</i>	<i>0.75</i>	<i>0.24</i>	<i>0.25</i>	<i>0.22</i>	<i>0.51</i>
Tester														
1	Challenger-3	-0.55	0.28	-2.46	0.82	0.15	-0.36	-2.90	-3.26	0.11	0.34	-0.41	-0.35	-7.30
2	SChal-5	-0.08	-0.31	0.43	0.71	0.31	0.67	5.70	6.46	1.07	0.20	-0.09	0.46	-12.60
3	SChal-10	0.63	0.03	2.02	-1.54	-0.46	-0.31	-2.70	-3.20	-1.19	-0.54	0.50	-0.11	19.90
	<i>S.E. (GCA)</i>	<i>0.33</i>	<i>0.25</i>	<i>0.80</i>	<i>0.40</i>	<i>0.43</i>	<i>0.34</i>	<i>0.52</i>	<i>1.29</i>	<i>0.53</i>	<i>0.17</i>	<i>0.18</i>	<i>0.16</i>	<i>0.36</i>
	<i>S.E. (gi - gj)</i>	<i>0.46</i>	<i>0.36</i>	<i>1.13</i>	<i>0.56</i>	<i>0.61</i>	<i>0.49</i>	<i>0.75</i>	<i>1.82</i>	<i>0.75</i>	<i>0.24</i>	<i>0.25</i>	<i>0.22</i>	<i>0.51</i>
Cross Combination														
1	SCBasn-1 × Challenger-3	-0.07	0.34	0.41	1.35	-0.30	0.35	1.80	-3.34	-0.36	0.82	0.09	0.31	5.00
2	SCBasn-1 × SChal-5	0.46	-0.27	1.56	-0.16	-0.11	0.22	-0.22	1.84	-0.45	-0.02	2.11	-0.11	-8.50
3	SCBasn-1 × SChal-10	-0.39	-0.08	-1.97	-1.20	0.41	-0.58	-1.58	1.50	0.81	-0.80	-2.21	-0.20	3.50
4	Shak-13 × Challenger-3	0.78	0.61	1.71	-0.17	1.80	0.52	1.64	4.36	-0.12	-0.98	-0.05	0.13	2.30
5	Shak-13 × SChal-5	-1.62	0.00	-3.41	2.09	-0.13	-1.02	-3.92	-6.06	1.26	1.11	-0.53	-0.69	-5.40
6	Shak-13 × SChal-10	0.84	-0.61	1.70	-1.93	-1.66	0.50	2.28	1.70	-1.15	-0.13	0.59	0.55	3.14
7	SPasn × Challenger-3	-0.71	-0.96	-2.12	-1.18	-1.50	-0.88	-3.44	-1.01	0.47	0.15	-0.03	-0.44	-7.20
8	SPasn × SChal-5	1.16	0.27	1.86	-1.94	0.24	0.79	4.15	4.21	-0.82	-1.09	-1.58	-0.36	13.40
9	SPasn × SChal-10	-0.45	0.69	0.27	3.13	1.25	0.08	-0.70	-3.20	0.34	0.93	1.62	0.80	-6.70
	<i>S.E. (SCA)</i>	<i>0.57</i>	<i>0.44</i>	<i>1.39</i>	<i>0.70</i>	<i>0.75</i>	<i>0.60</i>	<i>0.91</i>	<i>2.23</i>	<i>0.92</i>	<i>0.29</i>	<i>0.31</i>	<i>0.27</i>	<i>0.63</i>
	<i>S.E. (Sij - Skl)</i>	<i>0.80</i>	<i>0.62</i>	<i>1.96</i>	<i>0.98</i>	<i>1.06</i>	<i>0.85</i>	<i>1.30</i>	<i>3.15</i>	<i>1.30</i>	<i>0.41</i>	<i>0.44</i>	<i>0.39</i>	<i>0.90</i>

SE: standard error, NRPE: number of rows per ear, NKPR: number of kernels per row, EL: ear length, ED: ear diameter, CD: cob diameter, KD: kernel depth, SD: stem diameter, EH: ear height, PH: plant height, TL: tassel Length, TLN: Total leaf number, CGY: conservable grain yield, TP: tillering potential.

4. Discussion

Based on $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio and narrow-sense heritability (h^2_{ns}), plant height, tassel length, conservable grain yield, and tillering potential characters in the current experiment were affected by additive gene action. Selection might thus be used to enhance these qualities and find superior hybrids. The number of rows per ear, the number of kernels per row, the ear diameter, the cob diameter, the depth of the kernel, the stem diameter, the ear height, and the total number of leaves per plant were all significantly influenced by non-additive gene activity. The characteristics' broad-sense heritability varied from 81

to 99%, whereas their narrow-sense heritability was between (0) and 75%. The estimations of general combining ability impacts showed that the strongest general combiners for the majority of the analyzed characters were the parents SCBasn-1 and Shak-13 among the lines, Challenger-3 and SChal-10 among the testers. For the majority of the qualities under study, the cross combinations SPasn SChal-10, SPasn SChal-5, and Shak-13 SChal-5 recorded the greatest specific combining ability (SCA) impacts. While this was going on, the SCBasn-1 and SChal-5 combination had the highest levels of SCA impacts in terms of conservable grain yield and tillering potential features, making it

appear to be the best hybrid combination. This hybrid was linked to a high GCA of the SChal-5 in TP character and the SBasn-line CGY trait.

The results of the Estimates of genetic components are in accordance with the findings of [Amiruzzaman et al. \(2013\)](#), [Elmyhum \(2013\)](#), and [Sugiharto et al. \(2018\)](#). On the other hand, PH, TL, CGY, and TP characters with higher GCA variances than SCA variances caused the ratio of the $\sigma^2\text{GCA}/\sigma^2\text{SCA}$ to be more than one. It indicates that because these qualities are heavily influenced by additive effects, parental selection becomes more important for assessing them. The outcomes were identical to earlier publications from [Gissa et al. \(2007\)](#); [Kambegowda et al. \(2013\)](#); [Tessema et al. \(2014\)](#); and [Mogesse et al. \(2020\)](#).

According to studies from [Talukder and Banik \(2012\)](#) and [Ahmed et al. \(2016\)](#), testers generally offered the least overall variance. A large proportion of the line-tester interaction components were found in the results for the characters TLN, SD, NKPR, KD, EL, ED, and CD, which rules out the occurrence of significant SCA and significant non-additive variance effects.

Plant output may be predicted to display greater levels of heterosis since it has been proposed that this feature is a multiplicative variable that integrates variance from a number of other qualities ([Williams, 1959](#); [Lippman and Zamir, 2007](#)). It is preferable to have more leaves since they should produce more grain due to their high photosynthetic rate ([Fang et al., 2018](#)).

High values of heterosis in tillering potential trait agree with the results of [Sakr and Ghazy \(2010\)](#), [Ghazy \(2016\)](#), and [El-Adl et al. \(2018\)](#). In the current study, most hybrids recorded positive heterosis that revealed the existence of heterosis effects in the hybrid's performance.

High positive heterosis for grain yield and yield components and low heterosis for plant architecture are favorable in sweet maize genotypes ([Dermail et al., 2018](#)), enabling plant breeders to select lines and their promising hybrids.

[Chavan et al. \(2022\)](#) observed similar outcomes for grain yield. However, the SCBasn-1line revealed the lowest values for the undesirable characteristics that contribute to increasing grain yield: EL, RNPE, KNPR, CD, and TLN. Line Shak-13, which might be regarded a viable line for genetic enhancement of grain output through specified qualities by passing desired

characters to their progeny, demonstrated the strongest positive GCA effects for EL, RNPE, ED, CD, KD, and TP.

Observed high general combining abilities (GCA) were the result of additive and additive gene effects ([Sprague and Tatum, 1942](#)). For boosting cob and stem diameter as well as TLN characteristics, the tester Challenger-10 performed the best. In addition, the tester SPasn was selected as the best general combiner among the tested testers, which might be employed as a prospective parent in hybrid breeding projects, respecting CGY, TL, TP, EL, and KNRP traits. Based on the quantity of advantageous alleles with additive gene action, the parents' GCA assessment might help in finding superior parents for the development of superior genotypes ([Fasahat et al., 2016](#)). The results agreed with the earlier reports of [Amiruzzaman et al. \(2013\)](#), [Ejigu et al. \(2017\)](#), and [Gemechu et al. \(2018\)](#).

One of the genetic characteristics that represents the impact of non-additive influences on phenotypes is specific combining ability (SCA). In hybrid development, the SCA effects are more important than the GCA effects ([Yu et al., 2020](#)).

The number of desired alleles increases in hybrids formed from pairing parents with the best GCA and good SCA values ([Kamara et al., 2021](#)). Due to additive, additive, and additive dominant gene activities, crosses including strong general combiners (as well as good weak combiner) typically result in significant SCA effects. In terms of CGY characteristics, SPasn SChal-10 (involving a bad good general combiner) and SCBasn-1 SChal-5cross (involving a good average general combiner) showed the greatest levels of SCA. The crosses' high SCA impacts showed a considerable departure from what would have been expected based on their parents' behaviors. These crosses might be chosen based on their SCA for use in efforts to enhance maize ([Elmyhun et al., 2020](#)).

5. Conclusion

This study found that the sh2 populations had a broad range of genetic diversity for the 13 parameters, suggesting that there may be a chance to create high-yielding hybrids with particular breeding goals. The conservable grain yield trait exhibited the highest heterosis of all the characteristics examined, but tillering potential character showed negative heterosis

in the majority of the examined combinations. These findings might aid breeders in deciding how to select for desired features and cross-breed new types to produce high yields.

Conflict of interests

All authors declare no conflict of interest.

Ethics approval and consent to participate

No human or animals were used in the present research.

Consent for publications

All authors read and approved the final manuscript for publication.

Availability of data and material

All the data are embedded in the manuscript.

Authors' contributions

All authors had an equal role in study design, work, statistical analysis and manuscript writing.

Informed consent

The authors declare not to use any patients in this research.

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