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COMBINING ABILITY ANALYSIS FOR MATURITY AND YIELD ATTRIBUTES IN SWEET CORN ACROSS ENVIRONMENTS

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SUMMARY

Early maturity and genotype by environment interaction (GEI) have always been challenging concerns for breeders in selecting appropriate parents for breeding programs. The presented study aimed to investigate early maturity and the dimension of gene action, as well as, assess the performance of half-diallel populations using eight advanced sweet corn inbred lines and their 28 F_1 hybrids with two commercial checks for maturity and yield-related traits in the spring of 2018 at the Nowshera (plain) and Swat (hilly) areas, Khyber Pakhtunkhwa, Pakistan. Analysis revealed significant differences among the genotypes for the studied traits over both locations. General combining ability (GCA) effects were significant for all the traits at both the agro-climatic conditions, except 100-kernel weight, with the specific combining ability (SCA) effects relevant for grain yield at both locations. The GCA-SCA ratio for studied traits indicated dominance gene action, which also gained support by higher values of SCA than GCA variances. Based on the results, the identified inbred lines SWTS-1-8 and SODS-1 serve as good general combiners for traits like earliness and grain yield attributes, making them better parents to improve the stated characteristics in sweet corn. However, the F_1 hybrids, i.e., NARCCCRI-19 × CCRI-34 at Nowshera and CCRI-34 × SODS-1 at Swat, showed the best specific combiners for maturity. Likewise, F_1 hybrids, i.e., SWTS-1-4 × SWTS-1-8 and SWTS-1-8 × CCRIS-34, emerged as desirable for grain yield at Nowshera and Swat, respectively. The inbred lines for the mentioned hybrids can be a source of germplasm improvement, breaking through undesirable linkages in future sweet corn breeding programs.

Keywords: Sweet corn, combining ability, specific combining ability, general combining ability, Hayman's half diallel approach, gene action

Key findings: Combining ability analysis revealed that variations in the genetic magnitude over the two test locations indicated a significant role of environment on gene expression and would likely concentrate favorable alleles for the target corn yield attributes. Most of the traits showed non-additive gene linkage, which indicates that inter matting of selected progeny in the upcoming early segregating generation obtained by crossing these parents will release hidden genetic variability through the breakage of undesirable linkages. Over-dominance gene action revealed that delayed selection could be more effective in developing early maturing sweet corn hybrids with modified plant architectures.

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INTRODUCTION

Corn has a remarkable position in the world after wheat and rice in consumption as a human staple food, animal feed, and raw material for industry (Kusaksiz, 2010; Shojaei *et al.,* 2022). Sweet corn (*Zea mays* L. var. 'saccharata') is a type of corn with a creamy texture and mutant endosperm, which contains about three to eight times more sugar than other types of corn (Chozin *et al.,* 2017; Sheng *et al*., 2018; Zoric *et al*., 2022). Global production is relatively few grown on a small area of 1.06 million ha due to restricted research work, unexpected climatic changes, and tapered genetic makeup (Lertrat and Pulam, 2007; Fahad *et al*., 2022; Shojaei *et al.,* 2022).

Maximizing agricultural production depends mainly on promoting early maturing high-yielding corn hybrids to cover the mounting consumption of corn genotypes. It depends mostly on diallel crosses utilizing combining ability mating patterns for distinguishing early-maturing high-yielding hybrids and helps to identify the most appropriate parents along with their best combining ability and dimension of gene actions (El-Hosary and El-Fiki, 2015; Ibrar *et al*., 2021). In this regard, the application of Griffing's approach (Griffing, 1956) has been all-encompassing to understand the type and magnitude of the genetic effects in parents using offspring data for traits of interest (Glover *et al.,* 2005; Fahad *et al*., 2020; Revilla *et al*., 2021). General combining ability (GCA) expresses the additive portion of the total variance and average behavior of inbred lines, whereas specific combining ability (SCA) expresses the behavior of specific hybrid combinations, with a composition of a non-additive portion of the total variance, arising mainly from dominance and epistatic deviations (Mural, 2012; Aslam *et al.*, 2015; Haider *et al*., 2021).

Early maturity, with the good combining ability of the parents and their cross combinations, is a prerequisite to feed the ever-increasing demands of the current food security scenario. Early maturing high-yielding hybrids are more desirable for their commercial release into a particular target environment to reduce the climatic effect on sweet corn in Pakistan (Pacurar *et al*., 2018; Zoric *et al*., 2022). In addition, the phenotypic constitution of a crop is the function of genotype, environment, and the interactions due to genotype by environment (Smith *et al*., 2005; Adnan *et al.,* 2020; Shojaei *et al.,* 2022). Slight information is available about the implication of significant genotype and environment interaction (GEI), its source and importance, and its nature in plant breeding programs and on the net yield and resultant varieties (Fahad *et al*., 2021a; Ali *et al*., 2022).

Sweet corn genotypes that performed better under particular environments might not perform well across locations, or changes in the relative ranking of the genotypes are a grave concern to plant breeders (Stagnati *et al.,* 2020; Shojaei *et al*., 2022). Similarly, testing at various locations for morphological and yield traits is crucial if breeders are interested in germplasm having better adaptability to wider regions (Hassan *et al*., 2006; Hafiz *et al*., 2020). In contrast, corn genotypes are stable if they possess an unchanged expression or show non-significant changes regardless of variable environmental conditions (Smith *et al*., 2005; Harakotr *et al.,* 2016; Shojaei *et al*., 2022). The environment affects corn's quantitative traits, and the number of predominant genes increases as the effects increase. Thus, eliminating genotype × environment variances from the assessment of genetic variance forms an integral part of any endeavor to determine genetic variations without partiality (Wani *et al*., 2017; Al-Zahrani *et al*., 2022). Therefore, before the release of viable hybrids into a particular target environment, crop producers identify early maturing high-yielding sweet corn genotypes (Yan and Hunt, 2001; Mohammed, 2020; Zystro *et al*., 2021).

Early maturating high-yielding genotypes across environments and resistance to diseases occurring during yield growth stages are more desirable to escape abrupt environmental stresses that generally coincide with flowering and yield-causative traits. Considering all these things, the recent study identified, selected, and evaluated the breeding potential of sweet corn parental lines and F_1 hybrids based on gene action of the studied economic traits, along with broader range adaptability and stability across Nowshera and Swat diverse environments of Khyber Pakhtunkhwa, Pakistan.

MATERIALS AND METHODS

Breeding material and development of F_1 hybrids

The study material comprised 16 advanced sweet corn lines keeping the corn's cross-pollinated nature, with the eight diverse lines selected in the spring season of 2017 to manipulate its genetic makeup to identify the more promising hybrids in terms of vigor and earliness. For this purpose, eight sweet corn inbred lines, viz., NARCCCRI-17, NARCCCRI-19, SWTS-1-4, SWTS-1-8, CCRIS-29, CCRIS-34, KHWS-1, and SODS-1 undertook mating in diallel format (without reciprocals) during the summer season of 2017 at the Cereal Crop Research Institute (CCRI), Pirsabak, Nowshera, Khyber Pakhtunkhwa, Pakistan. Planting parental sweet corn lines with resultant F_1s was in RCB design with two replications. The plot area consisted of two rows, with the row length at 5 m. Plant-to-plant spacing was 25 cm maintaining a row spacing at 75 cm. The entire set of 38 sweet corn genotypes (including eight inbred lines, 28 F_1 hybrids, and two checks) proceeded to evaluation at two locations, viz., CCRI, Nowshera, and the Agriculture Research Institute (ARI), Mingora, Swat, Pakistan, in the spring season of 2018.

Meteorological data obtained came from the Agro-meteorological Stations of Khyber Pakhtunkhwa, Pakistan. The maximum and minimum temperatures of Nowshera during the summer season were 48 °C and -2 °C along with an annual rainfall of 450–500 mm and 32° N Latitude and 74° E Longitude. The ARI, Mingora, Swat, Pakistan, has a temperate environment with maximum and minimum temperatures of 42 °C and -4 °C. Additionally, annual recorded rainfalls were 737–1200 mm during the cropping season at 34.3° N Latitude and 72.5° E Longitude. The crop grown under uniform conditions received fertilizer applications of 120-60-60 NPK ha^{-1}, with all standard cultural practices adopted throughout the cropping season to minimize possible environmental effects. Soil analyses of the experimental fields show that the soil of Nowshera was sandy loam, having a pH of 7–8 and Swat, with silt loam, with a pH of 5–6.3.

Data recorded and analysis

Data recording was on parents and F_1 hybrids for days to tasseling and silking, 100-kernel weight, and grain yield. Upon observing significant differences among the sweet corn population, the computation of combining ability analysis used Griffing's approach (1956), Model-II Method-II, including parents with one set of progenies at each location of Khyber Pakhtunkhwa, Pakistan.

RESULTS AND DISCUSSION

Days to tasseling

Location-wise ANOVA revealed significant differences in sweet corn genotypes for days to tasseling at Nowshera (P = 0.05), but the differences were non-significant at Swat (Table 1). Similarly, general combining ability (GCA) mean squares for tasseling were highly significant at Nowshera (P = 0.01) but non-significant at Swat. However, specific combining ability (SCA) mean squares for tasseling were non-significant at both locations. Such results indicate that the location affects the non-additive gene actions more than additive genetic effects in tasseling. However, Aly and Mousa (2011) and Zoric *et al.* (2022) have reported significant GCA and SCA variances for most characters including tasseling in maize, emphasizing the function of both additive and non-additive components. GCA variances for tasseling were generally less in magnitude than SCA variances at both locations, revealing that a large part of total variability for tasseling inheritance was under non-additive gene legacy. As such, the resultant GCA-SCA ratio for days to tasseling was less than unity at Nowshera (0.70) and Swat (0.03), signifying the predominance of non-additive gene action (Table 2). Ravi and Chikkalingaiah (2018) and Revilla *et al.* (2021) also found the ratio of GCA and SCA less than 1 for days to tasseling in maize and indicated the role of non-additive gene action in the control of this trait. However, Zare *et al.* (2017) and Stagnati *et al.* (2020) indicated the additive type of gene action in the control of tasseling and other maturity traits.

Maize breeders focus on developing new genotypes with the least days to maturity, negative GCA and SCA magnitudes, and better adaptability to wider regions (Fahad *et al.,* 2021b). Mohammed (2020) studied that sweet corn inbreds having negative significant GCA and SCA variances were desirable for most of the maturity traits for developing early maturing corn lines. At Nowshera, the inbred SWTS-1-8 was the only desirable good general combiner for tasseling (GCA = -1.7, P = 0.05), while the same line (SWTS-1-8) was a poor general combiner at Swat test location. In test location Swat, none of the parents had a significant GCA effect for tasseling (Table 3). At Nowshera, the inbred line NARCCRI-17 was

Table 1. Combining ability ANOVA for days to tasseling, days to silking, 100-kernel weight, and grain yield of 38 sweet corn genotypes (derived from half diallel matting) evaluated at the two locations of Khyber Pakhtunkhwa, Pakistan.

Source of variation	d.f.	Days to tasseling		Days to silking		100-kernel weight		Grain yield	
		Nowshera	Swat	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat
Replications	1	25.7	9.4	88.9**	9.4	3.2	4.7	6470.2	165.0
Genotypes	35	15.6*	8.5	16.4**	9.8*	5.5	8.1**	711575.1**	1801337.4**
GCA	7	32.1**	6.8	33.1**	13.4*	4.6	3.5	723573.6**	1366099.5**
SCA	28	11.4	9.0	12.3*	8.9	5.8	9.2**	708575.5**	1910146.9**
Error	35	7.7	5.9	6.2	5.2	14.0	2.0	60137.0	61878.6

*,** = Significant at 5% and 1% probability level, respectively.

Table 2. Combining ability components due to GCA and SCA for different traits in sweet corn evaluated at the two locations of Khyber Pakhtunkhwa, Pakistan.

Traits	GCA component		SCA component		GCA-SCA ratio	
	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat
Days to tasseling	1.2	0.04	1.9	1.5	0.7	0.03
Days to silking	1.3	0.4	3.1	1.8	0.4	0.2
100-kernel weight	0.001	0.1	0.001	3.6	1.0	0.001
Grain yield	33171.8	65211.0	324219.3	924134.2	0.1	0.1

Table 3. General combining ability (GCA) effects among sweet corn parental genotypes for days to tasseling and silking, 100-kernel weight, and grain yield evaluated at the two locations of Khyber Pakhtunkhwa, Pakistan.

Parental genotypes	Days to tasseling		Days to silking		100-kernel weight		Grain yield	
	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat
NARCCCRI-17	1.8*	-0.7	1.9**	-0.7	0.3	0.3	-288.4**	-273.4**
NARCCCRI-19	1.4*	0.8	1.3*	-0.5	-0.5	-0.5	141.0*	24.8
SWTS-1-4	0.8	-0.8	0.5	-1.3*	-0.2	0.3	-9.1	134.0*
SWTS-1-8	-1.7*	0.3	-2.0**	-0.4	0.9	0.6*	51.8	369.5**
CCRIS-29	0.1	-0.5	0.3	0.7	-0.0	0.1	-1.9	-368.6**
CCRIS-34	0.0	0.5	0.1	0.7	0.3	-0.3	-71.4	-226.8**
KHWS-1	-1.0	0.5	-0.6	1.1	-0.5	0.0	-162.5*	208.8**
SODS-1	-1.3*	-0.2	-1.4*	0.4	-0.3	-0.6*	340.4**	131.7*
S.E for GCA effects	0.6	0.5	0.5	0.5	0.8	0.3	51.3	52.0

Table 4. Specific combining ability (SCA) effects in sweet corn F_1 hybrids for days to tasseling and silking, 100-kernel weight, and grain yield evaluated at the two locations of Khyber Pakhtunkhwa, Pakistan.

F_1 Hybrids	Days to tasseling		Days to silking		100-kernel weight		Grain yield	
	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat	Nowshera	Swat
NARCCCRI-17 × NARCCCRI-19	0.6	-0.2	0.1	1.2	0.4	-0.1	-51.4	-413.7**
NARCCCRI-17 × SWTS-1-4	3.2	0.3	2.8	0.5	-0.9	-0.8	-177.3	177.2
NARCCCRI-17 × SWTS-1-8	-2.3	-1.7	-1.2	-1.9	1.5	2.6**	-364.9*	181.6
NARCCCRI-17 × CCRIS-29	3.9*	-1.5	4.6**	-2.0	1.5	1.4	722.2**	106.8
NARCCCRI-17 × CCRIS-34	0.5	-0.9	0.7	-0.5	1.7	1.5	-408.3*	704.5**
NARCCCRI-17 × KHWS-1	0.5	-0.4	-0.1	-1.3	-0.1	-0.6	-23.9	128.9
NARCCCRI-17 × SODS-1	-0.7	-0.3	-0.8	-1.6	0.7	0.6	-126.8	-240.5
NARCCCRI-19 × SWTS-1-4	1.6	0.4	3.4*	-0.6	-1.1	-1.5	-344.6*	335.9*
NARCCCRI-19 × SWTS-1-8	2.6	-0.6	2.4	0.9	2.3	1.7	673.6**	266.9
NARCCCRI-19 × CCRIS-29	-2.2	-2.9*	-2.3	-2.6	-0.2	-0.8	407.4*	1141.5**
NARCCCRI-19 × CCRIS-34	-4.6*	-2.4	-3.7*	-2.1	-1.5	1.0	43.6	847.7**
NARCCCRI-19 × KHWS-1	0.9	-1.8	1.0	-1.0	0.2	0.7	394.7*	217.6
NARCCCRI-19 × SODS-1	2.2	-3.2*	0.8	-2.8	0.5	1.4	-289.6	227.7
SWTS-1-4 × SWTS-1-8	-3.4*	-2.6*	-3.3*	0.2	0.5	1.4	1219.3**	447.7**
SWTS-1-4 × CCRIS-29	-3.2*	-1.4	-3.6*	-2.3	1.5	3.4**	-577.1**	406.4*
SWTS-1-4 × CCRIS-34	0.5	-0.3	-0.4	-1.3	0.2	1.3	165.7	202.6
SWTS-1-4 × KHWS-1	-2.5	-0.8	-1.3	0.8	2.9	1.0	-96.6	952.0**
SWTS-1-4 × SODS-1	-3.3*	0.3	-2.9	1.5	1.7	1.7	657.4**	1103.6**
SWTS-1-8 × CCRIS-29	-0.2	0.6	-2.1	0.7	0.4	2.1*	-638.0**	989.8**
SWTS-1-8 × CCRIS-34	2.0	1.2	0.6	-0.8	3.6*	1.0	-189.1	1215.0**
SWTS-1-8 × KHWS-1	-2.0	0.2	-2.3	-0.6	0.3	-0.3	-30.8	739.4**
SWTS-1-8 × SODS-1	-0.8	-1.2	1.6	-1.9	-1.4	0.3	833.3**	370.0*
CCRIS-29 × CCRIS-34	-1.3	-0.6	-1.2	1.7	0.0	0.4	405.2*	-1440.3*
CCRIS-29 × KHWS-1	-0.3	-2.1	2.0	-1.2	0.3	1.1	-350.4*	-335.9*
CCRIS-29 × SODS-1	2.4	0.0	3.3*	-1.5	0.1	-0.2	626.9**	434.7**
CCRIS-34 × KHWS-1	-0.2	0.0	-1.4	-1.7	0.0	2.0*	485.8**	1042.3**
CCRIS-34 × SODS-1	-0.4	2.1	-1.5	3.5*	-0.2	-2.8**	676.2**	-213.6
KHWS-1 × SODS-1	1.1	-1.4	0.6	-0.8	0.0	1.9*	240.6	196.3
S.E for SCA effects	1.8	1.4	1.6	1.5	1.3	0.1	157.2	159.5

a poor general combiner with the highest positive significant GCA value of 1.8, but the same line (NARCCRI-17) had non-significant negative GCA at the Swat location. F_1 hybrid, NARCCRI-19 × CCRIS-34, was the best specific combiner for tasseling with significantly negative SCA (SCA = -4.6, P = 0.05) at Nowshera (Table 4). However, parents of the F_1 hybrid, NARCCRI-19 × CCRIS-34, showed non-significant GCA effects under both locations except NARCCCRI-19 at Nowshera, enlightening that heterozygosity in parental lines can refer to the variation in the genetic makeup of sweet corn inbreds. Other specific cross combinations for tasseling at Nowshera were F_1 hybrids, SWTS-1-4 × SWTS-1-8, SWTS-1-4 × SODS-1, and SWTS-1-4 × CCRIS-29, with significantly negative SCA values of -3.4, -3.3, and -3.2, respectively. Additionally, line SWTS-1-4 showed non-significant GCA with significant SCA mean squares in cross combinations, signifying the non-additive gene effects. Parent SWTS-1-8 of F_1 hybrid SWTS-1-4 × SWTS-1-8 was a good general combiner with the highest negative significant GCA estimate for tasseling at the Nowshera location. Analysis for the effects of SCA at the Swat location showed that F_1 hybrids, NARCCCRI-19 × SODS-1 (SCA = -3.2, P = 0.05) and NARCCCRI-19 × CCRIS-29 (SCA = -2.9, P = 0.05), exhibited significantly negative SCA; hence, the best specific combiners for tasseling. Thus, NARCCRI-19 × CCRIS-34 and SWTS-1-4 × SWTS-1-8 were best specific combiners for tasseling at Nowshera and Swat test locations, but parental lines of these hybrids (except SWTS-1-8) proved to be poor general combiners for the same trait.

Days to silking

Genotypes GCA and SCA mean squares for days to silking were highly significant at Nowshera while significant at Swat (Table 1). Further, GCA mean squares were greater than SCA at both locations. However, combining ability components due to GCA, SCA, and their ratio revealed that SCA was more than GCA, with the GCA-SCA ratio being less than unity indicating the role of non-additive gene action for silking at both test locations (Table 2). Chozin *et al.* (2017) and Revilla *et al*. (2021) also found the ratio of GCA and SCA less than 1 for maturity traits in maize, representing the function of non-additive gene action. Researchers like Stagnati *et al.* (2020), however, have suggested additive types of gene action for silking in maize. Jyoti *et al.* (2007), in a study of diallel analysis of six sweet corn inbreds, found that GCA and SCA variances were significant for most of the traits indicative of the role of additive, as well as, non-additive genetic mechanisms. In the same way, Zare *et al.* (2015), Aslam *et al.* (2017), and Ravi and Chikkalingaiah (2018) noted a lower value of GCA-SCA ratio (<1), emphasizing the function of non-additive over additive gene dimensions. On the contrary, Aly and Mousa (2011) and Ikram *et al*. (2021) determined additive types of gene action for silking. Significant GCA and SCA mean squares for days to silking have also been found by Al-Falahy (2015) and Zoric*et al.* (2022) signifying the magnitude of both additive and non-additive gene inheritance.

Two sweet corn parents, SWTS-1-8 (GCA = -2.0, P = 0.01) and SODS-1 (GCA = -1.4, P = 0.05), expressed desirable significantly negative general combining ability effects and hence, were good general combiners for silking at Nowshera. At Swat, inbred line SWTS-1-4 (GCA = -1.3, P = 0.05) displayed desirable negative significant GCA for silking, yet the same line (SWTS-1-4) was a poor combiner at Nowshera (Table 3). At Nowshera, parental line SODS-1 was a good general combiner but was non-significant at Swat. Specific combining ability for silking at Nowshera ranged from -3.7 to 4.6, and three F_1 hybrids, viz., NARCCCRI-19 × CCRIS-34 (SCA = -3.7, P = 0.05), SWTS-1-4 × CCRIS-29 (SCA = -3.6, P = 0.05), and SWTS-1-4 × SWTS-1-8 (SCA = -3.3, P = 0.05), were the best specific combiners for silking (Table 4). Parents of the same hybrids showed non-significant GCA, except SWTS-1-8, at the Nowshera location. Fluctuation of sweet corn hybrids from Nowshera to the Swat location appeared for the silking trait. Thus, the expression of a silking parameter controlled by several loci displayed greater genotype × environment interaction. Parent SWTS-1-8 of F_1 hybrid SWTS-1-4 × SWTS-1-8 was a good general combiner, with the highest negative GCA estimate at Nowshera for the said trait. Similarly, SCA for silking ranged from -2.8 to 3.5 at Swat, with hybrids NARCCCRI-19 × SODS-1, NARCCCRI-19 × CCRIS-29, and SWTS-1-4 × CCRIS-29 as the best specific combiners exhibiting highest negative SCA values of -2.8, -2.6, and -2.3, respectively. Hybrid NARCCCRI-17 × CCRIS-29 manifested the highest positive significant SCA at Nowshera and negative SCA at Swat. Parental inbred line NARCCCRI-17 of the same hybrid was also a poor combiner for silking at the Nowshera location. F_1 hybrid SWTS-1-4 × CCRIS-29 was a common good specific combiner with the highest negative SCA effect for silking at both (Nowshera and Swat) locations of Pakistan.

100-Kernel weight

Genotypes exhibited highly significant (P = 0.01) differences for 100-kernel weight at Swat only (Table 1). GCA mean squares were non-significant at both test locations, although SCA mean squares were highly significant (P = 0.01) at Swat. SCA mean squares were larger in magnitude than GCA at both locations for 100-kernel weight, pointing to a non-additive gene action in the control of the 100-kernel weight at the two locations (Table 2). Mohammed *et al*. (2014) and Ilyas *et al*. (2020) reported the importance of both additive and non-additive gene action, while Kumar *et al*. (2013) and Aslam *et al.* (2017) have reported the predominant role of non-additive gene action for the control of kernel weight in maize. However, Vafias and Ipsilandis (2005) and Asefa *et al*. (2008) have also reported that an additive gene action was more notable than a non-additive concerning the inheritance of 100-kernel weight in corn germplasm.

The inbred lines SWTS-1-8 (GCA = 0.91), NARCCCRI-17 (GCA = 0.31), and CCRIS-34 (GCA = 0.26) exhibited maximum positive but non-significant GCA estimates for 100-kernel weight at Nowshera. Parental line SWTS-1-8 (GCA = 0.6, P = 0.05) was a good general combiner for 100-kernel weight at Swat only. Additionally, parental line SODS-1 showed significantly negative GCA at Swat and non-significant negative GCA at Nowshera. Other parents with positive GCA values at Swat were NARCCCRI-17 and SWTS-1-4 (each with GCA = 0.3) for the 100-kernel weight (Table 3). Parental inbred line SWTS-1-8 exhibited significantly positive GCA for 100-kernel weight at Swat but showed non-significant GCA at Nowshera. Such results indicate that non-additive effects gain more impact from locations than additive genetic effects in 100-kernel weight. Specific combining ability effects for 100-kernel weight among F_1 hybrids ranged from -1.5 to 3.6 at Nowshera and -2.8 to 3.4 at Swat. F_1 hybrid SWTS-1-8 × CCRIS-34 was the only best specific combiner for 100-kernel weight due to a significantly positive SCA of 3.6 at Nowshera (Table 4). Under both locations, parental line CCRIS-34 showed non-significant GCA effects; however, the same line (CCRIS-34) showed significant SCA in cross combination at Nowshera, indicating the position of non-additive gene effects. In contrast at Swat, five F_1 hybrids were best specific combiners for 100-kernel weight: SWTS-1-4 × CCRIS-29 (SCA = 3.4, P = 0.01), NARCCCRI-17 × SWTS-1-8 (SCA = 2.6, P = 0.01), SWTS-1-8 × CCRIS-29 (SCA = 2.1, P = 0.05), CCRIS-34 × KHWS-1 (SCA = 2.0, P = 0.05), and KHWS-1 × SODS-1 (SCA = 1.9, P = 0.05).

Grain yield

Combining ability ANOVA showed that maize genotypes differed significantly (P = 0.01) for grain yield at Swat only (Table 1). Scientists, Gissa *et al.* (2007), Puttarach *et al*. (2016), and Ahmad *et al*. (2019) have also reported significant differences in grain yield in corn genotypes. Similarly, GCA and SCA variances for grain yield were highly significant (P = 0.01) at Swat while non-significant at Nowshera. GCA mean squares were higher than SCA at Nowshera, but the opposite was true at Swat. Such results designate that non-additive gene effects acquire more influence by location than additive genetic effects in grain yield. The same trend occurred for combining ability components; however, the GCA-SCA ratio was lower than unity, indicating an over-dominant type of gene action for grain yield (Table 2). Kumar *et al*. (2013) and Oyekunle and Apraku (2014) also observed a lower GCA-SCA ratio for grain yield in maize genotypes. On the other hand, Aly and Mousa (2011) and Zare *et al.* (2017) have reported that additive gene effects were predominant in the control of grain yield in maize. However, Werle *et al.* (2014), Baseer *et al*. (2019), and Zystro *et al.* (2021) noted that both additive and non-additive genetic effects showed involvement in the control of grain yield per plant in maize.

At Nowshera, the best general combiners for grain yield were parental lines SODS-1 (GCA = 340.4, P = 0.01) and NARCCCRI-19 (GCA = 141.0, P = 0.05), while at Swat, the best general combiners were parental lines SWTS-1-8 (GCA = 369.5, P = 0.01), KHWS-1 (GCA = 208.8, P = 0.01), and SWTS-1-4 (GCA = 134.0, P = 0.05) (Table 3). Parental line SODS-1 showed significantly positive GCA at Nowshera and Swat and, thus, a good general combiner for grain yield. Parental inbred line NARCCCRI-19 exhibited significantly positive GCA at Nowshera but had non-significant GCA at Swat. In contrast, inbred line NARCCCRI-17 was a poor general combiner for the trait due to considerably negative GCA estimates at both locations. Similarly, inbred line KHWS-1 expressed significantly negative GCA for grain yield at

Nowshera but notably positive GCA at Swat, revealing that a large part of total genetic variability for grain yield was under the non-additive gene legacy. Thus, the expression of a grain yield controlled by several loci displayed better genotype × environment interaction. Eleven F_1 hybrids at Nowshera and 14 hybrids at Swat expressed significantly positive SCA for grain yield, with a range of 394.7 ($P = 0.05$) to 1219.3 ($P = 0.01$) and 335.9 ($P = 0.05$) to 1042.3 ($P = 0.01$), respectively. Among these, six F_1 hybrids, viz., NARCCCRI-19 × CCRIS-29, SWTS-1-4 × SWTS-1-8, SWTS-1-4 × SODS-1, SWTS-1-8 × SODS-1, CCRIS-29 × SODS-1, and CCRIS-34 × KHWS-1 were the common best specific combiners for grain yield both at Nowshera and Swat locations (Table 4). Fluctuation of hybrids from Nowshera to the Swat location transpired for grain yield, and among six F_1 hybrids the parents showed significant GCA, except NARCCCRI-19, at the Swat location. Sweet corn hybrid CCRIS-29 × KHWS-1 was a poor specific combiner due to highly substantial ($P = 0.01$) negative SCA estimates for grain yield at both locations. At Swat, parents (SWTS-1-4 and SODS-1) of F_1 hybrid SWTS-1-4 × SODS-1 were also good general combiners with significantly affirmative GCA estimates for grain yield.

CONCLUSIONS

Determination of early maturity in sweet corn is imperative to determine the suitability of the crop to diverse locations in the cropping system. In the presented study, almost all parameters came under non-additive control, indicating that inter matting of selected progeny in the upcoming early segregating generation obtained by crossing their parents will release hidden genetic variability breaking through undesirable linkages involved in different characteristics like earliness and high yield. Over-dominance for most physiological traits revealed that delayed selection could be more effective. Combining ability analysis at both locations disclosed that inbred lines SWTS-1-8 and SODS-1 were good general combiners for morphological and yield-contributed traits and would likely concentrate favorable alleles for the target plant attributes. However, sweet corn hybrids SWTS-1-4 × SWTS-1-8, SWTS-1-4 × CCRIS-29, and SWTS-1-8 × CCRIS-34 were broad-spectrum outstanding hybrids at both locations for further testing in different sets of environments for release in coming years.

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