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COMBINING ABILITY ANALYSIS FOR NORTHERN CORN LEAF BLIGHT RESISTANCE AND YIELD IN SWEET CORN (*ZEA MAYS* L. VAR. *SACCHARATA*)

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SUMMARY

Northern corn leaf blight (NCLB) is a serious foliar disease in sweet corn (*Zea mays* L. var. *saccharata*) that considerably affects its productivity. This study evaluated the general combining ability (GCA) and specific combining ability (SCA) for NCLB resistance and yield-related traits in sweet corn. The crossing of five inbred lines and two testers using a line-by-tester design produced 10 F_1 hybrids. These F_1 hybrids and two commercial checks underwent evaluation through a randomized complete block design (RCBD) in 2025 at the PT BISI International, Pujon, Indonesia. The results showed Line B had a desirable negative GCA for disease severity and a positive GCA for yield, identifying it as a robust candidate parent for high-yielding and NLCB-resistant hybrids. Disease severity management was mainly with the non-additive gene action and revealed a weaker association between SCA and the hybrid performance, indicating that no single parameter was sufficient to predict hybrid success. Instead, an integrated selection approach is necessary considering the GCA, SCA, and field performance. The hybrid B × G emerges as the best candidate, showing significant resistance to NCLB and higher yield. The selection of parental genotypes based on combining ability and field evaluation could accelerate the development of disease-resistant and high-yielding hybrids.

Keywords: Sweet corn (*Z. mays* L. var. *saccharata*), *Exserohilum turcicum*, additive, dominance, variance components, hybrid performance

Key findings: The results revealed non-additive gene action predominantly influenced NCLB resistance in sweet corn (*Z. mays* L. var. *saccharata*). The identification of hybrid B × G succeeded as the best potential to use in developing sweet corn hybrids with NCLB resistance and higher yield.

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INTRODUCTION

Sweet corn (*Zea mays* L. var. *saccharata*) plays an important role in the national economy, as it serves as an ingredient in various valuable processed foods. In fresh daily use, sweet corn consumption is usually at the immature stage, generally boiled and steamed (Syukur and Rifianto, 2013). From nutritional perspectives, sweet corn provides more calories (86 calories per 100 g) than most vegetables and is also rich in many bioactive compounds that support health (Junpatiw *et al*., 2013; Swapna *et al*., 2020).

However, sweet corn productivity often incurs disruption from various diseases, and the Northern corn leaf blight (NCLB) is one of the crucial ones, caused by the *Exserohilum turcicum* (Et). Damage to the green leaf area during the grain-filling stage may result in yield losses of up to 50% in susceptible hybrids. This disease has the highest potential to cause severe damage and has received extensive studies in the past (De-Rossi and Reis, 2014). The initial symptoms that appear are small, chlorotic spots, which then develop into elliptical lesions about 12 mm wide and 2.5 to 15 cm long (Ijaz and Fan, 2024). The NCLB disease symptoms usually occur at all stages of plant growth and development (Meng *et al*., 2025).

The development of sweet corn cultivars with resistance to NCLB is essential to address the said issues, which can be attainable by utilizing the combining ability and heterosis. Heterosis is a phenomenon where hybrid offspring derived by crossing two different parental lines have superior performance compared with both parents (Fujimoto *et al*., 2018). A line-by-tester combining ability analysis is essential to optimize the heterotic effects in improving sweet corn resistance to NCLB. This approach emerged as highly effective in estimating combining ability and heterosis and in selecting the desirable parental genotypes for developing superior hybrids (Kamara *et al*., 2014).

Line-by-tester combining ability is a widely used method in plant breeding for estimating the genetic potential of parental lines through assessment of the general combining ability (GCA) and specific combining ability (SCA) effects among parental lines and their hybrids, respectively. Mane *et al*. (2024) reported several parental lines and testers showed considerable GCA effects for yield-related traits, while certain F_1 hybrids exhibited the highest desirable SCA effects, indicating their suitability for advancement in breeding programs. The GCA effects reflect the additive gene effects and represent the average performance of the parental genotype when crossed with multiple partners. In contrast, SCA captures the variants being associated with a particular hybrid combination and primarily influenced by non-additive gene action (Ali *et al*., 2014). Although line x tester analysis has reached wide application in sweet corn breeding, most previous studies have primarily focused on yield and its related traits. Limited information is available regarding the genetic control of NCLB resistance and its integration with yield performance in sweet corn. Therefore, simultaneous evaluation of combining ability for NCLB resistance and yield-related traits is essential to provide a more comprehensive basis for developing resistant and high-yielding hybrids. The following study aimed to estimate the GCA and SCA for NCLB resistance and yield-related traits in sweet corn.

MATERIALS AND METHODS

Study area and genetic material

The study transpired at the experimental field of PT BISI International, Tbk, Pujon, Malang, East Java, Indonesia, with an altitude of 1100 meters above sea level. The genetic material of sweet corn (*Z. mays* L. var. *saccharata*) used in this study comprised 19 genotypes, including five parental lines, two testers, 10 F_1 hybrids derived through line-by-tester crossing, and two commercial check cultivars (Table 1). In January 2024, five lines (A, B, C, D, and E) underwent crossing with two testers (F and G) to produce 10 F_1 hybrid combinations (A × F, A × G, B × F, B × G, C × F, C × G, D × F, D × G, E × F, and E × G). The

Table 1. Genetic material of sweet corn (*Z. mays* L. var. *saccharata*) used in the study.

Genotype	Type	Origin	Description		
			Leaf angle	Disease resistant	Ear shape
A	Line	PT BISI	erect	susceptible to NCLB	conical
B	Line	PT BISI	semi-erect	resistant to NCLB	cylindrical
C	Line	PT BISI	semi-erect	medium resistant to NCLB	conical
D	Line	PT BISI	erect	susceptible to NCLB	conical
E	Line	PT BISI	semi-erect	medium resistant to NCLB	cylindrical-conical
F	Tester	PT BISI	semi-erect	medium resistant to NCLB	cylindrical-conical
G	Tester	PT BISI	semi-erect	resistant to NCLB	conical

B × G with lowest NCLB severity

D × F with highest NCLB severity

Figure 1. Field performance of F_1 hybrids with the lowest (B × G) and highest (D × F) NCLB severity in sweet corn.

parental lines and testers were selected based on their genetic diversity, stable agronomic performance (Table 1).

Field experiment

The planted sweet corn genotypes totaled 19 in a randomized complete block design (RCBD) with three replications during January to April 2025. Each experimental plot comprised four rows, five meters long, with a spacing of 75 cm × 20 cm. Fertilization commenced by applying 8 g of NPK (15-15-15) per planting hole at the time of direct sowing. The second and third fertilizations proceeded at three and five weeks after planting, respectively, using 8 g of urea per planting hole. Artificial inoculation with *Exserohilum turcicum* followed 21 days after planting by spraying a spore suspension containing 4.5×10^4 spores mL^{-1}, following the procedure as described by Yang *et al*. (2017).

Observations and measurements

Field observations ensued to evaluate the maize F_1 hybrids for their resistance to NCLB and agronomic performance. Disease assessments occurred 30 days after inoculation (51 days after sowing) and continued every 10 days thereafter, 61, 71, and 81 days after sowing. Disease severity scoring ranged on a 1 to 9 scale, based on the percentage of infected leaf area (Suresh, 2023), where lower scores indicate resistance and higher scores indicate greater disease severity. Agronomic and yield-related traits observed included disease severity (DS), days to harvest (DH), ear length (EL), kernel row number (KR), yield (Y), and total soluble solids (TSS).

Data analysis

All the recorded data based on various variables underwent the analysis of variance (ANOVA) according to RCBD design using TNAUSTAT software. Line-by-tester analysis, as performed, followed the methodology of Kempthorne (1957) to estimate GCA and SCA effects. According to Hallauer *et al.* (2010), heterosis calculation was relative to the mid- and better parents.

RESULTS AND DISCUSSION

Analysis of variance and mean values

Sweet corn (*Z. mays* L. var. *saccharata*) genotypes with lower NCLB severity values were generally more resistant, while the higher severity values reflect the susceptibility. In this study, the analysis of variance for the line-by-tester cross combinations (Table 2) showed most sources of variation had a highly significant influence on disease severity. The significant genotype effect demonstrates the considerable genetic variability among parental lines and their hybrids (Tabu *et al*., 2023). The differences among the parents revealed the lines used in this study have substantial genetic diversity. The highly remarkable differences between the parental genotypes and the F_1 progeny indicate the heterosis for disease severity.

The significant differences among the F_1 hybrids suggested that selection can take place effectively to identify the cross combinations with lower disease severity values, with an improvement in resistance to NCLB. Significant effects of the lines and testers reflect the variability associated with GCA, while significant line-by-tester interactions revealed the contribution of SCA. The results enunciated that resistance to NCLB had the control of the combination of additive and non-additive gene effects. The wide genetic diversity among parental lines exhibited robust potential for improving sweet corn resistance to NCLB. These results align with the observations of Rice and Tracy (2013) and Belay (2022), who reported that genetic differences among parental cultivars provide opportunities to obtain hybrids with the desired heterosis and disease resistance. The significant line-by-tester interaction indicates the expression of NCLB resistance both depends on the individual genetic value of the parents and on the unique combination of dominance and epistatic interactions contributed by each cross.

ANOVA revealed maize genotypes have a highly significant effect on various traits, such as days to harvest, yield index, ear length, kernel row number, and total soluble solids, confirming considerable genetic difference among parental lines and their hybrids (Table 2). Therefore, these differences signified that each genotype has a different genetic potential to express a particular trait. Based on these results, breeders have an opportunity to select the desired cross combinations. The notable difference about the genetic makeup of parental lines indicates diverse genetic backgrounds, which is crucial to increasing the scope of finding superior hybrids. These results were consistent with Magar *et al.* (2021) and Abebe *et al.* (2020), who reported genetic variability among maize genotypes can be favorable in improving grain yield. Significant differences among parental genotypes and F_1 hybrids for traits, such as days to harvest, yield index, ear length, kernel

Table 2. Combined analysis of variance for disease severity, agronomic, and yield-related traits in sweet corn.

Source of variation	d.f.	Mean squares					
		DS	DH	Y	EL	KR	TSS
Replications	2	91.94**	1.90^{ns}	13.18**	0.94*	0.02	0.36
Genotypes	16	345.75**	28.31**	70.06**	16.70**	2.82**	1.67**
Parents	6	401.34**	15.49**	18.61**	2.47**	2.40**	3.034**
Parents vs. F$_1$	1	427.67**	259.23**	766.96**	213.93**	13.37**	5.54**
F$_1$ hybrids	9	315.59**	11.20**	26.93**	4.27**	1.92**	0.34^{ns}
Lines	4	295.27**	13.20^{ns}	47.15**	8.25**	2.98**	0.37^{ns}
Testers	1	1454.36**	19.20^{ns}	47.30**	0.02^{ns}	3.68**	0.11^{ns}
Line-by-tester	4	51.22**	7.20^{ns}	1.61^{ns}	1.36**	0.43^{ns}	0.35^{ns}
Error	32	11.43	3.01	0.80	0.27	0.31	0.26
Coefficient of variation (CV)		5.16	1.77	7.37	3.14	4.03	3.99

Remarks: *Significant at $P < 0.05$, **Significant at $P < 0.01$, ns: nonsignificant, DS: disease severity, DH: days to harvest, Y: yield, EL: ear length, KR: kernel row number, and TSS: total soluble solids.

Table 3. General combining ability effects among parental lines and testers for disease severity, agronomic, and yield-related traits in sweet corn.

No.	Parental lines/testers	DS	DH	Y	EL	KR	TSS
Lines							
1	A	4.96**	0.7^{ns}	-0.43^{ns}	0.87**	0.32^{ns}	0.11^{ns}
2	B	-11.33**	0.2^{ns}	4.34**	0.38^{ns}	0.51*	0.34^{ns}
3	C	-1.7^{ns}	-0.3^{ns}	-3.04**	1.12**	-0.63**	0.01^{ns}
4	D	6.07**	1.7*	0.75*	-0.66**	-0.88**	-0.33^{ns}
5	E	2^{ns}	-2.3**	-1.62**	-1.71**	0.68**	-0.13^{ns}
Testers							
6	F	6.96**	-0.8^{ns}	-1.26**	-0.03	-0.35*	0.06^{ns}
7	G	-6.96**	0.8^{ns}	1.26**	0.02	0.35*	-0.06^{ns}

Remarks: *Significant at $P < 0.05$, **Significant at $P < 0.01$, ns: nonsignificant, DS: disease severity, DH: days to harvest, Y: yield, EL: ear length, KR: kernel row number, and TSS: total soluble solids.

row number, and total soluble solids, disclosed that non-additive genes contribute to the heterosis.

General combining ability effects

The general combining ability effects for disease severity showed that parental Line B has a significantly negative GCA value, indicating that additive alleles could reduce disease severity (Table 3). As a lower disease severity indicates higher resistance, negative GCA effects were essential to identify the resistant parental lines. Those resistant lines can transmit the beneficial alleles to their offspring to ensure stable NCLB resistance across their generations. GCA effects enable the identification of superior parental lines for potential exploration to generate and select improved cross-combinations for hybrid development (El-Azeem *et al.,* 2022). In contrast, the parental lines A, D, and E showed positive GCA effects for disease severity, indicating limited suitability for resistance breeding. These results agreed with Rice and Tracy (2013), who reported negative GCA values for NCLB resistance effectively decreased the severity of the disease, identifying them as ideal for developing resistant hybrids in sweet corn.

Positive GCA effects are desirable for enhancing grain yield and its related traits, whereas negative GCA effects are advantageous for improving traits such as earlier maturity (El-Latif *et al.,* 2023). For days to harvest, negative GCA values were favorable for early maturity (Bhusal and Lal, 2020). The recorded line E had a significant negative GCA (-2.3), indicating superiority for early maturity, while the tester F showed a nonsignificant negative GCA value (-0.8), suggesting the tendency toward earlier maturity. The results signified additive gene effects could play an important role in controlling early flowering and maturity in sweet corn. Early-maturing genotypes appeared to be desirable in crop rotation systems and reduced risks of leaf diseases, such as NCLB, at later growth stages.

For yield index, positive GCA values are potentially beneficial. Parental line B had the highest and significant GCA for yield index (4.34), while tester G recorded the highest GCA (1.26) among the testers, identifying both as promising parental lines for yield improvement. Line C exhibited the topmost GCA for ear length (3.4) and line E for kernel row number (0.68), whereas tester G consistently showed positive GCA values across the traits. For TS, line B (0.34) and tester G (0.06) showed the maximum GCA values, indicating their contribution to sweetness. These results suggested parental lines B, C, and E possess favorable additive genes for yield and related traits, while tester G demonstrates a stable and broad combining ability. Belay (2022) and Sharma *et al*. (2020) also highlighted the importance of parental cultivars with high GCA values in transmitting desirable traits through the additive gene action. Notable GCA effects authenticate the greater role of additive gene effects controlling various traits.

Overall, parental line B exhibited the best GCA values for yield and sweetness, identifying it as a valuable donor for improving productivity and sugar content in sweet corn. Lines with the highest GCA values significantly contribute to the offspring performance, and additive gene effects played a substantial role. Inbred lines displaying significant and positive GCA effects for a specific target trait were considerably good general combiners, possessing the highest genetic potential to transmit beneficial alleles to their offspring through hybridization (Badu-Apraku *et al.*, 2021). Recurrent selection is an effective method to exploit the proportion of available additive genetic variance (Bhusal and Lal, 2020). According to Rodríguez-Pérez *et al*. (2025), inbred lines with the ultimate GCA values can serve to develop synthetic cultivars with high-yield potential and broader adaptability. In cross-pollinated crops, such as maize, hybrids generally exhibit a higher yield potential than synthetic varieties (Ahmed *et al*., 2022) due to the exploitation of both additive and non-additive gene effects. Lines C and E also showed potential for improving ear length and kernel row number, respectively. The consistent performance of tester G for various traits confirmed its reliability as a male parent in hybrid development. The results emphasized that selecting parental genotypes with robust GCA effects is crucial for accumulating beneficial additive genes and developing sweet corn hybrids with the highest potential for yield, good quality, and disease resistance.

Specific combining ability effects

For disease severity, hybrids with negative SCA values were desirable. The SCA analysis presented that F_1 hybrids A × F, B × G, C × F, D × G, and E × G exhibited negative SCA values for disease severity (Table 4). The F_1 hybrids with negative SCA values observed with the lower disease severity indicated a sustainable resistance. The results showed non-additive genes could significantly contribute to lower disease severity (Zhu *et al.*, 2023). The variance of SCA (13.65) was higher than that of GCA (8.97), suggesting that a non-additive gene action played a more important role than an additive gene action (Table 5). The hybrid A × F recorded the lowest and negative SCA value (-4.37) among all cross combinations; however, this hybrid expressed a high average disease severity (75.56%), emerging to be significantly different from other F_1 hybrids, such as B × F, B × G, C × G, D × G, and E × G (Figure 1). The hybrid with the best SCA value does not always show the best performance per se because the hybrid performance incurs influences from genotype (G), environment (E), and genotype-by-environment interaction (GEI) effects (Belay, 2022).

Table 4. Specific combining ability effects and performance per se of F_1 hybrids for disease severity, agronomic, and yield-related traits in sweet corn.

No.	F_1 hybrids	SCA	DS	SCA	DH	SCA	Y	SCA	EL	SCA	KR	SCA	TSS
1	A × F	-4.37^{*}	75.6^{ns}	0.3^{ns}	96.0^{ns}	-0.11^{ns}	13.6^{ns}	0.57^{ns}	19.7^{ns}	-0.09^{ns}	14.1^{ns}	-0.09^{ns}	13.1^{ns}
2	A × G	4.37^{*}	70.4^{ns}	-0.3^{ns}	97.0^{ns}	0.11^{ns}	16.3^{ns}	-0.57^{ns}	18.6^{ns}	0.09^{ns}	14.9^{ns}	0.09^{ns}	13.2^{ns}
3	B × F	2.3^{ns}	65.9^{ns}	-0.2^{ns}	95.0^{ns}	-0.39^{ns}	18.1^{ns}	-0.04^{ns}	18.6^{ns}	-0.07^{ns}	14.3^{ns}	0.01^{ns}	13.5^{ns}
4	B × G	-2.3^{ns}	47.4^{ns}	0.2^{ns}	97.0^{ns}	0.39^{ns}	21.4^{ns}	0.04^{ns}	18.7^{ns}	0.07^{ns}	15.1^{ns}	-0.01^{ns}	13.3^{ns}
5	C × F	-1.41^{ns}	71.8^{ns}	0.3^{ns}	95.0^{ns}	-0.5^{ns}	10.6^{ns}	-0.48^{ns}	18.9^{ns}	0.02^{ns}	13.2^{ns}	0.07^{ns}	13.2^{ns}
6	C × G	1.41^{ns}	60.7^{ns}	-0.3^{ns}	96.0^{ns}	0.5^{ns}	14.1^{ns}	0.48^{ns}	19.9^{ns}	-0.02^{ns}	13.9^{ns}	-0.07^{ns}	12.9^{ns}
7	D × F	2.67^{ns}	83.7^{ns}	1.3^{ns}	98.0^{ns}	0.78^{ns}	15.6^{ns}	0.39^{ns}	18.0^{ns}	0.43^{ns}	13.4^{ns}	-0.33^{ns}	12.5^{ns}
8	D × G	-2.67^{ns}	64.4^{ns}	-1.3^{ns}	97.0^{ns}	-0.78^{ns}	16.6^{ns}	-0.39^{ns}	17.3^{ns}	-0.43^{ns}	13.2^{ns}	0.33^{ns}	13.0^{ns}
9	E × F	0.81^{ns}	77.8^{ns}	-1.7^{ns}	91.0^{ns}	0.22^{ns}	12.7^{ns}	-0.44^{ns}	16.1^{ns}	-0.29^{ns}	14.2^{ns}	0.34^{ns}	13.3^{ns}
10	E × G	-0.81^{ns}	62.2^{ns}	1.7^{ns}	96.0^{ns}	-0.22^{ns}	14.8^{ns}	0.44^{ns}	17.1^{ns}	0.29^{ns}	15.5^{ns}	-0.34^{ns}	12.5^{ns}

Remarks: *Significant at $P < 0.05$, ns: nonsignificant, DS: disease severity, DH: days to harvest, Y: yield (t ha^{-1}), EL: ear length (cm), KR: kernel row number, and TSS: total soluble solids (°brix).

Table 5. Variance component for disease severity, agronomic, and yield-related traits in sweet corn.

Traits	Variance components			
	σ^2GCA	σ^2SCA	σ^2A	σ^2D
DS	8.97	13.65	35.91	54.61
DH	0.13	1.76	0.54	7.06
Y	0.86	0.15	3.46	0.63
EL	0.09	0.34	0.39	1.38
KR	0.05	0.08	0.20	0.32
TSS	0.00	0.0583	0.00	0.2333

Remarks: DS: disease severity, DH: days to harvest, Y: yield, EL: ear length, KR: kernel row number, and TSS: total soluble solids.

The correlation analysis showed the relationship between SCA and F_1 hybrid performance was weak and inconsistent across all traits (Table 6). The only trait of total soluble solids displayed a significant correlation, whereas other traits did not. The weak correlation between SCA and F_1 hybrid performance suggests the effects of the non-additive gene influencing SCA are not always evident in hybrid performance, possibly due to environmental influence and the contribution of additive gene effects for some traits. These results aligned with the findings of Solomon *et al.* (2012), who reported F_1 hybrid performance often has non-association with SCA effects. The SCA effects expressed by the different F_1 hybrids were highly environment dependent, making the identification of hybrids with stable performance across the environments crucial. Therefore, the SCA values proved specific to the combination of the genotype and environment, and their use as a selection criterion should be parallel with field phenotype validation. In relation to the performance per se of F_1 hybrids, the most resistant F_1 hybrid was B × G (Figure 1), as derived from parental lines with the best GCA values.

A negative SCA value for days to harvest indicates the contribution of non-additive gene effects leading to accelerated reproductive and maturation phases, which had a direct association with earliness. Based on Table 4, five F_1 hybrids (A × G, B × F, C × G, D × G, and E × F) exhibited nonsignificant negative SCA values for days to harvest, suggesting the contribution of non-additive gene effects toward early maturity. Meanwhile, other hybrids showed positive but nonsignificant SCA values, indicating a longer maturation period. The early-maturing F_1 hybrid, representing the most early-maturing plant with the best SCA value, was the cross E × F derived from the best general combiners (Table 6). Bhusal and Lal (2020) reported an early maturity from the parent with an average GCA × good GCA effects.

Table 6. Correlation among the specific combining ability and performance per se for disease severity, agronomic, and yield-related traits in sweet corn.

Traits	SCA vs. F_1 performance per se	MPH vs. F_1 performance per se	BPH vs. F_1 performance per se
DS	0.27^{ns}	0.29^{ns}	0.24^{ns}
DH	0.53^{ns}	0.79^{ns}	0.73^{*}
Y	0.16^{ns}	0.04^{ns}	-0.12^{ns}
LE	0.23^{ns}	0.81^{ns}	0.80^{ns}
KR	0.31^{ns}	0.74^{*}	0.58^{ns}
TSS	0.7^{*}	0.19^{ns}	0.30^{ns}

Remarks: *Significant at $P < 0.05$, ns: nonsignificant, MPH: mid-parent heterosis, BPH: better-parent heterosis, DS: disease severity, DH: days to harvest, Y: yield, EL: ear length, KR: kernel row number, and TSS: total soluble solids.

For yield index, four F_1 hybrids (A × G, C × G, D × F, and E × F) observed with positive and nonsignificant SCA values indicated a tendency toward higher yield potential (Table 4). Among these F_1 hybrids, the hybrid B × G succeeded in its identification as the best cross combination, with an SCA value of 0.39, derived from parents with the best × best GCA effects. These results were also greatly analogous to the findings of Tabu *et al.* (2023), who reported that for yield traits, the promising hybrids with significant higher SCA effects came from parental genotypes with higher GCA effects. Although the F_1 hybrid B × G did not have the highest SCA value, it exhibited the best performance per se, likely because the SCA expressed a non-correlation with performance per se (Table 6). A positive SCA for this desirable trait indicated better yield performance.

For ear length, the F_1 hybrids with positive SCA values are also desirable for longer ears. Five F_1 hybrids (A × F, B × G, C × G, D × F, and E × G) had positive SCA values of 0.57, 0.04, 0.48, 0.39, and 0.44, respectively, for ear length (Table 4). Based on per se performance, the F_1 hybrid C × G emerged with the longest ear length, derived from parental genotypes with the best GCA values. The F_1 hybrid A × F exhibited the best SCA value, being identified as the second best for performance per se, with the said hybrid derived from parental genotypes with high × low GCA effects. According to Arifin *et al.* (2018), the best F_1 hybrid with desirable yield components and higher yield generally involves one parent with a higher GCA effect.

For kernel row number, the F_1 hybrids with positive SCA values are also desirable, as a higher kernel row number is an advantageous trait. Five F_1 hybrids (A × G, B × G, C × F, D × F, and E × G) had nonsignificant positive SCA values for kernel row number. The hybrid with the highest kernel row number was E × G, derived from parental genotypes with higher GCA values. These results were consistent with the findings of Bhusal and Lal (2020), who reported hybrids with higher kernel row numbers entailed development from crossing parental genotypes with high × high GCA effects. In sweet corn, ear length is an important trait significantly influencing yield because it determines the number of kernels per ear and slightly affects kernel weight, whereas kernel row number considerably contributes to kernel size and total plant yield. For total soluble solids, positive SCA values were also favorable, as indicated by the higher sugar content, contributing to sweetness. Five F_1 hybrids (A × G, B × F, C × F, D × G, and E × F) showed nonsignificant positive SCA values for total soluble solids. The sweetest hybrid, B × F, resulted from parental cultivars with the best GCA values.

The SCA values represent the performance of a hybrid resulting from the cross between two parental genotypes, and the higher SCA values generally came from parental cultivars with higher GCA effects (Solomon *et al*., 2012). Negative SCA values for disease severity and days to harvest and positive SCA values for yield index, ear length, kernel row number, and total soluble solids indicate the contribution of non-additive gene effects. This leads to improved hybrid performance, suggesting the specific genetic interactions between parents generate heterotic effects.

CONCLUSIONS

In sweet corn (*Z. mays* L. var. *saccharata*), the parental line B exhibited the best GCA effects for resistance to the Northern corn leaf blight, as confirmed by the lowest GCA value for disease severity (−11.33) and a positive GCA value for yield index (4.34). The F_1 hybrid, B × G, showed the best SCA effects, along with high performance per se. Similarly, the F_1 hybrid B × G exhibited the highest heterosis accompanied by superior performance per se.

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