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Screening of Sesame Genotypes for Resistance to Major Sesame Disease in Bako Area and East Wollega Zone

Abay Guta [1*], **Addis Shiferaw** [2]
[1] Oromia Agricultural Research Institute, Bako Agricultural Research Center, P.O. box 3, Bako, Ethiopia
[2] Oromia Agricultural Research Institute, P.O. Box 81465, Addis Ababa, Ethiopia

* Corresponding Author: **Abay Guta**

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Abstract
Sesame (Sesamum indicum L.) is one of the most important and ancient oilseed crops valued for its high-quality edible oil, nutritional properties, and economic importance. Sesame is an excellent source of vegetable oil, and is known as the "queen of oil seeds" due to its high oil content with unsaturated fatty acids, proteins and carbohydrates. However, its productivity is constrained by several foliar diseases, particularly bacterial blight and Cercospora leaf spot, which are widely distributed in Ethiopia. The experiment evaluated 64 sesame genotypes to identify sources of resistance and high-yielding lines under natural disease pressure at Bako Agricultural Research Center in Western Ethiopia. The trial was conducted using an alpha lattice design with two replications. Two rows for one intery genotype with three replications and one block containing eight genotypes. Disease severity was assessed on eight tagged plants per plot using a 0–6 scale for bacterial blight and a 0–5 scale for Cercospora leaf spot, and converted into a percentage severity index (PSI). The area under the disease progress curve (AUDPC) was computed. Significant ($p < 0.01$) variation was observed among genotypes for disease severity, AUDPC, and grain yield. Final bacterial blight severity ranged from 9.0% to 41.2%, while Cercospora severity ranged from 5.0% to 33.2%. Several genotypes (e.g., SE42, SE51.4, SE14, SE39.1, SE49.1, SE4.1) exhibited strong resistance to one or both diseases. Yield varied widely, with SE42.1 (1039 kg ha^{-1}), SE20.2 (973.9 kg ha^{-1}), and SE54.2 (960.4 kg ha^{-1}) being the top performers. These genotypes represent promising candidates for breeding programs aimed at developing high-yielding and disease-resistant sesame varieties.

Keywords: Bacterial blight, Cercospora leaf spot Sesame, AUDPC, genotype screening, disease resistance

1. Introduction

Sesame (Sesamum indicum L.), a member of the family *Pedaliaceae*, is one of the world's most ancient and important oilseed crops (Falusi and Salako, 2001) [9]. It is a short-day plant, predominantly self-pollinated, with natural crossing rates ranging from 2% to 48% (Sarker, 2004; Gebremichael and Parzies, 2011) [11, 20]. The growth period may range from 70 days to 150 days, depending on the variety and the conditions of cultivation (Ashri, 1998) [3]. Sesame requires adequate moisture for germination and early growth, and a precipitation of 300 mm to 800 mm per season is necessary for reasonable yields (Terefe *et al*., 2012) [26].

Its seeds contain 44–58% high-quality oil rich in unsaturated fatty acids, 18–25% protein, and a range of health-promoting lignans, such as sesamin, sesamol, and sesamolin. These compounds contribute to its oxidative stability and long shelf life. Sesame is used for food, medicine, cosmetics, and industrial purposes, and is increasingly being explored for biodiesel production (Nupur *et al*., 2010; De Lima *et al*., 2020; Dias *et al*., 2017; Anastasi *et al*., 2017) [2, 6, 7]. In addition, sesame seeds are rich in minerals (calcium, iron, phosphorus) and vitamins (vitamin A, thiamin, and riboflavin). Ethiopia is one of the leading producers of sesame globally. Sesame is the country's second most important export crop after coffee, contributing significantly to national foreign exchange earnings, rural employment, and household livelihoods. In 2020, sesame covered over 375,000 hectares, accounting for nearly half of the national oilseed production area (Taghouti *et al*., 2017; Abebe, 2016; ECACC, 2020; Gebremedhn *et al*., 2019; FAOSTAT, 2019) [1, 13, 23].

Despite its importance, sesame production is constrained by biotic and abiotic factors. Among these, foliar diseases, particularly bacterial blight (caused by Xanthomonas campestris pv. sesami) and Cercospora leaf spot (Cercospora sesami), are major threats

(Terefe *et al*, 1992; Getinet *et al*., 1997; Zerihun, 2012) [15, 25, 28]. These diseases cause severe defoliation, reduce photosynthetic area, and significantly lower grain yield. In high-rainfall regions such as Western Ethiopia, bacterial blight can result in complete crop failure (Golla *et al*., 2019; Bashir *et al*., 2007) [4, 16].

Genetic resistance is the most economical, environmentally friendly, and sustainable method for managing sesame diseases. However, there is limited information on the resistance status of germplasm collections under high disease pressure in Western Ethiopia (Geremew *et al*., 2012) [14]. Therefore, this study aimed to screen 64 sesame genotypes for resistance to major foliar diseases and identify genotypes with high grain yield potential

2. Materials and methods

2.1. Description of the Study Area

The experiment was conducted during the 2023 main cropping season at Bako Agricultural Research Center (BARC) in Western Ethiopia. The site is located at 9°05'33" N and 37°02'41" E, at an altitude of 1654 m.a.s.l. The area receives an average annual rainfall of 1605 mm, with mean minimum and maximum temperatures of 14.5°C and 29.3°C, respectively.

2.2. Field Experimental materials and design

Sixty-four sesame genotypes obtained from the Ethiopian Biodiversity Institute were evaluated. The experiment was laid out in an alpha-lattice design (8 × 8) with two replications. Each plot consisted of two 3-m-long rows spaced 40 cm apart, with 10 cm spacing between plants. The spacing between plots and replications was 50 cm and 1.5 m, respectively.

2.3. Disease assessment

2.3.1. Bacterial Blight Severity

Eight plants per plot were tagged for disease scoring, and disease severity was rated using a 0–6 scale (Sarwar *et al*., 2006), where 0 = no infection and 6 = >70% leaf area infected (Table 1). Severity scores were converted into a percentage severity index (PSI) using the formula (Wheeler, 1969; ICARDA, 1986).

$$PSI(\%) = \frac{\sum Individual\ numerical\ ratings}{(Total\ number\ of\ plants\ assessed\ x\ Maximum\ score\ in\ the\ scale)} x\ 10$$

Table 1: Disease scale and Percent of infection rate for sesame bacterial blight disease

Disease scale	Description	disease reaction
0	no disease	Immune
1	0.1-5% leaf area affected	Highly Resistant
2	5.1-10% leaf area affected	Resistant
3	10.1-20% leaf area affected	Moderately Resistant
4	20.1-50% leaf area affected	Moderately Susceptible
5	50.1-70% leaf area affected	Susceptible
6	>70% leaf area affected	Highly Susceptible

Source: Sarwar *et al.* (2006).

2.3.2. Cercospora Leaf Spot Severity

Cercospora leaf spot severity was assessed using a 0–5 scale (Kushwaha & Kausal, 1970) [18]; similarly, Severity scores were converted into percentage severity index (PSI).

Table 2: Disease scale and Percent of infection rate for sesame Cercospora leaf spot disease

Disease scale	Description	disease reaction
0	no disease	Immune or Highly Resistant
1	1-10% leaf area infected	Resistant
2	11-25% leaf area infected	Moderately Resistant
3	26-50% leaf area infected	Moderately Susceptible
4	51-70% leaf area infected	Susceptible
5	>70% leaf area infected	Highly Susceptible

Source: Kushwaha and Kausal (1970)

2.4. Area under Disease Progress Curve (AUDPC)

The progression of bacterial blight was plotted over time using the mean percentage severity index (PSI) for each sesame genotype at each plot. The PSI values were also used to calculate the apparent infection rate (*r*). AUDPC was computed using the midpoint (trapezoidal) method (Berger, 1981; Campbell and Madden, 1990):

$$AUDPC = \sum_{i=1}^{n-1} 0.5(X_{i+1} + X_i)(t_{i+1} - t_i)$$

Where: Xi = disease severity of bacterial blight at ith assessment date, t_i = time of the ith assessment in days from the first assessment date, and n = the total number of disease assessments.

2.5. Growth and yield parameters

Days to 50% emergence, days of flowering, days of capsule setting, and 90% physiological maturity, Plant height (cm) at maturity (8 plants), Number of capsules per plant (8 plants), Grain yield (kg ha^{-1}), adjusted to recommended moisture levels

2.6. Statistical Analysis

Data were analyzed using R statistical software. ANOVA was performed using a linear mixed model appropriate for alpha-lattice designs. Treatment means were separated using Duncan's Multiple Range Test (DMRT) at $p < 0.05$ (Gomez and Gomez, 1984).

3. Results and Discussion

About 64 sesame genotypes, including two control varieties, were evaluated for screening major foliar diseases of sesame in the 2023 main cropping season under field conditions. The results revealed that Bacterial blight (*Xanthomonas campestris* pv. *sesami*) and Alternaria leaf spot (*Alternaria* *sesami*) were the major sesame diseases during the 2023 main cropping season in the study area. Similarly, previous studies indicated that bacterial blight (Yogesha *et al*., 2011) [27] and Cercospora leaf spot (Jayalakshmi *et al*., 2015) [17] are the major diseases affecting sesame.

3.1. Bacterial blight

3.1.1. Severity index

Bacterial blight disease was first observed on susceptible genotypes 74 days after sowing (DAS) in early September in the 2023 main cropping season. The disease spread to almost all genotypes within a few days after the first observation. A 100% incidence of bacterial blight disease was recorded across all genotypes.

The analysis of variance indicates that there were highly significant (p<0.01) differences among the genotypes, with a mean final Bacterial blight severity index ranging from 9.0% to 41.2% in the 2023 main cropping season. The lowest final Bacterial blight disease severity index was recorded for SE42 (9.0%) and SE51.4 (9.0%), followed by SE14 (9.3%), and SE39.1 (9.3), etc. Among the tested genotypes during the 2023 main cropping season, no genotypes were found immune and highly resistant. Still, eight genotypes were marked as resistant (5.1-10% severity), i.e., SE42, SE51.4, SE14, SE39.1, SE18, etc. With 9.0%, 9.0%, 9.3%, 9.3%, 9.5%, etc. disease severity index, respectively (Table 3). Seventeen genotypes of sesame were assigned moderately resistant (10.1-20% severity), SE43, SE44.1, Obsa, SE6.2, etc. With 10.2%, 10.2%, 10.3%, 11%, etc., respectively. Forty-one sesame genotypes were moderately susceptible (20.1-50% severity), SE43, SE44.1, SE6.2, SE9, etc. With 10.2%, 10.2%, 11%, 12.4%, etc., respectively, of sesame Bacterial blight disease severity index (Table 3).

Genotypic variation confirms earlier findings (Naqvi *et al*., 2012; Golla *et al*., 2019) [16, 19] showing the absence of complete resistance but presence of partial resistance in some lines (Table 3).

3.1.2. Area Under Disease Progress Curve (AUDPC)

The analysis of variance revealed that there were significant (P<0.01) differences among genotypes in the 2023 main cropping season for AUDPC value. Area under disease progress curve of Bacterial blight disease ranged from 174%-days to 663.8%-days in the 2023 cropping season. The lowest (174%- days) AUDPC value was computed from genotype SE51.4, followed by Obsa (180%-days), SE42 (183%-days), SE18 (183.9%-days), SE22.3 (187.8%-days), etc. (Table 3). Lower AUDPC values corresponded to genotypes with slower disease development and likely reduced yield loss (Table 3) (Singh and Rao, 1998).

Table 3: Mean disease severity index and AUDPC of bacterial blight on sesame genotypes at Bako during the 2023 main cropping season.

Genotypes	Severity Index	AUDPC	Genotypes	Severity Index	AUDPC
obsa	10.3	180.0	SE35.2	19.7	340.8
SE1	29.8	396.8	SE39.1	9.3	199.5
SE10.1	29.5	437.3	SE39.2	18.1	328.8
SE10.2	32.5	570.6	SE4.1	26.0	412.4
SE11.1	16.7	327.2	SE4.2	16.6	311.6
SE12.1	18.1	300.6	SE42	9.0	183.0
SE13	29.7	420.3	SE42.1	24.1	437.0
SE14	9.3	192.0	SE43	10.2	188.4
SE16	33.2	575.3	SE44.1	10.2	200.3
SE17.1	30.9	574.2	SE46.1	26.0	424.5
SE18	9.5	183.9	SE49.1	13.0	227.9
SE20.1	18.5	302.3	SE49.2	9.5	188.4
SE20.2	37.2	615.8	SE5.2	18.2	320.3
SE21.1	26.2	419.3	SE50.1	33.7	603.9
SE21.4	24.9	442.2	SE50.2	13.1	228.3
SE22.1	27.0	433.7	SE50.4	34.1	584.0
SE22.2	37.2	638.3	SE51.1	24.4	407.0
SE22.3	9.7	187.8	SE51.3	38.8	618.8
SE23.1	21.5	423.9	SE51.4	9.0	174.0
SE23.2	12.6	224.7	SE54.1	34.5	549.2
SE24	26.0	435.0	SE54.2	30.9	551.6
SE27.1	41.2	663.8	SE54.3	23.1	442.8
SE28.1	28.2	429.8	SE55	25.6	494.6
SE28.2	21.0	362.9	SE59.1	13.9	219.9
SE29	27.5	423.9	SE59.2	29.9	572.4
SE29.2	23.2	464.6	SE6.2	11.0	187.5
SE29.3	26.1	446.1	SE6.4	34.0	626.3
SE3.1	30.2	419.4	SE62.1	25.9	369.9
SE31.1	28.3	457.2	SE7	31.7	637.2
SE31.3	9.7	189.0	SE9	12.4	239.0
SE32.3	19.2	343.1	SE9.1	23.0	398.9
SE33.1	28.4	384.5	Walin	33.1	602.1
Mean				22.9	392.7
DMR (P<0.05%)				7.18**	114.15**
CV (%)				19.4	18

AUDPC= area under disease progress curve, DMR= Duncan's multiple range, CV= coefficient of variations, *= significant difference at (p< 0.05), **= highly significant difference at (p< 0.01)

3.2. Cercospora leaf spot

3.2.1. Severity Index

Cercospora leaf spot appeared slightly later than bacterial blight, at 76 DAS. Significant variation ($p < 0.01$) occurred among the genotypes. The disease spread to all genotypes within a few days after the first observation. Similar to bacterial blight, there was 100% disease incidence of Cercospora leaf spot recorded in all genotypes.

The analysis of variance indicates that there were highly significant ($p<0.01$) differences among the genotypes, with the mean final severity index ranging from 5.0% to 33.2% in the 2023 main cropping season. The lowest final Cercospora leaf spot disease severity index was recorded as SE49.2 (5%), followed by SE54.2 (8.6%), etc. Among the tested genotypes during the 2023 main cropping season, no genotypes were found immune, but twelve genotypes were marked as resistant (1-10% severity), i.e., SE49.2, SE4.1, SE4.2, SE54.1, etc. With 5%, 8.6%, 9.0%, 9.0%, etc. disease severity index, respectively (Table 4). Forty-three genotypes of sesame were assigned moderately resistant (11-25% severity), SE1, SE31.1, SE23.2, SE23.1, etc. With 10.5%, 11.7%, 12.6%, 13.5%, etc, respectively. Nine sesame genotypes were moderately susceptible (26-50% severity), SE50.1, SE62.1, SE51.1, SE54.2, etc. With 25.7%, 26%, 26.1%, 26.5%, etc., respectively, of sesame Cercospora leaf spot disease severity index (Table 4).

The variation in resistance level of the evaluated genotypes could be due to the different genetic resistance to Cercospora leaf spot disease infection. The result is in line with Gedifew *et al*. (2024) [12], who found similar survey results in Assosa and Kamash zones, in Western Ethiopia. Teshome *et al*. (2022) [24] report nearly similar results in the mid and lowland sesame growing districts of Bale zone, South-east, Ethiopia.

3.2.2. Area Under Disease Progress Curve (AUDPC)

The analysis of variance revealed that there were significant ($P<0.01$) differences among genotypes in the 2023 main cropping season for AUDPC value. AUDPC ranged from 149.8%·days to 582.8%·days. The lowest (149.8%- days) AUDPC value was computed from genotype SE49.1, followed by SE54.1 (175.5%-days), obsa (180%-days), etc. (Table 4). AUDPC values varied among the sesame genotypes depending on the resistance levels of the genotypes, and it is known that AUDPC is directly related to yield loss (Singh and Rao, 1998).

Table 4: Mean disease severity and AUDPC of Alternaria leaf spot on sesame genotypes at Bako during the 2023 main cropping season.

Genotypes	Severity Index	AUDPC	Genotypes	Severity Index	AUDPC
obsa	9.3	180.0	SE35.2	9.3	199.5
SE1	10.5	218.2	SE39.1	10.1	247.8
SE10.1	21.5	354.8	SE39.2	18.0	331.3
SE10.2	19.6	347.9	SE4.1	8.6	230.5
SE11.1	24.5	489.6	SE4.2	9.0	183.0
SE12.1	10.2	216.8	SE42	16.1	352.9
SE13	21.8	336.4	SE42.1	10.2	191.4
SE14	10.3	192.0	SE43	10.2	200.2
SE16	25.2	492.8	SE44.1	18.0	343.5
SE17.1	9.5	183.9	SE46.1	9.0	218.9
SE18	21.8	315.8	SE49.1	5.0	149.8
SE20.1	29.2	534.8	SE49.2	9.5	188.4
SE20.2	18.2	338.2	SE5.2	10.2	239.2
SE21.1	17.0	241.5	SE50.1	25.7	522.9
SE21.4	16.9	358.2	SE50.2	9.9	222.9
SE22.1	19.0	349.6	SE50.4	13.1	228.3
SE22.2	29.2	557.2	SE51.1	26.1	502.9
SE22.3	9.7	187.8	SE51.3	16.4	325.9
SE23.1	13.5	338.4	SE51.4	30.8	536.2
SE23.2	12.6	224.7	SE54.1	9.0	175.5
SE24	18.0	354.0	SE54.2	26.5	468.1
SE27.1	33.2	582.8	SE54.3	22.9	473.5
SE28.1	20.2	348.8	SE55	14.9	358.1
SE28.2	13.0	281.9	SE59.1	17.7	411.0
SE29	19.5	344.4	SE59.2	13.9	221.4
SE29.2	15.2	383.6	SE6.2	21.9	491.4
SE29.3	18.1	365.1	SE6.4	10.3	216.0
SE3.1	20.3	376.2	SE62.1	26.0	545.2
SE31.1	9.7	187.5	SE7	17.9	287.4
SE31.3	11.2	262.1	SE9	15.0	316.4
SE32.3	20.4	303.4	SE9.1	23.7	559.2
SE33.1	11.7	264.3	Walin	12.4	237.4
Mean				16.5	323.3
DMR (P<0.05%)				5.89**	100.5**
CV (%)				22.1	19.2

AUDPC= area under disease progress curve, DMR= Duncan's multiple range, CV= coefficient of variations, *= significant difference at ($p< 0.05$), **= highly significant difference at ($p< 0.01$)

3.3. Growth Parameters

The analysis of variance indicated that there were no significant ($P \leq 0.05$) differences in the days to 50% flowering and 50% capsule setting days among all genotypes. There were significant differences ($p<0.05$) among genotypes across the growth parameters considered in the current study. There were highly significant differences ($P \leq 0.01$) in the days to 90 % maturity of sesame genotypes. The largest (days 138.7) period of maturity was recorded on SE28.1, while the shortest (days 123) period of maturity was recorded on SE23.1 genotype (Table 5). The highest plant height of 151 cm was recorded by the genotype walin, whereas the shortest, 76.27 cm, was recorded by genotype SE20.1 (Table 5).

3.4. Yield and yield components

Data on yield parameters showed highly significant differences ($p<0.01$) among the treatments in the number of capsules per plant and grain yield. Analysis of capsules per plant indicated that there was a highly significant difference in the number of capsules per plant (0<0.01) among screened genotypes. It may depend on the genetic potential of genotypes, and different disease attacks on plants reduce the number of capsules per pod (Table 5). It may depend on the different disease pressure, which makes a highly significant contribution to reducing the number of capsules. The Analysis of variance showed that there were highly significant differences ($p<0.01$) on gran yield in kg/ha among the genotypes. Generally, the highest yield (1039kg/ha) was recorded on genotypes SE42.1, followed by SE20.2 (973.2kg/ha), SE35.2 (956.2kg/ha), SE49.2 (938.2kg/ha), etc. during the 2023 cropping season at the Bako area. Similar yield result reported by Baraki *et al*. (2016) [5] from northern Tigray, Ethiopia. Nearly similar result also found by Tadese *et al*. (2017) [22], from the Lowland Area of South Omo Zone, SNNPR of Ethiopia. Several high-yielding genotypes also exhibited desirable disease resistance, making them promising candidates for breeding. Furthermore, those genotypes that have good performance could serve to develop superior high-yielding and disease-resistant genotypes.

Table 5: Growth parameters, Yield and yield components of sesame genotypes at Bako during the 2023 main cropping season.

Genotype	DF	DCS	DM	PH	CPP	Yield/Kg
obsa	65.7	85.3	134.0	112.0	37.9	824.7
SE1	64.0	86.7	133.3	89.7	41.5	552.6
SE10.1	63.0	76.0	128.3	98.7	25.9	453.9
SE10.2	63.7	85.7	135.0	85.8	41.9	674.7
SE11.1	62.3	82.3	133.3	98.1	31.0	868.0
SE12.1	64.0	77.7	135.0	108.0	30.9	757.3
SE13	62.3	74.7	132.0	88.9	27.4	719.6
SE14	65.3	78.3	134.7	96.8	31.9	828.7
SE16	63.0	79.3	134.3	92.9	29.4	555.5
SE17.1	64.3	80.0	129.3	106.3	36.0	925.7
SE18	61.3	77.0	130.3	94.4	22.9	924.4
SE20.1	62.3	80.0	128.3	76.4	28.0	465.5
SE20.2	63.0	81.3	132.0	101.3	34.6	973.9
SE21.1	62.0	81.7	131.7	96.6	32.9	600.9
SE21.4	64.7	79.7	128.3	87.0	41.7	612.5
SE22.1	63.7	84.3	132.3	94.0	34.1	326.3
SE22.2	64.0	80.3	125.3	106.0	31.9	496.2
SE22.3	64.3	82.3	130.7	92.9	26.6	320.4
SE23.1	62.7	86.0	127.0	83.3	34.1	577.7
SE23.2	64.0	81.3	132.0	99.5	28.5	884.3
SE24	62.3	81.7	137.3	94.7	30.0	763.3
SE27.1	61.3	82.3	135.7	96.3	29.4	815.3
SE28.1	63.7	82.0	129.3	99.1	34.2	748.8
SE28.2	63.0	80.3	138.7	98.7	30.1	725.1
SE29	63.0	82.7	131.3	93.0	44.6	559.2
SE29.2	65.7	83.3	127.0	96.2	29.7	541.5
SE29.3	63.0	82.3	130.3	89.5	33.8	693.6
SE3.1	63.3	85.7	127.0	94.1	38.1	749.3
SE31.1	63.7	82.7	125.7	101.6	31.8	622.2
SE31.3	61.7	82.0	131.7	93.1	34.2	839.3
SE32.3	65.3	85.7	126.7	102.5	39.9	956.2
SE33.1	64.0	80.3	124.3	86.8	43.9	826.5
SE35.2	64.7	82.0	129.7	85.9	41.7	676.8
SE39.1	62.7	86.7	124.7	96.6	35.8	612.5
SE39.2	61.7	84.7	136.0	97.5	37.8	727.4
SE4.1	59.7	81.3	127.7	94.3	30.7	757.2
SE4.2	61.0	83.0	129.0	82.3	23.4	479.8
SE42	63.0	82.7	135.7	92.5	35.8	720.4
SE42.1	62.0	83.3	133.0	97.9	37.6	1039.0
SE43	61.7	82.0	133.7	79.0	28.5	381.7
SE44.1	62.3	87.0	132.0	86.7	30.9	722.6
SE46.1	63.0	82.3	127.3	108.4	34.6	535.8
SE49.1	66.7	86.7	133.7	103.1	26.9	817.0
SE49.2	63.0	82.7	133.0	93.3	23.9	938.2
SE5.2	62.3	85.3	136.3	107.9	28.7	661.2

SE50.1	62.3	81.0	135.3	88.6	33.1	781.2
SE50.2	64.3	84.7	136.3	80.3	36.4	383.4
SE50.4	63.0	82.7	133.7	97.2	31.3	753.9
SE51.1	61.7	84.3	129.7	74.8	35.0	336.6
SE51.3	63.0	81.7	136.7	90.3	40.1	734.7
SE51.4	62.7	82.0	132.3	91.0	23.7	776.0
SE54.1	60.7	82.0	132.0	108.0	46.6	862.2
SE54.2	62.0	82.7	129.7	95.1	28.1	960.4
SE54.3	62.0	80.7	129.3	90.0	34.3	503.0
SE55	62.0	83.7	129.7	97.4	32.8	804.7
SE59.1	61.7	81.3	128.7	92.0	27.2	860.0
SE59.2	64.0	83.3	126.7	97.3	32.2	411.7
SE6.2	64.0	85.0	124.3	103.0	38.7	592.7
SE6.4	66.0	85.0	129.0	98.0	24.8	875.9
SE62.1	61.7	81.3	129.3	74.1	34.2	757.1
SE7	61.3	83.3	130.7	94.1	29.6	780.8
SE9	63.3	85.0	128.7	86.2	28.0	735.3
SE9.1	62.3	83.7	129.0	98.6	37.1	678.7
walin	63.0	81.0	127.3	115.0	27.8	820.0
Mean	63.0	82.4	130.9	94.6	32.9	697.8
DMR(P<0.05%)	NS	NS	NS	15.60**	9.09**	136.96**
CV (%)	7.8	7.4	4.3	10.2	17.1	12.1

DF= days of flowering, DCS=days of capsule setting, PH= plants height, DM= days of maturity, CPP= capsules per plant, Kg/ha= kilogram per hectare, DMR= Duncan's multiple range, CV= coefficient of variations, *= significant difference at ($p < 0.05$), **= highly significant difference at ($p < 0.01$).

4. Conclusion and Recommendation

This study demonstrated substantial genetic variability among 64 sesame genotypes for resistance to bacterial blight and Cercospora leaf spot under natural field conditions. Eight genotypes showed resistance to bacterial blight, while twelve exhibited resistance to Cercospora leaf spot. Several genotypes, including SE42.1, SE20.2, SE49.2, and SE54.2, combined superior yield performance with moderate to high levels of disease resistance. These genotypes should be advanced for multi-location testing and incorporated into sesame breeding programs aimed at improving disease resistance and productivity in Western Ethiopia and similar environments.

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