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# Evaluation of sesame genotypes for resistance to bacterial blight (*Xanthomonas campestris* pv. *sesami*) under field conditions

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**Abstract**

Sesame is an important lowland oilseed crop cultivated in the tropical and subtropical regions of the world. In Ethiopia, the intensity of sesame bacterial blight varies depending on topography, altitude, and weather conditions. The study was initiated to evaluate the resistance level of sesame genotypes against bacterial blight disease. An inoculum suspension was prepared in sterile distilled water and standardized turbidometrically to an inoculum size of approximately $10^7$ CFU/ ml ($1\times10^7$ cfu/ml). A total of 77 treatments were laid out in an alpha lattice design ($7\times11$) having seven blocks. Two rows were designated for one genotype, with three replications, and one block includes seven genotypes. Disease severity was determined from 8 per-tagged plants as an estimate of the percentage of total leaf area covered by bacterial blight lesions. Out of the 77 genotypes evaluated during the 2019 cropping season, no any genotypes showed resistance, while 54 were identified as moderately susceptible (20.1 –50% severity) and 8 sensitive (50.1–70% severity). During the 2021 cropping season, among 77 genotypes, similar to the first year none were found immune or resistant but, 23 genotypes were found to be moderately resistant (10.1–20% severity), 57 genotypes were found to be moderately susceptible (20.1–50% severity index), and 7were found to be susceptible (50.1–70% severity). It was investigated that significant variation was observed in bacterial blight, growth, grain yield, and yield components among the 77 genotypes evaluated at Bako. Some sesame genotypes found as potential sources of resistance and better yield performance.

**Keywords** Sesame, Evaluation of genotypes, Resistance, Bacterial Blight

## 1 Introduction

Sesame (*Sesamum indicum L.*), grouped under the Pedaliaceae family, is one of the oldest oilseed crops domesticated well over 2000 years ago [14]. Sesame is an important lowland oilseed crop cultivated in the tropics, the subtropical region of India, and other parts of the world [23]. Sesame is used for food and flavoring. It is an annual self- pollinating plant with an erect, pubescent, branching stem. It has either single-stemmed or branched growth habits or two growth characteristics of indeterminate and determinate,

reaching up to 2 m in height. Sesame is a major oilseed crop in the ancient world because of its ease of extraction, great stability, and drought resistance.

Sesame is an important source of edible oil and is widely used as one of the ingredients in food products, especially in bakery foods and animal feed [3]. Sesame oil, which is gotten through conventional oil production methods, is wealthy in unsaturated greasy acids, fat-soluble vitamins, amino acids, etc. Studies have found that sesame seeds contain 21.9% protein and 61.7% fat, and are rich in minerals such as Fe and Ca [30] and digestible fiber 9.8% [10, 34]. It is also used in confectionery, cookies, cake, margarine and bread making and the oil is used in the manufacture of soaps, cosmetics, perfumes, insecticides, and pharmaceutical products [23]. Sesame oil has medicinal and pharmaceutical value and is being used in many health care products [3]. Furthermore, population pressure, urbanization, and the changing lifestyle have increased the global demand for sesame products [27]. India was the leading country in area followed by China, Myanmar, Ethiopia, Nigeria and Uganda, while in production Myanmar was followed by India, China, Tanzania, Ethiopia, Uganda and Nigeria [13]. Sesame is Ethiopia's second most important crop after coffee (*Coffee arabica*). In 2020, the area covered for sesame production was 735,119.95 ha, 45.7% of the total oil crop area production (CSA, 2021). It stands out as a key crop and major contributor to the gross domestic product of Ethiopia [15]

Sesame is used as one of the main cash crops and the second export commodity, next to coffee in Ethiopia and plays a significant role as the source of rural employment and ensuring food security of millions of people [1]. However, the yield of sesame in Ethiopia is very low, with a national average of 0.7 tons/ha [11], which is far below the potential grain yield of 3.6 tons/ha recorded in China [12]. Despite the importance of sesame at the national and regional level, its productivity is constrained due to inappropriate agronomic practices, low yield of existing varieties, weather uncertainties, lack of non-shattering, waterlogged, and disease and insect-resistant varieties. Bacterial blight (*Xanthomonas campestris* pv. *sesami*) disease is among the major diseases of sesame, which becomes a major threat in the study area and it is reported that yield losses due to bacterial blight disease on susceptible variety were up to 34.28% in Western Tigray, Northern Ethiopia [19].

Bacterial blight causes significant losses in tropical, subtropical and temperate climates and has been reported from all sesame growing areas of the world [18, 24, 32]. The disease is endemic in the county's high-rainfall and humid areas [16, 18]. It typically appears as dark brown ware-soaked spots that later merge, causing foliage blight and defoliation [7]. Disease incidence reaches up to 100% in areas such as Wellega, Pawe, and Gambella where high humidity persists for a longer time, while it is about 10–50% in semi-arid areas like Werer and Humera. Waterlogging encourages the spread of the disease [17].

Bacterial blight significantly impacts sesame production in East Wollega, causing substantial devastation in farmers' fields and posing a challenge for sesame producers [2]. Even if some management has been done in the area still the disease effect is critical in sesame quality reduction and yield loss [19]. Therefore, the present study was conducted to identify and select resistant sesame genotypes against bacterial blight with superior yield and agronomic performance.

## 2 Materials and methods

### 2.1 Description of the study area

The experiment was conducted at the Bako Agricultural Research Center (BARC). It is located at 9°05′33.366 N latitude and 37 ° 02′41.202 E longitudes and at an altitude of 1654 m.a.s.l. The yearly mean minimum and maximum temperatures in the 2019 cropping season were 13.70 °C and 28.67 °C, respectively, with the annual rainfall of 111.02 mm, while minimum and maximum temperatures were 14.02 °C and 27.98 °C, in 2021 copping season respectively, and the annual rainfall was 105.94 mm (Fig. 1).

### 2.2 Bacterial isolates and culture conditions

To ensure the causative agent of the disease, infected seeds were sown on plastic pots having a pot size of 20 cm height and 26 cm diameter, filled with sterile soil with a ratio of 3:2:1 loam, compost, and sand soil respectively up ¾ height of pots and maintained under a lath-house with the supply of water as needed for the growth of the crop. After the onset of symptoms (water-soaked and small, irregular spots) on leaves, the diseased plant parts were collected for isolation of the causing pathogen. Isolation of bacterial pathogens was conducted at the bacteriology laboratory of Ambo Agricultural Research Center (Ambo ARC).

### 2.3 Isolation and characterization of *X. campestris* from sesame

The pathogen was isolated using the sample maceration technique. Symptomatic sesame leaves were surface disinfected using 70% ethanol and washed with sterile distilled water to remove disinfectant residue. Surface-sterilized leaves were then crushed using a flame-sterilized pestle and mortar, and sterile distilled water was added to make a suspension. A loopful of the extract was streaked on plates containing pre-dried YDCA media (Yeast Dextrose Calcium Carbonate Agar) and incubated at 30 ℃ for 48 h. Bacterial colonies resembling *Xanthomonas campestris* were sub-cultured, and the pure cultures were kept for further characterization.

Both colonial and biochemical keys were considered to identify the isolates. Cultural characteristics such as colony color, texture, form, elevation, and margin, and

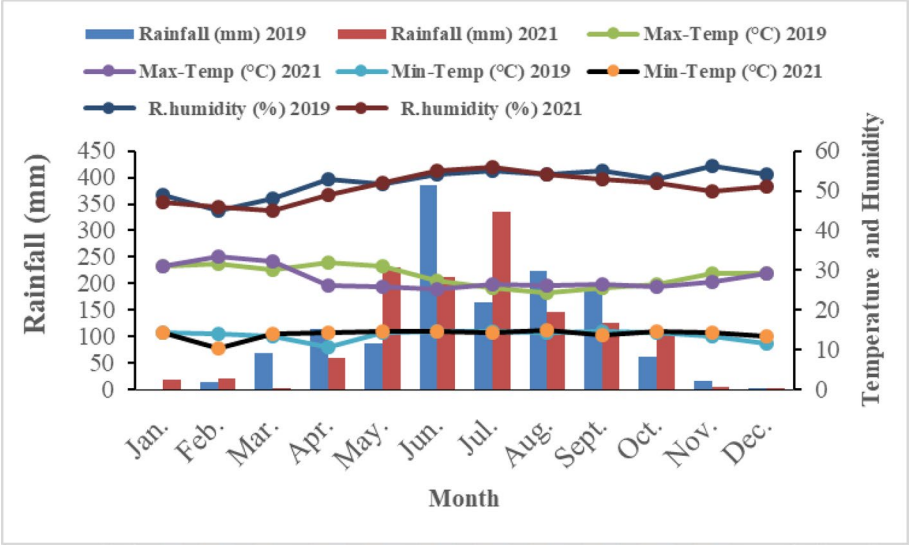


**Fig. 1** Monthly rainfall, Max. and min. Temperature and Relative Humidity of the two years

Biochemical tests such as KOH solubility, oxidase, and catalase, decomposition of macromolecules, and fermentative use of carbohydrates tests were employed to identify the pathogen.

### 2.4 Physiological characterization

#### *2.4.1 KOH solubility test*

The KOH string test, performed by mixing bacterial colonies with 2–3 drops of 3% HOH on a slide, identifies Gram-negative bacteria through cell lysis and DNA release. According to Ravi [29] *Xanthomonas campestris* pv. *Sesame* forms a thin thread or string upon lifting the loop.

#### *2.4.2 Oxidase test*

A filter paper fragment was saturated with the substrate tetramethyl-p-phenylenediamine dihydrochloride. An inoculation loop was used to apply a small quantity of culture to the paper. Observations were recorded ground on color change of the paper to a deep blue or purple within a 10–30 s time.

#### *2.4.3 Aesculin test*

Plates containing aesculin media were inoculated with bacterial suspension. The plates were incubated for 5 days. Positive response was recorded when a dark color is developed around the bacterial colonies.

#### *2.4.4 Catalase test*

The production of air bubbles within one minute was recorded after a few drops of 3% hydrogen peroxide were applied to the *X. campestris* culture, which gives a positive reaction for the catalase test. The result depicted that *X. campestris* is an aerobic bacterium. Similarly, Maji and Nath [26] reported that *X. campestris* isolates gave a positive test for catalase.

#### *2.4.5 Motility test*

Tubes half-filled with SIM motility media were single-stab inoculated with an inoculating needle immersed in bacterial suspension and the tubes were incubated at 30℃. After 72 h of incubation, a diffuse zone of growth flaring out from the line of inoculation was recorded.

#### *2.4.6 Starch hydrolysis*

The autoclaved and cooled starch agar medium was poured into a sterile glass Petri plate, and on solidification of the medium, streaked pure culture of the test bacterium, and incubated for 5 days at 28 °C. Then these plates were swamped with lugol's iodine and allowed to react for a few minutes. Reddish colored zones indicate a negative response, and the appearance of yellowish, clear zones around the bacterial growth indicates a positive reaction [4].

#### *2.4.7 Gelatin liquefaction*

To detect gelatinase enzyme production by the bacterium, tubes containing nutrient gelatin media were stabbed with the inoculum and incubated at 30℃ for two weeks.

Un-inoculated tubes were used as a check. After incubation, the tubes were placed inside the refrigerator until the un-inoculated tubes became completely solid. Partial or complete liquefication of inoculated tubes after refrigeration was recorded for positive reaction.

#### *2.4.8 Growth at 2% NaCl*

The ability to grow at 2% NaCl was tested by growing fresh cultures on nutrient broth media enriched with 2% concentrations of NaCl. Ten ml of broth media amended with NaCl was dispensed into 15 ml screw cap tubes. The tubes were inoculated with pure colonies and incubated at 30 °C. Tubes filled with nutrient broth without NaCl was inoculated with bacterial colonies and used as a positive check. After 48 h of incubation the percent transmittance was measured using a turbidimeter to determine bacterial growth.

#### *2.4.9 Growth at 36℃*

Ten ml of nutrient broth media was dispensed into 15 ml screw cap tubes. The tubes were inoculated with pure colonies and incubated at 36 °C. Tubes filled with nutrient broth were inoculated with bacterial colonies and incubated at 30 °C, and used as a positive check. After 48 h of incubation, the percent transmittance was measured using a turbidimeter to determine bacterial growth.

### 2.5 Field experimental materials and design

#### *2.5.1 Materials*

Seventy-seven sesame genotypes were used in this experiment. Seeds of sesame were obtained from the Bako Agricultural Research Center (BARC). BARC introduced the seeds from the Ethiopian Institute of Biodiversity. Every rule for treating seeds and plant parts has been adhered to in all plant-handling guidelines, i.e., despite the well-established system of the Ethiopian National Research Guideline [28].

#### *2.5.2 Treatment design*

A total of 77 treatments were arranged in an alpha lattice design (with three replications and eleven blocks per replication, each containing seven genotypes). Two rows for one genotype with three replications and one block contain seven genotypes. Two rows 3 m long with 40 cm wide (3 m X 80 cm = 1.2m$^2$) for one genotype. The block size consisted of a 3 m × 5.6 m area. Between block and replication 1 m and 1.5 m, an inter-row and intra-row spacing of 40 cm and 10 cm, respectively. The seeds were sown on June 25/2019, and June 23/2021each year in the field.

The bacterial pathogen isolated and identified was multiplied on Yeast Dextrose Calcium Carbonate Agar (YDCA) for field inoculation. The isolated bacterial suspension was foliar sprayed at a concentration of $10^8$ CFU/mL at a rate of 10-50µL of $10^8$ CFU/mL at 2 and 4 leaves growth stage (18–30 days after sowing.

### 2.6 Incubation period of bacterial blight in the field

The total duration of the bacterial blight cycle from initial contact to plant death is nearly 14 to 30 days in favorable field conditions [6].

- Inoculation and adhesion

- Entry (Penetration)
- Incubation period (internal multiplication)
- Manifestation (first symptom)
- Secondary spread

### 2.7 Disease assessment

*Disease incidence* Mean percentage of infected leaves showing typical symptoms of the disease per total leaves of plant units was assessed at nine-day intervals from the beginning of disease symptoms, seven days later (79 DAS), for four times. Both diseased and healthy plants were counted from the row plants, and the percentage of disease incidence (PDI) was calculated according to the formula used by Wheeler [33] and ICARDA [25]:

$$PDI\,(\%) = \frac{Number\ of\ diseased\ plants}{Total\ numberof\ plants\ inspected} \times 100$$

*Disease severity* disease severity was assessed from 8 per-tagged plants as the percentage of the total leaf surface covered with bacterial blight lesions on each expanded leaflet separately at regular intervals using a 0–6 scale (Table 1) [31]. The severity grades were converted into a percentage severity index (PSI) according to the formula by Wheeler [33] and [22].

$$PSI\,(\%\ ) = \frac{\sum Individualnumericalratings}{(Totalnumberofplantsassessedx Maximumscoreinthescale)} x100$$

### 2.8 Area under disease progress curve (AUDPC)

The progress of bacterial blight severity was plotted over time using the mean percentage severity index (PSI) for each sesame genotype in each plot, and the PSI values were also used to calculate the apparent infection rate (*r*). The AUDPC values (%-day) were calculated for each genotype using the mid-point rule formula [8, 9].

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

where *Xi* is the disease severity of bacterial blight at i$^{th}$ assessment date, *ti* is the time of the t$^{th}$ assessment in days from the first assessment date, and *n* is the total number of disease assessments. Disease severity was in percentage and time in days, and AUDPC was expressed as a proportion of the days.

**Table 1** Percent of infection and scale for sesame bacterial blight

| 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)

### 2.9 Growth parameters

A. Days to 50% emergence: Days from planting to 50% emergence of the plants per row was recorded.
B. Days to 50% flowering: Days to flowering were recorded for each plot when 50% of the plants in a plot flowered.
C. Days to 50% capsule setting: Days to capsule setting was recorded for each plot when 50% of the plants in a plot capsule setting.
D. Days to 90% maturity: days to 90% maturity of the crop recorded when 90% of the capsule reached physiological maturity.
E. Plant height (cm): The height of plants from the ground to the tip of plants was measured from eight randomly selected plants per row at maturity.

### 2.10 Yield and yield components

A. Number of capsules per plant: The number of capsules per plant was counted on five randomly taken plants from 8 pre-tagged plants, and means were recorded as the number of capsules/plant.
B. Seed yield per row (g): The grain yield per row was recorded.

$$\text{Adjusted yield per plot } = \text{FW}^* \left( \frac{100 - \text{Amc}}{RDW} \right)$$

where: Fw = Field weight; Amc = Actual moisture content; RDW = Recommended dry weight

C. Total grain yield (t $ha^{-1}$): The grain yield in grams per plot was calculated in per hectare basis.

### 2.11 Data analysis

The analysis of variance (ANOVA) was performed for the disease parameters (incidence, severity, AUDPC) and yield parameters using GenStat software (GenStat 18th ed.). Treatments mean separation were performed using Duncan multiple range test (DMRT) at $P \leq 0.05$. The analysis was performed followed the standard statistical procedures described by Gomez and Gomez [21].

## 3 Result and discussion

### 3.1 Isolation and characterization of *X. campestris*

Four bacterial blight causal agent suspected samples were isolated from sesame leaves for morphological and biochemical tests. *Xanthomonas* was isolated from all the assessed leaf samples. Both morphological and biochemical tests revealed that the isolate from the suspected symptom was the causal agent of bacterial blight of sesame *X. campestris* (Tables 2 and 3). In line with findings of the present study, *X. campestris* was reported as the causative agent of bacterial blight of sesame [25].

### 3.2 Disease incidence

Bacterial blight was first observed on susceptible genotypes 72 days after sowing (DAS) in early September in both years (2019 and 2021). The blight spread to almost

**Table 2** Morphological characteristics of *Xanthomonas* isolates from sesame leaf on YDCA after 48 h of incubation

| Isolate code | Cultural/colonial characterization keys | | | | |
|---|---|---|---|---|---|
| | color | Margin | Elevation | Texture | Cell shape |
| SLXc-1 | Creamy | Smooth | Raised | Mucoid | Rod |
| SLXc-2 | Creamy | Smooth | Raised | Mucoid | Rod |
| SLXc-3 | Creamy | Smooth | Raised | Mucoid | Rod |
| SLXc-4 | Creamy | Smooth | Raised | Mucoid | Rod |

**Table 3** Biochemical characterization of *Xanthomonas* isolates from sesame leaf

| Isolate code | Biochemical characterization keys | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | KOH solubility | Catalase | Oxidase | motility | Easculin | Growth at 36℃ | Growth at 2%NaCl | Gelatin liquefication | Starch hydrolysis |
| SLXc-1 | +ve | +ve | -ve | +ve | -ve | +ve | +ve | +ve | +ve |
| SLXc-2 | +ve | +ve | -ve | +ve | +ve | +ve | +ve | +ve | +ve |
| SLXc-3 | +ve | +ve | -ve | +ve | +ve | +ve | +ve | +ve | +ve |
| SLXc-4 | +ve | +ve | -ve | +ve | -ve | +ve | +ve | +ve | +ve |

all genotypes three to seven days later from the first observation. The disease incidence recording was started ten days later. There was a significant difference ($P<0.05$) was observed between genotypes in bacterial blight incidence (Table 4). The mean of final bacterial blight disease incidence ranged from 46.6 to 95.7% in 2019 and from 34.0 to 100% in 2021. The highest (95.7%) bacterial blight incidence was observed on genotype E4, followed by E16 (95.0%), E27 (95.0%), E6 (92.7%), etc., during the 2019 cropping season. In 2021, the highest final bacterial blight disease incidence was recorded on genotype E11 (100%) followed by E55 (100%), E45 (99.3), E20 (95.1%), etc. The disease spread more rapidly on susceptible genotypes, which exhibited the highest of final disease incidence (100%) (Fig. 2).

### 3.3 Disease severity

Screening in the 2019 cropping season revealed that, among seventy-seven genotypes evaluated, none was found to be immune or resistant. Fifteen genotypes were found to be moderately resistant (10.1–20% severity), and fifty-four genotypes were found to be moderately susceptible (20.1–50% severity), and eight genotypes were found to be susceptible (50.1–70% severity) (Table 4). In the 2021 cropping season, analysis of variance revealed that out of seventy-seven genotypes, similar to the first year, none were found immune or resistant, twenty-three genotypes were found to be moderately resistant (10.1–20% severity), E21, etc., and seven were found to be susceptible (50.1–70% severity).

Evaluated genotypes in both years (2019 and 2021) revealed that out of the 77, none of them were immune or resistant. It agrees with [20], and also [5] similar reports were made from Matama. But nine genotypes were found to be moderately resistant in both years (10.1–20% severity). The analysis of variance indicates that there were significant ($p<0.01$) differences among the genotypes in mean final blight severity, ranging from 13.3 to 60.7% in 2019 and from 15.5 to 59.7% in 2021. In 2019 the highest (60.7%) bacterial blight severity was recorded on genotype E45, followed by E25 (56.7%) in 2019. In 2021, the highest final disease severity index was recorded on E45 (59.7%) and PTY6 (59.7%) genotypes. Generally, Genotypes E-11, E-12, E-13, E-14, E-29, E-34, E-57, E-60,

**Table 4** Mean disease incidence, severity, and AUDPC of bacterial blight on sesame genotypes at Bako during the 2019 and 2021 main cropping seasons

| Genotypes | Disease parameters | | | | | |
|---|---|---|---|---|---|---|
| | 2019 | | | 2021 | | |
| | PDI (%) | PSI (%) | AUDPC (%-days) | PDI (%) | PSI (%) | AUDPC (%-days) |
| E-1 | 53.3 | 20.3 | 448.5 | 77.3 | 19.3 | 337.5 |
| E-10 | 65.7 | 41.0 | 736.5 | 52.3 | 30.0 | 436.5 |
| E-11 | 54.4 | 14.7 | 354.0 | 100.0 | 19.3 | 334.5 |
| E-12 | 63.5 | 19.7 | 393.0 | 35.7 | 16.7 | 255.0 |
| E-13 | 48.7 | 13.7 | 385.5 | 49.3 | 18.0 | 331.5 |
| E-14 | 53.3 | 18.0 | 429.0 | 59.3 | 19.3 | 355.5 |
| E-16 | 95.0 | 52.7 | 988.5 | 91.7 | 54.7 | 813.0 |
| E-17 | 60.1 | 24.0 | 532.5 | 53.2 | 26.3 | 549.0 |
| E-18 | 91.1 | 60.7 | 1135.5 | 78.3 | 45.3 | 799.5 |
| E-19 | 83.2 | 37.3 | 783.0 | 95.1 | 51.0 | 823.5 |
| E-2 | 54.4 | 26.3 | 589.5 | 56.7 | 19.7 | 318.0 |
| E-20 | 80.9 | 53.7 | 862.5 | 95.1 | 20.0 | 342.0 |
| E-21 | 85.0 | 20.0 | 415.5 | 65.7 | 35.0 | 562.5 |
| E-22 | 84.3 | 41.0 | 813.0 | 95.0 | 19.7 | 309.0 |
| E-23 | 74.8 | 42.0 | 852.0 | 72.7 | 35.7 | 598.5 |
| E-24 | 61.2 | 29.3 | 607.5 | 79.7 | 53.0 | 762.0 |
| E-25 | 80.9 | 56.7 | 879.0 | 78.6 | 47.7 | 786.0 |
| E-26 | 75.9 | 42.7 | 823.5 | 49.3 | 25.3 | 427.5 |
| E-27 | 95.0 | 48.3 | 891.0 | 64.3 | 32.3 | 463.5 |
| E-29 | 52.1 | 15.7 | 462.0 | 34.7 | 15.7 | 286.5 |
| E-3 | 62.3 | 30.0 | 580.5 | 84.9 | 50.0 | 769.5 |
| E-30 | 48.7 | 25.3 | 499.5 | 64.3 | 19.3 | 334.5 |
| E-31 | 90.0 | 50.0 | 972.0 | 67.7 | 36.0 | 592.5 |
| E-33 | 68.5 | 37.0 | 744.0 | 52.0 | 23.3 | 363.0 |
| E-34 | 77.1 | 19.7 | 385.5 | 76.5 | 17.3 | 322.5 |
| E-37 | 70.7 | 49.3 | 868.5 | 70.7 | 34.3 | 561.0 |
| E-38 | 77.5 | 39.7 | 754.5 | 69.3 | 44.0 | 673.5 |
| E-39 | 74.8 | 43.7 | 837.0 | 68.7 | 33.3 | 577.5 |
| E-4 | 95.7 | 54.7 | 988.5 | 43.3 | 22.7 | 418.5 |
| E-40 | 91.1 | 48.7 | 889.5 | 64.3 | 45.0 | 753.0 |
| E-41 | 82.1 | 45.0 | 816.0 | 52.3 | 19.7 | 346.5 |
| E-42 | 80.5 | 46.0 | 804.0 | 51.3 | 43.0 | 711.0 |
| E-43 | 64.6 | 37.3 | 741.0 | 48.7 | 19.3 | 298.5 |
| E-44 | 91.1 | 51.3 | 891.0 | 93.3 | 52.0 | 814.5 |
| E-45 | 63.5 | 41.0 | 802.5 | 99.3 | 59.7 | 910.5 |
| E-46 | 58.9 | 20.0 | 378.0 | 90.0 | 49.0 | 796.5 |
| E-48 | 72.5 | 36.7 | 808.5 | 74.4 | 41.7 | 630.0 |
| E-49 | 72.5 | 32.3 | 675.0 | 76.7 | 20.0 | 313.5 |
| E-5 | 83.9 | 44.3 | 801.0 | 55.7 | 36.0 | 568.5 |
| E-50 | 61.2 | 28.3 | 577.5 | 46.7 | 22.7 | 366.0 |
| E-51 | 58.9 | 18.3 | 447.0 | 60.9 | 39.0 | 646.5 |
| E-53 | 68.0 | 41.0 | 721.5 | 84.0 | 48.3 | 831.0 |
| E-54 | 47.6 | 23.3 | 489.0 | 53.3 | 19.7 | 334.5 |
| E-55 | 81.6 | 46.3 | 880.5 | 100.0 | 44.7 | 760.5 |
| E-56 | 44.2 | 13.3 | 283.5 | 75.5 | 44.7 | 727.5 |
| E-57 | 51.0 | 20.0 | 474.0 | 68.7 | 18.0 | 268.5 |
| E-58 | 57.8 | 35.7 | 699.0 | 71.0 | 16.3 | 315.0 |
| E-59 | 75.9 | 40.3 | 700.5 | 75.0 | 49.0 | 798.0 |
| E-6 | 92.7 | 52.3 | 951.0 | 73.3 | 37.7 | 601.5 |
| E-60 | 57.8 | 14.7 | 381.0 | 44.8 | 19.0 | 346.5 |

**Table 4** (continued)

| Genotypes | Disease parameters | | | | | |
|---|---|---|---|---|---|---|
| | 2019 | | | 2021 | | |
| | PDI (%) | PSI (%) | AUDPC (%-days) | PDI (%) | PSI (%) | AUDPC (%-days) |
| E-61 | 79.3 | 41.7 | 777.0 | 71.0 | 27.7 | 420.0 |
| E-62 | 72.5 | 42.0 | 709.5 | 54.0 | 25.3 | 450.0 |
| E-7 | 80.5 | 47.3 | 786.0 | 67.3 | 36.7 | 496.5 |
| E-8 | 71.4 | 35.7 | 721.5 | 52.3 | 25.3 | 369.0 |
| E-9 | 87.7 | 43.7 | 784.5 | 53.3 | 30.7 | 603.0 |
| Obsa | 90.0 | 43.0 | 814.5 | 94.0 | 47.3 | 796.5 |
| PYT-1 | 66.2 | 35.7 | 679.5 | 63.7 | 50.7 | 711.0 |
| PYT-10 | 82.1 | 37.0 | 679.5 | 52.0 | 36.3 | 531.0 |
| PYT-12 | 80.5 | 41.3 | 756.0 | 70.0 | 19.7 | 295.5 |
| PYT-13 | 77.1 | 19.3 | 385.5 | 73.3 | 31.3 | 600.0 |
| PYT-14 | 79.3 | 39.0 | 837.0 | 76.3 | 35.7 | 595.5 |
| PYT-15 | 72.5 | 37.3 | 672.0 | 45.7 | 33.3 | 504.0 |
| PYT-16 | 78.2 | 35.3 | 718.5 | 42.7 | 29.0 | 513.0 |
| PYT-17 | 78.7 | 44.3 | 787.5 | 34.0 | 18.0 | 270.0 |
| PYT-18 | 83.2 | 47.0 | 840.0 | 45.7 | 25.7 | 427.5 |
| PYT-2 | 74.8 | 19.7 | 361.5 | 62.3 | 32.3 | 567.0 |
| PYT-20 | 86.6 | 51.7 | 933.0 | 64.3 | 31.7 | 561.0 |
| PYT-21 | 74.8 | 38.0 | 739.5 | 51.7 | 23.3 | 393.0 |
| PYT-24 | 60.1 | 19.3 | 397.5 | 73.0 | 19.3 | 328.5 |
| PYT-3 | 82.7 | 48.3 | 892.5 | 62.3 | 19.7 | 291.0 |
| PYT-4 | 72.5 | 37.3 | 729.0 | 69.0 | 40.0 | 607.5 |
| PYT-47 | 73.7 | 32.7 | 673.5 | 47.3 | 31.3 | 510.0 |
| PYT-5 | 85.0 | 47.7 | 889.5 | 87.3 | 42.3 | 733.5 |
| PYT-6 | 79.8 | 49.3 | 930.0 | 95.0 | 59.7 | 906.0 |
| PYT-7 | 83.2 | 49.0 | 879.0 | 37.3 | 30.7 | 495.0 |
| PYT-9 | 63.5 | 42.7 | 826.5 | 69.0 | 40.0 | 652.5 |
| Walin | 83.7 | 43.0 | 822.0 | 45.3 | 22.0 | 345.0 |
| Mean | 73.2 | 36.8 | 704.5 | 66.2 | 32.5 | 527.5 |
| LSD (0.05) | 22.40** | 23.1** | 222.71** | 15.01** | 10.824** | 165.86** |
| CV (%) | 19.0 | 14.3 | 19.6 | 14.0 | 20.7 | 19.5 |

PDI = percentage disease incidence, PSI = percentage severity index, AUDPC = area under disease progress curve, LSD = least significant difference, CV = coefficient of variations, * = significant difference at $p < 0.05$), ** = highly significant difference at $p < 0.01$).

and PYT-24 were found to be moderately resistant in both years (10.1–20% severity) (Table 4).

### 3.4 Area under disease progress curve (AUDPC)

The analysis of variance indicates that significant ($p < 0.001$) differences were observed between genotypes in AUDPC value in both years. Area under disease progress curve ranged from 283.5%-days to 1135.5%-days in 2019 and from 255.0%-days to 910.5% in 2021. The lowest (283.5%-days) AUDPC value was computed from genotypes E-11(354.0%-days), followed by PYT-2(341.5%-days) in 2019. In 2021, the lowest (255.0%-days) AUDPC value was computed from genotypes E-12 followed by E-57 (268.5%-days) (Table 4 and Fig. 3).

### 3.5 Growth parameter

Combined analysis of growth parameters showed significant variation between genotypes in both cropping seasons, except for days to 50% emergence. The analysis of

**Picture 1** Sesame plant leaves affected by bacterial blight disease

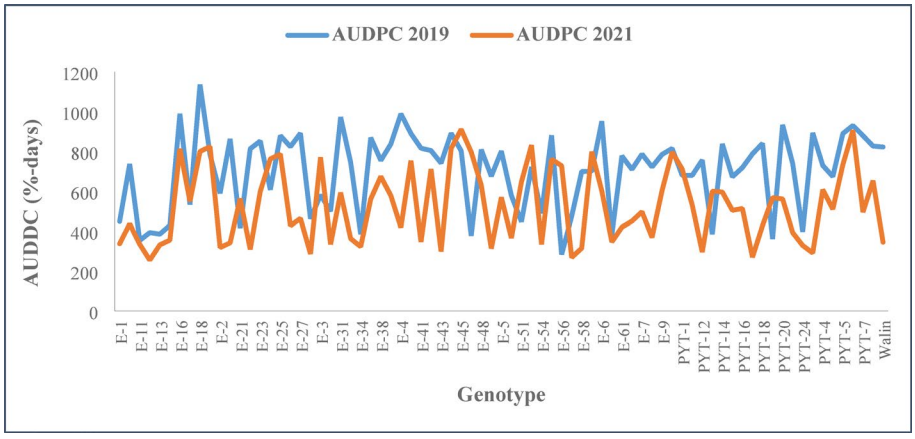


**Fig. 2** Area under disease progress curve

variance (ANOVA) on days to 50% emergence revealed that genotypes were not significantly different ($p < 0.05$) and emerged at uniform dates (Table 5). All the genotypes were not different in days to emergence, and seeds planted in all plots almost uniformly emerged (Table 5). The analysis of variance showed that there were no significant ($p < 0.05$) differences on the day to 50% flowering among all genotypes (Table 5). The longest (78.7 days) period of flowering was recorded on the genotype E61, while the shortest (74.0 days) period of flowering was statistically at par between the genotypes. In the days to capsule setting, statistical variation was not observed between the genotypes. However, the longest (93.7 days) of capsule setting was recorded on the genotype E30, while the shortest (84.3 days) was recorded in the genotype E31.

The analysis of variance showed that there were significant differences observed ($p < 0.05$) in the days to 90% maturity date of genotypes. The longest duration of 136.3 days was recorded on the genotype E56, while the shortest, 124.7 days, was recorded in genotype PTY2. There were significant differences ($p < 0.05$) in the height of

**Table 5** Pooled mean of Growth parameters, Yield, and yield components of sesame genotypes at Bako during the 2019 and 2021 main cropping seasons

| Genotypes | Growth parameters, Yield, and yield components | | | | | |
|---|---|---|---|---|---|---|
| | DF | DCS | PH | DM | CPP | Yield Kg/ha |
| E-1 | 75.7 | 90.7 | 91.3 | 133.3 | 28.2 | 788.8 |
| E-10 | 77.0 | 87.7 | 93.1 | 128.3 | 35.5 | 513.7 |
| E-11 | 76.0 | 87.3 | 99.8 | 131.3 | 32.7 | 810.2 |
| E-12 | 76.3 | 89.0 | 103.0 | 132.7 | 30.9 | 806.5 |
| E-13 | 75.3 | 90.3 | 95.5 | 134.3 | 22.5 | 748.6 |
| E-14 | 77.0 | 89.3 | 92.9 | 131.3 | 38.3 | 844.7 |
| E-16 | 77.3 | 88.7 | 122.2 | 130.7 | 42.6 | 380.9 |
| E-17 | 76.3 | 89.0 | 90.7 | 131.7 | 31.4 | 632.7 |
| E-18 | 74.7 | 86.3 | 92.4 | 127.0 | 31.8 | 350.5 |
| E-19 | 75.7 | 87.3 | 94.0 | 128.7 | 33.4 | 503.7 |
| E-2 | 77.7 | 89.3 | 100.3 | 130.0 | 33.5 | 690.2 |
| E-20 | 76.0 | 87.7 | 102.9 | 128.0 | 33.5 | 716.5 |
| E-21 | 78.3 | 89.0 | 107.0 | 130.3 | 33.3 | 624.9 |
| E-22 | 75.7 | 89.7 | 102.9 | 131.7 | 37.9 | 741.8 |
| E-23 | 77.3 | 87.3 | 95.1 | 127.0 | 25.9 | 499.0 |
| E-24 | 74.3 | 89.7 | 95.3 | 132.7 | 41.9 | 731.2 |
| E-25 | 74.0 | 85.7 | 95.6 | 127.0 | 31.0 | 480.5 |
| E-26 | 75.7 | 87.7 | 104.9 | 129.0 | 31.0 | 651.7 |
| E-27 | 75.7 | 86.7 | 99.8 | 127.0 | 27.4 | 454.0 |
| E-29 | 76.3 | 89.0 | 94.3 | 133.3 | 31.9 | 832.2 |
| E-3 | 75.3 | 87.0 | 97.9 | 130.7 | 29.4 | 731.5 |
| E-30 | 76.0 | 93.7 | 112.3 | 136.0 | 36.0 | 949.3 |
| E-31 | 76.7 | 84.3 | 86.6 | 127.3 | 22.9 | 503.0 |
| E-33 | 75.0 | 90.7 | 91.9 | 133.0 | 41.5 | 573.1 |
| E-34 | 74.0 | 88.3 | 93.1 | 132.7 | 28.1 | 754.2 |
| E-37 | 74.7 | 85.7 | 111.0 | 127.0 | 34.6 | 470.0 |
| E-38 | 76.0 | 88.0 | 101.9 | 130.3 | 32.9 | 685.2 |
| E-39 | 75.0 | 85.7 | 97.9 | 128.3 | 41.7 | 500.9 |
| E-4 | 78.0 | 88.0 | 93.9 | 127.0 | 34.1 | 647.0 |
| E-40 | 75.0 | 86.7 | 91.1 | 129.0 | 31.9 | 409.6 |
| E-41 | 76.3 | 87.3 | 96.1 | 126.7 | 26.6 | 423.6 |
| E-42 | 75.3 | 85.7 | 105.8 | 127.0 | 34.1 | 537.7 |
| E-43 | 77.7 | 90.0 | 97.3 | 132.0 | 28.5 | 576.5 |
| E-44 | 75.0 | 86.0 | 89.9 | 127.7 | 30.0 | 470.2 |
| E-45 | 74.0 | 86.7 | 90.3 | 131.0 | 29.4 | 498.4 |
| E-46 | 73.7 | 87.7 | 97.9 | 128.7 | 34.2 | 887.7 |
| E-48 | 74.0 | 86.7 | 92.3 | 130.3 | 30.1 | 372.3 |
| E-49 | 74.7 | 88.0 | 102.2 | 133.7 | 44.6 | 769.9 |
| E-5 | 77.3 | 90.3 | 92.5 | 132.0 | 29.7 | 484.6 |
| E-50 | 76.3 | 88.7 | 102.6 | 133.7 | 33.8 | 646.5 |
| E-51 | 73.7 | 87.7 | 101.7 | 131.3 | 38.1 | 814.6 |
| E-53 | 75.7 | 86.7 | 101.0 | 127.3 | 31.8 | 487.1 |
| E-54 | 77.3 | 91.7 | 103.4 | 136.0 | 34.2 | 948.1 |
| E-55 | 74.3 | 88.0 | 97.2 | 131.7 | 39.9 | 515.8 |
| E-56 | 74.7 | 89.3 | 100.5 | 136.3 | 43.9 | 1067.5 |
| E-57 | 76.0 | 89.3 | 107.7 | 133.7 | 41.7 | 847.5 |
| E-58 | 78.3 | 90.7 | 113.9 | 134.3 | 35.8 | 760.1 |
| E-59 | 76.3 | 91.0 | 95.5 | 133.7 | 37.8 | 487.7 |
| E-6 | 76.7 | 87.7 | 103.0 | 129.7 | 30.3 | 414.4 |
| E-60 | 73.7 | 90.0 | 97.4 | 134.0 | 23.4 | 815.4 |
| E-61 | 78.7 | 90.0 | 89.5 | 131.3 | 35.8 | 541.0 |

**Table 5** (continued)

| Genotypes | Growth parameters, Yield, and yield components | | | | | |
|---|---|---|---|---|---|---|
| | DF | DCS | PH | DM | CPP | Yield Kg/ha |
| E-62 | 74.7 | 86.7 | 102.3 | 130.3 | 37.6 | 510.8 |
| E-7 | 78.3 | 88.3 | 92.8 | 130.0 | 28.5 | 402.0 |
| E-8 | 77.0 | 89.7 | 102.2 | 131.3 | 30.9 | 664.0 |
| E-9 | 77.0 | 88.0 | 92.5 | 130.3 | 34.6 | 497.4 |
| Obsa | 74.0 | 87.0 | 85.1 | 128.7 | 26.9 | 545.8 |
| PYT-1 | 77.3 | 88.7 | 108.3 | 126.7 | 23.9 | 676.8 |
| PYT-10 | 76.0 | 85.7 | 87.6 | 125.7 | 28.7 | 572.9 |
| PYT-12 | 76.3 | 87.7 | 96.3 | 129.0 | 33.1 | 569.6 |
| PYT-13 | 76.0 | 88.7 | 94.7 | 129.3 | 36.4 | 728.7 |
| PYT-14 | 76.0 | 88.0 | 98.1 | 129.0 | 31.3 | 586.0 |
| PYT-15 | 77.3 | 88.0 | 91.7 | 129.0 | 35.0 | 572.3 |
| PYT-16 | 74.7 | 87.3 | 102.3 | 128.7 | 40.1 | 697.1 |
| PYT-17 | 75.7 | 85.3 | 84.5 | 127.3 | 23.7 | 453.1 |
| PYT-18 | 75.7 | 87.7 | 95.8 | 129.0 | 46.6 | 575.2 |
| PYT-2 | 75.0 | 85.7 | 101.2 | 124.7 | 28.1 | 485.4 |
| PYT-20 | 75.3 | 85.7 | 102.5 | 126.7 | 34.3 | 399.0 |
| PYT-21 | 77.3 | 88.7 | 92.8 | 130.7 | 32.8 | 398.9 |
| PYT-24 | 76.0 | 87.3 | 79.9 | 126.3 | 27.2 | 781.7 |
| PYT-3 | 75.0 | 85.7 | 93.1 | 125.7 | 32.2 | 486.8 |
| PYT-4 | 75.7 | 86.7 | 96.7 | 129.3 | 38.7 | 432.5 |
| PYT-47 | 72.7 | 86.7 | 102.6 | 129.3 | 24.8 | 682.2 |
| PYT-5 | 74.0 | 85.3 | 89.6 | 127.0 | 34.2 | 432.0 |
| PYT-6 | 76.0 | 87.0 | 90.3 | 129.3 | 29.6 | 384.9 |
| PYT-7 | 77.0 | 89.0 | 113.9 | 128.0 | 37.1 | 483.6 |
| PYT-9 | 77.3 | 88.0 | 104.5 | 127.0 | 28.0 | 513.7 |
| Walin | 75.3 | 86.3 | 90.3 | 127.3 | 27.8 | 686.2 |
| Mean | 75.9 | 88.0 | 97.7 | 129.9 | 32.9 | 605.3 |
| LSD (0.05) | NS | NS | 16.95* | 4.85** | 8.99** | 125.23** |
| CV (%) | 3.1 | 2.9 | 10.8 | 2.3 | 16.9 | 12.8 |

DF = days of flowering, DCS = days of capsule setting, PH = plants height, DM = days of maturity, CPP = capsules per plant, Kg/ha = kilo gram per hectare, LSD = least significant difference, CV = coefficient of variations, * = significant difference at $p < 0.05$), ** = highly significant difference at $p < 0.01$).

the genotypes. The highest plant height of 122.2 cm was recorded by the genotype E16, whereas the shortest 84.5 cm was recorded in genotype PTY17 (Table 5).

### 3.6 Yield and yield components.

In the combined analysis of variance, yield and yield components showed significant variations among genotypes in both cropping seasons (2019 and 2021). The Number of capsules per plant was significantly different ($p < 0.05$) between the genotypes. The highest number of capsules per plant (46.6) was recorded from the PTY18 genotype, while the smallest number of capsules per plant (22.5) was recorded in genotype E13 (Table 5). There were highly significant differences ($p < 0.001$) in grain yield (Kg/ha) among the genotypes. The highest (1067.5 kg/ha) yield was recorded from genotype E56, followed by E30 (969.3 kg/ha). From the result of the analysis, a higher yield was obtained from moderately resistant and susceptible genotypes. Generally, Genotypes E-1, E-11, E-12, E-13, E-14, E-29, E-34, E-57, E-60, and PYT-24 were found to be moderately resistant as well as promising yield performances. Genotypes E-20, E-22, E-24, E-3, E-30, E-46, E-49, E-51, E-54. E-56, E-58, and PYT-13 were moderately susceptible and showed good yield performances. Because they tolerated the disease. Tolerant genotypes, affected by

disease, but give better yield due to their ability to give high yield even if affected by disease. Therefore, 22 genotypes recorded higher sesame grain yield compared to other genotypes.

### 3.7 Conclusion and Recommendation

This study's results showed that sesame genotypes had different reactions to the bacterial blight disease under field conditions. Significant variation was recorded in bacterial blight disease reaction, growth, grain yield, and yield components among the 77 genotypes evaluated at Bako. The two-year field evaluation demonstrated that significant variation in bacterial blight response among 77 sesame genotypes at Bako. Although no genotype showed complete resistance, 10 genotypes in 2021 and 15 in 2019 expressed moderately resistant reactions (10–20% PSI), and 12 genotypes were moderately susceptible (21–50% severity), and showed good yield performances, tolerating the disease. Which also exhibits comparatively higher yield performance. Totally 22 genotypes represent potential parents for resistance breeding and varietal improvement, as well as sources of resistance to bacterial disease.

## 4 Experimental crop care

Every rule of treating seeds and plant parts has been adhered to in all plant handling guidelines, i.e., despite a well-established system for the Ethiopian National Research Guideline (2014).

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Abay Guta:—wrote the main manuscript, data collection analysis, Abreham Nagera: -edition and supervision Denberu Kebede:—Laboratory assist and some data analysis.

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**Data availability**
Data to support this manuscript will be sent upon request.

## Declarations

**Conflict of interest**
The authors declare no competing interests.

**Ethical approval**
Not applicable.

**Consent to participate**
Not applicable.

**Consent for publicatiom**
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## Publisher's Note