

Research Article

Resistance of Sesame (*Sesamum indicum* L.) Genotypes Against Bacterial Blight (*Xanthomonas campestris* pv. *sesami*) in Benishangul Gumuz Region, Northwestern Ethiopia

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Abstract

Bacterial blight poses a significant threat to sesame production in Ethiopia, especially in regions with high rainfall. It causes yield reduction and affects seed quality by inducing premature leaf defoliation. To address these challenges, evaluating existing germplasm for disease resistance is crucial. This study assessed various sesame genotypes for resistance to bacterial blight and their performance in seed yield and seed yield related traits. Seventeen genotypes were evaluated in a randomized complete block design at Kamashi research sub-station. Resistance evaluations were conducted every 14 days from emergence up to 72 days, along with recording seed yield and related agronomic and morphological traits. The mean area under the disease progress curve (AUDPC) varied from 673.86 to 825.01, indicating differing susceptibility levels to disease advancement. Approximately 46.67% of the tested genotypes exhibited lower AUDPC compared to Benishangul-1, a variety specifically developed for its adaptability and resistance for bacterial blight-prone regions. Initially, at 14 and 28 days after emergence (DAE), no noticeable bacterial blight symptoms were observed across the genotypes. However, at 42, 56, and 72 DAE, the average severity index steadily rose to 16.92%, 20.78%, and 27.71%, respectively. This transition from immunity to moderate susceptibility underscores the dynamic nature of disease progression and the significant challenge posed by bacterial blight in later sesame growth stages. Notably, significant differences ($P < 0.05$) were noted in days to 50% flowering, days to 90% maturity, plant height to the first branch, overall plant height, length of the capsule-bearing zone, and seed yield. This comprehensive evaluation offers valuable insights into the genetic diversity to improve crop performance and yield potential.

Keywords

Area Under Disease Progress Curve, Bacterial Blight (*Xanthomonas campestris* pv. *sesami*), Disease Reaction, Percentage of Severity Index, Seed Yield

1. Introduction

Sesame (*Sesamum indicum* L.), a member of the Pedaliaceae family, stands as one of the oldest oilseed crops [1].

Hence most wild species of the genus *Sesamum* thrive in Africa, sesame is widely believed to have originated on the

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Received: 15 July 2024; **Accepted:** 9 August 2024; **Published:** 30 August 2024



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continent [2]. Despite its susceptibility to rainy conditions [3], sesame exhibits remarkable tolerance to drought and thrives in relatively high temperatures, enabling it to maintain substantial seed yield [1].

The majority of global sesame production occurs in Africa and Asia [4]. Notably, Ethiopia is a key player in sesame production and exportation on a global scale. In 2018, Ethiopia contributed approximately 200,000 tons of sesame, cultivated on 294,819 hectares of land [5]. The regions of Amhara, Tigray, Oromia, Benishangul Gumuz, and Somali in Ethiopia boast favorable agro-ecological conditions for sesame cultivation [6].

Despite the favorable agro-ecologies conducive to sesame production and its pivotal role as a source of income for both the country and its farmers, productivity has been hindered by various biotic and abiotic factors. Among these factors, bacterial blight (*Xanthomonas campestris* pv. *sesami*) stands out as the primary disease threatening sesame cultivation in Ethiopia, particularly in regions with high rainfall and humidity [6], such as Benishangul Gumuz, Northwestern Ethiopia. In Northwestern Ethiopia, such as Wollega and Benishangul Gumuz, Wollega and Gambella, bacterial blight can lead to complete crop failure, especially when farmers use varieties non-adaptable to these high rainfall areas. Bacterial blight typically manifests during the rainy season when humidity levels are high, resulting in defoliation and sterility under severe conditions [7]. Studies have shown a notably high severity index of bacterial blight in areas with substantial rainfall in Northwestern Ethiopia [8], whereas its severity is comparatively lower in semi-arid areas [9] and in areas with optimal moisture levels [10] when contrasted with the high rainfall areas of Northwestern Ethiopia. In high rainfall areas such as Wollega, Kamashi, and certain parts of Metekel, frequent heavy rains can exacerbate sesame susceptibility to bacterial blight due to waterlogging. This disease not only diminishes sesame yields but also adversely affects seed quality by causing defoliation of leaves before seeds reach full maturity.

To address the challenges of seed yield loss and seed quality deterioration in sesame, it is imperative to harness the potential of existing germplasm by systematically evaluating and screening elite breeding plant materials for resistance to bacterial blight, particularly in regions hot spot to the disease. Therefore, the current study aims to assess various sesame genotypes for their resistance to bacterial blight disease and to evaluate their performance in terms of yield and related traits under field conditions in the high rainfall areas of Northwestern Ethiopia.

2. Materials and Methods

2.1. Experimental Site, Plant Materials and Design

The experimental site is situated in the Kamashi zone, within the Benishangul Gumuz region of Northwestern Ethiopia, at a

latitude of 09°30'N and longitude of 35°45'E. It is positioned at an altitude ranging from 1000 to 1350 meters above sea level (m.a.s.l). This area experiences an average annual rainfall of 1150 mm, along with a minimum and maximum mean daily temperature of 25 °C and 30 °C, respectively. Notably, the Benishangul Gumuz region is known as a hotspot for bacterial blight infestation, often reaching a severity index of up to 100% due to persistent rainfall and humidity ([6]. During the 2017/18 cropping season, seventeen genotypes (as listed in Table 1) were evaluated for their resistance against bacterial blight disease (*Xanthomonas campestris* pv. *sesami*). These genotypes comprised three varieties (Acc-51-02-sel-6(2), Benishangul-1, and Tate) and 14 advanced lines. The advanced lines were screened from a larger pool of genotypes evaluated for bacterial blight resistance in the preceding 2016/17 season. The experimental design employed was a Randomized Complete Block Design (RCBD) with three replications. Each plant material was sown on plots measuring 2 meters in width and 5 meters in length, with intra-row spacing of 10cm and inter-row spacing of 40cm.

Table 1. Description of plant materials used in the experiment.

S. No	Genotype	Status
1	Acc-202-374	Advanced line
2	Acc-51-02-sel-6(2)	Released variety
3	Benishangul-1	Released variety
4	Tate	Released variety
5	WARC-100	Advanced line
6	WARC-103	Advanced line
7	WARC-59	Advanced line
8	WARC-63	Advanced line
9	WARC-70	Advanced line
10	WARC-72	Advanced line
11	WARC-74	Advanced line
12	WARC-81	Advanced line
13	WARC-84	Advanced line
14	WARC-87	Advanced line
15	WARC-88	Advanced line
16	WARC-92	Advanced line
17	WARC-93	Advanced line

2.2. Data Collected

Days to 50% flowering (DF) and 90% maturity (DM) were meticulously recorded on a plot-by-plot basis for each replicate. In assessing bacterial blight disease severity, data were gath-

ered from 10 randomly chosen and pre-tagged plants situated within the middle rows of every plot. The assessment of bacterial blight disease severity took place at five times, every 14 days from 14 up to 72 days after emergence, utilizing the scale established by Sarwar and Haq [11], where severity levels were categorized as follows: 0 = 0%, 1 = 0.1–5%, 2 = 5.1–10%, 3 = 10.1–20%, 4 = 20.1–50%, 5 = 50.1–70%, 6 = >70%, corresponding to immune, highly resistant, resistant, moderately resistant, moderately susceptible, susceptible, and highly susceptible, respectively. Subsequently, these severity grades were converted into a percentage severity index (PSI) using Wheeler's [12] formula, which is as follows: -

$$\text{PSI (\%)} = \frac{\text{Sum of all disease scores}}{\text{Number of ratings} \times \text{Maximum disease grade}} \times 100$$

The area under the disease progress curve (AUDPC) was estimated for each observation as suggested by Madden et al. [13] as follows:-

$$\text{AUDPC} = \sum_{i=1}^{n-1} \frac{(y_i + y_{i+1})}{2} (t_{i+1} - t_i)$$

Where, y_i is an assessment of a disease at the i^{th} observation, t_i is time in days at the i^{th} observation, and n is the total number of observations. During harvesting, data were recorded for yield and yield-related traits at three levels: plant basis, capsule basis, and plot basis. Data collection for seed yield and morphological traits followed the sesame descriptor [14]. Plant height to the first branch (PHFB), overall plant height (PH), the length of the capsule-bearing zone (LCBZ), number of primary branches per plant (PBPP), and number of capsules per plant (CPP) were recorded for 10 randomly selected plants in each plot. Additionally, the number of seeds per capsule (SPC) was assessed by examining five capsules from the bottom towards the tip on the main stem of each plant. Seed yield (SY) per plot was determined from three middle rows, while the thousand-seed weight (TSW) was measured after counting 1000 seeds which sampled from the harvest per plot.

2.3. Data Analysis

Analysis of variance (ANOVA) for the traits considered in this study was conducted using the *doebioresearch* package [15] within the R software [16]. The model employed for the analysis of variance is as follows:

$$y_{ij} = \mu + G_i + R_j + \varepsilon_{ij}$$

Where, y_{ij} is the observation of the i^{th} genotype (G) in the j^{th} replication (R); μ is the overall mean; G_i is the i^{th} genotype (G) effect; R_j is the j^{th} replication (R) effect; and ε_{ij} is an error term. Tukey test was utilized to compare means among genotypes at a significance level of 5% probability.

3. Result and Discussion

3.1. Resistance of Sesame Genotypes Against Bacterial Blight (*Xanthomonas campestris* pv. *sesami*)

The data collected subjected to an analysis of variance to examine variability among genotypes concerning disease resistance and their performance in yield and related traits (Table 2). Notably, there were no statistically significant variation observed among the genotypes for the area under disease progress curve (AUDPC). The AUDPC serves to quantify the cumulative disease severity or advancement across time intervals. This parameter offers a thorough evaluation of disease evolution dynamics and proves valuable in contrasting disease progression across various genotypes. Across the sesame genotypes assessed, the mean AUDPC ranged from 673.86 to 825.01 (Table 3), indicating varying levels of susceptibility to disease progression. The highest AUDPC (825.01) was recorded on WARC-63 and the lowest AUDPC (673.86) was recorded on WARC-81. This discrepancy underscores the potential for genotype-specific resistance mechanisms against bacterial blight disease, shedding light on avenues for sesame improvement for bacterial blight resistance through genotypic selection. About 46.67% of the tested genotypes demonstrated low AUDPC compared to Benishangul-1, a variety released for its adaptability in high rainfall and bacterial blight hot spot areas, such as Kamashi, Assosa, and Metekel zones, and similar agro-ecologies. Despite its initial acclaim, Benishangul-1's yield potential has shown signs of deterioration over time. This decline can be attributed, in part, to the increasingly harsh weather conditions, characterized by intensified and prolonged rainfall in the region. Such environmental stresses pose formidable challenges to crop resilience and productivity, highlighting the imperative for ongoing research and breeding efforts aimed at bolstering the resilience of sesame varieties to evolving climatic conditions. The progression of bacterial blight infection in sesame genotypes unfolds in a nuanced manner, as depicted in Figure 2. Initially, at 14 and 28 days after emergence (DAE), no discernible symptoms of bacterial blight were observed across the genotypes. However, as the plants advanced through their growth stages, notably at 42, 56, and 72 DAE, the mean percentage of severity index steadily increased to 16.92%, 20.78%, and 27.71%, respectively. This escalation in disease severity notably coincides with the onset of flower initiation, marking the transition into the critical reproductive phase of sesame development. Similarly, bacterial blight disease was found as prominent in West Gondar, Northwestern Ethiopia [17]. In a testing site, located in Kamashi zone, the mean percentage of severity index in landrace collections ranges from 24.76 to 40.34% [18]. Further, higher percentage of severity index reaching 77.40% has been observed in other sesame genotypes at the same testing site [8].

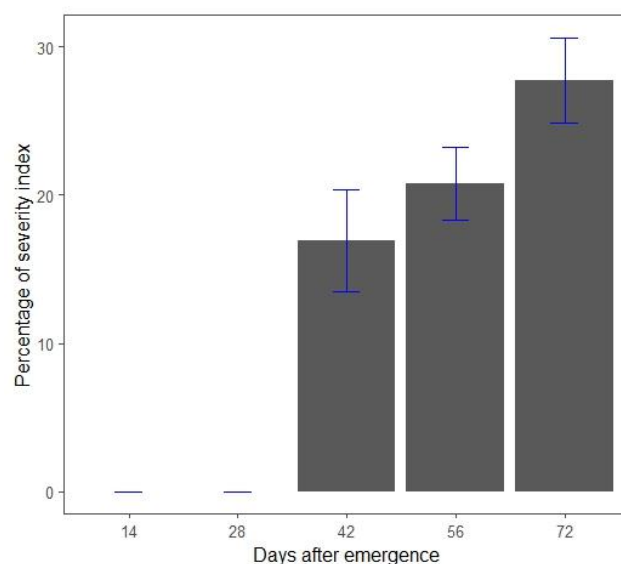
Table 2. Mean square values for disease and seed yield related traits of sesame genotypes evaluated at Kamashi during 2017/18 cropping season.

Character	Mean squares		
	Block (df=2)	Genotype (df=16)	Error (df=32)
Days to 50% flowering	5.70	17.59**	5.99
Days to 90% maturity	1.19	24.06***	4.50
Area under disease progress curve	71889	4128 ^{ns}	5435
Plant height to first branching (cm)	120.30	67.52**	25.07
Plant height (cm)	970.57	224.78**	72.30
Length of capsule bearing zone (cm)	146.65	78.99*	32.00
Number of primary branches per plant	0.79	0.69 ^{ns}	0.45
Number of capsules per plant	483.07	181.50 ^{ns}	118.07
Number of seeds per capsule	56.61	32.20 ^{ns}	21.39
1000 seeds weight (g)	0.20	0.30 ^{ns}	0.18
Seed yield per hectare (kg)	121397	34016*	14462

df=degree of freedom

The incidence and severity of bacterial blight vary depending on agroecological conditions, reaching up to 100% in Northwestern Ethiopia where rainfall and humidity levels are high [6], and ranging from 10% to 50% in semi-arid areas such as Werer and Humera [9]. In optimum moisture areas of Norther Ethiopia, bacterial blight disease severity index (%) ranges from 9.30 to 39.15% [10]. Remarkably, certain genotypes exhibited a remarkable resilience to bacterial blight at key time points. WARC-81 was found as a standout performer, showing the lowest percentage of severity index at 42 DAE, closely followed by WARC-92 and WARC-59. Similarly, at 72 DAE, WARC-81 and WARC-70 demonstrated notable resistance, underscoring their potential as valuable genetic resources for breeding programs aimed at enhancing disease tolerance in sesame cultivars. Conversely, the variety Tate, alongside genotypes WARC-63 and WARC-92, succumbed to higher levels of bacterial blight infection, particularly evident at 72 DAE, where they exhibited the highest percentage of severity index. This discrepancy shows the inherent variability in disease susceptibility among sesame genotypes, underscoring the importance of intensive evaluation of available sesame germplasm to overcome the impact of the disease in sesame production. Beyond the confines of this study, these findings carry profound implications for sesame cultivation practices and breeding strategies. By elucidating the dynamics of bacterial blight infection across critical growth stages, stakeholders gain valuable insights into optimal disease management practices and the identification of resilient genotypes for future breeding endeavors. Moreover, this study underscores the imperative for ongoing research aimed at

unraveling the genetic mechanisms underpinning disease resistance in sesame, paving the way for the development of tailored interventions to safeguard yield stability and enhance agricultural sustainability in sesame-growing regions.

**Figure 1.** Mean percentage of severity index of sesame genotypes at 14, 28, 42, 56, and 72 days after emergence during 2017/18 at Kamashi.

Despite the absence of visible symptoms of bacterial blight disease infection at 14 and 28 days after emergence (DAE)

(Figure 1), a notable shift in disease response emerged as the sesame plants progressed through their growth stages. By 42 DAE, a significant development unfolded: all genotypes displayed a uniform pattern of moderate resistance, characterized by a 10.1 – 20% range in the percentage of severity index (Figure 2). This collective resilience across the genotypic spectrum underscores the inherent capacity of sesame plants to mount an effective defense against bacterial blight at this crucial juncture of growth. However, the resilience observed at 42 DAE began to wane as the plants advanced in age. As shown in Table 3, by 56 DAE, only 35.29% of the genotypes retained their moderate resistance, signaling a shift in disease dynamics. Notably, among the remaining genotypes exhibiting moderate resistance at this stage were two varieties, Benishangul-1 and Tate, alongside four advanced lines, including WARC-59, WARC-74, WARC-81, and WARC-84. This subset of genotypes demonstrates a sustained ability to mitigate bacterial blight infection, highlighting their potential

as key genetic resources for breeding programs aimed at enhancing disease resistance in sesame cultivars. However, by 72 DAE, moderate susceptibility, defined by a 20.1 – 50% range in the percentage of severity index, permeated across all genotypes (Figure 2). This marked transition from moderate resistance to moderate susceptibility underscores the dynamic nature of disease progression and the formidable challenge posed by bacterial blight in later stages of sesame development. These findings carry significant implications for sesame breeding and disease management strategies. The transient nature of moderate resistance observed during the critical growth stages underscores the importance of timely interventions and vigilant monitoring to curtail disease spread. Moreover, the identification of resilient genotypes, such as Benishangul-1 and select advanced lines, offers promising avenues for future breeding efforts aimed at fortifying sesame cultivars against bacterial blight disease.

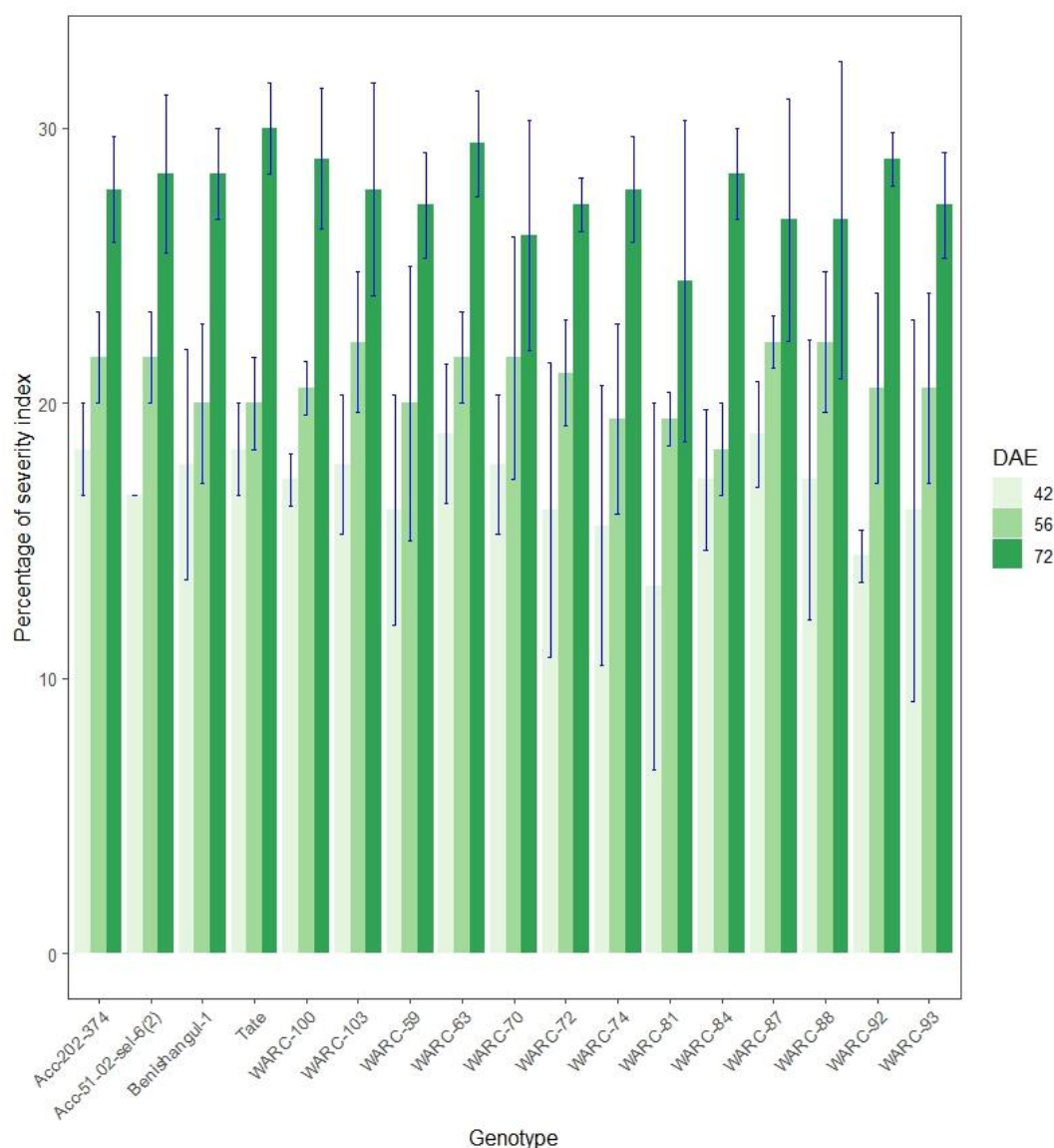


Figure 2. Percentage of severity index in sesame genotypes at 42, 56, and 72 days after emergence during 2017/18 at Kamashi.

Table 3. Resistance reaction of sesame genotypes against bacterial blight at 14, 28, 42, 56, 72 days after emergence.

Genotype	14 DAE		28 DAE		42 DAE		56 DAE		72 DAE	
	PSI	DR	PSI	DR	PSI	DR	PSI	DR	PSI	DR
Acc-202-374	0.00	NS	0.00	NS	18.33	MR	21.67	MS	27.78	MS
Acc-51-02-sel-6(2)	0.00	NS	0.00	NS	16.67	MR	21.67	MS	28.34	MS
Benishangul-1	0.00	NS	0.00	NS	17.78	MR	20.00	MS	28.33	MS
Tate	0.00	NS	0.00	NS	18.33	MR	20.00	MS	30.00	MS
WARC-100	0.00	NS	0.00	NS	17.22	MR	20.56	MS	28.89	MS
WARC-103	0.00	NS	0.00	NS	17.78	MR	22.22	MS	27.78	MS
WARC-59	0.00	NS	0.00	NS	16.11	MR	20.00	MS	27.22	MS
WARC-63	0.00	NS	0.00	NS	18.89	MR	21.67	MS	29.44	MS
WARC-70	0.00	NS	0.00	NS	17.78	MR	21.67	MS	26.11	MS
WARC-72	0.00	NS	0.00	NS	16.11	MR	21.11	MS	27.22	MS
WARC-74	0.00	NS	0.00	NS	15.56	MR	19.44	MR	27.78	MS
WARC-81	0.00	NS	0.00	NS	13.33	MR	19.44	MR	24.44	MS
WARC-84	0.00	NS	0.00	NS	17.22	MR	18.33	MR	28.33	MS
WARC-87	0.00	NS	0.00	NS	18.89	MR	22.22	MS	26.67	MS
WARC-88	0.00	NS	0.00	NS	17.22	MR	22.22	MS	26.67	MS
WARC-92	0.00	NS	0.00	NS	14.44	MR	20.56	MS	28.89	MS
WARC-93	0.00	NS	0.00	NS	16.11	MR	20.56	MS	27.22	MS
Mean	NA		NA		16.92		20.78		27.71	
Standard error of mean	NA		NA		1.70		1.42		1.58	
P-value	NA		NA		0.672		0.823		0.770	
Coefficient of variation	NA		NA		17.39		11.90		9.92	

DAE=days after emergence; PSI=percentage of severity index; DR=disease reaction; NS=no symptom; MR=moderate resistant; MS=moderate susceptible; NA=not applicable

3.2. Performance of Sesame Genotypes for Seed Yield and Its Related Traits

The analysis of variance unveiled significant difference among the sesame genotypes, particularly concerning critical agronomic traits (Table 2). Notably, significant differences ($P < 0.05$) were observed for days to 50% flowering, days to 90% maturity, plant height to the first branch, overall plant height, length of the capsule-bearing zone, and seed yield. Similarly, significant variability reported among sesame genotypes for days to 50% flowering, 90% days to maturity, plant height to first branch, length of capsule bearing zone, number of branches per plant, and seed yield [8, 19]. This comprehensive assessment provides invaluable insights into the genetic diversity underlying sesame cultivation, offering a roadmap for

targeted breeding efforts to enhance crop performance and yield potential. However, certain traits exhibited remarkable consistency across genotypes. Notably, no significant differences were detected for the number of primary branches per plant, number of capsules per plant, number of seeds per capsule, and 1000-seed weight. The mean number of days to 90% maturity spanned a range from approximately 102 to 112 days, highlighting the variability in growth duration among the genotypes. Notably, WARC-84 emerged as the tallest genotype, followed by WARC-87, whereas WARC-103 and WARC-81 exhibited comparatively shorter stature (Table 4). Genotype WARC-84 also exhibited the highest number of primary branches per plant, number of capsules per plant, and seed yield. This genotype significantly outperformed the two released varieties, Acc-51-02-sel-6(2) and Tate, in terms of seed yield (Figure 3). However, the maximum yield recorded

is lower than the national sesame productivity average (680 kg ha⁻¹) [5], as well as the maximum yield recorded on elite genotypes at the same site [8, 18]. Furthermore, within the tested genotypes, Tate and Acc-202-374 were characterized by their larger seed size, with 1000-seed weights of 2.84 g and

2.72 g, respectively. This distinction underscores the significance of seed morphology in influencing yield potential and market value, highlighting avenues for future breeding efforts aimed at enhancing seed quality and commercial viability.

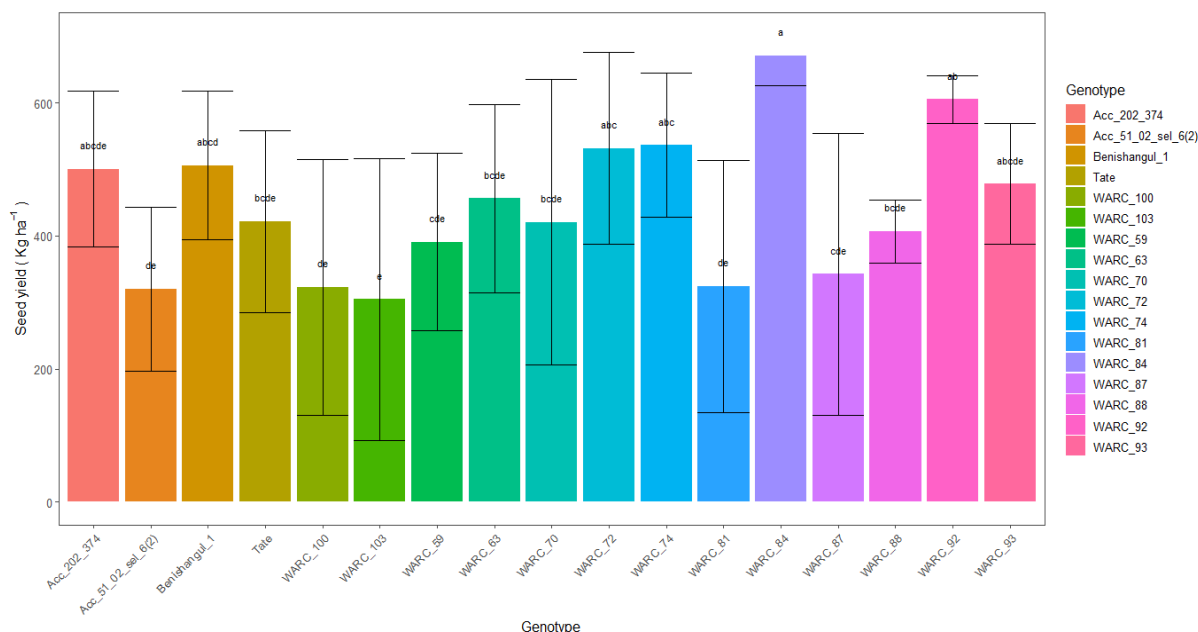


Figure 3. Mean seed yield comparisons of sesame genotypes evaluated at Kamashi during 2017/18 cropping season.

Table 4. Performance of sesame genotypes for bacterial blight disease resistance and seed yield related traits at Kamashi during 2017/18 cropping year.

Genotype	50%DF	AUDPC	90%DM	PHFB	PH	LCBZ	PBPP	CPP	SPC	TSW	SY
Acc-202-374	51.67c-e	803.91	106.00bcd	38.50ab	100.63b-e	49.73b-f	3.03	43.13	71.70	2.72	500.51a-e
Acc-51-02-sel-6(2)	56.33ab	785.07	108.67bc	42.77a	103.47b-e	46.07def	3.40	37.47	75.37	2.25	319.99de
Benishangul-1	57.00a	775.59	109.33ab	42.70a	102.30b-e	47.57c-f	3.40	36.83	74.97	2.30	505.81a-d
Tate	55.67a-c	796.67	105.33cd	30.47bcd	102.83b-e	54.50a-e	3.70	44.90	72.70	2.84	421.57b-e
WARC-100	52.67b-e	780.60	102.67de	39.10a	107.70abc	44.47f	2.80	37.60	68.03	2.60	322.83de
WARC-103	51.67cde	804.44	102.67de	29.87cd	91.43e	47.63c-f	3.23	37.50	69.77	1.71	304.78e
WARC-59	53.33a-d	743.35	106.00bcd	40.33a	105.77a-d	45.43ef	2.73	26.70	69.70	2.27	390.87cde
WARC-63	55.00abc	825.01	107.00bc	37.60a-d	98.80cde	45.93def	3.50	42.83	72.93	2.60	456.19b-e
WARC-70	53.67a-d	782.78	108.33bc	37.10a-d	90.70e	44.17f	2.57	39.33	74.73	2.32	420.55b-e
WARC-72	50.00de	759.98	108.33bc	39.00a	111.33abc	56.70abc	2.90	44.70	76.67	2.37	531.74abc
WARC-74	55.67abc	731.68	106.00bcd	43.83a	110.73abe	59.30a	3.30	40.23	77.37	2.47	536.27abc
WARC-81	56.00ab	673.86	108.67bc	39.01a	92.10de	44.77f	2.73	29.60	74.20	2.10	324.46de
WARC-84	55.67abc	742.79	108.67bc	42.57a	118.90a	53.23a-f	4.30	58.43	75.90	2.15	671.23a
WARC-87	52.33b-e	811.14	109.33ab	38.07abc	117.77a	54.60a-e	3.87	52.97	72.87	1.70	342.75cde
WARC-88	54.33abc	787.81	109.33ab	43.00a	113.17ab	54.87a-d	3.78	46.47	76.30	2.41	406.67b-e
WARC-92	49.00e	741.65	101.67e	29.33d	106.57abc	57.30ab	2.80	49.47	69.47	2.48	605.26ab

Genotype	50%DF	AUDPC	90%DM	PHFB	PH	LCBZ	PBPP	CPP	SPC	TSW	SY
WARC-93	57.00a	751.65	112.33a	43.90a	113.13ab	53.13a-f	3.47	41.23	80.37	2.72	478.03a-e
Mean	53.94	770.46	107.07	38.65	105.13	50.55	3.26	41.72	73.70	2.35	443.50
Standard error of mean	1.41	42.56	1.22	2.89	4.90	3.26	0.39	6.27	2.67	0.25	69.43
P-value	0.004	0.715	2.885e ⁻⁰⁵	0.008	0.003	0.014	0.156	0.146	0.158	0.116	0.019
Coefficient of variation	4.54	9.56	1.98	12.95	8.08	11.19	20.72	26.03	6.27	18.43	27.11

DF= days to flowering; AUDPC=area under disease progress curve; DM=days to maturity; PHFB=plant height to first branching in cm; PH=plant height in cm; LCBZ=length of capsule bearing zone in cm; PBPP=number of primary branches per plant; CPP=number of capsules per plant; SPC=number of seeds per capsule; TSW=1000 seeds weight in g; SY=seed yield per hectare

4. Conclusion

Surprisingly, certain genetic types displayed notable resistance to bacterial blight at crucial stages. Among these, WARC-81 emerged as a standout, exhibiting the lowest severity index at 42 days after emergence (DAE), closely trailed by WARC-92 and WARC-59. Throughout the evaluation period, the genotypes exhibited varying responses to bacterial blight, ranging from immunity between 14 and 28 DAE to moderate susceptibility from 42 to 72 DAE. This transition from immunity to moderate susceptibility highlights the dynamic nature of disease progression and the significant challenge posed by bacterial blight during later stages of sesame growth. Furthermore, these findings hold significant implications for sesame cultivation methods and breeding approaches. By unraveling the dynamics of bacterial blight infection across critical growth phases, stakeholders can gain valuable insights into effective disease management practices and the identification of resilient genotypes for future breeding efforts.

Abbreviations

AUDPC	Area Under Disease Progress Curve
DAE	Days After Emergence
PSI	Percentage of Severity Index

Acknowledgments

The Ethiopian Institute of Agricultural Research is duly acknowledged for its financial support.

Author Contributions

Sintayehu Gedifew is the sole author. The author read and approved the final manuscript.

Conflicts of Interest

The author declares no conflicts of interest.

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