

Research Article

Incidence, Severity, and Distribution of Cassava Bacteria Blight Disease in Sierra Leone

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Abstract

Cassava Bacterial Blight Disease (CBBB) is a major constraint in cassava production, initially manifesting on the lower leaves as scattered, cigar-shaped, water-soaked lesions. This study aimed to evaluate cassava bacterial blight disease in Sierra Leone. A field trial was conducted at the School of Agriculture and Food Sciences research site to evaluate disease susceptibility of various cassava genotypes and identify elite genotypes for population improvement. The experiment followed an augmented randomized complete block design (ARCB). Additionally, a farmer field survey was carried out across all districts to assess the distribution and prevalence of CBBB. The cassava genotypes were classified into three categories: resistant (17.6%), susceptible (80.9%), and mildly susceptible (1.5%). Resistant genotypes, such as TME419, SLE0201, and SLE0087, exhibited no disease progression ($rAUDPC = 0.0$, $SSV = 0.0$), while susceptible genotypes, including SLICASS 4 and SLE0109, demonstrated $rAUDPC$ values between 1100 and 2999. Genotype SLE0092 was the most severely affected, displaying the highest disease incidence (50%) and severity (3.1) nine weeks post-planting. The highest root weight (14.2 kg) was recorded for genotype SLE0185, while most genotypes showed moderate yields. A survey of 276 cassava fields across Sierra Leone revealed a widespread occurrence of CBBB, with a national mean incidence of 60.4%, which was notably higher in the Eastern region (69.2%) and Kambia District (78.6%). These findings emphasize the urgent need for the widespread cultivation of CBBB-resistant genotypes.

Keywords

Incidence, Severity, Prevalence, Distribution, Genotypes, Resistance

1. Introduction

Cassava (*Manihot esculenta*, Crantz) is an essential food crop for Africa, Latin America, and Asia [1]. The crop provides daily calories to more than 800 million people globally, and its production ranks fourth globally among tropical crops [2]. Its starchy roots provide valuable sources of carbohydrates compared to most cereal [3]. The roots can be utilized

fresh as food or processed into various products. Some people consume cassava leaves as a source of proteins, vitamins, and micronutrients [4]. Furthermore, it is documented that cassava cultivation has more significant potential in improving the living standards of farmers in rural areas [5]. Cassava can also play a crucial role in relieving hunger and poverty [6]. The

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product of cassava are integral in the daily lives of nearly every household in cassava growing regions [7].

Recently, cassava has received considerable interest from various governments and industries to counter prevailing food security threats owing to its exclusive and desirable characteristics, including adaptability to climate change and appreciable productivity in poor soils. In Sierra Leone, cassava is the second most important food crop after rice the country's staple. It is also the most important root and tuber crop [8]. Cassava has also grown all over the country, which has shown remarkable progress in cassava processing at both domestic and commercial scales, although to varying degrees. Some common cassava products processed in the country include gari, foo-foo, gbodor, dried chips, starch and boiled cassava with beans. Cassava-based products such as raw tubers, gari and cassava bread (very thin, small, flat, round pieces) are traded mainly in Sierra Leone [9]. Cassava leaves provide a source of income for women. The leaves are used to prepare a very popular national cassava leaf sauce [9]. Much of this success may be attributed to its adaptability, its capacity to provide acceptable yields under marginal farming conditions and its tolerance to drought [9]. However, cassava production has been strained by several biotic factors, including cassava bacteria blight (CBB). Cassava bacterial blight is one of the most severe bacterial diseases that constrain cassava production worldwide [10]. The bacterium *Xanthomonas axonopodis* pv. *Manihotis* (Xam) is the causal agent of CBB that is distributed by infected cuttings [11]. Symptoms associated with CBB include; water-soaked angular leaf spotting, leaf blighting and wilting, defoliation, exudation, vascular necrosis, and dieback [12]. Cassava bacterial blight can lead to 100% yield loss depending on cassava variety and environmental conditions [13]. High atmospheric temperature and humidity, wounds and bruises caused on cassava stems, and susceptibility of cassava genotypes favor the proliferation of cassava bacterial blight. In Sierra Leone, Cassava bacterial blight (CBB) is one of the most damaging diseases affecting cassava production in Sierra Leone. The prevalence of CBB was found to be 100% and 92% in the rainy season and dry season, respectively in Sierra Leone. Breeding for resistance against CBB and farmers using CBB-resistant cassava varieties is the most practical way of managing this disease [14]. Therefore, this study aimed to evaluate the resistance of different cassava genotypes against cassava bacteria blight in Sierra Leone.

2. Materials and Methods

2.1. Description of the Experimental Sites

This study involves two activities. The first activity was to screen 260 cassava genotypes including 15 dominant varieties that are widely used by farmers in all five regions for their susceptibility of cassava bacteria. Therefore, field experiment was carried out in the upland at the experimental site of the

school of Agriculture and Food Science, Njala campus in Kori chiefdom Moyamba district, South of Sierra Leone. School of Agriculture and Food Science is located at an elevation of 50 m above sea level on latitude 8 °N and longitude 12 °W of the equator. Njala University, Njala campus is located at about one hundred and fourteen miles (114) from the capital city, Freetown or Southern Sierra Leone at approximately 7 miles off the Bo-Freetown highway. Njala University, Njala campus experiences a distinct dry and wet season because of the denial nature of the area, the rainy season starts from May to October and the dry season starts from November to April. The mean monthly air temperature ranges from 21 °C to 23 °C for a greater part of the day and night especially during the rainy season.

The second activity was to determine the prevalence and distribution of cassava bacteria blight disease in Sierra Leone through farmers field survey. The survey was carried out in all five regions of Sierra Leone. Sierra Leone, a country located on the west coast of Africa between latitudes 7 ° and 10 ° North and longitudes 10 ° and 13 ° West, offers a rich and complex field of study encompassing disciplines such as history, political science, anthropology, economics, environmental studies, and public health. Covering a total land area of approximately 71,740 square kilometers (27,699 square miles), Sierra Leone boasts a diverse landscape with a wide array of geographical features important for survey studies.

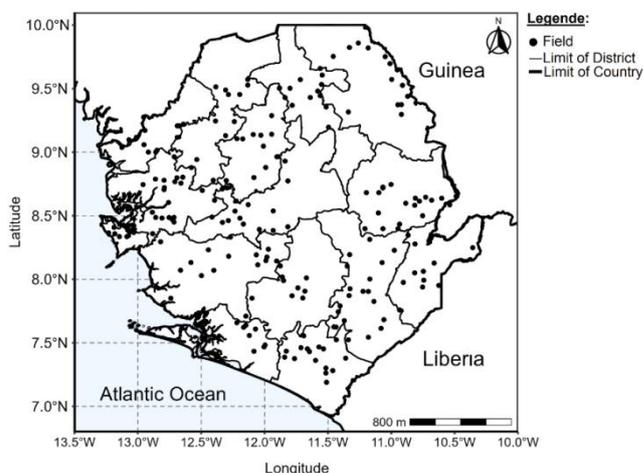


Figure 1. Locations of the 276 farms surveyed in the five regions for CBB in 2023-2024.

2.2. Experimental, Survey Design and Layout

Cassava genotypes including local accessions and improved varieties was collected from all districts of Sierra Leone and evaluated against cassava bacteria blight.

The experiment was laid in a 110 m × 22 m Augmented randomized Design with four blocks, each block measured 28 m × 10 m with 2 m apart between blocks. Equal number of genotypes was planted in every block, and they were assessed

in one year. Stem cuttings (20-30 cm long) of each of the local genotypes collected were planted on a 10 m long ridges and spaced 1 m between ridges and 1 m between hills. Secondly The research used a survey design (farm survey research method) to elicit information from 278 farms.

2.3. Data Collection

Incidence was calculated as a percentage of the total plants infected over the total number of plants assessed.

Formula:

$$\text{Mean incidence (\%)} = \frac{\sum \text{Infected plants}}{\sum \text{plants}} \times 100$$

The severity of cassava leaf symptoms of cassava blight was scored using a scale of visual rating ranging from 1 to 5, depending on the expression of the bacteria symptoms on the leaves as described by Wydra and Msikita, [15].

1= No visible symptoms on the leaves

2= Appearance of slight spots on the leaves

3= Presence of lesion on almost all the leaves of the plant (2/3 of the leaves of the plant)

4= Sever lesion on almost all leaves in leaf area

5= very severe lesion on all the leaves

The yield data such as root air weight, root water weight and biomass were collected from five plants out of the plants in the ridge. The root air weight was obtained by weighing the harvested roots from the five plants using digital scale, whilst the root water weight was obtained by weighing the root in water and biomass which is the above ground of the plants were also weighed using the digital balance.

A total of 20 farms per district were visited. The fields surveyed were separated on average by 10 km, the diagonal (\times) method was used in this study to assess the plants and a total of 30 plants was evaluated in each field, with 15 plants randomly selected along each diagonal. A tablet which has Kobo application and GPS facility that made it possible to identify the geographical coordinates (longitude, latitude, altitude) in each field was used to collect in each field.

2.4. Data Analysis

The disease severity score values for CBBD were converted to percentages and then used to estimate the area under the disease progress curves (AUDPC), as described by Forbes *et al.* [16]. The formula for computing AUDPC is shown below:

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

where y_i = disease severity of the i^{th} observation, t_i = time (days) for the i^{th} observation, and n = total number of observations.

The susceptibility scale values of the disease CBBD were

estimated by first calculating the resistance-scale values, as described by Forbes *et al.* [16]:

$$S_x = S_y \frac{D_x}{D_y}$$

where S_y = the assigned susceptibility scale value, D_y = observed disease score (AUDPC or relative AUDPC (rAUDPC)) for the standard variety, S_x = estimated susceptibility-scale value, and D_x = observed disease score for the studied clones. The quotient of the assigned susceptibility value and the resistance measure of the check variety (AUDPC or rAUDPC) was used to obtain a constant. The resistance value of each clone was then multiplied by the constant to obtain the susceptibility value of the clone. An analysis of variance with one classification criterion (ANOVA) was carried out to determine the incidence and severity of the disease. The differences between the means were compared by using Fisher's LSD test to distinguish homogeneous groups at the significance level $P = 0.05$ and the distribution maps were drawn using the Geomfunction in R studio.

3. Results

3.1. SSV and rAUDPC for 260 Cassava

The result also showed significant ($p \leq 0.05$) variation among genotypes for CBBD infection. The resistance class comprises genotypes with (0.0) rAUDPC and (0.0) SSV, mildly susceptible class comprises of genotypes with rAUDPC comprises genotypes with rAUDPC ranging from 1100-2999 and SSV ranging from 1.1-2.9 whilst the susceptibility class range from 3000-4000 and SSV ranging from 3.0-4.0.

From the results, 210 (80.9%) out of the 260 genotypes were assessed were mildly susceptible to cassava bacteria blight disease (CBBD) with the relative area under disease progress curve (rAUDPC) ranging from 1100-2999 and the susceptibility scale value (SSV) ranging from 1.1-2.9, 46 (17.6%) out of the 260 genotypes were resistance to cassava bacteria blight disease (CBBD) with zero (0.0) rAUDPC and SSV (0.0) and 4 (1.5%) out 260 genotypes were susceptible to the disease with rAUDPC ranging from 3000-4000 and SSV ranging from 3.0-4.0.

3.2. SSV and rAUDPC for 15 Cassava

The result also showed significant ($p \leq 0.05$) variation among genotypes for CBBD infection among 15 dominant cassava varieties. The relative area under disease progress curve (rAUDPC) and susceptibility scale value (SSV) analysis revealed three classes (resistance, susceptible and mildly susceptible). The resistance class comprises genotypes with (0.0) rAUDPC and (0.0) SSV, mild susceptibility class comprises genotypes with rAUDPC ranging from 1100-2999 and

SSV ranging from 1.1-2.9 whilst the susceptible class comprises of genotypes with rAUDPC range from 3000-4000 and SSV ranging from 3.0-4.0 (Table 2). From the results, the genotypes that were resistant to cassava bacteria blight disease (CBBB) were TME419, SLE0201, SLE0082, SLE0205, and SLE0087 with rAUDPC and SSV of 0.0. The susceptible class includes genotypes like SLICASS SLE0109, 0078, 0028, 0056, 0127, 0182, 0115 and 0234 though with different levels of susceptibility and only genotype SLE0092 were found susceptible class with rAUDPC and SSV of 3500 and 3.1 respectively (Table 1).

Table 1. Susceptibility scale value and relative area under disease progress curve for 15 dominant cassava varieties in Sierra Leone.

Variety	rAUDPCBBD	SSVCBBD
TME419	0	0.0
SLICASS 4	1400	1.1
SLE0109	2500	2.3
SLE0078	1500	1.5
SLE0028	2200	1.9
SLE0056	2200	1.9
SLE0092	3500	3.1
SLE0127	1400	1.1
SLE0201	0	0.0
SLE0082	0	0.0
SLE0205	0	0.0
SLE0182	1400	1.1
SLE0087	0	0.0
SLE0115	2100	1.7

Table 2. Incidence and severity of 15 dominant cassava genotypes.

Variety	Incidence 3MAP	Incidence 6MAP	Incidence 9MAP	Severity 3map	Severity 6MAP	Severity 9MAP
TME419	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.0	1.0±0.0	1.0±0.0
SLICASS 4	10.0±0.60	10.0±1.0	20.0±1.2	1.1±0.0	1.1±0.0	1.5±0.0
SLE0109	10.0±0.78	20.0±1.7	40±2.3	1.6±0.01	2.0±0.2	2.3±0.2
SLE0078	10.0±1.0	10.0±1.0	20±2.0	1.2±0.0	1.2±0.0	1.5±0.0
SLE0028	10±0.8	30±2.6	40±3.0	1.2±0.0	1.8±0.0	1.9±0.0
SLE0056	20±2.0	20±1.7	40±3.0	1.1±0.0	1.5±0.0	1.9±0.0
SLE0092	20±0.0	40±3.6	50±4.0	2.0±0.1	2.5±1.0	3.1±0.2
SLE0127	10±1.0	20±1.0	30±1.7	1.1±0.0	1.1±0.0	1.1±0.0
SLE0201	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.0	1.0±0.0	1.0±0.0

Variety	rAUDPCBBD	SSVCBBD
SLE0234	2100	1.7
SE	150.3	0.3
LSD (0.05)	764.8	0.5036
F pr.	<.001	<.001
CV (%)	10.11	10.14

LSD = least significance difference; SE= standard error; CV = coefficient of variation

3.3. Incidence and Severity of 15 Dominant

The assessment of bacteria blight disease revealed significant ($p \leq 0.05$) variation among genotypes in the incidence and severity at all evaluation periods. The results showed that genotype SLE0092 recorded that highest incidence of CBBB at 3 (20.0±0.0%), 6 (40.0±0.0%) and 9 (50.0±0.0%) weeks after planting, closely followed by SLE0056 at 3 (20.0±0.0%), 6 (20.0±0.0%), 9 (40.0±0.0%), SLE0115 at 3 (20.0±0.0%), 6 (20.0±0.0%), 9 (30.0±0.0%), SLE0028 at 3 (10.0±0.0%), 6 (30.0±0.0%), 9 (40.0±0.0%) and SLE0109 at 3 (10.0±0.0%), 6 (20.0%) and at 9 (40.0±0.0%). Genotypes TME419, SLE0201, SLE0082, SLE0205, and SLE0087 were all resistant to CBBB with an incidence of 0.0%. Significant ($p \leq 0.05$) variations in severity were also observed among genotypes assessed. Genotypes SLE0092 recorded the highest at 3 (2.0), 6 (2.5) and 9 (3.1) followed by SLE0109 at 3 (1.6), 6 (2.0) and 9 (2.3), SLE0028 at 3 (1.2), 6 (1.8) and 9 (1.9), SLE0056 at 3 (1.1), 6 (1.5) and 9 (1.9), and SLE0115 at 3 (1.5), 6 (1.7) and 9 (1.7) and genotypes TME419, SLE0201, SLE0082, SLE0205, and SLE0087 were resistant with severity score of 1.0±0.0 (Table 2).

Variety	Incidence 3MAP	Incidence 6MAP	Incidence 9MAP	Severity 3map	Severity 6MAP	Severity 9MAP
SLE0082	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.0	1.0±0.0	1.0±0.0
SLE0205	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.0	1.0±0.0	1.0±0.0
SLE0182	10±1.0	10±1.0	10±0.8	1.1±0.0	1.1±0.0	1.1±0.0
SLE0087	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.0	1.0±0.0	1.0±0.0
SLE0115	20±1.7	20±1.8	30±2.0	1.5±0.0	1.7±0.0	1.7±0.0
SLE0234	10±0.7	20±2.0	30±3.0	1.2±0.0	1.6±0.0	1.7±0.0
F pr.	<.001	<.001	<.001	0.05	0.002	<.001
CV (%)	14.6	16.1	12.0	7.8	10.3	9.6

Note: MAP = Month after planting, CV (%) = coefficient of variance, ± = mean standard error (Mean ±se)

3.4. Yield and Yield Component of 260 Cassava Genotypes

The yield and its components analysis of 260 cassava genotypes revealed significant ($p \leq 0.05$) difference among cassava genotypes in yield. The results showed that root weight ranges from 0.5 ha to 14.2 ha and out of the 260 cassava genotypes assessed, 17 (6.5%) of genotypes recorded root weight ranging from 10.0 ha-14.2 ha with genotype SLE0185 recording the highest root weight (14.2 ha) followed by Genotype SLE0201 (13.8 kg). Out of 260 genotypes, 67 (25.7%) recorded root weight ranging from 5.0-9.9 ha with genotypes SLE0010 recording root weight of 9.9 ha, followed by genotypes SLE0257 (9.6 kg), SLE0140 (9.5 kg) and SLE0092 (9.0 kg), the remaining 176 (67.8%) genotypes recorded fruit weight ranging from 0.5- 4.9 kg with genotypes SLE0014, SLE0070, SLE0071, SLE0255, SLE0199, SLE0204, SLE0205, SLE0102, SLE0074, SLE0077, SLE0167, SLE0029 and SLE0034 recording the lowest root weight of 0.5 kg. The water root and biomass weight were also significant among genotypes assessed with root water weight and root biomass ranging from 0.1 kg to 10.1 kg. Out of the 260 genotypes 26 (10.0%) of them recorded root water weight ranging from 5.0-10.0 kg with genotype SLE0185 recording root water weight of 10. kg and the remaining 234 (90.0%) genotypes recorded root water weight ranging from 0.5-4.9 kg. Genotypes SLE0077, SLE0167, SLE0029 and SLE0034 recorded the best root water weight of 0.1 kg. Out of the 260 genotypes the root biomass was high for 56 (19.2%) with biomass weight ranging from 5.0-10 kg and the remaining 210 (80.8%) recorded biomass weight ranging from 0.5-4.9 kg and the least biomass weight (0.1 kg) was observed for genotypes SLE0077, SLE0167, SLE0029 and SLE0034.

The yield and its components analysis of 15 dominant cassava genotypes (Table 3), revealed significant ($p \leq 0.05$) difference among cassava genotypes in yield. The evaluation, SLICASS 4 recorded the highest root yield (13.5 kg) followed

by TME419 (11.5 kg), SLE0082 (10.6 kg), SLE0201 (10.4 kg), and SLE0087 (10.0 kg) and the lowest root weight was recorded for genotypes SLE0092 (2.0 kg) and SLE0056 (2.6 kg). The root was best for SLICASS 4 (5.3 kg) followed by SLE0201 (4.5 kg), TME419 (4.0 kg), and SLE0087 (3.7 kg) whilst genotypes SLE0092 and SLE0056 recorded root water weight of 1.0 kg. The root biomass was higher than SLICASS 4 (7.4 kg), TME419 (7.0 kg), SLE0087 (6.0 kg), SLE0201 (5.7 kg), SLE0109 (5.1 kg) and SLE0082 (5.0 kg) and lowest biomass was recorded with genotype SLE0092 (1.0 kg), SLE0115 and SLE0234 (2.0 kg).

Table 3. Yields and its components of 15 dominant cassava genotypes in Sierra Leone.

Variety	Weight (kg)	Water weight (kg)	Biomass (kg)
TME419	11.5±1.3	4.0±0.3	7.0±0.6
SLICASS 4	13.5±1.20	5.3±0.5	7.4.0±0.4
SLE0109	7.3±0.7	3.0±0.2	5.1±0.3
SLE0078	6.8±0.4	2.8±0.2	20±2.0
SLE0028	4.3±0.2	1.8±0.0	2.6±0.2
SLE0056	2.6±0.2	1.0±0.0	2.0±0.2
SLE0092	2.0±0.0	1.0±0.0	1.0±4
SLE0127	6.0±1.0	2.0±0.2	4.0±0.3
SLE0201	10.4±1.0	4.5±0.4	5.7±0.5
SLE0082	10.6±0.9	3.7±0.3	5.0±0.5
SLE0205	9.6.0±0.6	3.2±0.2	4.7±0.4
SLE0182	5.6±0.3	2.3±0.2	2.6±0.2
SLE0087	10.0±1.0	3.6±0.3	6.0±0.4
SLE0115	4.3±0.2	1.7±0.0	2.0±0.0
SLE0234	4.6±0.3	2.0±0.0	2.0±0.0

Variety	Weight (kg)	Water weight (kg)	Biomass (kg)
F pr.	<.001	<.001	<.001
CV (%)	17.1	10.0	9.3

Note: CV (%) = coefficient of variance, \pm = mean standard error (Mean \pm se)

3.5. Correlation Analysis

The relationship between bacteria blight incidence and severity showed significant positive correlation between incidence and severity which clearly indicate an increase in incidence lead to an increase in severity whilst there was a significant negative correlation between incidence and yield and between severity and yield which indicate that an increase in incidence and severity will lead to decrease in yield (Table 4).

Table 4. Correlation between incidence, severity and yield of 260 cassava genotypes.

	Incidence	Severity	Yield
Incidence	1	0.57***	-
Severity	-	1	-0.76***
Yield	-0.65***	-	1

*** =significant at 0.001

3.6. Prevalence and Distribution of Cassava Bacteria Blight Diseases in Sierra Leone

The survey assessed 276 cassava fields and 8,281 plants of which the findings revealed that 141 (51.1%) out of 276 fields

recorded high CBBB incidence (>50 to 70%), 80 (29.8%) fields recorded very high CBBB incidence (>70-78%) and the remaining 55 (19.1%) fields recorded low CBBB incidence (>25-50%). The assessment revealed that the country mean Incidence of CBBB was 58.4% which is moderately high. At regional level, the mean CBBB incidence ranges from 37.5% in the Western area to 76.6% in the Eastern region and the district level assessment revealed that Kono district recorded the highest mean incidence of CBBB (78.2%) followed by Kenema district with a mean incidence of 74.7%. The incidence in the Eastern region was relatively highly than other regions with each district in the region recording mean CBBB incidence above 60.0%. This clearly explained that cassava genotypes in the eastern region are susceptible to the CBBB, and environment is favorable for the pathogen since is a rain forest region and the pathogen that cause cassava bacterial blight favors moist environment (Figure 2).

The country meant CBBB severity was low with a mean CBBB severity of 2.2 (Table 5). The lowest mean CBBB severity (1.2) was recorded in the Western area region and highest mean CBBB severity was recorded in the Northern region (2.7). The district level assessment revealed that the highest mean CBBB severity was recorded in Kono district with a mean CBBB severity of 3.5 followed by Kenema district (3.1) and the lowest mean CBBB severity was recorded in Western area urban rural with both districts recording CBBB severity of 1.2. The low severity observed in Western urban and rural areas can be attributed to that fact most of the cassava varieties cultivated in these districts are resistant and most of the fields visited fall within CBBB of 1-2 which is low to CBBB symptoms. The distribution map showed the widespread CBBB severity with many fields having a CBBB of 1.1-3.2. Fields with no CBBB symptoms or asymptomatic (healthy) were mostly found in districts in the Western region and few districts in the northern and northwest regions (Figure 2).

Table 5. Number of fields Incidence and severity of bacteria blight disease across Sierra Leone.

Regions	District	Number of Fields	Incidence (%)	Severity (score)
Southern			66.5 \pm 5.6	2.8 \pm 0.0
	Bo	20	56.7 \pm 4.6	2.1 \pm 0.0
	Bonthe	14	70.0 \pm 4.7	2.8 \pm 0.0
	Moyamba	20	65.0 \pm 5.6	2.7 \pm 0.0
	Pujehun	20	74.3 \pm 4.5	3.5 \pm 0.0
Northern			54.1 \pm 3.4	1.7 \pm 0.0
	Bombali	20	46.9 \pm 3.0	1.7 \pm 0.0
	Koinadugu	18	45.6 \pm 2.8	1.3 \pm 0.0
	Tonkolili	20	68.0 \pm 7.0	2.7 \pm 0.2

Regions	District	Number of Fields	Incidence (%)	Severity (score)
Eastern	Falaba	15	55.9±5.3	1.9±0.0
	Kenema	20	74.7±6.0	3.1±0.2
	Kono	19	78.2±6.0	3.5±0.0
	Kailahun	20	76.9±5.0	3.0±0.0
Northwest	Portloko	20	60.3±6.0	2.5±0.0
	Kambia	20	68.6±6.3	3.2±0.1
	Karene	13	46.8±4.6	1.6±0.1
	Mean±Se	276.0	58.6±5.5	2.2±0.0
Western area	Western Area Rural	10	40.1±3.4	1.2±0.0
	Western area Urban	7	35.0±3.0	1.2±0.0
	Mean±Se	276.0	58.6±5.5	2.2±0.0

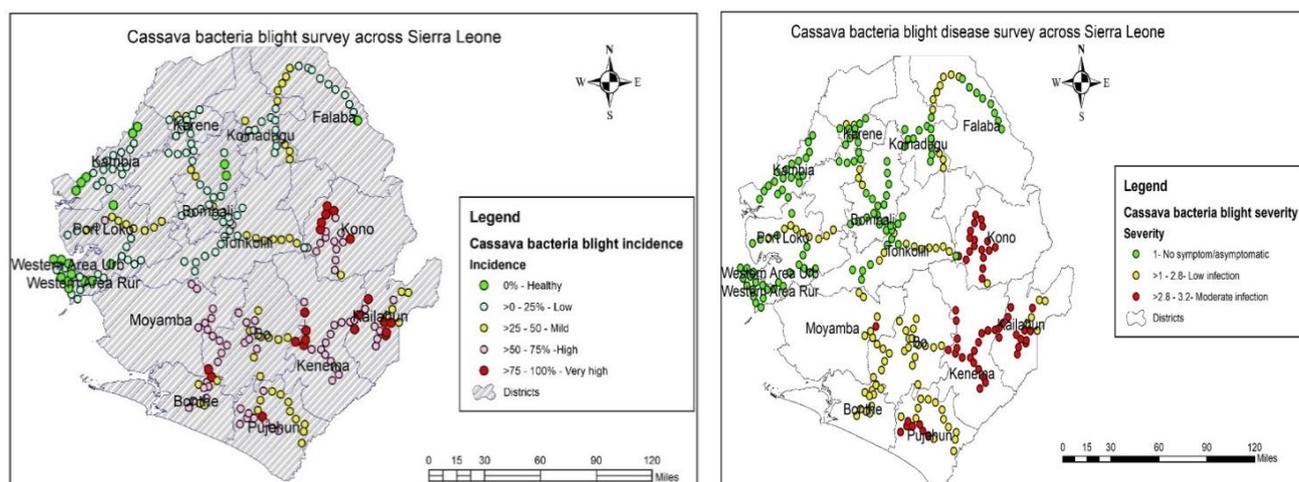


Figure 2. Map of Sierra Leone showing the distribution, Spread and severity of CBBB incidence across the country.

4. Discussion

The results of this study provide a comprehensive evaluation of cassava bacterial blight disease (CBBB) across a diverse set of 260 genotypes. The onset of CBBB was first observed on the lowest leaves of infected plants, progressing to other leaves as the plants matured. The lesions were characterized by small, scattered, cigar-shaped spots, and greyish, water-soaked blights. A thorough assessment of disease progression, based on the relative area under disease progress curve (rAUDPC) and susceptibility scale value (SSV), categorized the genotypes into three distinct classes: resistance, susceptible, and mildly susceptible. This classification revealed significant differences among the genotypes in their

response to CBBB, underscoring the genetic diversity and variability in disease resistance. Ohunakin *et al.* [17], who determined the relative resistance of northern leaf blight of maize by comparing sum rank and AUDPC and proposed classes of resistance and susceptibility of maize genotypes.

Most genotypes evaluated were susceptible to CBBB, comprising a large proportion of the total genotypes. These susceptible genotypes exhibited considerable disease progression and severity, which could have significant implications for cassava production, particularly in regions where CBBB is prevalent. In contrast, a smaller fraction of the genotypes demonstrated complete resistance, showing no signs of disease progression (rAUDPC and SSV values of 0.0). These resistant genotypes, including TME419 and several SLE lines, offer potential as breeding material for developing CBBB-resistant

varieties. Similar observation was made Malik *et al.* [18], who observed why evaluating six popular Southeast Asian industrial cassava varieties in Cambodia that KU50 and HB60 demonstrated significantly superior tolerance to CMD caused by SLCMV over other varieties. Further analysis revealed that the incidence and severity of CBBB were highly variable across the genotypes and at different stages of plant growth. Genotypes such as SLE0092 and SLE0056 were identified as having the highest CBBB incidence and severity, especially at later stages of plant development. This suggests that these genotypes may be more vulnerable to CBBB as the plants mature. On the other hand, resistant genotypes maintained low incidence and severity scores throughout the evaluation periods, confirming their robust resistance to the disease. Samura *et al.* [19] reported that most of the cassava varieties in Sierra Leone are susceptible to cassava bacteria blight disease. In terms of yield, significant differences were also observed among the genotypes. The resistant genotypes generally exhibited higher root yield and biomass compared to the susceptible ones, reinforcing the negative correlation between CBBB incidence and yield. Genotypes that were more severely affected by the disease, such as SLE0092, exhibited the lowest yields, while resistant genotypes like SLICASS 4 and TME419 had notably higher yields and root biomass. This relationship highlights the detrimental impact of CBBB on cassava yield and the potential benefits of cultivating resistant varieties. Samura *et al.* [19] reported that though most of the cassava varieties are susceptible to the cassava bacteria blight but most studies have not been done to estimate the yield loss as the result of this disease.

The survey of cassava fields across different regions further demonstrated the widespread nature of CBBB in the country, with more than half of the fields recording high disease incidence. The Eastern region was heavily affected, with many fields showing both high incidence and severity of CBBB. This geographic distribution suggests that certain environmental or agricultural practices in the Eastern region may be contributing to the higher susceptibility of cassava crops to the disease. The work of Samura *et al.* [19] reported that CBBB was prevalent across country with Eastern region recording the highest CBBB incidence and severity.

5. Conclusion

This study provides valuable insights into the varying levels of resistance and susceptibility to CBBB among 260 genotypes. The significant differences in disease progression and severity among the genotypes highlight the genetic diversity present in cassava, which can be leveraged to mitigate the effects of CBBB. A large proportion of the genotypes exhibited susceptibility to the disease, leading to lower yields and biomass, while a smaller group of resistant genotypes, including TME419 and several other genotypes, showed no disease progression and maintained higher yield performance. The relationship between disease incidence, severity, and yield clearly demonstrates the detrimental impact of CBBB

on cassava production, particularly in regions where the disease is widespread, such as the Eastern and Northern areas of the country. Overall, the findings emphasize the importance of identifying and promoting CBBB-resistant genotypes to enhance cassava productivity and resilience.

Abbreviations

CBBB	Cassava Bacteria Blight Disease
AUDPC	Area Under Disease Progress Curve
rAUDPC	Relative Area Under Disease Progress Curve
CMD	Cassava Mosaic Disease
ARCBDB	Augmented Randomized Complete Block Design
SLCMV	Sri Lankan Cassava Mosaic Virus

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Conflicts of Interest

The authors declare no conflict of interest.

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