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Research Article

Cassava Mosaic Disease (CMD) and Its Whitefly Vector in Sierra Leone: Incidence, Severity and Whitefly Population from Field Surveys in 2020

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ABSTRACT

The role played by cassava is vital in ensuring food security and bolstering the economy in Sierra Leone. However, the production of this crop has been hindered by cassava mosaic disease (CMD). Despite CMD being the most devastating cassava disease, a comprehensive study or survey assessing its prevalence in Sierra Leone is still lacking. The aim of this study was to assess the status of CMD and its whitefly vector in the country. In 2020, a field disease assessment survey was conducted, following a standardized protocol for sampling, diagnostics, and data storage, which was coordinated across 10 West and Central African countries for comparative purposes. The survey covered 268 fields, with 30 plants assessed per field for CMD severity, whitefly population, and sources of infection. The findings revealed the presence of CMD across all five regions and sixteen districts of Sierra Leone. Out of the 8,018 plants assessed, only 896 (11.17%) were found to be asymptomatic (healthy). At the farm level, only 6 (2.23%) farms were classified as healthy. The mean CMD incidence throughout the country was 88.38%, with the highest severity scores observed in the North (3.30), South (3.30), Northwest (3.09), and East regions (3.33). The lowest severity score was recorded in the Western Area region, contributing to the country's overall mean severity score. Cutting-borne infection was identified as the primary source of CMD infection across the country. Additionally, each assessed field had an average mean whitefly count of 4.64. Significant negative relationships were found between CMD incidence and whitefly abundance, while the relationship between CMD severity and whitefly numbers was negative but not statistically significant. PCR screening of 224 samples detected various viruses, including ACMV-like and EACMV-like viruses, both as single infections and co-infections. This study complements previous survey studies of CMD conducted throughout Sierra Leone, providing detailed insights that can contribute to improving intervention and management strategies for CMD in the country.

Keywords: Manihot esculenta; Cassava Mosaic Begomoviruses; Bemisia tabaci; Sierra Leone.

INTRODUCTION

Cassava (Manihot esculenta Crantz) is grown throughout Sierra Leone. The falls in the rain forest zone, with derived savanna due to climate change, human activities such as deforestation, savannah highlands in the north as well as the coastal plains which border the Atlantic Ocean [1]. Rainfall is above 3,000 mm with an average temperature range from 25°C to 35°C. Cassava is the important root and tuber crops and the second most important food crop after rice which is the country's staple and it is consumed by many Sierra Leoneans [2]. It is widely grown in Sierra Leone on different soils varieties and ecologies, lowlands and uplands inclusive. Cassava is tolerant to drought and is productive without intensive inputs. Cassava production and processing have shown remarkable progress at both domestic and commercial scales.;. Some common cassava dishes processed in the country include gari, foo-foo, gbodor, dried chips, starch and boiled cassava with beans. Cassava leaves are traded raw or as a popular sauce consumed by millions of Sierras Leones and contribute to the livelihood of women who dominate the cassava products market [2, 3].

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Cassava mosaic disease (CMD) posed major threats to the production and productivity of cassava in Sierra Leone. The disease is caused by a virus that affects cassava plants, with yield losses of up to 100%, leading to food insecurity and economic hardship for farmers. The diseased cassava plants become stunted, produce fewer roots, and have yellowing and mosaic-like patterns on their leaves. The gravity of chlorosis on the surface cassava leaves sometimes varies between <5% to almost 100% [4]. Symptoms can be varied by both season and cassava cultivars (Chikoti et al., 2019). Symptoms exhibited by plants can be influenced by factors such as the virus species and environmental factors. Fondong et al. (2000) observed variation in showed symptoms of cassava mosaic disease on a cassava plant due to double infection by African Cassava Mosaic Virus Cameroon Strain (ACMV) and East African Cassava Mosaic Virus Cameroon Virus (EACMCMV) which exacerbate the infection of the disease in cassava plants. Revealed that their molecular diagnostic from cassava collected during their study showed that cassava mosaic disease in Sierra Leone is mainly caused by the African cassava mosaic virus (ACMV) although they also detected East African cassava mosaic virus (EACMV) [5].

Since farmer-to-farmer exchange of planting materials remain the most common mode of cutting-distribution, the risk of new viruses such as the cassava brown streak virus (CBSV) being introduced into the farming system unchecked is high, thus posing serious threat to the livelihood of millions of farmers in Sierra Leone. In addition to the introduction of new viruses, these practices also contribute to the spread of the viruses associated with CMD. Whiteflies play vector role in spreading cassava viral diseases, such as cassava mosaic disease (CMD) and cassava brown streak disease (CBSD); The viral diseases can significantly reduce yield by up to 40%-100% depending the cassava variety [6-8]. Whitefly (Bemisia tabaci) serves as major vectors of cassava mosaic begomoviruses (CMBs) and cassava brown streak viruses (CBSVs) which are causative agents of CMD and cassava brown streak diseases (CBSD), respectively [9]. In a recent report of indicate that the population of whitefly in Sierra Leone is generally low, and that the source of cassava mosaic virus disease infection is predominantly through contaminated cassava cuttings which most farmers used in their farm for cultivation [10]. There is limited quantitative data on whitefly population dynamics and transmission mode in Sierra Leone. The aim of this study was to provide data that can be used to help strengthen the surveillance system for cassava viruses in Sierra Leone. The specific objectives were to determine the incidence and severity of cassava viruses and the whitefly population dynamics in Sierra Leone alongside the 9 other Central and West African countries of the WAVE programme.

Materials and Methods

Locations

The survey was conducted across the whole country (Figure 1) to assess the distribution of the cassava mosaic disease in the different agroecologies.

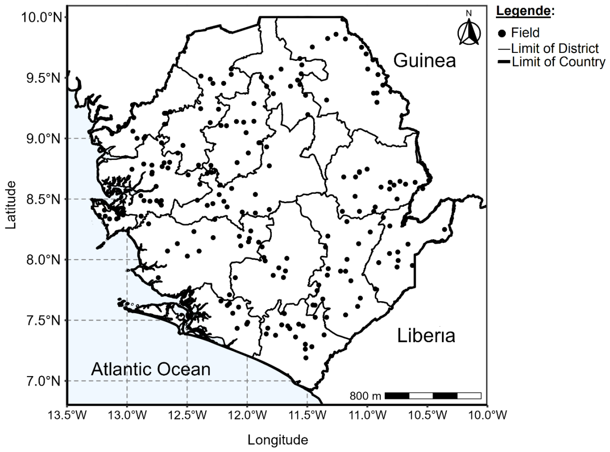

Figure 1: Locations of the 268 farms surveyed in the Northern, Eastern Southern and Western Area for CMD in 2020-2021

Survey

A field Survey was conducted in 2020 and 2021 to assess the cassava mosaic disease using the Central and West African Virus Epidemiology (WAVE) harmonized sampling and diagnostic protocols [11]. This survey involved collecting data and samples (cassava leaf and whitefly vector) from cassava plants between 3-6 months after planting. A total of 268 fields were surveyed in the five regions and sixteen districts of Sierra Leone covering areas of rain forest, coastal plains, savannah lowlands and savannah highlands.

Cassava fields within villages and towns were sampled with distance between survey sites varied generally 10-20 Km or availability of cassava farms.

Data recording and storage

Data were recorded at each survey site using a tablet with survey software iForm Zerion (version 9.1.6) developed by Cambridge, UK's Epidemiology Modelling Group. Data recorded at each site comprised the name of the village or town, the district, the region and the geographical coordinates (latitude and longitude), altitude of sampling sites, the CMD symptoms observed, and whitefly counts. Additional information on cassava variety, date and time, field size, planting type and distance between surveyed fields was also recorded. The recorded data were uploaded to iForm's cloud-based database and then integrated into the WAVE Cube. A total of 30 cassava plants were assessed along two diagonals in an X shape (15 plants chosen randomly on each diagonal). The distance between plants assessed varied depending on the size of the field. On each selected plant, data were collected on CMD severity, whitefly abundance and where the plant was infected, the source of infection was determined as either from cuttings or by the vector. According to from three to six MAP, a distinction is possible between cutting-borne and whitefly-borne infections [12]. Symptoms appearing only on upper leaves were taken to have resulted from whitefly-transmitted infection, whereas plants that showed symptoms either only on the lower leaves or on all leaves were taken as having been infected through cassava cuttings.

Disease Assessment

The severity of the symptoms was recorded using the standard scale of 1 = Symptom-less plants, severity score 2 = Mild chlorotic patterns affecting most leaves; mild distortions at the bases of most leaves and remaining part of the leaves are normal, severity score 3 = Pronounced chlorosis on most leaves, narrowing and distortion of the lower one-third of the leaflets. Severity score 4 = Severe chlorosis and distortion of two-thirds of most leaves and general reduction of leaf size and some stunting and severity score 5 = Most severe symptoms (severe chlorosis, leaf distortion, twisting, misshapen leaves, severe reduction of most leaves and severe plant stunting)

The CMD incidence was calculated as the percentage of CMD symptomatic plants out of the total plants assessed using the formula provided by below [12].

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

The incidence was then visually categorized into five percentage bands: fields with 0 incidence were recorded as Healthy; >0–25% as Low incidence; >25–50% as medium incidence; >50–75% as High incidence; and >75–100% as Very High incidence.

The whitefly population was estimated by counting the number of whiteflies on the top five fully expanded leaves of each plant. The mean of whiteflies per plant was calculated as the total number of whiteflies recorded on 30 plants divided by 30. The mode of infection in each plant was determined based on the location of the symptomatic leaves as previously described by [12].

Leaf samples were collected from plants in every field assessed, a total of 222 leaf samples from 198 plants with symptoms and 24 without symptoms were collected for laboratory analysis using polymerase chain rection (PCR).

Molecular detection of cassava mosaic begomoviruses

The total DNA was extracted from cassava leaf samples using the protocol described by Doyle and Doyle (1987). The concentration of each extracted DNA was measured using the Eppendorf spectrophotometer and adjusted to 50 ng for subsequent use in polymerase chain reaction (PCR). For the detection of ACMV, EACMV, and EACMCMV, partial DNA was amplified using specific primer pairs listed in Table 1. The PCR reactions were performed with Gotaq polymerase (Promega). The reaction mixture contained 1X colorless Gotaq Reaction Buffer (Promega), 0.625 U GoTaq polymerase (Promega) ,0.4µM each primer (synthesized by Eurogentec), 0.2 mM of dNTP (NEB), and 1 Mm of MgCl2 (Promega). The PCR protocol consisted of an initial denaturation step at 94°C for 4 min, followed by 35 cycles of 94°C for 1 min, 55°C for 1 min and 72°C for 1 min and a final extension of 72°C for 10 min. The PCR products (10 µl) were subjected to 1% agarose gel electrophoresis, stained with ethidium bromide, and visualized under UV light using a gel imager.

Virus	Primer name	Primer sequence	DNA target	Size/amplified region
ACMV	JSP001	5′-ATG-TCG-AAG-CGA-CCA-GGA-GAT-3′	DNA-A	783 bp/CP
	JSP002	5′-TGT-TTA-TTA-ATT-GCC-AAT-ACT-3′		
	ACMVB1	5′-TCG-GGA-GTG-ATA-CAT-GCG-AAG-GC-3′	DNA-B	628 bp/BV1-BC1
	ACMVB2	5′-GGC-TAC-ACC-AGC-TAC-CTG-AAG-CT-3′		
EACMV	JSP001	5′-ATG-TCG-AAG-CGA-CCA-GGA-GAT-3′	DNA-A	780 bp/CP
	JSP003	5′-CCT-TTA-TTA-ATT-TGT-CAC-TGC-3′		
	CMBRep	5′-CRT-CAA-TGA-CGT-TGT-ACCA-3’	DNA-A	650 bp/AC1
	EACMVRep	5′-GGT-TTG-CAG-AGA-ACT-ACA-TC-3’		
EACMCMV	VNF031	5′-GGA-TAC-AGA-TAG-GGT-TCC-CAC-3′	DNA-A	560 bp/AC2-AC3
	VNF032	5′-GAC-GAG-GAC-AAG-AAT-TCC-AAT-3′		

Table 1: PCR primer pairs for ACMV, EACMV, and EACMCMV detection

Figure 2: CMD symptoms in Survey fields : A, asymptomatic ; B, mild infection ; C, moderate infection ; D, severe infection ; and E, very severe infection

Severity Score	Number of Plant	Cutting-derived infection	Whitefly - derived infection
Severity 1	896	-	-
Severity 2	696	670	26
Severity 3	5,530	5,220	310
Severity 4	890	750	140
Severity 5	6	5	1
Total	8,018	6,645	477

Table 2: Number of plants for CMD severity scores and infection sources.

Number of fields within the CMD incidence

Out of 268 fields assessed, 231 recorded very high above 75% to 100%, 12 fields recorded high incidence (50 to 75%), 11 fields recorded medium incidence levels (> 25% to 50 %) and 8 fields recorded low levels (0 to 25%). Of all fields sampled, only 6 were classified as healthy (asymptomatic) and these 6 farms were found in Bonthe district in the Southern region (Figure 3).

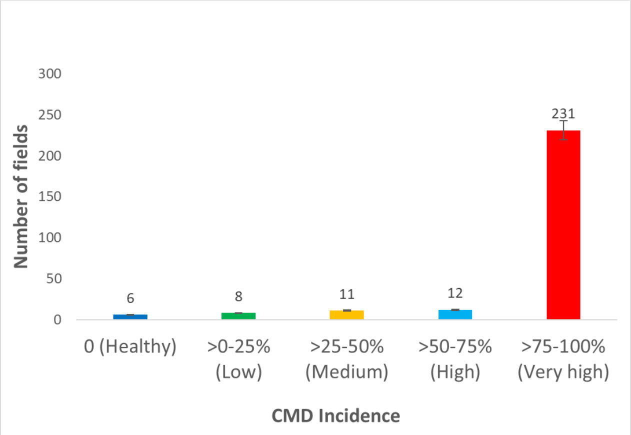

Figure 3: Number of fields within the CMD incidence

Number of fields assessed per region, Cassava mosaic severity and Incidence per region and district in Sierra Leone

The mean CMD incidence across the country was 88.38% which is considered very high. This might be as a result of many fields having high incidence scores with 231 fields having incidence score ranging from 75-100% (Table 3). Across the regions, the CMD incidence ranges from 68.52% in the Southern region to 99.77% in the Eastern region (Table 3). Among all the districts surveyed, lowest cassava mosaic disease incidence of 22. 86% was recorded for Bonthe district, Southern region. Higher CMD incidence recorded in the Eastern region were consistent among all the three districts assessed. In contrast, among all the district, cassava mosaic disease incidence of 100% was recorded in Kailahun and Kono in the Eastern region, Falaba in the Northern and Karena in the Northwest region. The distribution map of CMD incidence showed that fields with high CMD incidence (75-100%) were widely spread across the country followed by fields with CMD band of 50-75%. Fields with low CMD band (0-25%) were mostly found in Southern region (Figure 4). The mean CMD severity across the country was 3.03. The Western Area had the lowest mean CMD severity (2.78). This is simply because the two districts in the Western Area recorded lower CMD severity although they recorded CMD incidence above 75%. Among all the regions assessed, Southern and Northern regions recorded highest mean CMD severity (3.30). Nonetheless, among all the districts, the lowest CMD severity (2.43) was observed in Moyamba and the highest mean CMD severity (3.97 and 3.31) were observed in Falaba and Koinadugu respectively (Table 3). The distribution of CMD severity showed a very high CMD incidence (75-100%) across the county. Severity scores showed that fields with mild CMD severity symptoms (2-3) and high CMD severity symptoms (3-4) were widely distributed across the country (Figure 5). Fields with very high CMD severity (4-5) was only found in fields in the Northern region of Sierra Leone.

Region	Number of fields	District	CMD severity mean	CMD incidence mean
Eastern	61		3.05	99.77
		Kenema	3	99.3
		Kailahun	3.13	100
		Kono	3.04	100
Southern	70		3.3	68.52
		Bo	3.02	76.79
		Moyamba	2.43	74.63
		Pujehun	3.16	99.81
		Bonthe	2.96	22.86
Northern	67		3.3	94.25
		Bombali	2.98	84.67
		Tonkolili	3.03	93.19
		Koinadugu	3.31	99.14
		Falaba	3.97	100
Northwest	55		3.09	91.86
		Port Loko	3.04	85.76
		Kambia	3.05	89.82
		Karena	3.97	100
Western Area	15		2.78	87.5
		Western area rural	2.75	85
		Western area urban	2.81	90
Mean	268		3.03	88.38

Table 3: Number of fields surveyed per region, CMD severity, and CMD Incidence per region and district in Sierra Leone

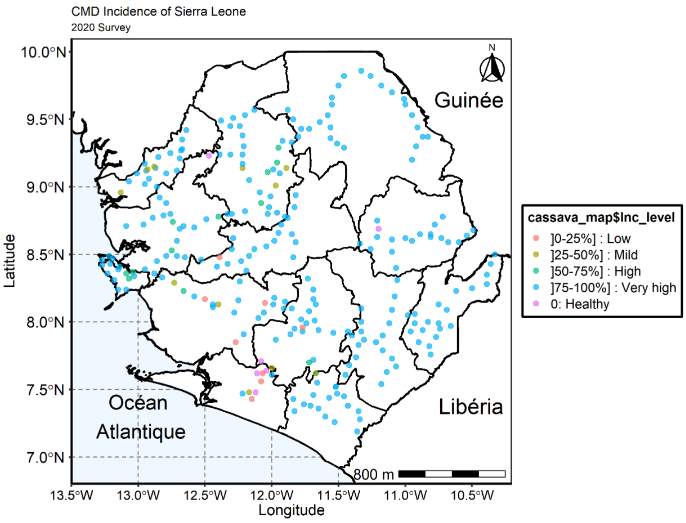

Figure 4: Map of Sierra Leone showing the distribution and spread of CMD incidence across all regions.

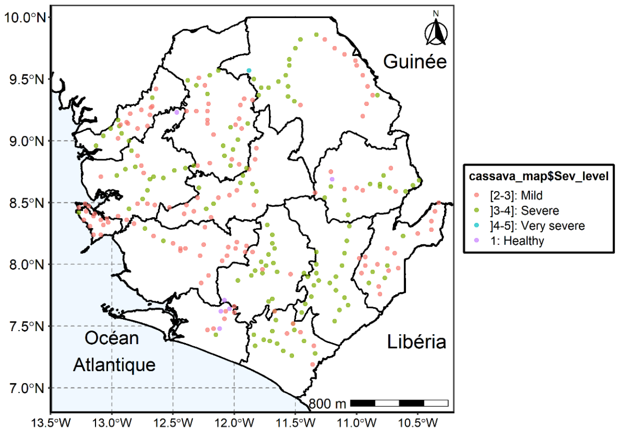

Figure 5: Map of Sierra Leone showing the distribution and spread of CMD severity across all regions

Whitefly Population

Mean whitefly count varied with survey site (Table 3). The mean count across the country was 4.64. At regional level, the mean whitefly count varied from 2.69 in the Southern Region to 6.89 in the West area region. Among the 268 fields assessed, the mean whitefly counts per plant ranges from 0.08 in the Southern region to 0.22 in the Western Area. Higher number of whiteflies was found in Western area region (56.00) and the lowest number of whiteflies was observed in the Southern region (8.00). In total 188 whiteflies were counted in 70 fields in the Southern region whereas 103 whiteflies were counted in just 15 fields in the Western Area (Table 3)

Regions	Maximum no. of whitefly per plant	Minimum no. of whitefly per plant	Mean no. of whitefly per plant	Total no. of whitefly	No. of fields surveyed	Mean no.of whitefly per field (based on 30 plants/field
Eastern	10	0	0.10 ± 0.00	187	61	3.07 ± 0.02
Southern	8	0	0.08 ± 0.00	188	70	2.69 ± 0.01
Northern	16	0	0.15 ± 0.00	305	67	4.56 ± 0.02
Northwest	20	0	0.20 ± 0.00	331	55	6.02 ±0.05
Western area	56	0	0.22 ± 0.00	103	15	6.87 ±0.05
Mean/sum	22	0	0.15	1,114.00	268	4.64

Table 4: Whitefly numbers observed in surveyed fields, per region.

Whitefly population by CMD severity level

The highest whitefly mean count (6.5) was counted on plants with CMD severity score of 3 and the highest CMD severity of 5 records whiteflies mean count of 4. As CMD severity increased, the whitefly population gradually decreased. It was observed that whitefly was found on health plant (asymptomatic plant), plants with severity score of 1 records whitefly mean count of 3.1(Fig 4)

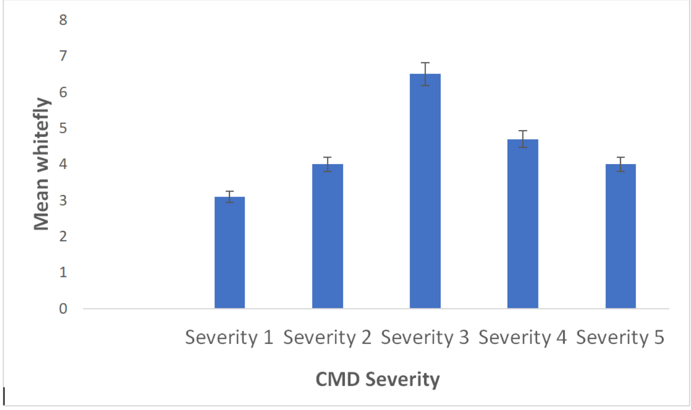

Fig 6: Mean whitefly by CMD severity level.

Variation of CMD Incidence and Severity According to the Mean Number of Whitefly Per Plant

There was no proportional relationship between the incidence of cassava mosaic disease (CMD), severity and mean number of whiteflies per plant (Table 4). For instance, in the Eastern region, a low number of whiteflies was associated with very high CMD incidence (99.77%) and moderate severity (3.05). This was observed for all the region, low whiteflies population was observed in all the regions with associated high CMD incidence and moderate CMD severity.

Regions	Mean CMD incidence	Mean CMD severity	Mean no. of whitefly per plant
Eastern	99.77 ± 5.00	3.05 ± 0.19	0.10 ± 0.00
Southern	68.52 ± 4.00	3.30 ± 0.21	0.08 ± 0.00
Northern	94.25 ± 4.75	3.30 ± 0.21	0.15 ± 0.00
Northwest	91.86 ± 4.50	3.09 ± 0.19	0.20 ± 0.00
Western Area	87.50 ± 4.25	2.78 ±0.12	0.22 ± 0.00
Overall mean	88.38 ± 4.25	3.03 ± 0.19	0.15 ± 0.00

Table 5: Variation of CMD incidence and severity according to the mean number of

whitefly per plant

Cassava Mosaic Begomoviruses (CMBs) s detected by PCR in cassava leaf samples

A total of 224 leaf samples of cassava were collected during the 2020 disease assessment, with 200 cassava leaves obtained from cassava plants exhibiting symptoms and 24 leaves samples from symptomless cassava plants. These samples were subjected to PCR analysis to determine the presence of different CMBs species. Among the samples with observable symptoms and symptomless, 41.52% (93/224) tested positive for ACMV-like virus, 14.73% (37/224) tested positive for EACMV-like virus, and 8.93% (20/224) tested positive for EACMCMV-like virus. Conversely, 56.70% (127/224) of the samples tested negative for these viruses (Fig 5 and 6). About 43.30% (97/224) of the collected samples were found to be positive for CMGs (cassava mosaic geminiviruses). Among these CMG-positive samples, the most common type of infection was single ACMV-like virus, accounting for 17.85% (40/224) of the total samples. The second most frequent infection was a mixed infection of ACMV and EACMV, which accounted for 14.73% (33/224) of the samples.

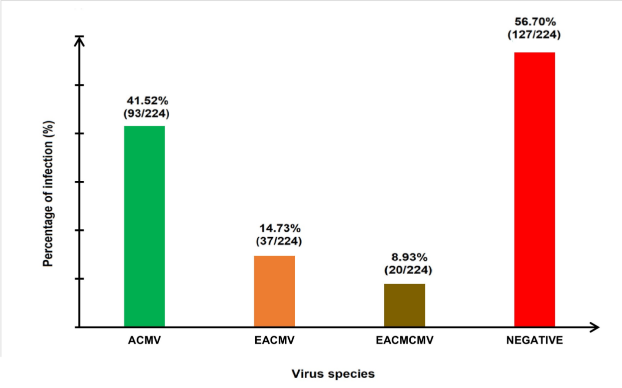

Figure 7: Incidence of cassava mosaic begomoviruses in Sierra Leone in 2020

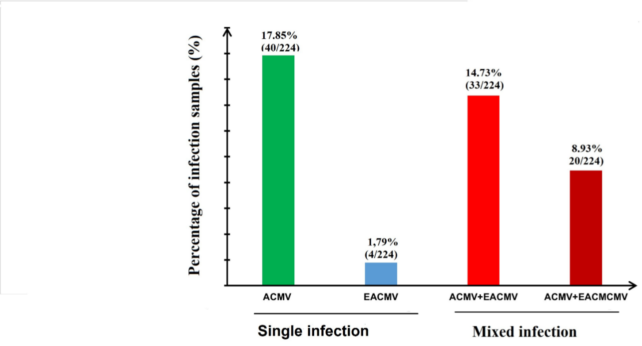

Figure 8: Percentage of single and mixed of cassava mosaic begomovirus infection in Sierra Leone

CMBs distribution across Sierra Leone

The distribution map of CMBs showed that ACMV-like virus was predominated and distributed in most of the surveyed regions with the highest in North and Northwest region followed by EACMV-like virus which are dominant in the South and East region. However, mixed infection (ACMV+EACMV) occurs most part of the country although in not large number. Symptomatic negative samples were found in all surveyed regions.

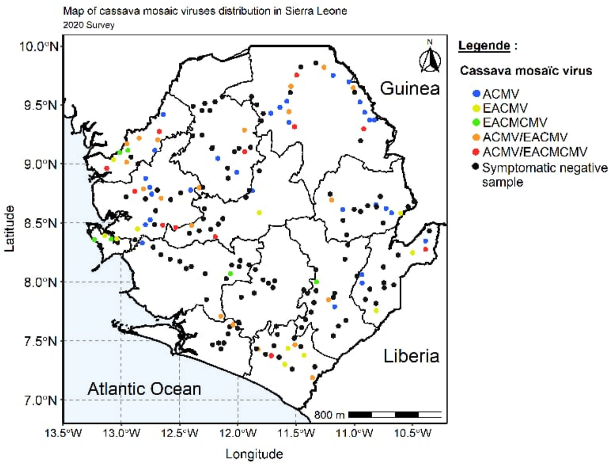

Figure 9: Map of Sierra Leone showing the distribution of CMBs

Relationship between whitefly population and other variables

There was significant positive correlation ($P < 0.01$) between CMD incidence and severity but significant negative between CMD incidence and whitefly popualtion (Table 5). There was a negative correlation between CMD severity and whitefly count. The altitude of the survey fields varies from 20 m above sea level in the Western area region up to 529 m in the Northern region. The analysis revealed that a strong significant positive correlation (P 0.01) between altitude and whitefly abundance (Table 5)

Parameters	CMD Incidence	CMD Severity	Whitefly Abundance	Altitude
CMD Incidence	1	0.423**	-0.530**	0.200**
		0	0	0
CMD Severity	--	1	-0.019	-0.801**
			0.467	0
Whitefly abundance	--	--	1	0.752**
				0
Altitude	--	--	--	1

**, significant at P < 0.01 (two-tailed), n = 268.

Table 6: Pairwise Spearman rank correlation coefficients rs (normal text) and P-values (italics).

DISCUSSION

The country's high CMD incidence and severity can be attributed to the facts that most farmers in the country cultivate local varieties that are susceptible to the cassava mosaic disease. A similar situation was observed in Ghana, where the predominant cassava cultivars were also susceptible to CMD [13]. Moreover, many farmers in the country do not perceive cassava mosaic disease as a significant threat, which hampers production and productivity of cassava. Furthermore, our local farmers often neglect good management practices, thus they lack awareness of the disease's cause and vector, as reported by other researchers [14, 15]. A Few healthy farms were found in the Southern Region and the Region recorded low CMD incidence compared to other Regions, however, like other regions, the Southern Region experienced moderate CMD severity. The moderate CMD severity observed in the Southern can be attributed to the presence of SLICASS 4,6, and 7 which are improved varieties in the region, although only a small number of farmers have adopted and benefited from them [16]. emphasizes the strong cultural attachment to local varieties in this region. These varieties are favored for their ease of cooking, low cyanide content, and their role in providing immediate calories and supporting farming activities. The tubers of these varieties are commonly consumed raw or cooked and constitute a significant portion of the diet for many Sierras Leoneans. The preference for local varieties can also be attributed to their mosaic-like symptoms, which are desirable for the preparation of cassava leaf sauce, a popular dish in some Africa countries especially Sierra Leone, Guinea, Madagascar, Nigeria, and the Democratic Republic of Congo [17, 18]. Based on feedback from the survey, Sierra Leonean women reported that the low chlorophyll content in the mosaic-infected leaves reduces the amount of palm oil required for cooking compared to improved cassava genotypes. Palm oil is an expensive yet crucial ingredient in preparing cassava leaf sauce in Sierra Leone. It is not clear to what extent environmental condition most importantly climate change influenced CMD incidence and severity in Sierra Leone. The disease symptoms observed were more indicative of cutting-borne infection than whitefly derived infection which suggests that farmer-to-farmer exchange of cassava cuttings was the main source of acquiring planting materials within the districts. However, new evidence from ecological-niche modeling indicates that the geographic distribution of cassava mosaic disease and its whitefly association, as well as cassava brown streak disease and its cassava mealybug association, is projected to undergo changes. These changes may be attributed to the emergence of new areas where these pests and diseases can thrive, as well as the likelihood of pests and diseases leaving or reducing their impact in existing areas. Our study revealed a negative correlation between whitefly presence and CMD incidence and severity which the indicate that in Sierra Leone, the presence or absence of whitefly does not significantly affect CMD incidence and severity levels. This result is consistent with the work of where no correlation was found between whitefly number and CMD incidence [19]. In the Western Area Region, despite high abundance of whiteflies, CMD severity did not increase. However, plants with a low number of whiteflies had higher CMD mean severity. This could be because virus-infected cassava leaves create a repellent or unattractive environment for whiteflies to settle [20]. The work of Legg and Winters (2021) revealed that cassava mosaic virus is primarily transmitted through persistent infections from the whitefly Bemisia tabaci but is also widely propagated through infected stem cuttings. This observation was consistent with the results of this study which largely attributed CMD prevalence to the continuous cultivation of susceptible cassava cultivars and whiteflies. Our field observations revealed that resistant varieties, mainly used for commercial purposes, were also planted alongside local varieties as secondary options. It is unclear whether this mixed cultivation of varieties was a strategy for CMD management or a deliberate action to maintain local varieties for food alongside improved varieties for industrial purposes. The survey conducted across the country revealed an average adult whitefly population of 4.65 per plant. This figure is lower than the recent report from Cameroon but higher than the reports from Ghana and Burkina Faso [21]. The variations in whitefly population across the country can be attributed to factors such as climate change, whitefly biotype, cassava variety types, and cultural practices, as documented by and [22, 23]. that have been shown to impact whitefly populations. The study also revealed regional differences in whitefly populations, with higher abundance observed in the Western Area and Northwest regions compared to other regions. The elevated whitefly abundance in these regions may be influenced by their proximity to the Atlantic Ocean, resulting in higher relative humidity and lower altitude [24]. Similar findings were inficated in Madagascar by and in Tanzania by,where whitefly counts decreased with higher altitude. Although previous studies have shown a clear correlation between whitefly abundance and the transmission of whitefly-borne infections, it is challenging to establish a direct causal relationship due to temporal variations in whitefly populations and the latency period of 3 to 5 weeks between transmission and the appearance of the first symptoms. In our survey, we accounted for the variations in whitefly populations and cassava mosaic disease incidence and found that whitefly number was low in the eastern and southern regions, whereas CMD incidence was very high or medium. This indicates that whiteflies don't act only as vectors for CMD viruses but contribute to the spread of other viruses. Similar observations were made by in the Alibori and Borgou regions of Benin, where they reported low whitefly populations despite high or medium CMD incidence. The active nature of the whitefly and the high incidence and severity of the cassava mosaic disease in Sierra Leone have serious implications for the epidemiology of the disease for the Mano River Union countries and the Economic communities of West African states (ECOWAS) region. Studies in Sierra Leone indicate that the level of cassava production will remain low and uncompetitive for the emerging small and medium scale industries (gari and flour enterprises) in the cassava subsector. This study revealed the presence of ACMV-like and EACMV-like viruses in all cassava growing regions. These viruses were found to occur as single infections or in combination with each other. The exchange of planting materials between Sierra Leone and neighboring countries is believed to be a potential factor contributing to the spread of these. Among the two types of viruses, ACMV-like viruses were found to be the most predominant and widely spread CMGs (Cassava Mosaic Geminiviruses) species in all cassava-growing regions. It was observed that the majority of cassava mosaic disease (CMD) cases resulted from single ACMV-like virus infections. This pattern of single ACMV-like virus infection in West Africa has been previously reported. On the other hand, the occurrence of single EACMV-like virus infections was relatively low. The present assessment also discovered that most of the EACMV-like virus infections occurred in combination with ACMV. More than 54% of the samples positive for EACMV-like virus were found to have East African cassava mosaic Cameroon virus (EACMCMV). This finding suggests that EACMCMV may be more prevalent in Sierra Leone than previously thought. Similar results were reported by in Burkina Faso, where EACMV-like virus isolates were also found to occur as mixed infections with ACMV. This indicates that the prevalence of EACMCMV may be higher in Burkina Faso as well. Interestingly, the study also detected the occurrence of CMGs in a few symptomless cassava samples. This shows that the viruses can be latent in the plants without manifesting any visible symptoms. As a result, the use of symptomless cassava landraces as a strategy to manage CMD could unintentionally lead to increased transmission of the viruses through infected cuttings. It is important to be aware of this potential risk and take appropriate measures to prevent the spread of CMGs [25-30]. Overall, this study provides important insights into the prevalence and distribution of ACMV-like and EACMV-like viruses in Sierra Leone. It highlights the need for continued monitoring and management strategies to mitigate the impact of cassava mosaic disease on cassava production in the region [30-36].

CONCLUSION

This study established that CMD is widespread in all regions of Sierra Leone, with evidence of its continuous spread to new cassava-growing areas. In some districts, the prevalence of CMD reached 100%, posing a significant risk of high yield losses due to severe mosaic symptoms observed in most growers' fields. The incidence and severity of CMD recorded during the survey are alarming. The high count of whiteflies and the exchange of contaminated planting materials among farmers across regions and countries create favorable conditions for the introduction and expansion of virulent CMG species or strains, potentially leading to a severe CMD pandemic. To effectively manage CMD and enhance cassava productivity, an integrated strategy is needed. This strategy should involve the multiplication, distribution, and adoption of improved cassava planting materials that are resistant or tolerant to CMD for local farmers. Additionally, training farmers to recognize the disease and encouraging the use of healthy cuttings when establishing new plots are crucial steps. In the future, efforts should focus on characterizing the viruses and vectors associated with CMD, strengthening phytosanitary and quarantine measures, and implementing frequent surveillance or monitoring programs. These measures will help prevent the further spread of CMD and minimize its impact, thus mitigating the potential for widespread outbreaks.

ABBREVIATIONS

CMD, Cassava mosaic disease; CMG, Cassava Mosaic Gemini viruses; ACMV, Africa Cassava Mosaic Virus; EACMV, East Africa Cassava Mosaic Virus; EACMCMV; East African cassava mosaic Cameroon virus; ECOWAS, Economic communities of West African states

COMPETING INTERESTS

The authors declare that they have no competing interest.

AVAILABILITY OF DATA

All data relating to this work can be found in WAVE data base.

AUTHORS CONTRIBUTIONS

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