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RESEARCH PAPER

Assessment of cassava mosaic disease (CMD) intensity and whitefly (*Bemisia tabaci*) population in Cameroon based on field surveys

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ABSTRACT

Cassava mosaic disease (CMD) remains a major constraint to cassava (*Manihot esculenta* Crantz) production in Cameroon. This study aimed to generate updated epidemiological data on CMD across the country. Surveys were conducted in 342 fields across the ten administrative regions of Cameroon between January and September 2022, following a standardized protocol adopted by all fourteen countries participating in the Central and West African Virus Epidemiology for Food Security (WAVE) program. In each field, 30 plants were assessed for CMD incidence, severity, whitefly population, and mode of infection. CMD symptoms were observed in all ten regions. The overall mean CMD incidence was 54.72%, with a mean severity score of 2.39. Incidence, severity, and whitefly populations varied significantly among regions. The South Region recorded the highest mean incidence (74.34%), while the Far North had the lowest (18.97%). The Adamawa Region exhibited the highest mean severity (2.63), whereas the South West Region had the lowest (2.19). Whitefly abundance per plant was greatest in the South West (21.44) and lowest in the Far North (0.40). PCR amplification and sequencing confirmed the presence of cassava mosaic geminiviruses (CMGs) in leaf samples. A positive correlation was detected between mean whitefly abundance and CMD incidence, while altitude was negatively correlated with whitefly numbers. Both CMD incidence and whitefly populations were higher in intercropped fields than in monocropped fields. Notably, intercropping cassava with maize reduced whitefly populations, while intercropping with sweet potato lowered CMD incidence. The primary source of CMD infection was the use of infected cuttings. These findings provide valuable insights for the development of targeted interventions and improved management strategies for CMD in Cameroon.

Key words: *Bemisia tabaci,* cassava mosaic geminivirus, CMD symptoms, epidemiology

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is essential for food security and income generation, as both its roots and leaves are widely consumed. Globally, it is the fourth most important staple food after rice, wheat, and maize, contributing 2.6% of total caloric intake (Hareesh et al., 2023). Beyond its role as food, cassava is also used in animal feed and in various industries such as starch, ethanol, and biofuel production (FAO, 2017). In Cameroon, cassava is particularly important due to its large arable land area (6.16 million ha) and a rural population representing 51% of the country's 25.9 million inhabitants (INS, 2019). The nation is the leading food producer in Central Africa (Evouna & Ngounou, 2024), with cassava contributing 60% of roots and tubers consumed—40% as processed products and 20% as fresh roots—making it the second most consumed crop after bananas (Kegah et al., 2019). In 2022, cassava production in Cameroon reached 6.3 million tons from 465,097 ha, averaging 13.48 t/ha, which accounts for 1.9% of global production (FAOSTAT, 2025). However, this yield remains below that of Asian countries, where yields can reach up to

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21.5 ton/ha (Kongsil et al., 2024). Factors contributing to this yield gap include limited availability of quality planting materials, poor adoption of good agricultural practices, inadequate disease management, and insect pest damage (Legg et al., 2014).

Among the most constraints to cassava production in sub-Saharan Africa are viral diseases, particularly cassava mosaic disease (CMD) and *Cassava brown streak disease* (CBSD). CMD can cause yield losses of 40–70%, while CBSD may result in up to 100% losses (Changadeya et al., 2016). In Cameroon, CMD is widespread and significantly impacts production (Fondong et al., 2000; Akinbade et al., 2010; Tize et al., 2021), whereas CBSD has not been scientifically reported. CMD is caused by *Cassava mosaic geminiviruses* (CMGs) (Family: *Geminiviridae*, Genus: *Begomovirus*), which have circular single-stranded DNA genomes. The bipartite genome consists of DNA-A and DNA-B components, encapsidated in twinned icosahedral particles (~2.7 kb each) (Hareesh et al., 2023). DNA-A encodes replication, encapsidation, and anti-host defense functions, while DNA-B encodes movement proteins, including the nuclear shuttle protein and the movement protein (Dye et al., 2023). The International Committee for Taxonomy of Viruses (ICTV) recognizes 11 CMG species, nine of African origin and two from Asia (Soro et al., 2021; Chikoti & Tembo, 2022; Hareesh et al., 2023). In Cameroon, *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV), and *East African cassava mosaic Cameroon virus* (EACMCV) are particularly important (Fondong et al., 2000; Akinbade et al., 2010).

Transmission of CMGs is mediated by the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae), a cryptic species complex of more than 35 morphologically indistinguishable species (Chikoti et al., 2020; Namuddu et al., 2023). Cassava-colonizing *B. tabaci* belongs to the sub-Saharan Africa (SSA) group, identified through mitochondrial COI sequencing. This group comprises five subgroups (SSA1–5), with SSA1 further divided into subgroups SG1–SG5 (SSA1-SG1 to SG5) (Chikoti et al., 2020; Macfadyen et al., 2021; Caspary et al., 2023). Whiteflies damage plants directly through phloem feeding by nymphs and adults, and indirectly by producing honeydew, which supports sooty mold growth on leaves (Ally et al., 2019). Environmental factors such as temperature, rainfall, and humidity strongly influence their population dynamics (Chikoti & Tembo, 2022). CMD is also spread through the use of infected cuttings for planting (Namuddu et al., 2023).

CMD symptoms include chlorotic mosaic patterns on leaves, distortion, deformation, stunting, and in severe cases, leaflet shrinkage. These symptoms reduce photosynthetic surface area, impair plant growth, and ultimately lower yields (Legg et al., 2014; Chikoti et al., 2019; Eni et al., 2021). Symptom severity depends on factors such as virus species, synergistic effects of mixed infections, host susceptibility, plant age at infection, and environmental conditions including soil fertility and moisture (Chikoti et al., 2019; Houngue et al., 2022; Claude et al., 2023). High CMD incidence is usually associated with infected cuttings and abundant whitefly populations, while severity often reflects high virus concentrations within plants (Houngue et al., 2019).

CMD management strategies include the production of virus-free planting materials via in vitro culture, selection of clean cuttings, roguing of diseased plants, and cultivation of resistant or tolerant varieties (Biola et al., 2022; Chikoti & Tembo, 2022). In Cameroon, cassava varieties can be categorized into local landraces, which are generally low-yielding and CMD-susceptible, and improved varieties, which are higher-yielding and more tolerant or resistant (Tchuente et al., 2024). Despite these options, CMD remains highly prevalent due to limited farmer awareness (Houngue et al., 2018), continued use of susceptible varieties, poor adoption of cultural practices (Chikoti et al., 2019; Houngue et al., 2019) high whitefly populations (Chikoti & Tembo, 2022; Namuddu et al., 2023), mixed infections (Eni et al., 2021), and the presence of virulent strains such as the recombinant *East African cassava mosaic virus* Ugandan strain (EACMV-Ug), reported in Cameroon's East and Adamawa regions (Akinbade et al., 2010). More recent surveys (Doungous et al., 2022) confirm that CMD is widespread across all ten regions of Cameroon, with high incidence.

Given the complexity of factors influencing CMD epidemiology, updated information is essential for effective disease management. In particular, little is known about how cropping systems affect CMD incidence, severity, and whitefly populations in Cameroon. Regular epidemiological surveys are therefore crucial to guide integrated control strategies and reduce CMD's impact on cassava production.

This study aims to provide updated epidemiological data on CMD in Cameroon, focusing on its incidence, severity, causal agents, and vector populations. In addition, it assesses the influence of cropping systems on CMD incidence and whitefly abundance.

MATERIALS AND METHODS

Research Site. The survey was conducted across all ten administrative regions of Cameroon: Adamawa, Centre, East, Far North, Littoral, North, North West, South, South West, and West. These regions encompass the country's five agro-ecological zones, each characterized by distinct geographical features and soils suitable for cassava cultivation. Climatic conditions and average altitudes of the study areas correspond to those described by Doungous et al. (2022).

Field Surveys. Field surveys were conducted between January and September 2022, following a harmonized protocol established for the fourteen target countries of the Central and West African Virus Epidemiology (WAVE) program (Sseruwagi et al., 2004; Eni et al., 2021; Soro et al., 2021; Doungous et al., 2022). Data collection included epidemiological information, GPS coordinates, and samples from both symptomatic and asymptomatic cassava leaves of plants aged 3–6 months. A total of 342 fields were surveyed across the 10 regions (Figure 1). In each farm, a systematic visual inspection was carried out to assess CMD symptoms. Survey site spacing depended on cassava field availability: in low-density areas, maximum distances were determined by field presence, while minimum distances generally ranged from 10–20 km.

Data Collection and Recording. Data were collected at each site using a tablet equipped with iForm Zerion version 9.12.7 survey software, developed for the WAVE program by the Epidemiological Modeling Group, University of Cambridge (UK). Recorded information included: locality, administrative district, GPS coordinates (longitude, latitude, altitude), observed CMD symptoms, and whitefly counts on the top five apical leaves. Additional metadata—such as cassava variety, intercropping type, survey date and time, field size, cropping system (mono- or intercropping), number of cassava varieties per field, and distance between surveyed fields—was also collected. Data were uploaded to the iForm cloud database and integrated into the WAVE Cube, a multidimensional platform for WAVE program data storage.

Field Data Evaluation. In each field, 30 plants were evaluated along two X-shaped diagonals, with 15 plants randomly selected on each diagonal. For each plant, CMD severity symptoms, whitefly population on apical leaves, and infection source (cuttings or vectors) were recorded.

CMD Severity Symptom. CMD severity was scored on

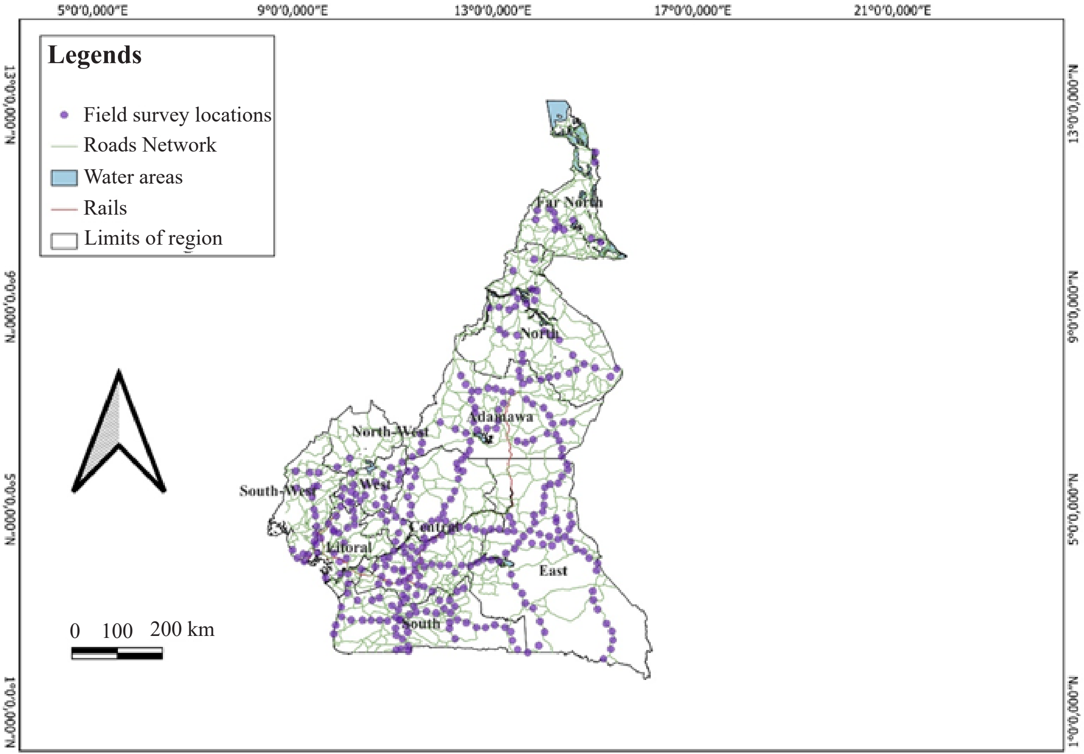

Figure 1. Map showing the locations of cassava fields surveyed in Cameroon.

a 1–5 scale (Hahn et al., 1980; Sseruwagi et al., 2004):

1 = No symptoms;
2 = Slight chlorotic pattern on ≤20% of the leaf blade, no deformation;
3 = Strong mosaic pattern on across leaf, deformation in lower third of leaflets, no size reduction;
4 = Severe mosaic; deformation of two-thirds of leaflets, reduced size, leaf distortion;
5 = Very severe mosaic; chlorosis, deformation, and plant stunting.

Representative CMD symptoms are shown in Figure 2. The mean CMD severity was calculated for each field, division, region, and for the whole country using the method described by Mouketou et al. (2022):

$$CS = \frac{\sum_{2}^{5} P}{\sum I} = \frac{S}{C}$$

CS= Mean CMD Severity;
P = Plant severity score;
I = Infected plants;
S = Sum of severity scores >1;
C = Count of infected plants (severity >1).

Mean CMD Incidence. CMD incidence (%) was calculated as the proportion of symptomatic plants relative to total plants assessed, following Mouketou et al. (2022).

$$CI = \frac{IP}{TP} \times 100$$

CI= Mean CMD incidence;
IP = Infected plants;
TP= Total plants.

Incidence values were categorized as: 0% = Healthy; 0–25% = Low; 25–50% = Medium; 50–75% = High; 75–100% = Very high.

Whitefly Population. Whiteflies were counted on the five apical leaves of each plant by gently turning leaves to examine the underside. Mean whitefly density per plant was obtained by dividing the total number of whiteflies recorded across 30 plants by 30. Mean densities were calculated for each field, division, region, and nationally.

Source of Infection. The source of infection was determined according to Sseruwagi et al. (2004), which states that vector-caused infections show symptoms only on the upper leaves, while cuttings cause symptoms on the lower leaves.

Detection of Cassava Mosaic Geminiviruses (CMGs). To identify CMD causal agents, molecular analyses were performed on 60 randomly selected symptomatic samples. Genomic DNA was extracted from cassava leaves using the CTAB method (Permingeat et al., 1998). DNA concentration was quantified with a NanoDrop™ Lite spectrophotometer (Thermo Scientific) and adjusted to 200 ng/µL. PCR amplification was carried out with specific primers (Table 1) in 25 µL reactions containing: 16.4 µL

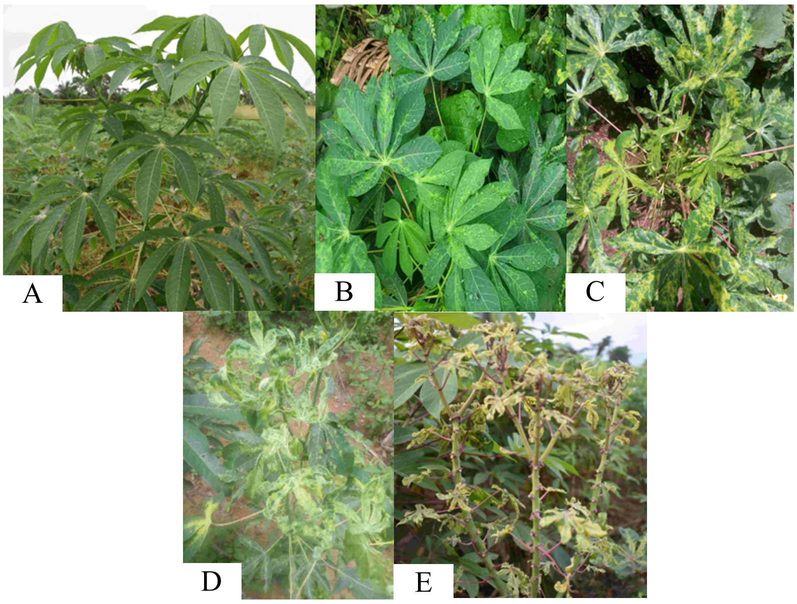

Figure 2. Types of cassava mosaic disease (CMD) symptoms observed in the field, based on a 1–5 severity scale: A = 1 (no symptoms); B = 2 (slight symptoms); C = 3 (moderate symptoms); D = 4 (severe symptoms); E = 5 (very severe symptoms).

nuclease-free water (Solis BioDyne), 2.5 µL 10× FIREPol Reaction Buffer BD (Solis BioDyne), 2.5 µL 25 mM $MgCl_2$ (Solis BioDyne), 0.5 µL 10 µM dNTPs, 0.5 µL of each 0.5 µM primers (GenCust), 0.1 µL FIREPol DNA polymerase (5 U/µL; Solis BioDyne), and 2 µL DNA template. Thermal cycling conditions were: initial denaturation at 94 ºC for 4 min; 35 cycles of denaturation at 94 ºC for 1 min, annealing at 55 ºC for 1 min, and extension at 72 ºC for 1 min; with a final extension at 72 ºC for 10 min.

PCR products were analyzed by electrophoresis on a 1% agarose gel stained with ethidium bromide. Electrophoresis was run at 100 V for 45 min in 1× TAE buffer using a Midigel 2 system (Apelex). Bands were visualized with a Vilber Lourmat E-Box CX5 TS Edge system. Positive amplicons were sequenced bidirectionally by the Sanger method (Sanger et al., 1977) at Macrogen Europe BV (Amsterdam, Netherlands).

Data Analysis and Visualization. Epidemiological data were analyzed at plant, field, division, regional, and national scales. Results were presented as tables, graphs, and histograms. Statistical analyses were conducted using Python 3.12. Normality of continuous variables (CMD incidence, severity, whitefly density, infection source, cropping system) was tested with the Shapiro–Wilk test. Mean comparisons were performed with the Wilcoxon test ($P < 0.05$). Correlations among variables were assessed using Spearman's rank correlation ($P < 0.05$).

Maps of survey sites, CMD incidence, and severity distributions were generated with QGIS 3.28. Sequencing results were analyzed using the NCBI BLAST tool (Altschul et al., 1997) to identify homologous sequences in GenBank based on alignment scores and metrics.

RESULTS AND DISCUSSION

CMD Symptoms in the Field. Out of the 342 fields surveyed, 317 (92.69%) were infected with CMD, while 25 (7.31%) were asymptomatic. Prevalence was highest in the Littoral, North West, and West Regions, where all fields (100%) were infected. In contrast, the Far North Region recorded a lower prevalence, with 61.54% of fields showing infection (Table 2). Among the 25 healthy fields, 8 were located in Adamawa, 6 in the North, 5 in the Far North, 2 each in the East and South West, and 1 each in the Centre and South.

The widespread distribution of CMD across Cameroon is largely driven by the use and exchange of infected planting materials among farmers, a finding consistent with earlier reports from across Africa (McGuire & Sperling, 2016; Chikoti et al., 2019; Houngue et al., 2022; Mouketou et al., 2022).

CMD Incidence, Severity, and Causal Agents. CMD was present in all ten regions with a national mean incidence of 54.72%. Significant variation was observed across fields ($W = 0$, $df = 341$, $P < 0.0001$), with incidences ranging from 18.97% to 74.34%. High incidences (>50–75%) were recorded in the South, Littoral, East, and Centre, while the Far North had the lowest (18.97%). CMD was absent in three divisions of the Far North (Mayo-Danay, Mayo-Kani, Mayo-Tsanaga), whereas very high incidences (>75–100%) were observed in nine divisions, including Ndé, Bamboutos, Ndian, Meme, and Vallée-du-Ntem (Table 3). At the field scale, 112 fields exhibited very high incidence, 85 had medium incidence, and 49 showed low incidence (Figures 3–4).

The mean CMD severity across all surveyed plants was 2.39, with significant differences among fields ($W = 0$, $df = 341$, $P < 0.0001$). Of the 10,233 plants assessed, 4,634 showed no symptoms (score 1), 3,583 had slight symptoms (score 2), 1,865 showed moderate symptoms (score 3), 137 had severe symptoms (score 4), and 14 had very severe symptoms (score 5) (Figure 5). Regional mean severities ranged from 2.19 in the South West to 2.63 in Adamawa (Figure 6). At the divisional level, Mayo-Louti had the lowest severity (2.00), while Djerem recorded the highest (2.69) (Table 3, Figure 7).

Molecular diagnostics confirmed the presence of ACMV, EACMV, and EACMCV in both single and mixed infections. BLAST analyses revealed high nucleotide identity (95.58–98.76%) between Cameroonian isolates and GenBank reference sequences (Table 4). One isolate exhibited 97.52% identity with the DNA-A component of the EACMV-Ug strain previously reported in Chad and the Central African Republic (HE814064). Past studies also documented co-infections involving ACMV, EACMV, and EACMCV in Cameroon (Akinbade et al., 2010). EACMV-Ug, in particular, is known as a highly virulent strain associated with severe CMD symptoms in Gabon and East Africa (Legg et al., 2004; Chikoti & Tembo, 2022).

The distribution of CMD in all ten regions is consistent with earlier surveys by Doungous et al. (2022), who reported a higher mean incidence (66.93%) and severity (2.28). Similarly, Alain et al. (2024), reported a mean incidence of 57.58% and a

Table 1. Primers used for the detection cassava mosaic begomoviuses (CMBs)

Primer	Sequence (5′-3′)	Target region	Expected size (bp)	Virus species	Reference
ACMV21F	GCAGTGATGAGTTCCCCGGTGCG	DNA-A (AC3-AC2-AC1)	552	ACMV, EACMV, EACMCV, EACMKV, EACMMV, EACMZV and SACMV	Matic et al. (2012)
ACMV21R	ATTCCGCTGCGCGGCCATGGAGACC				
VNF031F	GGATACAGATAGGGTTCCCAC	DNA-A (AC2/AC3)	560	EACMCV	Fondong et al. (2000)
VNF032R	GACGAGGACAAGAATTCCAAT				
CMBRepF	CRTCAATGACGTTGTACCA	DNA-A(AC1)	650	EACMV	Alabi et al. (2008)
EACMVRepR	GGTTTGCAGAGAACTACATC				

Table 2. Number of cassava mosaic disease (CMD)-infected fields by region

Regions	Surveyed fields	Infected fields	Infected fields (%) within region
Adamawa	45	37	82.22
Centre	75	74	98.67
East	62	60	96.77
Far North	13	8	61.54
Littoral	21	21	100.00
North	31	25	80.65
North West	2	2	100.00
South	53	52	98.11
South West	20	18	90.00
West	20	20	100.00
Total	342	317	92.69

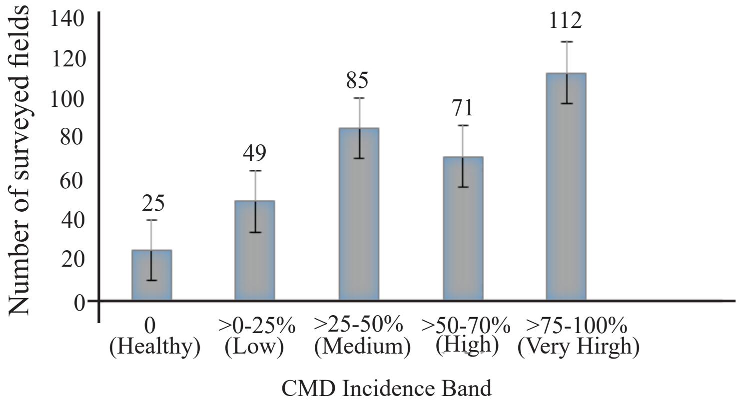

Figure 3. Number of fields surveyed by cassava mosaic disease (CMD) incidence level. Bars represent the standard error of the mean (SEM).

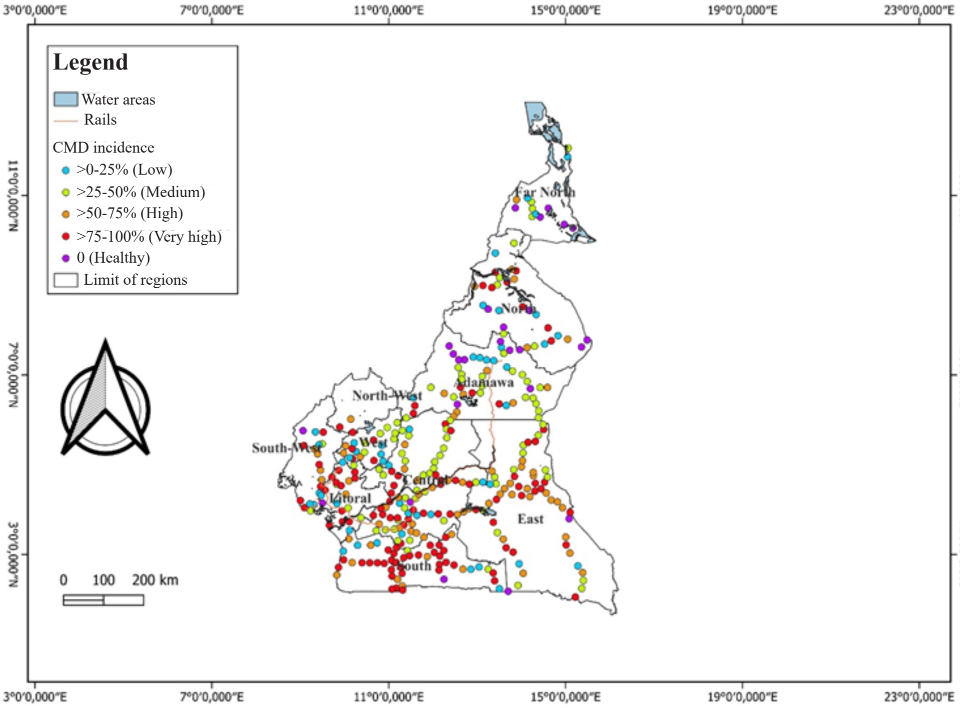

Figure 4. Cassava mosaic disease (CMD) incidence levels in 342 cassava farms surveyed in Cameroon.

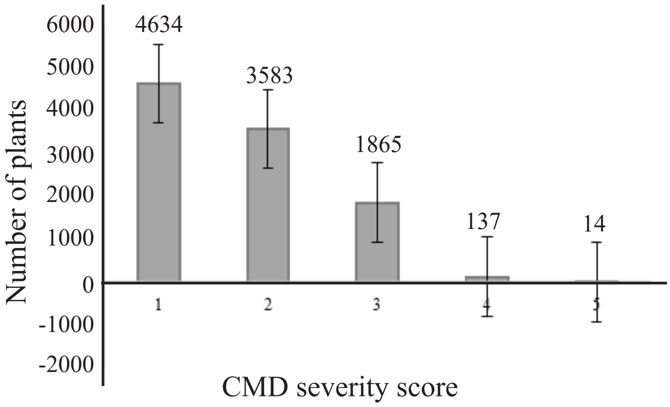

Figure 5. Distribution of cassava mosaic disease (CMD) severity scores across 10,233 plants surveyed. Bars represent the standard error of the mean (SEM).

Table 3. Mean CMD Incidence, mean severity and mean whitefly population in the Divisions within Cameroon

Regions	Divisions	Surveyed fields	Mean CMD severity	Mean CMD incidence (%)	Mean No. Whitefly
Adamawa		45	2.63	36.67	1.99
	Djerem	10	2.69	55.33	3.98
	Faro-Et-Déo	8	2.68	10.48	1.58
	Mayo-Banyo	5	2.66	51.33	4.08
	Mbéré	9	2.61	46.30	1.70
	Vina	13	2.54	26.92	0.22
Centre		75	2.41	56.51	6.77
	Haute-Sanaga	12	2.37	66.67	15.08
	Lekié	8	2.57	51.67	9.13
	Mbam-et-Inoubou	7	2.61	65.24	4.56
	Mbam-et-Kim	20	2.40	46.00	4.35
	Méfou-et-Afamba	3	2.22	40.00	8.38
	Méfou-et-Akono	2	2.35	43.33	2.45
	Mfoundi	3	2.48	57.78	2.90
	Nyong-et-Kéllé	11	2.29	62.12	6.14
	Nyong-et-Mfoumou	3	2.48	76.83	3.13
	Nyong-et-So'o	6	2.30	60.00	3.08
East		62	2.52	60.41	4.90
	Boumba-et-Ngoko	10	2.46	51.85	4.41
	Haut-Nyong	17	2.60	61.76	5.61
	Kadey	15	2.53	68.22	8.32
	Lom-et-Djérem	20	2.46	57.39	2.08
Far North		13	2.26	18.97	0.40
	Diamaré	4	2.10	17.50	0.23
	Logone-et-Chari	2	2.23	21.67	0.08
	Mayo-Danay	2	1.00	0.00	0.50
	Mayo-Kani	1	1.00	0.00	1.57
	Mayo-Sava	3	2.35	44.44	0.52
	Mayo-Tsanaga	1	1.00	0.00	0.00
Littoral		21	2.27	73.69	11.64
	Moungo	7	2.13	78.13	9.34
	Nkam	6	2.23	70.00	8.64
	Sanaga-Maritime	6	2.42	78.89	13.06
	Wouri	2	2.48	55.00	23.75
North		31	2.42	42.90	0.66
	Bénoué	10	2.38	70.33	1.11
	Faro	4	2.23	21.67	0.07
	Mayo-Louti	1	2.00	36.67	0.03
	Mayo-Rey	16	2.54	31.46	0.57
North West		2	2.35	71.67	14.35
	Momo	2	2.35	71.67	14.35

Table 3. Continued. Mean CMD Incidence, mean severity and mean whitefly population in the Divisions within Cameroon

Regions	Divisions	Surveyed fields	Mean CMD severity	Mean CMD incidence (%)	Mean No. Whitefly
South		53	2.25	74.34	5.75
	Dja-et-Lobo	20	2.27	71.17	4.95
	Mvila	11	2.27	92.42	8.66
	Océan	13	2.18	55.64	6.04
	Vallée-du-Ntem	9	2.24	86.30	3.54
South West		20	2.19	47.83	21.44
	Fako	8	2.17	31.25	22.90
	Kupe Manenguba	2	2.19	60.00	16.58
	Manyu	5	2.19	34.67	14.30
	Meme	4	2.20	81.67	27.62
	Ndian	1	2.19	86.67	30.40
West		20	2.34	46.33	3.70
	Bamboutos	1	2.18	93.33	2.30
	Haut Nkam	2	2.13	51.67	16.80
	Hauts Plateaux	2	2.36	46.67	0.73
	Koung Khi	1	2.33	40.00	0.10
	Menoua	3	2.38	57.78	0.63
	Mifi	1	2.50	26.67	1.83

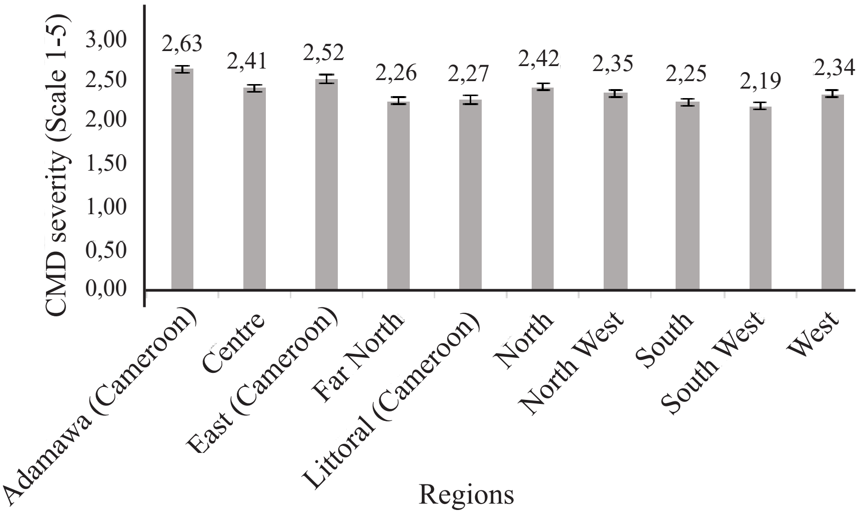

Figure 6. Mean cassava mosaic disease (CMD) severity scores across 10 regions of Cameroon. Bars represent the standard error of the mean (SEM).

mean severity of 2 across two agro-ecological zones in Cameroon. The observed decline in incidence after 2020 may reflect the impact of WAVE program interventions, including farmer sensitization, use of the PlantVillage Nuru application for real-time disease diagnosis, and the establishment of clean seed fields in major production areas.

High to very high CMD incidences in the Centre, South, North West, and Littoral regions mirror trends reported in neighboring countries such as Gabon (64.29%), the Central African Republic (85%), and the Republic of Congo (86%) (Ntawuruhunga et al., 2007; Zinga et al., 2013; Mouketou et al., 2022). In these regions of Cameroon, access to improved varieties remains limited, and farmers commonly recycle susceptible local planting materials without

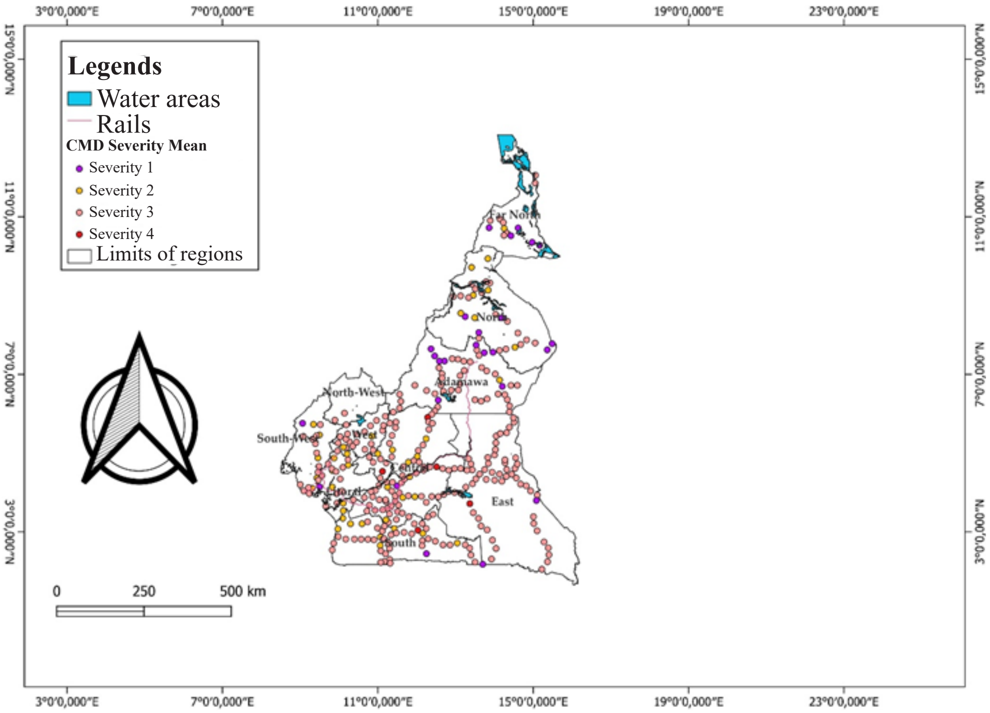

Figure 7. CMD severity mean in 342 cassava farms assessed in Cameroon.

considering their phytosanitary status. In their study, McGuire & Sperling (2016) reported that 90.2% of planting materials in such areas are sourced from the informal sector. Farmers also tend to underestimate CMD severity and neglect recommended cultural practices, further driving disease spread (Chikoti & Tembo, 2022; Houngue et al., 2022; Mouketou et al., 2022). Kuate et al. (2017) demonstrated that proper phytosanitary measures can significantly reduce CMD incidence in Cameroon's tropical rainforest zone. Combining resistant or tolerant varieties with improved phytosanitation offers a promising approach to reducing CMD prevalence.

In the Southern Region, the Vallée-du-Ntem and Mvila divisions recorded very high incidences of 86.30% and 92.42%, respectively, indicating that these are potential hotspots for CMD in Cameroon. Immediate action is needed to promote farmer access to virus-free planting materials, either through certified seed multipliers or subsidized programs. Conversely, the relatively low incidence observed in the Far North may be linked to the recent introduction of cassava, which occupies less than 1% of cultivated land in the region. Similarly, the low incidence in Adamawa likely reflects the distribution of improved varieties by humanitarian and development programs supporting local populations and refugees from the Central African Republic (Kegah et al., 2019; Tchuente et al., 2024).

Whitefly Population. The mean number of whiteflies per plant across all surveyed fields in Cameroon was 5.86. This difference was statistically significant, confirming that the variation in whitefly abundance among the 342 surveyed fields was not due to chance ($W = 0$, $df = 341$, $P < 0.0001$). Regional means varied considerably, ranging from 0.40 in the Far North Region to 21.44 in the South West Region (Table 5). At the divisional scale, Ndian recorded the highest mean (30.40), while Mayo-Louti had the lowest (0.03). No whiteflies were detected in Mayo-Tsanaga (Far North Region).

At the field level, exceptionally high mean densities (>50 whiteflies/plant) were recorded in Mabanda (Meme Division, 82.03), Mabeta (Fako Division, 57.80), Bwasa (Fako Division, 56.40), and Koukoue (Sanaga-Maritime Division, 54.93). Maximum counts per plant ranged from 6 in the Far North to 222 in the South West (Table 5). The overall mean (5.86) was consistent with values previously reported by Doungous et al. (2022) in Cameroon. Comparable infestations have been documented in North-Eastern Nigeria (42.39), the North-Western Democratic Republic of Congo (5.74), and Zambia (11.1 in 2013 and 10.8 in 2015) (Abubakar et al., 2019; Chikoti et al., 2020; Likiti et al., 2023). Notably, Legg (2010) suggested that threshold of five whiteflies per plant on apical leaves is sufficient to trigger epidemic risk.

High whitefly abundance in Cameroon is likely influenced by multiple factors, including

Table 4. Results of the BLAST analysis based on sequences of Cassava Mosaic Geminiviruses (CMGs) isolated in Cameroon.

Sequence IDs	Virus species	Total score	Query coverage (%)	Nucleotid sequence Identity %	NCBI Acession No	Country
ACMV_S2-CM	ACMV	863	28	97.25	LC721739	Côte d'Ivoire
ACMV_S4-CM	ACMV	868	36	98.02	KJ887762	Madagascar
ACMV_S12-CM	ACMV	823	32	97.53	EU685322	Nigeria
ACMV_S15-CM	ACMV	835	32	97.38	MN809986	Nigeria
ACMV_S16-CM	ACMV	847	49	98.76	HE979765	Africa
ACMV_S22-CM	ACMV	856	32	98.38	MG250102	Ghana
EACMV_S28-CM	EACMV	837	27	97.38	AY211887	Cameroon
EACMV_S30-CM	EACMV	918	34	98.04	AY211887	Cameroon
EACMV_S35-CM	EACMCV	1358	43	95.58	MT856195	Cameroon
EACMV_S54-CM	EACMV-Ug	1012	40	97.52	HE814064	Central African Republic and Chad

varietal susceptibility, differences in whitefly species, cropping systems (monoculture vs. intercropping), and phytosanitary practices. Environmental conditions, particularly altitude, temperature, humidity, and rainfall, also play critical roles in vector survival, reproduction, and dispersal (Fondong et al., 2002; Abubakar et al., 2019; Chikoti et al., 2020; Chikoti & Tembo, 2022; Houngue et al., 2022). These findings highlight the need for efficient, integrated control measures targeting whitefly populations.

Interestingly, some CMD-free fields also showed relatively high mean whitefly densities (~ 5.13/plant). A similar observation was made by Omongo et al. (2012), who reported that the improved cassava variety I92/0067 supported more eggs and nymphs of *B. tabaci* than the local Njule red. This suggests that improved varieties grown in some surveyed areas may be more attractive to whiteflies.

Furthermore, whitefly densities were particularly high in the Littoral and South West Regions. This aligns with findings by Aregbesola et al. (2020), who reported that the optimal survival temperature for *B. tabaci* (SSA-ESA subgroup) ranges from 26–28 ºC. The mean annual temperatures and rainfall patterns in these regions are therefore highly favorable for the development and persistence of *B. tabaci.*

Relationship between Whitefly Population, CMD Incidence, CMD Severity, and Cropping System. The mean number of whiteflies per field showed a weak but significant positive correlation with CMD incidence ($r = 0.3$; $P < 0.0001$). As illustrated in Figure 8, whitefly populations tended to increase when CMD incidence exceeded 25%. CMD severity was also weakly correlated with incidence ($r = 0.2475$; $P < 0.0001$) (Table 6). The highest mean number of whiteflies (7.20) was recorded on plants with severity score 2, while the lowest (3.57) occurred at severity score 5. This resulted in a very weak and non-significant negative correlation between severity and whitefly abundance ($r = -0.0568$; $P = 0.2947$) (Table 6). Notably, whitefly density decreased progressively as severity increased from score 2 onward (Figure 9). These findings are consistent with results from Zambia (Chikoti et al., 2020), Nigeria (Eni et al., 2021), and Cameroon (Doungous et al., 2022), although other studies have reported different trends. For example, Kuate et al. (2017) observed a negative correlation between whitefly numbers and CMD incidence in the TMS 92/0326 variety, while Houngue et al. (2022) found no correlation in Benin. These differences suggest that CMD incidence is not solely determined

Table 5. Mean CMD incidence, mean CMD severity, and mean whitefly population in cassava across ten regions of Cameroon

Regions	Number of fields surveyed	CMD Severity Mean	CMD Incidence Mean	Whitefly Mean	Whitefly Max	Whitefly Min	Whitefly Sum	Whitefly Infected Plants Count	Whitefly Infected Plants Count (%)
Adamawa	45	2.63 ± 0.0215	36.67 ± 0.0130	1.99 ± 0.0866	116	0.00	2683	1350	13.19
Centre	75	2.41± 0.0143	56.51 ± 0.0107	6.77 ± 0.1886	136	0.00	15,185	2242	21.90
East	62	2.52 ±0.0192	60.41 ± 0.0150	4.90 ± 0.2764	107	0.00	9101	1859	18.16
Far North	13	2.26 ± 0.0484	18.97 ± 0.0211	0.40 ± 0.0316	6	0.00	156	390	3.81
Littoral	21	2.27 ± 0.0209	73.69 ± 0.0179	11.64 ± 0.6816	180	0.00	7125	612	5.98
North	31	2.42 ± 0.0245	42.90 ±0.0160	0.66 ± 0.0648	18	0.00	614	930	9.09
North West	2	2.35 ± 0.0735	71.67 ± 0.0623	14.35 ± 2.5040	89	0.00	861	60	0.58
South	53	2.25 ± 0.0119	74.34 ± 0.0103	5.75 ± 0.1912	91	0.00	9140	1590	15.53
South West	20	2.19 ± 0.0214	47.83 ± 0.0148	21.44 ± 0.9973	222	0.00	12,861	600	5.86
West	20	2.34 ± 0.0262	46.33 ± 0.0178	3.70 ± 0.3443	152	0.00	2219	600	5.86
Overall mean		2.39	54.72	5.86					
SEM		0.0067	0.0050	0.1153					
P-value		P < 0.0001	P < 0.0001	P < 0.0001					

Values are presented as mean ± standard error of mean. SEM = Standard Error of Mean

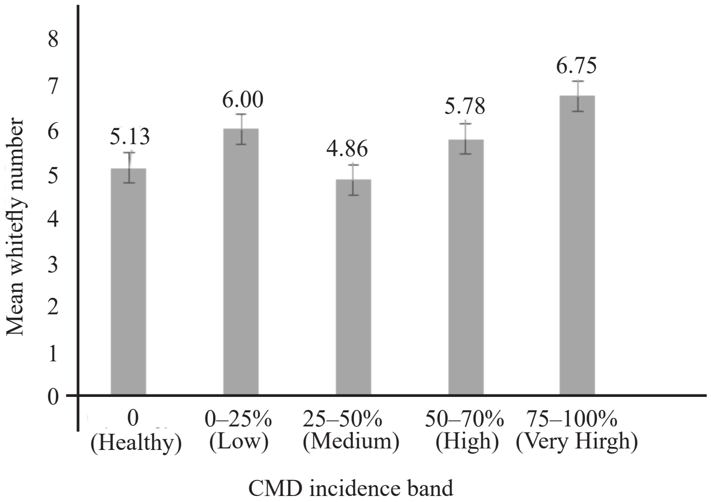

Figure 8. Mean number of whiteflies per plant by CMD incidence band. Bars represent the standard error of the mean SEM.

Table 6. Pairwise Spearman's correlations among mean whitefly number per field, mean CMD severity, mean CMD incidence, and altitude

Variables		r	CI95%	P-value	Power
CMD severity	CMD incidence	0.2475**	[0.15 ; 0.34]	3.62×10^{-6}	0.996525
CMD severity	Whitefly abundance	-0.0568	[-0.16 ; 0.05]	0.2947	0.182346
CMD severity	Altitude	0.2703**	[0.17 ; 0.37]	3.87×10^{-7}	0.999185
CMD incidence	Whitefly abundance	0.3000**	[0.2 ; 0.39]	1.55×10^{-8}	0.999909
CMD incidence	Altitude	-0.1044	[-0.21 ; 0]	0.0537	0.488919
Whitefly abundance	Altitude	-0.2849**	[-0.38 ; -0.18]	8.29×10^{-8}	0.999711

**, significant at $P < 0.0001$ (two-sided), n = 342

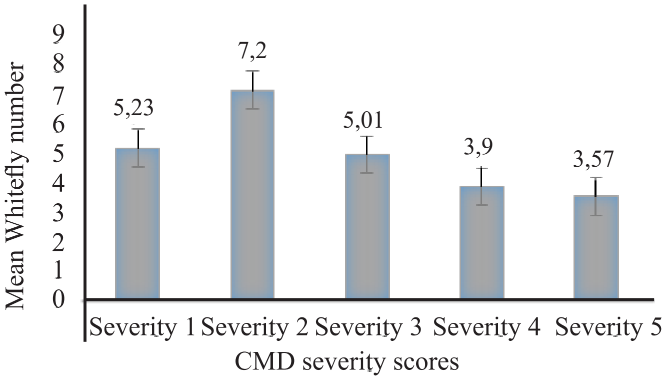

Figure 9. Mean number of whiteflies per plant at each CMD severity score. Bars represent the standard error of the mean (SEM).

by vector abundance but also influenced by factors such as the use of infected cuttings and cross-field transmission.

Surveyed fields spanned a wide altitudinal range, from 0.3 m above sea level in coastal regions to 1,549.1 m in the western highlands. Statistical analysis showed a weak but significant negative correlation between whitefly abundance and altitude ($r = -0.28$; $P < 0.0001$) (Table 6), confirming earlier observations that whitefly populations decline with increasing elevation (Doungous et al., 2022).

To evaluate the effect of cropping systems, boxplots were generated for CMD incidence, severity, and whitefly abundance. Of all surveyed fields, 50.88% were intercropped, while 49.12% were monocropped. Intercrops included groundnut, cocoyam, maize, yam, sweet potato, beetroot (*Beta vulgaris*), folere (*Hibiscus sabdariffa*), beans, pepper, plantain, millet, okra, egusi, and bitter-leaf. No significant differences in CMD incidence and severity were observed between systems.

However, incidence was higher in intercropped fields (66.80%) compared with monocropped ones (46.50%). Severity was similar, with median values of 2.28 (intercropped) and 2.35 (monocropped) (Figure 10).

Whitefly abundance, however, varied significantly with cropping system. Intercropped fields averaged 3.5 whiteflies per plant, compared with 1.3 in monocropped fields (Figure 11). Notably, fields intercropped with bitter-leaf recorded very high whitefly densities (57.8/plant), while those intercropped with maize (2.5), groundnut, and yam (0.2) had much lower densities (Figure 12). CMD incidence was highest in cassava–maize–plantain systems (median = 0.88) and lowest in cassava–sweet potato systems (median = 0.48) (Figure. 13).

These observations contrast with findings from other regions, where intercropping cassava with maize, cowpea, or green gram significantly reduced CMD incidence, severity, and vector populations (Fondong et al., 2002; Uzokwe et al., 2016; Sam et al., 2021). Similarly, Ewusie et al. (2010) reported fewer *B. tabaci* eggs, nymphs, and adults in cassava bordered by cotton or *Jatropha curcas*, highlighting the potential of strip cropping as a management strategy. In addition, Togni et al. (2018) demonstrated that tomato–coriander intercropping with sprinkler irrigation reduced *B. tabaci* infestations in organic tomato systems. These studies indicate that the effectiveness of intercropping in reducing vector populations depends heavily on crop combinations, local ecology, and management practices. In the present study, some intercrops may have acted as alternative hosts for *B. tabaci*, potentially increasing vector abundance and CMD incidence.

Source of Infection. Field observations indicated that the main source of CMD infection in Cameroon was the use of infected cuttings for planting, accounting for 98.37% of symptomatic plants. Only 1.63% of infections were attributed to whitefly transmission. However, vector-borne transmission was considerably higher in the Far North Region (Table 7). These findings underscore the importance of strengthening

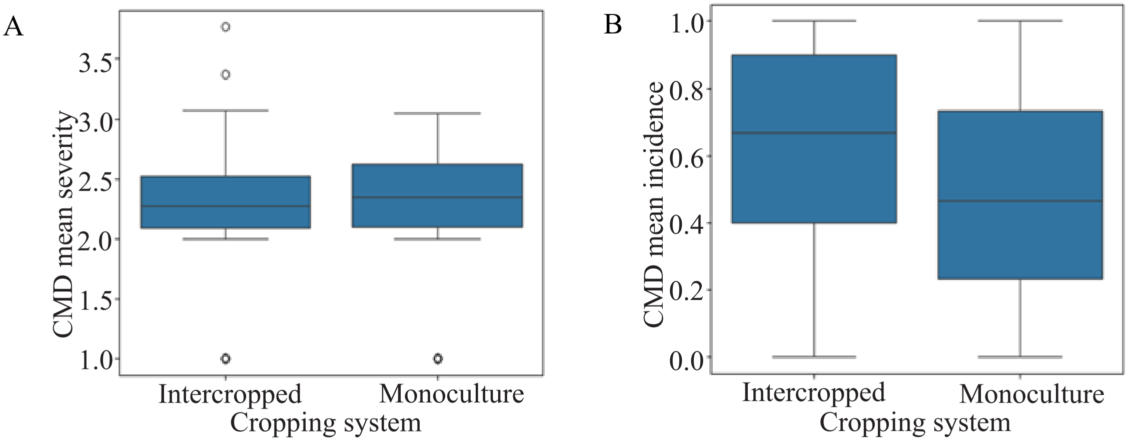

Figure 10. Cassava mosaic disease (CMD) severity and incidence according to cropping system in Cameroon. A. CMD severity; B. CMD incidence.

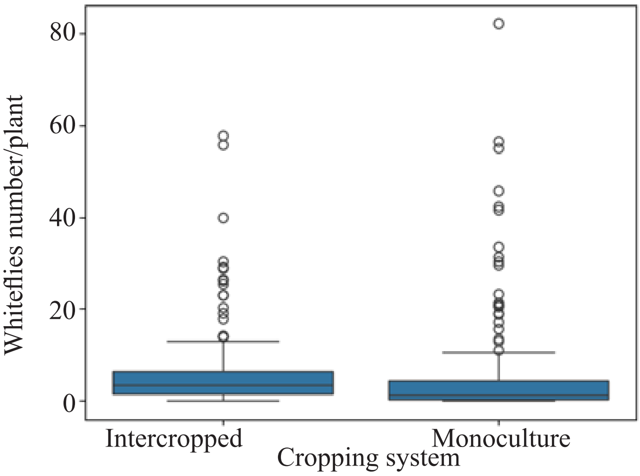

Figure 11. Whitefly population according to cropping system in Cameroon.

phytosanitary practices, particularly the distribution and use of clean planting materials. Other potential sources of inoculum—such as alternative hosts, weeds, and infected neighboring fields—also require attention

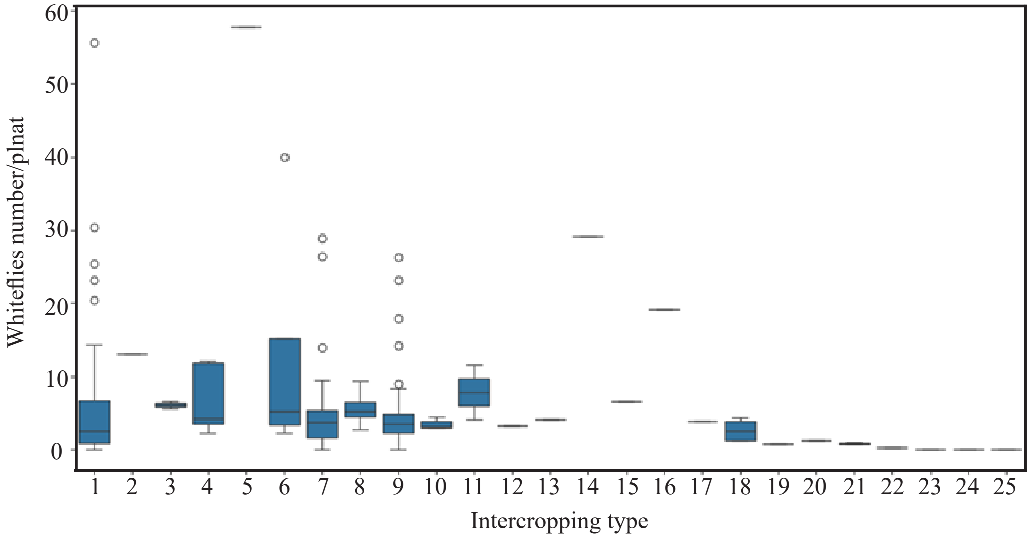

Figure 12. Whitefly population according to intercropping systems in cassava fields. Intercrops: 1 = Maize; 2 = Maize–Egusi; 3 = Maize–Sweet potato; 4 = Groundnut–Plantain; 5 = Bitter leaf; 6 = Plantain; 7 = Groundnut; 8 = Maize–Plantain; 9 = Maize–Groundnut; 10 = Maize–Groundnut–Plantain; 11 = Maize–Groundnut–Sweet potato; 12 = Maize–Groundnut–Cocoyam–Plantain; 13 = Maize–Plantain–Cocoyam; 14= Plantain–Pepper; 15 = Egusi; 16 = Maize–Okra; 17 = Cocoyam; 18 = Sweet potato; 19 = Maize–Sweet potato–Millet; 20 = Groundnut–Sweet potato; 21 = Maize–Beans; 22 = Maize–Groundnut–Beans–Sweet potato; 23 = Beetroot; 24 = Folere; 25 = Groundnut–Yam.

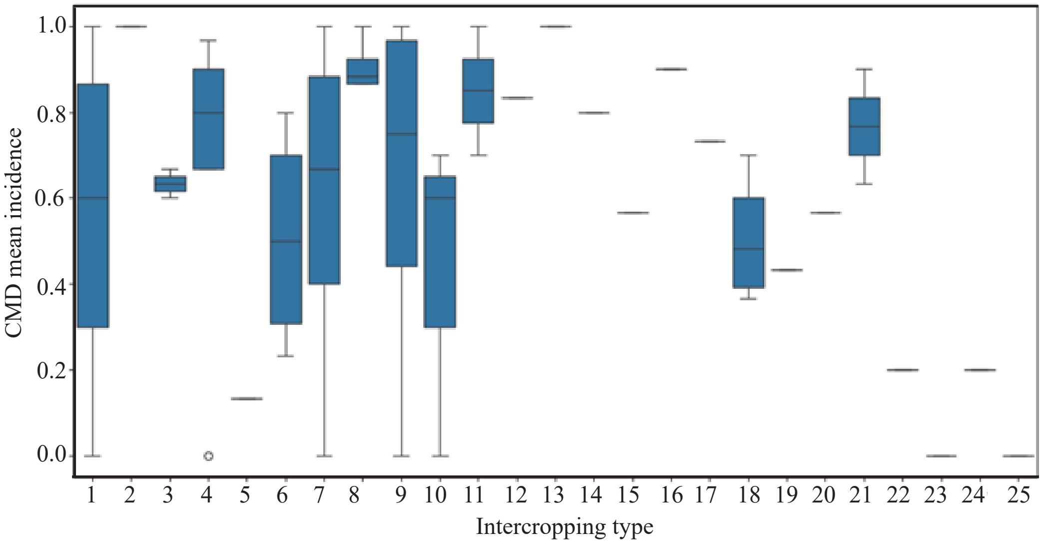

Figure 13. Mean cassava mosaic disease (CMD) incidence according to intercropping system in cassava fields. Intercrops: 1 = Maize; 2 = Maize–Egusi; 3 = Maize–Sweet potato; 4 = Groundnut–Plantain; 5 = Bitter leaf; 6 = Plantain; 7= Groundnut; 8 = Maize–Plantain; 9 = Maize–Groundnut; 10 = Maize–Groundnut–Plantain; 11 = Maize–Groundnut–Sweet potato; 12 = Maize–Groundnut–Cocoyam–Plantain; 13 = Maize–Plantain–Cocoyam ; 14 = Plantain–Pepper; 15 = Egusi; 16 = Maize–Okra; 17 = Cocoyam; 18 = Sweet potato; 19 = Maize–Sweet potato–Millet; 20 = Groundnut–Sweet potato; 21= Maize–Beans; 22 = Maize–Groundnut–Beans–Sweet potato; 23 = Beetroot; 24 = Folere; 25 = Groundnut–Yam.

Table 7. Source of cassava mosaic disease (CMD) infection by region

Region	Number of infected plants	Cutting derived infection (%)	Whitefly-derived infection (%)
Adamawa	495	96.97	3.03
Centre	1267	99.45	0.55
East	1123	99.55	0.45
Far North	74	41.89	58.11
Littoral	451	99.33	0.67
North	399	98.50	1.50
North West	43	100.00	0
South	1182	99.92	0.08
South West	287	97.56	2.44
West	278	98.56	1.44
Overall	5599	98.37	1.63

as part of integrated disease management (Uzokwe et al., 2016; Sam et al., 2021; Doungous et al., 2022).

CONCLUSION

This study reveals that cassava mosaic disease (CMD) is widespread across all ten regions of Cameroon, with high incidence and severity particularly in the South, Littoral, East, and Centre regions. The main driver of CMD spread is the use of infected cuttings, while whitefly-mediated transmission is more important in the Far North. Incidence and whitefly populations were higher in intercropped fields, though cassava–maize and cassava–sweet potato systems showed potential to suppress whiteflies and reduce CMD incidence, respectively. These findings underscore the need for clean planting materials, improved phytosanitary practices, and vector control within integrated management strategies. Future research should investigate the genetic diversity of cassava mosaic geminiviruses and *Bemisia tabaci* biotypes in Cameroon to support more effective disease management.

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AUTHORS' CONTRIBUTIONS

OD, JSP, FTI, and AOE conceived and designed the study. OD, JALB, LDL, and DNN conducted the surveys, data collection, and field recording. JALB performed the formal data analysis. The original draft was prepared by JALB and LDL. JALB, LDL, PFK, DNN, EYM, AOE, FTC, NN, FTI, JSP, and OD contributed to reviewing and editing the manuscript. OD, FTC, and NN supervised the study. All authors have read and approved the final version of the manuscript.

COMPETING INTEREST

The authors declare no competing interests. The funders had no role in the design of the study; in the collection, analysis, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

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