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Analysis of Whitefly (*Bemisia tabaci*) Prevalence and Developmental Stages and Its Effects on Cassava Plant Height and Infection by Cassava Mosaic Disease under Field Conditions

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Abstract

Whiteflies (*Bemisia tabaci*) serve as a vector for transmitting phytopathogens that inhibit the normal development of plants, affecting crop performance. This study assessed the seasonal dynamics of whitefly developmental stages in relation to plant height, cassava mosaic disease (CMD) severity and incidence in cassava; and the influence of whitefly prevalence and developmental stages on cassava plant height and infection by CMD under field conditions. The trial was conducted under natural cassava production conditions during 2020/2021 cropping season at the upland experimental site of the School of Agriculture and Food Sciences, Njala University. A total of 270 cassava genotypes comprising 268 local varieties and 2 improved checks (SLICASS 4 and SLICASS 6) was laid out in an augmented randomized design with four blocks. Results revealed that whitefly eggs dominated early colonization at 3 months after planting (MAP) but had little epidemiological influence, whereas adults and nymphs strongly predicted severity and incidence of CMD from 6 - 9 MAP. Findings on correlation circles revealed seasonal associations, with adults clustering closely with CMD variables at epidemic peak (9 MAP), but decoupling occurring at 12 MAP due to symptom persistence. The CMD trend analysis showed a characteristic sigmoidal pattern, while data on mode-of-infection confirmed dual pathways: early cutting-borne infections and mid-to-late seasonal whitefly-borne CMD infections. These findings suggest that CMD epidemiology is probably governed by shifting whitefly population structure and environmental heterogeneity. Future studies will explore better understanding of these dynamic relationships that provide a framework for timely integrated pest management (IPM) interventions for sustainable cassava production.

Keywords

Bemisia tabaci, Whitefly Developmental Stages, Cassava Mosaic Disease, Prevalence, Correlation Circle, Vector-Virus Interactions, Cassava

1. Introduction

Cassava (*Manihot esculenta* Crantz) is a major food security crop in sub-Saharan Africa, providing carbohydrates to more than 800 million people globally. Despite its resilience to drought and poor soils, cassava production is heavily constrained by biotic factors including whitefly (*Bemisia tabaci* Gennadius) and cassava mosaic disease (CMD). Whiteflies comprise 1556 species, of which, *Bemisia tabaci* [Hemiptera: Aleyrodidae] remains one of the most economically important pests of vegetable and ornamental crops worldwide [1] [2]. The insect feeds on several crops, including cassava, potato, brinjal, chili, cotton, okra, tomato, and tobacco [3] [4]. The economic damage caused by *B. tabaci* ranges between mild and severe with global annual loss reaching up to billions of USD in many crops [5]-[7]. The adults of this insect are minute (usually 1 to 3 mm in length) and they feed and oviposit in large quantities on the underside of leaves [8].

Bemisia tabaci may decrease the rate of photosynthesis in plants through the excretion of honeydew during feeding, besides being able to transmit a large number of plant pathogenic viruses such as cassava mosaic begomoviruses (CMBs), carlaviruses, criniviruses, ipomoviruses, and torradoviruses [9]-[13]. CMD is considered one of the most economically damaging diseases in the African cassava belt caused by CMBs, with yield losses ranging from 20% to 95%, depending on cultivar susceptibility and infection timing [14] [15].

Whitefly population dynamics play a central role in CMD epidemiology. The adult stage plays key role in viral acquisition and transmittal, while the egg and nymphal stages account for the reproductive buildup and colonization potential of the insect. Patterns in the abundance of these life stages influence not only vector pressure but also the temporal progression of CMD severity and incidence in the field [16] [17]. Seasonal population shifts are well-documented in whitefly systems but have not been thoroughly integrated with CMD expression across cassava growth stages. Recent epidemiological evaluations indicate variability in the occurrence and severity of CMD across different agroecologies, influenced by the susceptibility of cultivars, the quality of planting materials, and the pressure from vectors; combining laboratory diagnostics with field monitoring has revealed shortcomings in traditional monitoring methods for early detection and effective management [18]. In Sierra Leone, recent research integrating CMD detection with the evaluation of agronomic traits emphasizes the interaction between variety performance and local seed systems in relation to disease impact, providing strategies to synchronize breeding, the distribution of disease-free seeds, and vector control in order to minimize yield reductions [19].

Plant height and canopy architecture also influence whitefly colonization through effects on microclimate, visibility, and suitability of feeding sites [20] [21]. However, there is lack of dynamic, season-long analyses that link specific whitefly developmental stages to CMD epidemiology. The direct relationships among plant height, whitefly developmental stages with CMD severity and incidence are not fully understood. Meanwhile, CMD expression arises through two primary pathways: (1) Cutting-borne infection from contaminated planting materials and (2) Whitefly-borne infection occurring during the growing season. Disentangling the contributions of these pathways is essential to improving disease forecasting and integrated pest management (IPM). Establishing a connection between whitefly developmental variations and CMD epidemiology necessitates a focus on the synchronization among vector life stages, cassava growth patterns, and the windows for virus acquisition and transmission. Elevated temperatures and arid-season circumstances can speed up the development of *B. tabaci* and reduce their generational span, thereby increasing the number of effective adult vectors during the period when cassava is most physiologically susceptible. Meanwhile [22] observed changes in natural predator dynamics or crop patterns can influence nymph survival rates and adult emergence, ultimately altering inoculum pressure and the trajectories of epidemics [23].

Modern multivariate statistical tools, including principal component analysis (PCA), offer robust frameworks for visualizing ecological and epidemiological relationships among variables [24]. Correlation-circle (PCA plots), in particular, reveal variable clustering patterns that reflect seasonal interactions among whitefly developmental stages, plant height, and CMD. Thus, the objectives of this study were to 1) assess the seasonal dynamics of whitefly developmental stages in relation to plant height, CMD severity and incidence in cassava; and 2) determine the influence of whitefly prevalence and developmental stages on cassava plant height and infection by CMD under field conditions.

2. Materials and Methods

2.1. Description of the Study Area

The field trial was conducted under natural cassava production conditions during the 2020/2021 cropping season at the upland experimental site of the School of Agriculture and Food Sciences, Njala University. The site is located at an elevation of approximately 50 masl, at latitude 8˚6'N and longitude 12˚6'W. The experimental site is predominantly covered by secondary bush vegetation. The area experiences a rainy season from April to November and a dry season extending from October to May. The soil type, temperature range, and prevailing humidity during the experimental season were typical of cassava-producing regions in sub-Saharan Africa and comparable to environmental conditions noted in previous whitefly-CMD epidemiological studies [15] [25]. During the rainy season, monthly air temperatures typically range from 21˚C to 23˚C throughout both day and night.

2.2. Plant Material, Experimental Design and Layout

The experimental materials included stem cuttings of 268 cassava genotypes, collected from all districts of Sierra Leone and 2 improved released varieties (SLICASS 4 and SLICASS 6) utilized as checks. The experiment was laid out in an augmented randomized design with four blocks, each measuring 28 m × 10 m with 1 m distance between the blocks. This enabled robust assessment of block effects (micro-environment) and treatment effects (genotype), consistent with modern entomological field methods [24]. The total experimental area utilized was 43 m × 28 m. About 10 stem cuttings per genotype, each measuring 30 cm in length, were planted on a standard plot size of 10 m long ridges while uniform plant-to-plant and row spacing was used 1 m × 1 m spatial arrangement. No irrigation, fertilizer and pesticide application were done, whereas manual weeding schedule was employed monthly to avoid interference with the natural whitefly vectors and the resultant disease dynamics.

2.3. Data Collection

2.3.1. Whitefly and Cassava Mosaic Disease Assessments

Assessment of whitefly populations necessitates a systematic and standardized approach to guarantee precision, consistency, and relevance across various agricultural systems. The subsequent procedures merge established entomological sampling techniques with field-based monitoring practices. Following standardized IITA and FAO whitefly monitoring protocols, the initial step in population assessment involved identifying representative sampling locations within the crop field [26]. A stratified random sampling approach was used to capture spatial variability, including edge effects and variations in canopy structure. Sampling typically occurred on a weekly basis, corresponding with the developmental cycle of *B. tabaci* under field conditions [27]. Following the procedures of Abdullahi *et al.* [26], 10 plants were randomly selected per plot, of which, 10 leaves were examined for the presence of *B. tabaci* in the upper, middle and lower canopies of each plant. 9Adult populations were evaluated on the undersides of the youngest fully developed leaves (preferred sites for egg-laying and feeding). Direct counts were conducted by gently tilting leaves to reduce disturbance while recording the number of adults observed. Counting was done using a hand lens of 20 - 30× magnification per unit leaf.

The immature life stages, such as eggs, nymphs, and pupae, were assessed using a hand lens with a magnification of 10 - 20×. To maintain uniformity, standardized leaf ranks were chosen, usually from mid-canopy leaves. The counts of egg, nymph, and adult on the plants for 3, 6, 9 and 12 months (Naranjo & Ellsworth, 2017) were done [28].

For Cassava Mosaic Disease (CMD), sampling was conducted at 3, 6, 9, and 12 months after planting (MAP), representing early vegetative stage, canopy establishment stage, peak growth and peak whitefly abundance stage, and mature cassava nearing harvest, respectively. These time points align with known seasonal shifts in CMD expression and whitefly population dynamics [29].

Evaluating the severity and incidence of CMD requires a uniform methodology for field surveys, thus guaranteeing comparability between various sites and seasons. Stratified random sampling of fields was done, with each field chosen at regular intervals along sets of transects. In each plot, 10 plants were assessed along two diagonals to capture variability in disease prevalence. Following the methods described by Sseruwagi *et al.* [30], incidence of CMD was calculated as the ratio of plants exhibiting CMD symptoms to the total number evaluated, represented as a percentage. This metric provided an estimate of CMD's propagation within a specific population. In contrast, severity was rated using a standardized visual scale from 1 to 5, where 1 signified no observable symptoms and 5 represented severe leaf distortion and stunting [30]. In order to minimize bias, data on CMD symptoms, such as chlorotic mosaic patterns, leaf distortion, and reduced leaf size were conducted through scoring. An average severity index was determined by calculating the mean severity across all affected plants within a plot using the formula of Sseruwagi *et al.* [30].

Equation (1) is the CMD incidence:

$$\text{CMD Incidence}\left(\%\right)=\frac{\text{Number of symptoms per plant}}{\text{total number of plants observed}}\times 100. \tag{1}$$

$$\text{Mean CMD Severity}=\frac{\text{Number of symptomatic plants}}{\text{Total number of infected plants}}. \tag{2}$$

Assessments were conducted at all MAP periods on all sampled plants. For epidemiological studies, data collection included quantification of *B. tabaci* populations, the primary vector of CMB. Whitefly developmental stages were counted on the top ten leaves of each plant, providing data that can be correlated with CMD incidence and severity. This integration of vector population data strengthened the interpretation of disease pressure and transmission dynamics [30].

2.3.2. Plant Height and Leaf Measurements

Plant height serves as a crucial agronomic indicator that reveals growth performance, differences among genotypes, and reactions to management techniques. The measurement procedures started with the careful identification of representative plants within each experimental plot or treatment. Plants along the border were excluded to reduce edge effects, and a consistent number of plants usually

10 per plot were selected to ensure treatment comparability and statistical validity [31]. Measurement was done at established growth stages, such as three, six, nine and twelve months after planting, with the timing standardized across treatments for valid comparisons [32].

Plant height was measured as the distance from the soil surface at the base of the stem to the highest point of the main stem apex. In instances of branching, the tallest primary stem was utilized as the reference point to maintain uniformity. A graduated measuring stick or tape rule was used, held vertically next to the plant, with the base positioned at ground level adjacent to the stem. The height was recorded to the nearest centimeter to ensure precision [20].

A total of 30 farmers were randomly selected for the participatory identification and selection of their five best preferred, five moderately preferred, and five least preferred cassava accessions based on leaf and petiole aboveground traits for marketability and consumption of foliage leaves. These qualitative traits were evaluated based on the agro-morphological descriptor of cassava by Fukuda *et al.* [33].

2.3.3. Classification of Mode of Infection

Infected plants from cutting-borne infections appearing before or at 2-MAP generally display symptoms uniformly throughout the field, particularly in young crops, because the virus spreads systemically through the infected stem cuttings. On the other hand, whitefly-borne infections were identified by their irregular distribution, often starting at the edges of fields or in specific patches, and tend to increase in prevalence as the crops mature [17] [34]. This pattern of distribution served as a crucial diagnostic factor for distinguishing between the different modes of infection.

To enhance classification accuracy, the timing of symptom emergence was documented following the methodology of Saffa *et al.* [19]. Symptoms of cutting-borne CMD typically manifest at an early stage (3 - 6-MAP), whereas symptoms from whitefly-transmitted infections develop later, frequently emerging after 6-MAP, aligning with peak activity of the whitefly vector. The severity of the disease was assessed using a standard 1 - 5 CMD rating scale, and affected plants were marked for tracking the progression of the disease. At the same time, whitefly populations were measured by counting the adult insects on the upper 10 leaves of every plant. Elevated whitefly counts related to emerging infections provided crucial epidemiological support for vector transmission.

Data analysis combined rates of occurrence, severity levels, and vector population counts to classify the modes of infection. Plots exhibiting a high and uniform rate of occurrence along with early symptom development were classified as cutting-borne, whereas those showing irregular incidence, a delay in symptom appearance, and a connection to elevated whitefly populations were designated as whitefly-borne. Mixed infections were recognized when both infection patterns were present in the same plot. This classification system is essential for understanding CMD epidemiology, as it guides management approaches: cutting-borne infections necessitate the implementation of clean seed systems, while whitefly-borne infections stress the importance of controlling the vector and deploying resistant genotypes.

2.4. Statistical Analysis

Data analysis included computing the average incidence and severity for each location, then aggregating regions to pinpoint areas with high CMD prevalence. Statistical comparisons across various locations and seasons were conducted using either ANOVA or non-parametric tests, based on how the data is distributed. The spatial mapping of incidence and severity also aided in identifying disease patterns and possible epidemiological factors [35].

Statistical analyses were conducted in R (version 4.3) using the packages factoextra (for PCA and correlation circles), stats (for correlation matrices) and ggplot2 (for CMD trend visualization) [15] [29]. Pearson's correlation coefficients were computed to assess linear relationships among whitefly eggs, whitefly nymphs, whitefly adults, plant height, CMD severity, and CMD incidence. Principal Component Analysis was used to explore multivariate associations that visually represented the contribution of each variable to PC1 and PC2. For seasonal trend analysis, CMD severity and incidence mean values sampled at 3, 6, 9 and 12 MAP were plotted to produce a seasonal epidemic curve. This multi-analytic approach parallels methodologies used in recent vector-virus epidemiology studies [15] [29] is believed to clearly underscore the seasonal dynamics of whitefly developmental stages in relation to plant height, CMD severity and incidence in cassava and the influence of whitefly prevalence and developmental stages on cassava plant height and CMD transmission under field conditions.

3. Results and Discussion

3.1. Correlations among Whitefly Life Stages, Cassava Mosaic Disease and Plant Height across Cassava Growth Stages

Plant height, whitefly infestation parameters, and disease incidence show dynamic correlations across the four growth phases (3, 6, 9 and 12-MAP) (**Table 1**). As the crop ages, these correlations were observed to change, providing insight on pest pressure and disease development throughout time. At 3 MAP (the early growth stage), whitefly nymphs and whitefly eggs had a strong positive association (r = 0.672***), suggesting early reproductive buildup or coordinated development between both life stages, whereas adults exhibited weak correlations with CMD severity and incidence. Additionally, there is a weak positive correlation between adult whiteflies and nymphs (r = 0.222***) and eggs (r = 0.127*), indicating that early infestation is well established throughout all stages. Interestingly, adult whiteflies had a weak and positive correlation with both disease incidence (r = 0.164**) and severity (r = 0.633***), respectively, suggesting that pest pressure starts to affect disease outcomes even at this early stage. The relationship between pest activity and disease manifestation is further supported by the strong correlation (r = 0.633***) between severity and occurrence.

Table 1. Correlation coefficient among whitefly developmental stages, CMD severity, CMD incidence, and plant height sampled at 3, 6, 9 and 12 MAP.

Trait	PHT	NWFE	NWFN	NWFA	CMDS	CMDI
Correlation coefficient at 3 MAP						
PHT	1.000					
NWFE	−0.025	1.000				
NWFN	−0.054	0.627***	1.000			
NWFA	0.200***	0.127*	0.222***	1.000		
CMDS	−0.045	−0.045	−0.052	0.090	1.000	
CMDI	0.053	−0.015	0.050	0.161**	0.633***	1.000
Correlation coefficient at 6 MAP						
PHT	1.000					
NWFE	0.001	1.000				
NWFN	−0.024	0.399***	1.000			
NWFA	−0.073	0.220***	0.489***	1.000		
CMDS	−0.107	0.159**	0.357***	0.415***	1.000	
CMDI	−0.021	0.154*	0.310***	0.365***	0.736***	1.000
Correlation coefficient at 9 MAP						
PHT	1.000					
NWFE	0.013	1.000				
NWFN	−0.017	0.237***	1.000			
NWFA	−0.004	0.128*	0.592***	1.000		
CMDS	−0.061	0.100	0.294***	0.323***	1.000	
CMDI	−0.025	0.082	0.190**	0.255***	0.710***	1.000
Correlation coefficient at 12 MAP						
PHT	1.000					
NWFE	−0.070	1.000				
NWFN	−0.063	0.033	1.000			
NWFA	−0.093	−0.001	0.416***	1.000		
CMDS	−0.002	0.011	0.078	0.192**	1.000	
CMDI	−0.018	0.002	0.002	0.069	0.714***	1.000

*, **, and *** = significant at $p < 0.05, 0.01, 0.001$, respectively; PHT = plant height; NWFE = number of whitefly eggs; NWFN = number of whitefly nymphs; NWFA = number of whitefly adults; CMDS = cassava mosaic disease severity and CMDI = cassava mosaic disease incidence.

At 6-MAP, correlation patterns changed considerably. Adult whiteflies and nymphs had a positively intermediate correlation (r = 0.489***), and their correlation with disease severity was relatively strong (r = 0.435***), highlighting the transition to vector-mediated CMD spread. The correlation between severity and incidence became considerably stronger (r = 0.739***), indicating an increase in the visibility and prevalence of disease symptoms. Whitefly eggs were still correlated with nymphs and adults, but the intensity of these correlations started to decline, maybe due to shifting environmental factors, population dynamics or a shift from reproductive expansion to adult-driven transmission.

Correlations between disease indicators and whitefly stages started to declining at 9-MAP, the mid-reproductive stage. The total strength of the correlations between adult whiteflies and nymphs (r = 0.592***) and illness severity (r = 0.170**) decreases. Additionally, a modest decrease in the correlation between severity and incidence (r = 0.170**) was observed suggesting a possible change in host resistance or disease progression. Pest pressure may be less indicative of disease outcomes at the period, which could be a transitional phase. The correlation between disease severity and occurrence (r = 0.714***) at 12-MAP, the late growth stage, is similar to the higher correlation detected between severity and incidence at 6 MAP (r = 0.739***), highlighting the cumulative effect of previous insect attacks. The correlation between adult whiteflies and disease severity remained robust (r = 0.714***), but it becomes minimal when compared to other stages of whiteflies and disease incidence. This implies that while adult whiteflies still have an impact on the severity of the disease, additional factors might be involved in its persistence and transmission at this point. Findings also indicate that CMD expression at this stage was primarily driven by cumulative infections rather than current vector pressure.

Plant height does not significantly correlate with any other characteristic at any stage, suggesting that it is not a good indicator of disease pressure or pest infestation. Adult whiteflies are important drivers of illness dynamics, as evidenced by the persistent and strong correlation between them and disease measures, particularly severity and incidence. These results imply that, especially during the early and late phases of crop development, tracking whitefly numbers may be a useful early warning system for disease outbreaks.

3.2. Multivariate Structure from Correlation-Circle Principal Component Analysis

Correlation-circle PCA plots (**Figure 1** and **Figure 2**) provided deeper insight into ecological clustering patterns across MAP periods. **Figure 1(a)** shows strong interaction between eggs and nymphs of whitefly in PC1, thus forming a cluster of early reproductive buildup while adults displayed low influence and did not cluster with CMD variables. Represents early whitefly colonization. CMD severity and incidence loaded independently on PC2. Disease variables operate on a different axis showing independent causation. Adults displayed low influence and did not cluster with CMD variables. Transmission stage is not yet active. This confirms minimal vector-mediated CMD spread at early growth stages.

At 6 MAP, close clustering of adults and nymphs with CMD severity and incidence on PC_1 was detected, while eggs did not form CMD cluster (**Figure 1(b)**).

Findings indicate that reproduction is not a strong indicator of transmission. Adults and nymphs cluster with CMD variables whitefly life stages now influence disease expression. Weak separation of plant height early influence but no strong CMD predictiveness. CMD spread is adult-driven, with partial influence from nymphs reflecting onset of whitefly-driven epidemic spread.

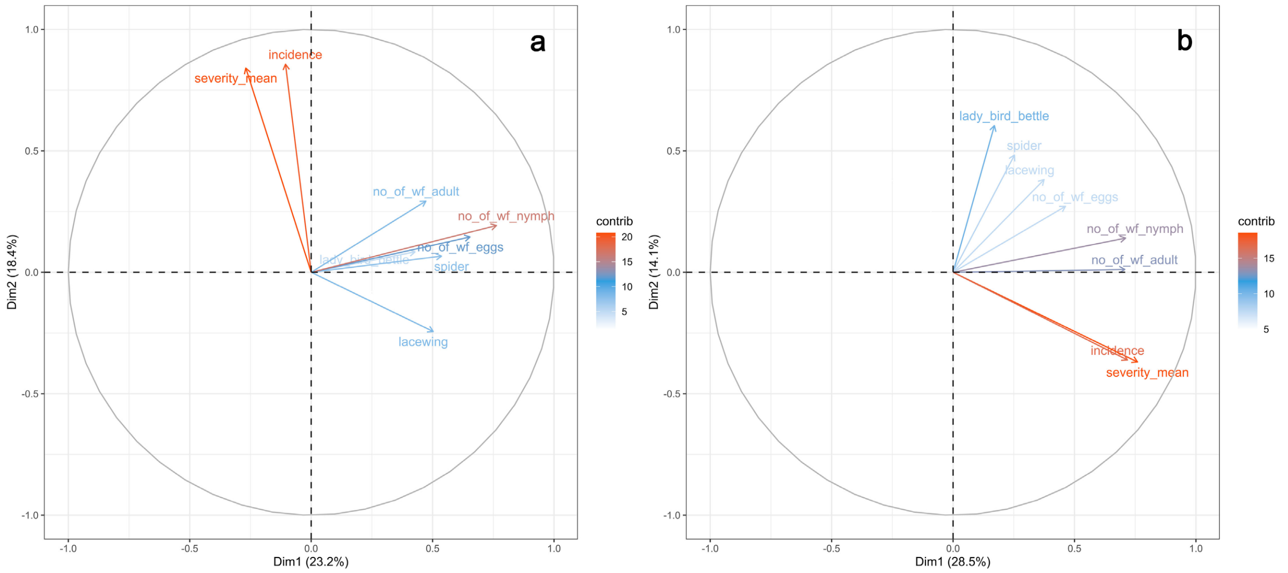

Figure 1. Correlation-circle principal component analysis at (a) 3 months after planting, and (b) 6 months after planting.

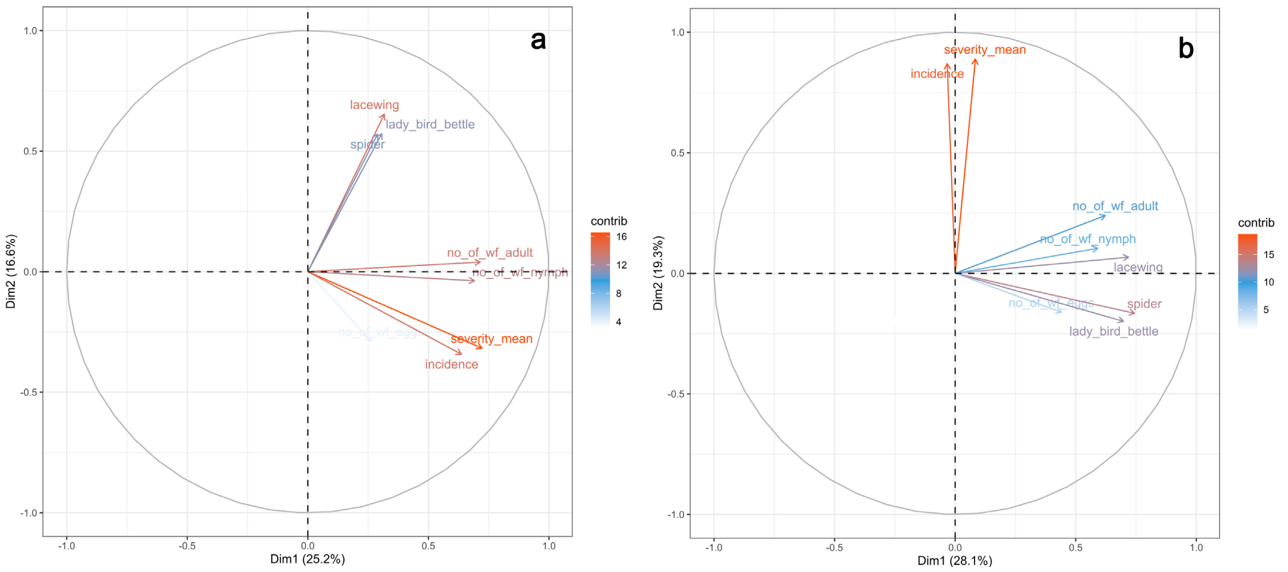

Figure 2. Correlation-circle principal component analysis at (a) 9 months after planting, and (b) 12 months after planting.

A strong co-alignment of adults, nymphs, CMD severity, and CMD incidence was observed which represent peak CMD transmission and vector pressure. At 9 MAP, strongest relationship observed in the alignment of adults and nymphs with CMD metrics (Figure 2(a)) Plant height was still peripheral indicating that height alone does not protect from infection. Eggs are fully detached as they no longer inform CMD patterns. Moreover, findings indicate a peak biological synchrony between vector and virus.

At 12 MAP, whitefly developmental stages did not cluster with CMD metrics (Figure 2(b)). The CMD parameters shift onto PC2 indicating that the persistence of the disease in host is disconnected from the vectors. Whitefly stages were not aligned with the vector population wanes; thus, the disease becomes systemic. The CMD symptoms persist independent of late-stage symptom expression suggesting no ongoing spread of the disease. The late-stage CMD expression reflects earlier infection rather than new transmission. These multivariate shifts clearly demonstrate the temporal decoupling of vector presence and disease symptoms in late-seasonal infection of cassava.

The accumulation of eggs and nymphs indicated colonization rather than epidemiological significance, indicating that contaminated planting materials are the primary source of CMD infection. This finding is in line with recent studies that highlight how important planting material health is to the epidemiology of CMD [17] [34].

3.3. Whitefly Infestation and Cassava Mosaic Disease Infection Trends

Genotype effects are weak or non-significant across most MAP periods. Varieties did not differ greatly regarding whitefly attractions. Environmental effects dominant site-specific conditions overpowered genetic differences. CMD management must prioritize environmental strategy (planting pattern, spacing, IPM) over varietal resistance alone suggesting that cassava genotypes utilized in this experiment did not differ substantially in whitefly attractiveness or suitability. Strong environmental effects overshadowed genotype differences.

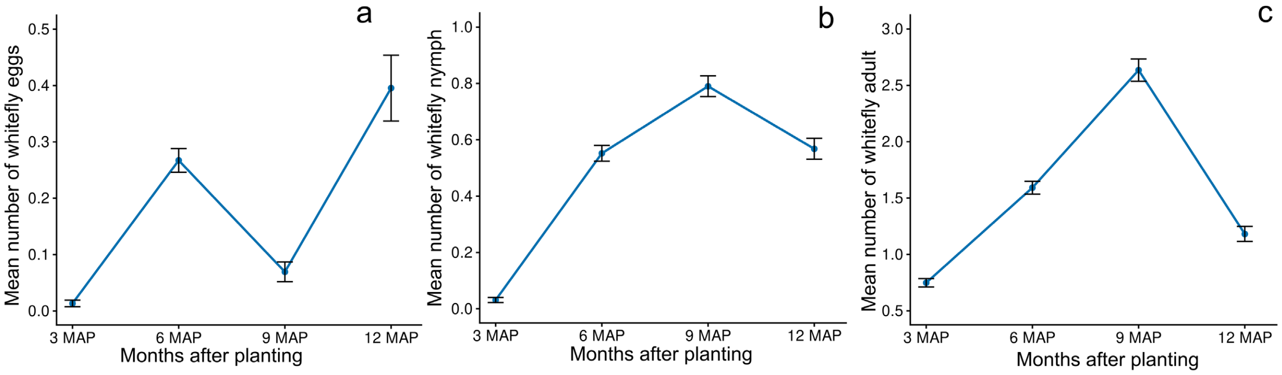

Figure 3. Whitefly infestation trends showing (a) Number of whitefly eggs; (b) Number of nymphs; and (c) Number of adult whiteflies across four sampling regimes.

Figure 3 shows CMD temporal trajectory that clearly followed a sigmoidal progression typical of systemic viral diseases at 3-MAP, 6 to 9-MAP and 12-MAP, respectively, representing initial phase, rapid escalation and plateau phase. These three phases showed low severity and incidence that is dominated by cutting-borne infections; conspicuous increase in severity and incidence that seemed to be driven by adult-mediated whitefly transmission and high but stable CMD severity and incidence. Additionally, it was observed that symptom persistence was independent of vector dynamics (also see Figure 4).

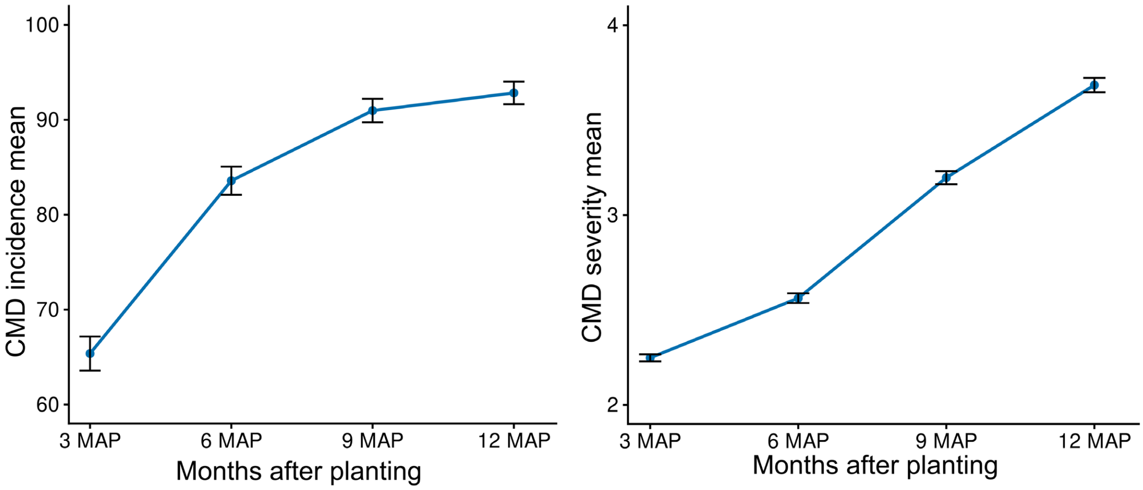

Figure 4. Cassava mosaic disease infection trends showing (a) Incidence and (b) Severity across four sampling regimes.

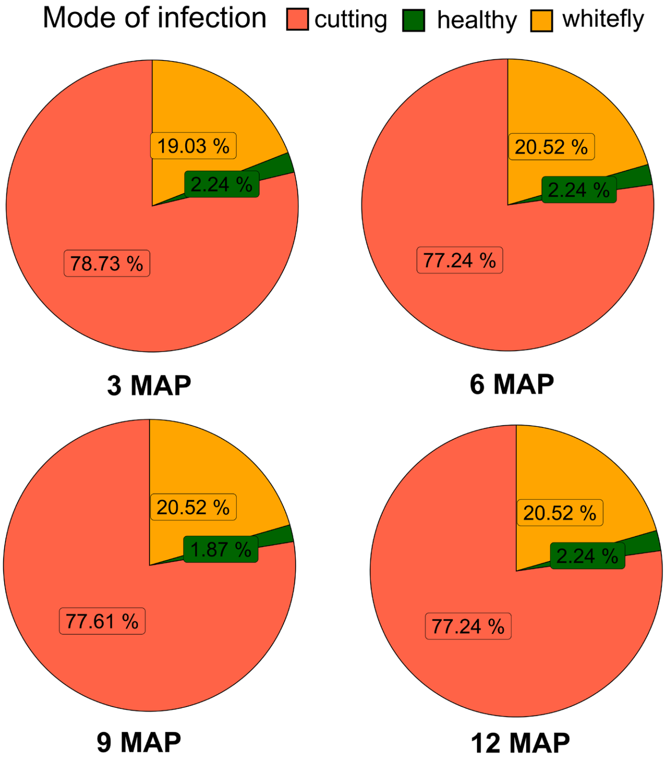

Figure 5. Mode-of-infection of cassava cuttings across sampling regimes.

3.4. Mode of Disease Infection Profiles

The mode-of-infection analysis revealed a clear partitioning of infection pathways throughout the cassava cropping season (Figure 5). Cutting-borne infections constituted most early infections at ≤3 MAP. Whitefly-borne early infections between 3 - 6 MAP, increasing sharply as adult activity intensified. Whitefly-borne late infections between 6 - 9 MAP became dominant during peak vector transmission. This confirms that CMD epidemics involve combined primary (planting material) and secondary (vector-mediated) infection pathways. Cutting-borne infection was the main cause of early CMD expression (≤3 months after planting, MAP), and correlation and PCA analyses revealed no significant relationship between whitefly life stages and CMD variables at this time. Cutting-borne infection dominates the early phase (0 - 3 MAP) of CMD epidemics, but vector-borne infection drives epidemic development from 3 - 9 MAP, with peak transmission happening during maximal adult activity, according to mode-of-infection studies. These results support the combined significance of seasonally timed vector control and clean planting material in the management of CMD [36] [37]. Limited epidemiological significance was shown by plant height, which had an impact on early colonization (3 MAP) but not after 6 MAP. This bolsters the idea that vector ecology and colonization dynamics are affected by canopy microstructure and leaf arrangement rather than just height [20] [21].

3.5. Analysis of Cassava Varieties along Whitefly Developmental Stages

The results projects cassava varieties onto the principal component axes, are reflective of differential genotypic response to whitefly pressure and CMD expression across months after planting (MAP). The multivariate patterns (whitefly life stages vs CMD infection), show different trends across the four sampling regimes studied. Early season (3 MAP) infection reflects colonization without epidemiological impact. Most cassava varieties cluster centrally, indicating low differentiation in response to whitefly pressure (**Figure 6(a)**). This suggests that at 3 MAP, most cassava genotypes responded similarly to early colonization. The lack of divergence implies that genotype-level traits (such as biochemical defenses or leaf anatomical structures) do not significantly influence whitefly behavior. Whiteflies are probably selecting plants randomly or based on initial visibility rather than resistance traits. Varieties with slightly higher scores on PC1 may have early visibility or leaf expansion, attracting more eggs.

Genotypes positioned slightly toward PC1 likely exhibited faster vegetative growth or larger leaf surface area, making them more attractive to whitefly adults during the oviposition phase. However, this attraction does not yet influence disease risk, as eggs do not transmit CMD. Varieties are yet to be epidemiologically differentiated, since CMD is still primarily cutting-borne. Although some varieties may have higher egg numbers, whitefly-driven transmission has not begun, and CMD severity/incidence reflects virus already present in the cuttings at planting. Genotypic differences are not reflected in CMD status at this stage leading to uniform response to vector colonization. Thus, the CMD infection reflects only material purity, rather than genetic resistance or vector dynamics.


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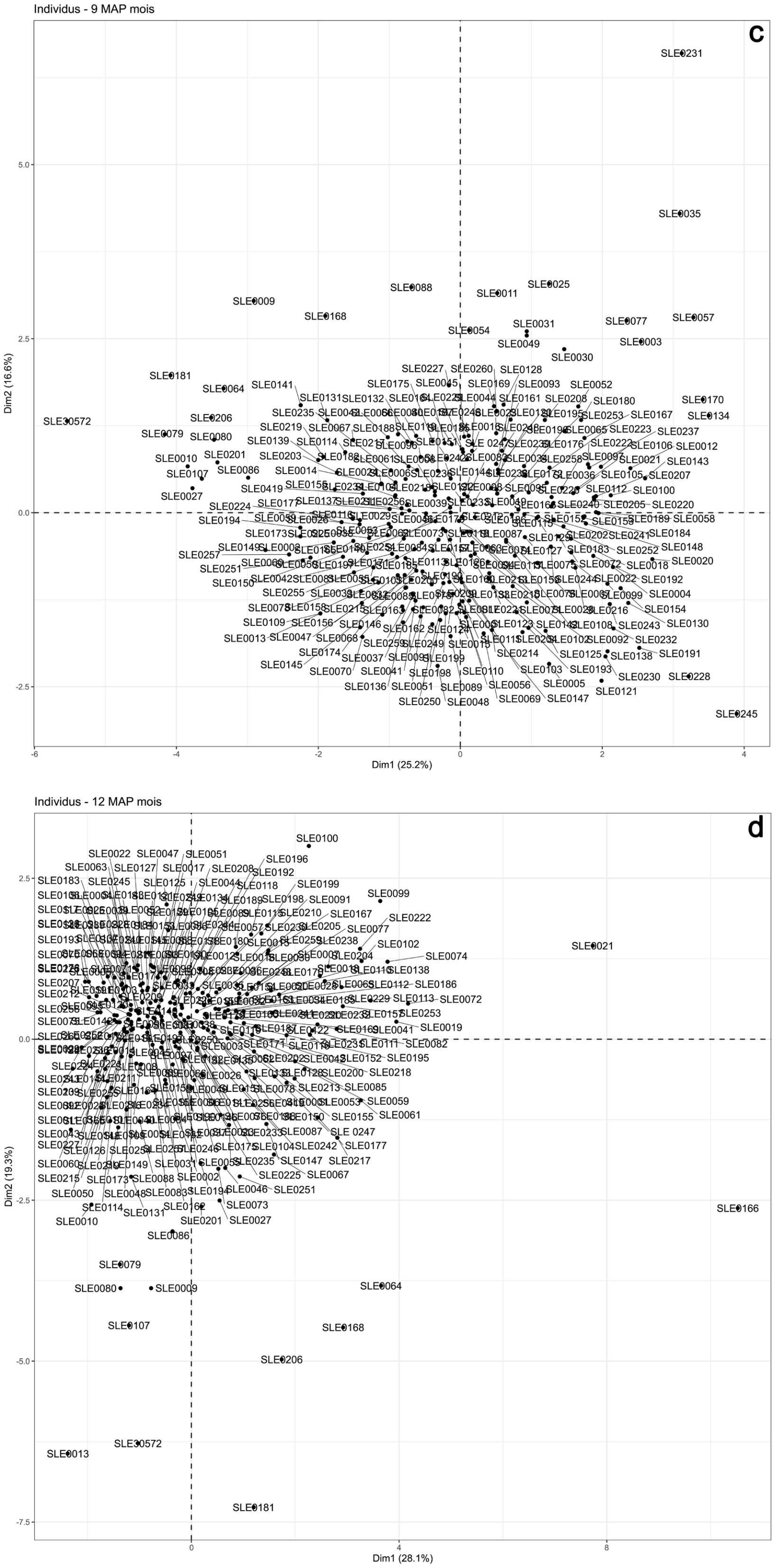

Figure 6. Cassava genotypic response to dynamics in whitefly development stages and CMD expression across four sampling regimes.

Strong relationships between adult and nymph populations and CMD severity and incidence emerged by mid-season (6 MAP), indicating a distinct epidemiological change. The shift from passive infection to active epidemic development was highlighted by the clustering of adult whiteflies with CMD factors shown by PCA correlation circles. According to earlier epidemic research [36] [38], this pattern illustrates the epidemiological significance of mobile adult stages in virus transmission.

The highest vector-to-disease connections were found at 9 MAP, which also happened to be the peak of the epidemic. In line with recent findings that peak adult whitefly pressure speeds up the progression of CMD, adult populations were found to be the most significant drivers of CMD spread [15] [29]. Interestingly, CMD severity rose faster than incidence, indicating that existing illnesses rather than new infections were the cause of the increased symptom manifestation. Although whitefly reproduction was reducing, the severity and incidence of late-season CMD persistence (12 MAP) remained high, decoupling it from vector activity. PCA verified that there was no longer a correlation between CMD variables and vector abundance, suggesting that viral buildup rather than continuous transmission was the cause of disease persistence. This confirms that CMD epidemics involve combined primary (planting material) and secondary (vector-mediated) infection pathways. This is consistent with new research showing that once CMD is established, it cannot be reversed and that viral load, not vector dynamics, determines the severity of symptoms [39] [40].

Mid-Season (6 MAP) infection reflects onset of genotype differentiation due to whitefly activity. At this stage, genotypes begin separation into 2 - 3 clusters (**Figure 6(b)**). Genotypes near adult/nymph vectors indicate high susceptibility/vector preference. These genotypes likely possess leaf textures, chemical profiles, or canopy microclimate that favor whitefly settlement, making them more vulnerable to early transmission during the vector activation phase. Genotypes farther from CMD variables indicate their inherent ability of deploying better early defense traits. It is probable that the tolerant genotypes may have expressed a denser trichomes or tougher leaf cuticles, antifeedant compounds and lower visual detectability contributing to delayed whitefly settlement and reduction of CMD transmission. Since these traits were not assessed in the present study, these aspects are suggested to be included in future research. Genotypes closer to planting height may reflect rapid canopy development, indirectly influencing vector establishment. Early height advantage may increase exposure to incoming whiteflies and alter humidity and light distribution. Thus, contributing to indirect susceptibility due to structural traits rather than biochemical resistance. These genotypes begin to differentiate based on their interaction with vector life stages, suggesting early differences in susceptibility or tolerance before peak CMD pressure.

Peak epidemic (9 MAP) infection reflects maximum genotype differentiation. Strongest separation observed in PCA individuals with genotypes visually align according to their epidemiological performance under pressure (**Figure 6(c)**).

Highly susceptible varieties are clustered close to adult whiteflies and CMD metrics this shows high transmission rate of the CMD. Moderately susceptible varieties are positioned between eggs/nymphs and CMD axes showing possibly delayed infection. Tolerant/resistant varieties are far from CMD vectors (toward PC2 residual space) showing a lower infection or symptom suppression. The PCA demonstrates strong biological stratification under epidemic conditions. This is the most accurate reflection of true CMD impact resistance, as whitefly pressure and virus load peak simultaneously. Traits likely displayed by tolerant genotypes are lower adult whitefly attraction with the leaf surface characteristics or chemical signals reduce vector settling. More robust physiological stress tolerance, varieties may better maintain photosynthesis and energy production under infection. Possibly earlier activation of resistance pathways with early viral replication suppression limits symptom development and severity. Conclusion (9 MAP): This phase gives the clearest visual separation between susceptible and tolerant genotypes, indicating optimal timing for genotype efficacy assessment in CMD resistance screening trials.

Late season (12 MAP) infection reflects symptom stabilization and CMD persistence. Genotypes no longer differentiate based on vector pressure (whitefly declining. At 12 MAP, whitefly populations (especially adults and nymphs) have significantly decreased due to natural ecological decline (senescing leaves, climatic changes, reduced nutritional value) (**Figure 6(d)**). At this stage, Whiteflies are crucial during the infection phase; once infection has occurred and symptoms stabilized, vector dynamics have limited further influence on disease expression. Separation now reflects internal CMD tolerance and symptom suppression capacity. In the PCA plot at 12 MAP, variation between genotypes is predominantly based on their ability to withstand CMD after infection, not their resistance to becoming infected. Varieties far from CMD vectors are genotypes plotted away from CMD severity/incidence vectors on PCA axes (particularly on PC2, representing unexplained/residual variability). At this stage, tolerance matters more than resistance to new infections since infection has already occurred. This shows that Resistance (preventing infection) is no longer the key factor and tolerance (coping with infection) has become the dominant trait of agricultural importance. Late-stage differentiation is less about avoiding the disease and more about surviving and producing under disease pressure. This phase indicates functional CMD tolerance, not vector resistance. This phase is best used to assess long-term physiological tolerance markers. Whitefly distribution patterns in this study support previous reports that whitefly distribution is influenced by the microenvironmental temperature gradients, soil moisture retention, and nearby vegetation [41] [42].

Early CMD is best controlled by cutting-stage therapies, epidemic development is suppressed by mid-season interventions, and late-season control is not very beneficial because of the persistence of viral symptoms. This time-specific paradigm promotes sustainable cassava production across a range of agro-ecological circumstances. A comprehensive and integrated approach that starts even before planting is necessary for the effective management of Cassava Mosaic Disease (CMD). The first line of defense is prevention, and in order to reduce the possibility of introducing CMD into new fields, farmers should give priority to using certified planting material free of viruses during the pre-planting stage. Three to six months after planting, once crops are established, vector monitoring becomes crucial (MAP). To identify early indicators of whitefly populations, which are the main carriers of CMD, both visual inspections and trap-based surveillance should be used. Integrated pest management (IPM) measures must be initiated between six and nine MAP as the crop develops, especially when epidemic thresholds are reached. In order to lessen the need for broad-spectrum chemical pesticides, the focus at this point should be on adult suppression utilizing biological or biorational controls. This selection strategy maintains long-term ecological balance while simultaneously safeguarding useful creatures.

3.6. Marketable Cassava Leaves Assessment against Whitefly and CMD

There are five elite varieties selected by farmers based on the desired leaf traits for selling and consumption included Tangaigboi, Coco cassava, Cookson, Butter cassava, and Ndiamonyamalo, followed by the moderately preferred varieties Tapiyoka, Yaa kanu, Nikaneh, Mende tangai, and Kendemeh (**Table 2**). However, the varieties of SLICASS 4, SLICASS 6, Pink lady, and Munafa are not usually consumed and sold.

Table 2. List of 15 varieties selected by farmers for marketability and consumption.

Varieties	**Genotypes Rating**	Whitefly Rating	CMD Rating
Butter cassava	Highly preferred	High	Susceptible
Cook soon	Highly preferred	High	Susceptible
Coco cassada	Highly preferred	High	Susceptible
Ndiamonyamalo	Highly preferred	High	Susceptible
Tangaigboi	Highly preferred	Low	Healthy
Yaa kanu	Moderately preferred	High	Susceptible
Tapiyoka	Moderately preferred	High	Susceptible
Kendemeh	Moderately preferred	High	Susceptible
Mende tangai	Moderately preferred	High	Susceptible
Nikaneh	Moderately preferred	Moderate	Susceptible
Munafa	Not preferred	Low	Healthy
Pink Lady	Not preferred	Moderate	Susceptible
SLICASS 4	Not preferred	Moderate	Susceptible
SLICASS 6	Not preferred	Low	Healthy

4. Conclusion

This study established functional relational relationship among whitefly prevalence, developmental stages, cassava mosaic disease (CMD) infection and plant height under field conditions. Whitefly eggs dominated early colonization at three months after planting (MAP) but had little epidemiological influence, whereas adults and nymphs strongly predicted severity and incidence of CMD from 6 - 9 MAP. Correlation circles exhibit close clustering of adult whiteflies with CMD variables at the 9 MAP epidemic peak, but decoupling occurring at 12 MAP due to symptom persistence. The CMD trend analysis shows a characteristic sigmoidal pattern, while data on mode-of-infection confirms dual pathways including early cutting-borne infections and mid-to-late seasonal whitefly-borne CMD infections. Findings demonstrate that CMD epidemiology is governed by shifting whitefly population structure and environmental heterogeneity. Understanding these dynamic relationships provide a framework for adequate application of integrated pest management (IPM) interventions for sustainable cassava production. Farmers should be encouraged to utilize the established recommended management strategies such as barrier hedges and diversify their cropping systems as part of ongoing landscape-based management. These methods improve resistance to the spread of CMD and lessen vector movement. Using CMD-tolerant or resistant genotypes at planting offers an extra layer of protection, making fields less susceptible to infection.

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Conflicts of Interest

The authors declare no conflict of interest.

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