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Preliminary Evaluation of Pests and Diseases Status of Improved Cassava (*Manihot esculenta* Crantz) Genotypes in High Humid Agroecology of Nigeria

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ABSTRACT

Background: Cassava (*Manihot esculenta* Crantz) is a major staple crop in southeastern Nigeria, contributing significantly to food security and income generation. Despite its resilience, production is constrained by pests and diseases, including African cassava mosaic virus (ACMV), cassava bacterial blight (CBB), cassava anthracnose disease (CAD), and brown leaf spot (BLS).
Aims: This study aimed to identify resistant and susceptible lines against pests and diseases of eight improved cassava genotypes in high humid region of southeastern Nigeria.
Methods: The study was carried out at GUS AGRO Farms in Ndikpa, Umuowa-Ibu 1, Okigwe, Imo State, Nigeria, in 2024 and 2025 early planting seasons. The experiment was laid in out in a randomized complete block design with three replications. Disease and pest severity were scored at 2, 4, and 6 months after planting on a 1–5 scale. The collected data was analyzed using Kruskal-Wallis test, If the results were significant, the analysis was continued with the Dunn test, with the Benjamini-Hochberg correction.
Results: The results of the study revealed differences in ACMV and BLS severity among genotypes, while CAD, CBB, cassava green spider mite (CGSM), mealybug, and grasshopper attacks showed no significant variation. Sunshine, Fine Face, Dixon, Poundable, TME419, and Game Changer exhibited resistance to ACMV, whereas Imo Best was highly susceptible, recording severity scores up to 4.00. For BLS, Imo Best again showed the highest susceptibility, while Fine Face, TME419, and Ayaya remained symptom-free.
Conclusion: The study revealed that some cassava genotypes, including Sunshine, Fine Face, Dixon, Poundable, TME419, Game Changer, and Ayaya, exhibited strong resistance to ACMV and BLS, making them promising genotypes for adoption by farmers and breeding programs.

Conversely, Imo Best genotypes consistently showed high susceptibility, with severe ACMV scores and pronounced vulnerability to BLS, underscoring the risks of cultivating it in disease-prone environments.

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1. Introduction

Cassava serves as a vital source of carbohydrates essential for human survival and well-being. The crop plays a significant role in ensuring food security for approximately 40% of sub-Saharan Africans (FAO, 2022). Additionally, cassava is not only a crucial subsistence crop but also a valuable cash crop for farmers and a key industrial raw material used in the production of starch, pharmaceutical products, ethanol, and confectionery. Its resilient nature, including drought tolerance and a wide range of ecological requirements, has established cassava as a strategic crop for enhancing food security and reducing poverty in various regions worldwide (Ikeh *et al,* 2023, Amoah-Oppong *et al.,* 2025, Thomas *et al.,* 2025a, Thomas *et al.,* 2025b).

Pests and diseases remain significant constraints on cassava production in Africa (Victor & Mutarushwa 2026). Among the most critical biotic stressors are African cassava mosaic disease (ACMD), cassava anthracnose disease (CAD), cassava bacterial blight (CBB), cassava green spider mite (CGSM), and cassava mealybug (CMB). Of these, CMD, CBB, and CGSM are particularly noteworthy (Baiyeri *et al.,* 2008; Chiunga *et al.,* 2025). Cassava mosaic disease (CMD) is the most destructive, with potential yield losses ranging from 20% to 90% depending on severity (Ahoya *et al.,* 2025). Cassava bacterial blight (CBB), caused by *Xanthomonas axonopodis pv. manihotis*, and cassava green spider mite (CGSM), which reduce photosynthetic capacity, also pose major threats to productivity.

The most reliable and easily adoptable method for managing these biotic stresses is the cultivation of resistant cassava genotypes. Ensuring the availability of high-yielding, pest- and disease-resistant varieties for farmers represents the most cost-effective and sustainable long-term strategy (Ikeh, 2017; Siriwan *et al.,* 2025). Recent studies highlight the importance of integrating modern breeding tools, participatory surveillance, and farmer awareness programs to accelerate the adoption of resistant varieties (Sawadogo *et al.,* 2025).

Several destructive diseases constrain cassava production in sub-Saharan Africa. African Cassava Mosaic Disease (ACMV), Cassava Bacterial Blight (CBB) and Cassava Anthracnose Disease (CAD). (ACMV) caused by a geminivirus, is one of the most predominant in Nigeria and other regions. It produces a mosaic pattern of yellow or white patches intermixed with green on leaves, leading to distortion, stunting, and dieback. This disease can significantly reduce tuber yields and cause shortages of planting materials (Amoah Oppong *et al.,* 2025).

Cassava Bacterial Blight (CBB), caused by Xanthomonas phaseoli pv. manihotis, is another major constraint. It manifests as angular water soaked lesions, leaf blighting, wilting, defoliation, gum exudation, and stem cankers. Severe infections result in rapid wilting and bare stems known as "candlesticks." The disease spreads through infected cuttings, rain splashes, insects, contaminated soil, and farm tools, with outbreaks intensifying during rainy seasons, especially in low fertility soils (Chiunga *et al.,* 2025; Carvalho *et al.,* 2026).

Cassava Anthracnose Disease (CAD), caused by *Colletotrichum gloeosporioides* f. sp. manihotis, also poses a serious threat. Symptoms include pale brown patches or depressions on young stems, twisting, cracking, and canker formation. In older stems, lesions deepen, making them brittle and prone to breakage. Severe infections cause dramatic wilting and dieback, often facilitated by punctures from

the sap sucking insect *Pseudotheraptus devastans*. The disease typically begins with rainfall and results in yield reductions and loss of planting material (IITA, 1990; Ikeh, 2017).

Cassava production in Nigeria and other parts of West Africa faces serious constraints from foliar diseases and insect pests that significantly reduce yield and planting material quality. Cercospora Leaf Spot (CLS) is one of the most widespread foliar diseases, comprising brown leaf spot, leaf blight, and white leaf spot. The most common form, brown leaf spot, is caused by *Cercosporidium henningsii* and is characterized by small circular lesions that expand, coalesce, and lead to premature defoliation. Yield losses are typically around 20% under moderate infection but can rise to 40% in severe outbreaks (IITA, 1990; da Costa *et al.,* 2020; FAO, 2023). Resistant cassava germplasm has been identified, and breeding programs in Nigeria and Brazil have reported promising lines with reduced susceptibility (Oliveira *et al.,* 2022).

The Cassava Mealybug (CMB) (*Phenacoccus manihoti*) is another major pest, feeding on phloem sap and primarily attacking terminal shoots. Infestation results in bunchy top symptoms, wilting, and defoliation, giving shoots a candle stick appearance. Disseminated by wind and infected cuttings, CMB is particularly prevalent during the dry season. Yield losses range from 20% to 80%, with severe infestations causing up to 80% crop loss in Africa (Udoh & Ndon, 2016). Mealybug attacks also weaken stem cuttings used for propagation, leading to poor quality planting material and reduced crop establishment.

The variegated Grasshopper (*Zonocerus variegatus*) is another major pest, feeding on cassava leaves, petioles, and stems. Infestations result in defoliation, die back, and sometimes plant death, with losses between 20% and 80% (Onwueme & Sinha, 1991; Udoh & Ndon, 2016). The Elegant Grasshopper, also Zonocerus variegatus, is especially damaging to seedlings, chewing leaves and stems, which can cause die back and poor crop establishment (Ikeh, 2017).

In addition, termites (*Nasutitermes* sp.) represent a significant pest problem in cassava growing regions. They attack newly planted stem cuttings and tunnel through the stem bases of older plants, leading to tuber rot and substantial yield losses (Udoh & Ndon, 2016).

The validation for this study lies in the urgent need to address these persistent threats through sustainable solutions. Resistant cassava genotypes represent the most reliable and cost effective strategy for long term management of pests and diseases. The aim of this research is therefore to evaluate the pest and disease status of improved cassava genotypes under Southeastern Nigerian agroecology, identifying resistant and susceptible lines to guide farmer adoption and breeding programs.

2. Materials

2.1 Experimental site and cropping history

The field experiment was carried out at GUS AGRO Farm in Ndikpaezeala, Umuowa-Ibu1 community, Okigwe, Imo State, Nigeria. Okigwe is located between latitudes 5°49' 45"N and longitudes 7° 21' 2" E. It has a mean annual range of rainfall of 2000 to 2500 mm; mean relative humidity of 79%; and mean temperature of 22.7 to 34°C. The area, which lies within the humid tropical rainforest zone of Nigeria, has two distinct seasons. The seasons are wet and dry. The wet season starts between March and April and lasts until October, with a brief break in August traditionally referred to as the “August Break”. The dry season begins in November and extends to February and late March.

The experimental site was previously cropped to fluted pumpkin, maize, and okra before it was fallowed for two years. The predominant weeds in the farmland before planting were *Chromolaena odorata*, *Pennisetum purpureum* (elephant grass), *Sida acuta*, *Centrosema pubescens*, *Calopogonium mucunoides*, and *Ageratum conyzoides*.

2.2 Experimental treatments and design

The eight cassava genotypes (sunshine, fine face, Dixon, poundable, TME 419, game changer, ayaya and Imo best) were appraised for pest and disease status in the high-humid agroecology of southeastern Nigeria.

2.3 Experimental plot size

The entire experimental area measured 60 meters by 40 meters, totaling 2,400 square meters. Each plot measured 8 meters by 8 meters, covering an area of 64 square meters. There were 8 plots in each replication, resulting in a total of 24 plots overall. The plots were separated by paths: a spacing of 1.5 meters between plots and 2 meters between replications. Each plot measuring 8 m × 8 m contained 80 stands. Each replication had 640 stands, and the total plant population across the entire experimental site was 1,920 stands.

2.4 Agronomic practices

i) Land preparation and planting: The experimental site was ploughed, harrowed and ridged with a tractor and marked out with measuring tapes, rope, and pegs.

ii) Planting was done on the crest of ridges, using 25cm stem cuttings long. Cutting was planting in an inclined position (45º) at 1.0 m x 0.8 m spacing.

iii) Fertilizer Application: Compound fertilizer, NPK (20:10:10) fertilizer was applied at rate of 400kg/ha at two (2) months after application (MAP). The ring method of application was used.

iv) Weeding: Manual weeding was carried out using a native weeding hoe at 1 and 3 MAP, while slashing was done at 5 MAP.

v)

2.5 Data collection and analysis

The following diseases: African cassava mosaic virus (ACMV), Cassava bacterial blight (CBB), Cassava anthracnose disease (CAD), and Brown leaf spot (BLS) were assessed for their severity at 2, 4, and 6 MAP using the scale of 1-5 (IITA, 1990) (In scale: 1 = No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe). The following pests were also assessed: Cassava green spider mite (CGSM), Cassava mealy bug (CMB), and variegated grasshopper. In scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

Disease and pest severity were assessed on a scale of 1–5 (IITA, 1990), thus the data were ordinal. The Shapiro-Wilk and Levene tests indicated that the data were not normally distributed and the variances were not homogeneous ($p < 0.001$), thus the ANOVA assumptions were not met. Therefore, differences between varieties were analyzed using the non-parametric Kruskal-Wallis test (Kruskal & Wallis, 1952), which is suitable for ordinal data and does not require the assumption of normality or homogeneity of variance. If the results were significant, the analysis was continued with the Dunn test (Dunn, 1964) with the Benjamini-Hochberg correction (Benjamini & Hochberg, 1995) to control for errors due to multiple comparisons. All tests were conducted at a significance level of 5%.

3. Results

3.1 African cassava mosaic virus severity as influenced by some improved cassava genotypes

The severity or resistance to African Cassava Mosaic Virus in the 4th and 6th months of 2024 and 2025 (Tabel 1), based on the Kruskel-Wallis test, was highly significant among varieties. The Dunn test with Benjamini-Hochberg correction showed that Sunshine, TME419, and Game Changer varieties had higher resistance than Fine Face, Dixon, Ayaya, and Poundable. Imo Best was the most susceptible.

Table 1. Comparison of african cassava mosaic virus (ACMV) severity of improved cassava genotypes

Cassava Genotypes	2024			2025		
	Months after Planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.33 ab	1.00 a	1.00 a	1.33 ab
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.33 ab	1.33 ab
Poundable	1.00 a	2.11 b	2.33 ab	1.00 a	2.00 ab	2.00 ab
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	2.00 ab	1.00 a	1.00 a	2.00 ab
Imo Best	1.00 a	3.33 b	3.33 b	3.00 b	3.00 b	4.00 b

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.2 Comparison of cassava anthracnose disease (CAD) severity as influenced by cassava genotypes

CAD severity as influenced by cassava genotype showed no significant difference ($p>0.05$) (Table 2). Cassava Anthracnose Disease (CAD) severity was not influenced by genotype ($p>0.05$). Across both seasons, all genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 weeks after planting, indicating no observable symptoms of CAD. The uniformity of results suggests either the absence of CAD pressure in the environment or broad tolerance among the tested genotypes. These findings highlight the stability of cassava performance under the prevailing conditions, though further evaluation under higher disease pressure is recommended to confirm genetic resistance.

Table 2. Comparison of cassava anthracnose disease (CAD) severity as influenced by cassava genotypes

Cassava Genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Poundable	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.3 Comparison of brown leaf spot (BLS) severity as influenced by cassava genotypes

Brown leaf spot (BLS) as influenced by cassava genotypes varied significantly ($p<0.05$) only at 4 and 6 MAP in both cropping seasons (Table 3). Brown Leaf Spot (BLS) severity varied significantly among cassava genotypes at 4 and 6 months after planting ($p<0.05$). Imo Best consistently recorded the highest severity (3.00 and 4.00), indicating high susceptibility. Dixon and Poundable showed slightly severe symptoms (2.00), while Fine Face, TME419, and Ayaya remained symptom-free across both seasons. The progression of BLS severity from 4 to 6 MAP suggests increased vulnerability with plant age. These findings highlight Imo Best as highly susceptible to BLS, whereas Fine Face, TME419, and Ayaya

demonstrate potential resistance, making them suitable candidates for breeding and farmer adoption in BLS-prone environments.

Table 3. Comparison of brown leaf spot (BLS) severity as influenced by cassava genotypes

Cassava genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	2.00 ab	2.00 ab	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	2.00 ab	2.00 ab	1.00 a	2.00 ab	2.00 ab
Poundable	1.00 a	2.00 ab	2.00 ab	1.00 a	2.00 ab	2.00 ab
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.33 ab	1.33 ab
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	3.00 b	4.00 b	1.00 a	3.00 b	4.00 b

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.4 Comparison of cassava bacterial blight disease severity as influenced by cassava genotypes

Cassava bacterial blight disease severity as influenced by cassava genotypes showed no significant difference in all the months under observation (Table 4). No severity of cassava bacterial diseases was recorded in all the cassava genotypes under investigation. Cassava Bacterial Blight (CBB) severity was not influenced by genotype ($p>0.05$). All genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 months after planting in both seasons, indicating no observable symptoms of CBB. The uniformity of results suggests either absence of CBB pressure in the environment or broad tolerance among the tested genotypes.

Table 4. Comparison of Cassava Bacterial Blight Disease Severity as Influenced by Cassava Genotypes

Cassava Genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Poundable	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.5 Comparison of cassava green spider mite (CGSM) severity as influenced by cassava genotypes

Cassava Green Spider Mite (CGSM) severity was not influenced by genotype ($p>0.05$). All genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 months after planting in both seasons, indicating no observable symptoms of CGSM. The uniformity of results suggests either the absence of CGSM pressure in the environment or broad tolerance among the tested genotypes. Further evaluation under higher pest pressure is recommended to confirm genetic resistance.

Table 5. Comparison of cassava green spider mite (CGSM) severity as influenced by cassava genotypes

Cassava Genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.33 a	1.00 a
Poundable	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.33 a

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.6 Comparison of severity of grasshopper attack as influenced by cassava genotypes

The severity of grasshopper attack on cassava as influenced by genotypes varied not significantly (P>0.05) at 2, 4, and 6 MAP (Table 6). Grasshopper attack severity was not influenced by genotype (p>0.05). All cassava genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 months after planting in both seasons, indicating no observable symptoms of grasshopper damage. The uniformity of results suggests either the absence of grasshopper pressure in the environment or broad tolerance among the tested genotypes. Further evaluation under higher pest pressure is recommended to confirm genetic resistance.

Table 6. Comparison of Severity of Grasshopper Attack as Influenced by Cassava Genotypes

Cassava Genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.33 a	1.00 a
Poundable	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

3.7 Comparison of severity of cassava mealybug (CMB) attack as influenced by cassava genotype

The severity of cassava mealybug (CMB) attack across eight improved cassava genotypes is presented in Table 7. In both 2024 and 2025, all cassava genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 weeks after planting. According to the adopted severity scale (1 = no symptom, 5 = very severe), this uniform score indicates complete absence of visible mealybug symptoms throughout the observation periods.

Table 7. Comparison of severity of cassava mealybug (CMB) attack as influenced by cassava genotype

Cassava Genotypes	2024			2025		
	Weeks after planting					
	2	4	6	2	4	6
Sunshine	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Fine face	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Dixon	1.00 a	1.00 a	1.00 a	1.00 a	1.33 a	1.00 a
Poundable	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
TME419	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Game Changer	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Ayaya	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a
Imo Best	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a	1.00 a

Means with the same letter are not significantly different according to Dunn test with Benjamini-Hochberg correction at $p \leq 0.05$. Scale: 1= No symptom, 2 = slightly sever, 3 = moderately severe, 4 = severe and 5 = very severe.

4. Discussion

The severity of African cassava mosaic virus (ACMV) was significantly influenced by cassava genotypes, with local varieties showing moderate to severe symptoms between 4–8 MAP, while improved morphotypes such as TME 419, Sunshine, and Game Changer exhibited complete resistance. This aligns with recent findings that the CMD2 gene confers durable resistance in West African cassava landraces (Sheat & Winter, 2023). Marker-assisted selection has further confirmed the genetic basis of resistance in African germplasm (Codjia *et al.,* 2022), while diversity studies emphasize the role of genotype in disease response (Sesay *et al.,* 2023). Advances in cassava genomics continue to strengthen breeding programs, ensuring resistant varieties like TME 419 remain central to sustainable cassava production (Ntui & Tripathi, 2023; NRCRI, 2024).

The results of this study revealed no significant differences in Cassava Anthracnose Disease (CAD) severity among the tested genotypes ($p > 0.05$). All genotypes consistently recorded a severity score of 1.00 across both seasons, indicating no observable symptoms of CAD. This uniformity suggests either an absence of CAD pressure in the trial environment or broad tolerance among the cassava lines. Similar outcomes have been reported in environments with low pathogen inoculum, where disease symptoms fail to manifest and genotypic variation remains undetectable (Nascimento *et al.,* 2024).

CAD, historically attributed to *Colletotrichum gloeosporioides f. sp. manihotis*, remains one of the most destructive diseases of cassava in humid regions. However, recent studies have demonstrated that CAD is not caused by a single pathogen species. Multiple *Colletotrichum* species, including *C. fructicola*, *C. siamense*, and *C. truncatum*, have been implicated in cassava anthracnose outbreaks, complicating resistance screening and management strategies (Machado *et al.,* 2021; Silva *et al.,* 2023; Aumentado & Balendres, 2025). This pathogen diversity means that genotypes appearing tolerant in one environment may succumb under different pathogen pressures, reinforcing the importance of multi-location trials.

Genetic studies further confirm that resistance to CAD is controlled by both additive and non-additive genetic effects, with general and specific combining ability contributing to resistance expression. Recent evaluations of cassava germplasm in Brazil and Nigeria have demonstrated phenotypic variability in resistance to CAD and other foliar diseases, underscoring the need for hotspot screening and controlled inoculation to validate resistance (Nascimento *et al.,* 2024; Oliveira *et al.,* 2025). Without such evaluations, breeding programs risk overestimating tolerance based on trials conducted under low disease pressure.

Beyond genetic resistance, emerging research highlights complementary strategies for CAD management. Cassava-associated endophytic bacteria have shown promise as biocontrol agents against

Colletotrichum species, offering an environmentally friendly alternative to chemical control (Owino *et al.,* 2026). Integrating such biocontrol approaches with genetic resistance could provide durable protection against CAD, particularly in regions where pathogen diversity undermines genetic resistance.

The study demonstrated that BLS severity varied significantly among cassava genotypes at 4 and 6 months after planting (MAP), highlighting the role of genotype in disease response. *Imo Best* consistently showed the highest severity scores (3.00–4.00), confirming its high susceptibility. In contrast, *Fine Face*, *TME419*, and *Ayaya* remained symptom-free, suggesting strong genetic resistance. This agrees with recent reports that cassava germplasm exhibits wide variability in foliar disease resistance, with certain improved lines showing complete tolerance under field conditions (Nascimento *et al.,* 2024).

The progression of BLS severity from 4 to 6 MAP indicates that disease intensity increases with plant age, likely due to canopy development and favorable microclimates for pathogen growth. Similar observations were made in multi-season trials in Southeastern Nigeria, where foliar diseases intensified as cassava matured (Baiyeri *et al.,* 2008).

The identification of resistant genotypes such as *TME419* and *Ayaya* is particularly significant for breeding programs and farmer adoption. These varieties can serve as sources of durable resistance, reducing reliance on chemical control. Recent evaluations of cassava germplasm in Brazil and Nigeria emphasize the importance of hotspot screening and multi-location trials to confirm resistance stability across environments (Oliveira *et al.,* 2025).

The results showed no significant differences in CBB severity among cassava genotypes ($p > 0.05$), with all lines recording a score of 1.00 at 2, 4, and 6 months after planting. This suggests either an absence of CBB inoculum in the environment or broad tolerance across the tested genotypes. Similar outcomes have been reported in Southeastern Nigeria, where cassava fields under low pathogen pressure exhibited negligible bacterial blight symptoms (Baiyeri *et al.,* 2008).

CBB, caused by *Xanthomonas axonopodis* pv. *manihotis*, remains a major constraint in humid cassava-growing regions. However, recent studies emphasize that disease severity is strongly influenced by environmental conditions, with resistant genotypes appearing symptom-free under low inoculum but showing variable responses under hotspot conditions (Nascimento *et al.,* 2024). The uniform tolerance observed in genotypes such as *TME419*, *Ayaya*, and *Fine Face* is encouraging, but multi-location trials and controlled inoculation are necessary to confirm durable resistance. Recent cassava improvement programs stress the importance of validating resistance stability across diverse agro-ecological zones to ensure reliable farmer adoption (Oliveira *et al.,* 2025).

The study revealed that CGSM severity was not influenced by cassava genotype ($p > 0.05$). All tested genotypes consistently recorded a severity score of 1.00 at 2, 4, and 6 months after planting across both seasons, indicating no observable symptoms of mite infestation. This uniformity suggests either an absence of CGSM pressure in the environment or broad tolerance among the cassava lines. Similar outcomes have been reported in Southeastern Nigeria, where cassava fields under low pest pressure showed negligible mite damage across diverse genotypes (Baiyeri *et al.,* 2008; Ikeh, 2017).

Although the cassava green spider mite (*Mononychellus tanajoa*) is a major pest in tropical cassava-growing regions, capable of causing severe yield losses under high infestation. However, recent studies emphasize that mite severity is strongly influenced by environmental conditions, with outbreaks more common in dry seasons and under stressed crop conditions (Yaninek & Herren, 2023). Improved genotypes such as *TME419* have been noted for their tolerance. The absence of symptoms across all genotypes in this study is encouraging, but multi-location trials under higher pest pressure are recommended to validate true genetic resistance. Recent cassava improvement programs highlight the importance of integrating resistant germplasm with biological control strategies (e.g., predatory mites) to ensure sustainable management of CGSM (Akinbo *et al.,* 2024).

4. Conclusion

The study shows that cassava genotype selection is crucial for effective disease management and yield stability. Significant differences were observed in the severity of ACMV and BLS among varieties, whereas other biotic stresses, such as CAD, CBB, cassava green spider mite, mealybug, and grasshopper attacks, showed no significant variation. Resistant genotypes, including Sunshine, Fine Face, Dixon, Poundable, TME419, Game Changer, and Ayaya, exhibited strong resistance to ACMV and BLS, making them promising candidates for adoption by farmers and breeding programs. Conversely, *Imo Best* consistently showed high susceptibility, with severe ACMV scores and pronounced vulnerability to BLS, underscoring the risks of cultivating it in disease-prone environments. The study recommends that multi-location trials under higher disease pressure be conducted to validate resistance stability and guide breeding programs.

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6. Conflict of Interest Declaration

The authors declare that there is no conflict of interest regarding the publication of this article. The Authors confirmed that the paper was free of plagiarism.

7. Author Contribution Statement

All authors contributed equally to the research, data analysis, and writing and preparation of this scientific article.

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