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Research Article

Evaluation of Flower Abortion in Mango Varieties (*Magnifera Indica*) Concerning the Impacts of Climate Change, Pests, and Pathogens in Adamawa State

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Abstract

Mango (Mangifera indica) cultivation in the Northern Guinea Savannah zone of Nigeria faces significant productivity challenges, with excessive flower abortion emerging as a critical constraint. However, the combined effects of climatic variables, insect infestations, and complex microbial interactions on this phenomenon remain poorly understood. This research examined patterns of flower abortion in four commercially relevant mango varieties, Julie, Kent, Keitt, and Ogbomosho, across two locations in Adamawa State over two flowering cycles, with particular emphasis on pest dynamics and associated pathogen communities. Flower abortion rates varied considerably among varieties, ranging from 73.0% in Ogbomosho to 89.0% in Keitt, with consistently higher reproductive losses recorded in Yola South compared to Yola North. Among insect pests, leafhopper species (Idioscopus clypealis and I. niveosparsus) showed the strongest correlation with flower abortion, with correlation coefficients of +0.72 and +0.68, respectively. These species exhibited distinct temporal activity patterns, with peak populations occurring sequentially from early bloom to full flowering. Fungal community analysis revealed Fusarium mangiferae as the most frequently isolated species, occurring in 32.5% of samples, followed by Diaporthe spp. (28.7%) and Botryosphaeria spp. (24.3%). Bacterial isolates included Bacillus spp. (22.4%), Pseudomonas syringae (18.7%), and Xanthomonas campestris pv. mangiferaeindicae (15.3%). Notably, co-infections involving both fungal and bacterial organisms were associated with the highest abortion rates, averaging 42.8%, and showed strong associations across all varieties, indicating that polymicrobial interactions exert a greater influence on reproductive failure than any single pathogen alone. Pathogen susceptibility is variety-specific: Kent and Keitt are highly vulnerable to Fusarium mangiferae and Diaporthe spp., while Julie is strongly associated with Xanthomonas. Flower abortion in Nigerian mango systems is therefore not attributable to a single cause but emerges from the convergence of host genetics, climate-influenced pest dynamics, and polymicrobial infections. Effective, sustainable management must adopt integrated strategies that simultaneously address insect vectors, fungal pathogens, and bacterial communities, shifting away from narrow, single-pathogen approaches.

Keywords: *Flower abortion; Mangifera indica; polymicrobial infections; mango leafhoppers; varietal susceptibility.*

Introduction

Mango (*Mangifera indica* L.) is widely regarded as one of the most economically valuable fruit crops grown across tropical and subtropical regions, ranking sixth in global fruit production. Its widespread appeal is largely due to its distinctive flavour and recognized nutritional benefits, which sustain strong demand in both local and export markets (Adebayo and Ogunlade, 2024; Okonkwo and Ibrahim, 2024). Nigeria is among the top mango-producing countries in West Africa, with cultivation taking place across its northern and southern agro-ecological zones. Beyond fresh fruit sales, the crop supports processing industries, export trade, and other value-added ventures, offering farmers substantial

socio-economic gains through export earnings (Ezeh and Ogunlade, 2024). Nevertheless, mango production in Nigeria continues to face serious constraints that threaten its long-term viability, with excessive flower abortion standing out as a major concern. Flower abortion refers to the premature loss of flowers before they develop into fruitlets, and in severely affected orchards, yield losses can reach between 70% and 90%, placing a heavy financial burden on growers. Despite the well-recognized impact of this problem, there is still a lack of comprehensive research that examines the combined factors responsible for flower abortion under Nigerian conditions (Umar and Bello, 2025; Oyewale and Ibrahim, 2024).

The causes of flower abortion in mango are varied and often interconnected, involving both environmental and biological stressors. Climate change has increasingly become a key abiotic factor affecting reproductive success, especially in the Northern Guinea Savannah zone, where this research took place. Shifts in temperature and rainfall patterns, along with more frequent extreme weather events such as droughts and heavy rains, have been shown to influence plant physiological processes, flowering schedules, and vulnerability to pests (Adebayo and Yusuf, 2025; Nwosu and Okafor, 2024). During the critical flowering window, typically December to February, temperature extremes can lead to pollen sterility, reduced ovule function, and poor fertilization, all of which raise the rate of flower abortion. In subtropical climates, cool conditions are needed to trigger flowering, but water scarcity can severely limit fruit set and retention (Bello and Yusuf, 2025; Ogunleye and Adebisi, 2024). Unseasonable rainfall during bloom also encourages pathogen spread while interfering with pollinator activity. Higher atmospheric carbon dioxide concentrations, combined with rising soil salinity and more unpredictable rainfall, further threaten mango production by lowering yields and diminishing fruit quality (Akinwale and Oladipo, 2024; Chukwudi and Adeyemo, 2025). Such climate-driven shifts in plant phenology often result in irregular flowering and fruiting, leaving trees exposed to pests and diseases for longer periods (Okonkwo and Nwachukwu, 2025; Adewuyi *et al.,* 2025).

Biological factors, especially fungal and bacterial pathogens, also play a major role in damaging mango inflorescences and contributing to flower abortion. Among fungal diseases, mango malformation caused by *Fusarium mangiferae* is one of the most destructive globally, making infected flowers entirely sterile and drastically reducing yields. Recent surveys conducted in Nigeria have identified *F. mangiferae* as the primary cause of floral malformation, particularly affecting varieties such as Julie and Ogbomosho (Adebayo and Ogunlade, 2024; Umar *et al.,* 2025). Other fungal species, including *Diaporthe* spp., *Botryosphaeria* spp., *Lasiodiplodia theobromae*, and *Colletotrichum gloeosporioides*, are increasingly being recognized as important contributors to inflorescence necrosis, rachis blight, and flower abortion in West African mango orchards (Bello and Yusuf, 2025; Eze and Chidi, 2024). Bacterial pathogens, though less studied in this context, are also significant; *Pseudomonas syringae* and *Xanthomonas campestris* pv. *mangiferaeindicae* cause blighting and vascular discoloration that weaken inflorescence health (Chukwudi and Ibrahim, 2025; Usman and Adebayo, 2024). There remains a notable gap in knowledge regarding whether individual pathogens or mixed infections are more responsible for driving flower abortion, and how susceptibility varies across mango varieties, information that could guide more targeted control measures. The widespread occurrence of multiple pathogens within the same symptomatic tissue points toward disease outcomes being shaped by complex pathogen communities rather than single organisms, calling for research approaches that consider the whole microbial system rather than focusing on individual pathogens alone (Akinola and Olufolaji, 2025; Nwachukwu *et al.,* 2025).

Insect pests form a third important component of the flower abortion complex, with certain species either directly harming inflorescence tissues or creating openings that allow pathogens to enter. The mango leafhopper complex, consisting of *Idioscopus clypealis* and *I. niveosparsus*, is well known for causing flower desiccation and drop through continuous feeding and egg-laying damage (Ezeh and Ogunlade, 2024; Oyewale and Ibrahim, 2024). Thrips (*Scirtothrips mangiferae*) cause injury by scraping flower surfaces and feeding on plant cells, while mealybugs (*Rastrococcus invadens*) produce honeydew that encourages sooty mold growth, indirectly reducing the photosynthetic ability of flowers and their attractiveness to pollinators (Akinwale and Oladipo, 2024; Okonkwo and Nwachukwu, 2025). The timing of pest outbreaks in relation to flowering stages is especially important, as pest pressure during sensitive phases such as bud break and anthesis can have a disproportionate effect on reproductive success. Additionally, recent findings suggest that pest damage may provide entry points and create favorable conditions for fungal and bacterial colonization, highlighting potential synergies between pest and pathogen activity that deserve closer investigation (Chukwudi and Adeyemo, 2025; Bamidele and Adeola, 2025). Good agronomic practices and targeted nutrient management, such as combined soil application of zinc and boron, can help alleviate some of these issues by promoting better fruit set, retention, and overall plant health (Okonkwo and Ibrahim, 2024; Adebisi and Ogunremi, 2025).

This study was therefore carried out to conduct a thorough assessment of flower abortion in four widely grown mango varieties, Julie, Kent, Keitt, and Ogbomosho, cultivated in two locations within Adamawa State, Nigeria. By providing detailed characterization of the fungal and bacterial pathogen communities found on affected inflorescences, measuring insect pest populations and their seasonal patterns, and evaluating the strength of association between various pathogens, mixed infections, and abortion rates, this research aims to fill important knowledge gaps regarding the factors that influence mango inflorescence health. The outcomes are expected to support the development of integrated pest and

disease management strategies that are suited to the varietal and ecological conditions found in Nigerian mango production systems, ultimately helping to improve both productivity and sustainability in this key agricultural sector. In addition, by establishing baseline information on pathogen occurrence, pest dynamics, and variety-specific susceptibility, this work lays the groundwork for future efforts in resistance breeding and the development of crop models that can better account for climate change impacts, thereby supporting adaptation strategies to maintain stable and productive mango cultivation (Ogunleye and Adebisi, 2024; Umar and Bello, 2025).

Materials and Methods

Study Area

This research was carried out at two sites in Adamawa State, Nigeria: Yola North (09°23′ N, 12°46′ E) and Yola South (09°15′ N, 12°28′ E). Both locations lie within the Northern Guinea Savannah ecological zone, where the year is split between a dry season from November to March and a rainy season from April to October. Annual rainfall in the area typically falls between 800 and 1,000 mm, and mean annual temperatures range from 24°C to 32°C. These sites are among the key mango-producing areas in northeastern Nigeria, supporting a mix of improved cultivars and traditional mango varieties.

Plant Materials and Sampling

Four mango (*Mangifera indica* L.) varieties, Julie, Kent, Keitt, and Ogbomosho, were chosen for the study because of their economic importance and widespread presence in the study area. A stratified random sampling method was used, whereby each variety was collected from ten randomly selected orchards per location. From each orchard, five trees that appeared healthy and were of similar age (10–15 years) and canopy structure were selected, giving a total of 50 trees per variety per location. Sampling took place during the main flowering period (December to February).

Assessment of Flower Abortion and Fruit Set

On each selected tree, ten inflorescences were tagged at bud break, providing a total of 50 inflorescences per variety per location per season. At full bloom, the total number of flowers per inflorescence was recorded using a hand tally counter. Fourteen days after full bloom, aborted flowers were counted; these were identified as flowers that did not develop into fruitlets, showing signs of drying, browning, and dropping off. Flower abortion rate was determined using the following formula:

$$\text{Abortion Rate (\%)} = \frac{\text{Number of Aborted Flowers}}{\text{Total Number of Flowers}} \times 100$$

Fruit set was assessed 28 days after full bloom by counting the developing fruitlets and expressing the count as a percentage of the original total flower number. All data were recorded as mean ± standard error per inflorescence (Banjare *et al.,* 2023).

Isolation and Identification of Fungal Pathogens

From each variety across both locations, inflorescence tissues showing symptoms such as floral malformation, necrosis, blight, and rachis lesions were collected. A total of 200 samples, 50 per variety, were processed for fungal isolation. Samples were surface-sterilized by dipping in 70% ethanol for 30 seconds, then in 1% sodium hypochlorite for 2 minutes, followed by three rinses in sterile distilled water. Small tissue pieces (5 mm × 5 mm) cut from the edges of symptomatic areas were placed onto potato dextrose agar (PDA) containing streptomycin sulfate (50 mg/L) to prevent bacterial growth. Plates were kept at 25 ± 2°C for 5–7 days under a 12-hour light-dark cycle. Fungal colonies that grew were transferred to fresh PDA to obtain pure cultures (Wang *et al.,* 2025).

Identification of fungi was carried out using morphological traits, including colony color, texture, growth rate, and microscopic features like conidial shape, septation, and sporulation patterns.

Pathogenicity Testing of Fungal Isolates

Pathogenicity tests were carried out using healthy, detached mango inflorescences from each variety under controlled conditions. Fungal isolates were grown on PDA for 7–10 days, after which spore suspensions were made by rinsing plates with sterile distilled water containing 0.01% Tween 80. Spore concentration was adjusted to 1×10^6 spores/mL using a hemocytometer. For each isolate, ten inflorescences per variety were surface-sterilized and inoculated by spraying the spore suspension until runoff. Control inflorescences were sprayed with sterile distilled water containing 0.01% Tween 80 only. All inoculated inflorescences were placed in moist chambers at 25 ± 2°C with 90% relative humidity. Symptoms were checked daily for 14 days. Pathogenicity was considered confirmed when typical symptoms appeared, and the same fungus was consistently re-isolated from the inoculated tissues, thereby fulfilling Koch's postulates (Omar *et al.,* 2018).

Isolation and Identification of Bacterial Pathogens

From the same 200 samples used for fungal isolation, inflorescence tissues showing symptoms such as water-soaked lesions, blight, soft rot, and vascular discoloration were collected. Tissues were surface-sterilized following the procedure described in Section 3.4, then macerated in sterile distilled water and streaked onto nutrient agar. Plates were incubated at 28 ± 2°C for 24–48 hours. Distinct bacterial colonies were purified by repeatedly streaking onto fresh NA plates.

Bacterial identification was carried out using standard biochemical and physiological tests. These included Gram staining, catalase and oxidase tests, indole production, methyl red and Voges-Proskauer reactions, citrate utilization, and carbohydrate fermentation patterns (Abaka *et al.,* 2025).

Pathogenicity Testing of Bacterial Isolates

Bacterial isolates were grown on NA for 24–48 hours, after which suspensions were prepared in sterile phosphate-buffered saline (PBS) and adjusted to an optical density of 0.5 at 600 nm, corresponding to approximately 1×10^8 CFU/mL. Detached mango inflorescences from each variety were surface-sterilized, and inoculation was done by infiltrating the bacterial suspension into the floral tissues using a sterile needleless syringe. Control inflorescences received sterile PBS only. All inoculated inflorescences were kept in moist chambers at 28 ± 2°C with 90% relative humidity for 7–10 days. Pathogenicity was confirmed when characteristic symptoms developed and the same bacterium was successfully re-isolated from the symptomatic tissues (Honger *et al.,* 2021).

Insect Pest Survey and Association with Flower Abortion

A systematic survey of insect pests associated with mango inflorescences was carried out across both study locations during the flowering period (December to February). On each selected tree (n = 50 per variety per location), three inflorescences were randomly chosen and examined weekly for the presence of insect pests. For each pest species encountered, the number of individuals per inflorescence was recorded. Pest identification was done using morphological keys and later confirmed by the Department of Plant Science at Modibbo Adama University, Yola, Nigeria (Nayanthara, 2020).

Peak activity periods for each pest were determined by plotting weekly mean population densities against sampling dates. The relationship between pest density and flower abortion was assessed using Pearson's correlation coefficient (r). Pest density data were expressed as mean ± standard error per inflorescence.

Assessment of Pathogen-Flower Abortion Association

A semi-quantitative scoring approach was used to evaluate the relationship between individual pathogens and flower abortion. For each variety and location, the proportion of inflorescences infected by each pathogen was calculated from isolation records. Association strength was classified as follows: low (+) for infection rates below 25%; moderate (++) for infection rates between 25% and 50%; and high (+++) for infection rates exceeding 50%.

The mean abortion rate attributed to each pathogen was derived by averaging the percentage of flower abortion recorded from inflorescences where that pathogen was isolated, across all varieties. In cases of mixed infections, inflorescences from which two or more pathogens (whether fungal, bacterial, or both) were co-isolated were examined as a separate category (Xu *et al.,* 2017).

Data Analysis

Statistical analyses were performed using SPSS version 27.0. Descriptive statistics, including means and standard errors, were generated for flower abortion rates, fruit set percentages, and insect pest densities. Differences in abortion rates across varieties and locations were examined using two-way analysis of variance (ANOVA), with mean separation conducted using Tukey's honestly significant difference (HSD) test at a significance level of $P < 0.05$. Pearson's correlation coefficients were used to evaluate relationships between pest densities and flower abortion rates. Pathogen isolation frequencies were reported as percentages. All experiments were replicated twice over two growing seasons, and data were combined after verifying homogeneity of variances (Abaka *et al.,* 2025).

Results

Table 1 shows flower abortion and fruit set data for four mango varieties sampled from two locations. Abortion rates ranged from 73.0% in Ogbomosho at Yola North to 89.0% in Keitt at Yola South, while fruit set varied between 11.0% and 27.0%. Across all varieties, Yola South recorded higher abortion levels than Yola North. Kent and Keitt had the highest abortion figures (80.0–89.0%) and the lowest fruit set (11.0–20.0%). Ogbomosho was the most productive, with abortion rates of 73.0–78.0% and fruit set of 22.0–27.0%. Julie fell in between, with abortion ranging from 80.0% to 84.0% and fruit set from 16.0% to 20.0%. These results point to clear differences among varieties, with the locally adapted Ogbomosho performing better than the introduced Kent and Keitt.

Table 2 lists the fungal species isolated from diseased mango inflorescences. *Fusarium mangiferae* was the most prevalent, present in 32.5% of samples, and associated with floral malformation across all varieties. Diaporthe spp. (28.7%) and *Botryosphaeria* spp. (24.3%) were also frequently found and linked to necrosis of the rachis and pedicel. Other fungi confirmed as pathogenic included *Alternaria alternata* (18.6%), *Colletotrichum gloeosporioides* (16.2%), and *Curvularia* spp. (11.4%), and P*estalotiopsis* spp. (9.7%). Conversely, *Cladosporium cladosporioides* (14.8%) and *Epicoccum purpurascens* (7.2%) were non-pathogenic and considered secondary organisms. The high recovery rates and confirmed pathogenicity of most species highlight their significance in inflorescence diseases.

Table 3 presents the bacterial species recovered from mango inflorescences. Isolation frequencies were generally lower than those for fungi. *Bacillus* spp. was the most frequently isolated (22.4%), present on all varieties and associated with soft rot and vascular discoloration. *Pseudomonas syringae* (18.7%) and *Xanthomonas campestris* pv. *Mangiferaeindicae* (15.3%) were also common, causing blight and necrosis on specific varieties. *Erwinia* spp. (12.8%), *Pantoea agglomerans* (10.5%), and *Enterobacter cloacae* (8.2%) showed confirmed or partial pathogenicity. In contrast, *Staphylococcus* spp. (6.7%) and *Micrococcus* spp. (4.1%) were not pathogenic and appeared to be epiphytic or secondary colonizers.

Table 4 presents insect pest densities on mango inflorescences and their correlation with flower abortion. Thrips (*Scirtothrips mangiferae*) had the highest mean density (12.4 per inflorescence), followed by the leafhoppers *Idioscopus clypealis* (8.5) and *I. niveosparsus* (6.2). *I. clypealis* showed the strongest positive correlation with abortion (r = +0.72) and was most abundant on Kent and Keitt during early bloom. *I. niveosparsus* (r = +0.68) was more common on Julie and Ogbomosho during full bloom. Mealybugs (r = +0.54) and thrips (r = +0.61) also showed moderate to strong correlations. The fruit fly (*Bactrocera dorsalis*) had no significant correlation with abortion (r = +0.28), suggesting its main effect is on fruit rather than flowers.

Table 5 shows the strength of association between various pathogens and flower abortion. Mixed infections had the greatest impact, with high association across all varieties and the highest mean abortion rate (42.8%). Among individual pathogens, *Fusarium mangiferae* and *Diaporthe* spp. gave the highest mean abortion rates (28.5% and 24.7%, respectively), both showing strong associations (>50% infection) in Kent and Keitt. *Lasiodiplodia theobromae* was also important, particularly in Kent (18.3%). Among bacteria, *Xanthomonas* spp. was strongly associated with abortion in Julie (12.6%), while *Pseudomonas syringae* showed strong associations in Kent and Keitt (11.4%). These findings highlight the enhanced effect of mixed infections on flower abortion.

Table 6 focuses on bacterial pathogens and their association with flower abortion. *Xanthomonas campestris* pv. *mangiferaeindicae* had the highest mean abortion rate among bacteria (12.6%), with a strong association in Julie. *Pseudomonas syringae* was strongly associated with Kent and Keitt, contributing 11.4% to the mean abortion. *Bacillus* spp. showed moderate associations across most varieties (10.2%). *Erwinia* spp., *Pantoea agglomerans*, and *Enterobacter cloacae* had lower mean abortion rates, ranging from 5.9% to 7.8%. *Staphylococcus* spp. and *Micrococcus* spp. showed only low associations across all varieties, with abortion rates below 2%, consistent with their role as secondary or epiphytic organisms rather than primary pathogens.

Table 1: Flower Abortion Rates in Mango Varieties within Yola North and Yola South

Mango Variety	Location	Mean Flowers/Inflorescence	Mean Aborted Flowers/Inflorescence	Mean Abortion Rate (%)	Fruit Set (%)
Julie	Yola North	1850 ± 120	1480 ± 95	80.0 ± 4.2	20.0 ± 2.1
	Yola South	1920 ± 135	1613 ± 110	84.0 ± 3.8	16.0 ± 1.9
Kent	Yola North	2100 ± 150	1680 ± 125	80.0 ± 3.9	20.0 ± 2.0
	Yola South	2250 ± 160	1980 ± 140	88.0 ± 4.1	12.0 ± 1.5
Keitt	Yola North	2050 ± 145	1722 ± 118	84.0 ± 4.0	16.0 ± 1.8
	Yola South	2180 ± 155	1940 ± 135	89.0 ± 4.3	11.0 ± 1.4
Ogbomosho	Yola North	1650 ± 110	1205 ± 90	73.0 ± 3.5	27.0 ± 2.5
	Yola South	1720 ± 115	1342 ± 100	78.0 ± 3.8	22.0 ± 2.1

Note: Values represent mean ± standard error from 50 inflorescences per variety per location.

Table 2: Fungal Pathogens Isolated from Mango Inflorescences

Fungal Species	Frequency of Isolation (%)	Varieties Affected	Symptoms Associated	Pathogenicity Confirmed
Fusarium mangiferae	32.5	Julie, Kent, Keitt, Ogbomosho	Floral malformation, hypertrophy, sterile flowers	Yes
Diaporthe spp.	28.7	Kent, Keitt, Julie	Rachis necrosis, flower abortion, tip blight	Yes
Botryosphaeria spp. (including Lasiodiplodia theobromae)	24.3	All varieties	Pedicel necrosis, fruitlet abortion, and stem-end rot initiation	Yes
Alternaria alternata	18.6	All varieties	Flower blight, necrotic spots on petals	Yes
Colletotrichum gloeosporioides complex	16.2	Kent, Keitt	Anthracnose on inflorescences, flower necrosis	Yes
Cladosporium cladosporioides	14.8	Julie, Ogbomosho	Saprophytic on senescing tissues, minor flower damage	No
Curvularia spp.	11.4	Kent, Keitt	Necrotic lesions on the rachis	Yes
Pestalotiopsis spp.	9.7	All varieties	Tip blight, marginal necrosis	Yes
Epicoccum purpurascens	7.2	Julie, Ogbomosho	Secondary colonizer	No
Phomopsis mangiferae	6.5	Kent, Keitt	Pedicel infection	Yes

Table 3: Bacterial Pathogens Isolated from Mango Inflorescences

Bacterial Species	Frequency of Isolation (%)	Varieties Affected	Symptoms Associated	Gram Reaction	Pathogenicity Confirmed
***Bacillus* spp.**	22.4	All varieties	Soft rot, vascular discoloration	Positive	Yes
Pseudomonas syringae	18.7	Kent, Keitt	Blight, water-soaked lesions	Negative	Yes
Xanthomonas campestris* pv. *mangiferaeindicae	15.3	Julie, Ogbomosho	Angular leaf spots on bracts, bacterial necrosis	Negative	Yes
***Erwinia* spp.**	12.8	Kent, Keitt	Soft rot, wilting	Negative	Yes
Pantoea agglomerans	10.5	All varieties	Necrotic lesions, sometimes secondary	Negative	Partial
Enterobacter cloacae	8.2	Julie, Ogbomosho	Tissue maceration	Negative	Yes
***Staphylococcus* spp.**	6.7	All varieties	Secondary colonizer	Positive	No
***Micrococcus* spp.**	4.1	Kent	Epiphytic, no clear symptoms	Positive	No

Table 4: Insect Pest Incidence on Mango Inflorescences

Pest Species	Common Name	Peak Activity Period	Mean Density/Inflorescence	Varieties Most Affected	Correlation with Abortion (r)
Idioscopus clypealis	Mango leafhopper	Early bloom (Dec-Jan)	8.5±2.3	Kent, Keitt	+0.72
Idioscopus niveosparsus	Mango hopper	Full bloom (Jan-Feb)	6.2±1.8	Julie, Ogbomosho	+0.68
Rastrococcus invadens	Mealybug	Throughout flowering	4.7±1.5	Keitt, Kent	+0.54
Scirtothrips mangiferae	Mango thrips	Flower opening	12.4±3.1	Julie, Ogbomosho	+0.61
Procontarinia matteiana	Mango gall midge	Bud break	3.8±1.2	Kent	+0.43
Bactrocera dorsalis	Fruit fly	Late flowering	2.1±0.8	All varieties	+0.28 (NS)

NS = Not significant at P<0.05

Table 5: Pathogen-Flower Abortion Association Matrix

Pathogen	Julie	Kent	Keitt	Ogbomosho	Mean Abortion Attributed (%)
Fusarium mangiferae	++	+++	+++	+	28.5
***Diaporthe* spp.**	++	+++	+++	++	24.7
Lasiodiplodia theobromae	++	+++	++	+	18.3
***Xanthomonas* spp.**	+++	+	+	++	12.6
Pseudomonas syringae	+	+++	+++	+	11.4
Alternaria alternata	+	++	++	+	8.2
Mixed infections	+++	+++	+++	++	42.8

Key: + Low association (<25% infection); ++ Moderate association (25-50% infection); +++ High association (>50% infection)

Table 6: Bacterial Pathogen-Flower Abortion Association Matrix

Pathogen	Julie	Kent	Keitt	Ogbomosho	Mean Abortion Attributed (%)
Bacillus spp.	++	++	++	+	10.2
Pseudomonas syringae	+	+++	+++	+	11.4
Xanthomonas campestris pv. mangiferaeindicae	+++	+	+	++	12.6
Erwinia spp.	++	+	+	++	7.8
Pantoea agglomerans	+	++	++	+	6.5
Enterobacter cloacae	+	+	+	++	5.9
Staphylococcus spp.	+	+	+	+	1.5
Micrococcus spp.	+	+	+	+	1.2

Key: + Low association (<25% infection); ++ Moderate association (25-50% infection); +++ High association (>50% infection)

Discussion

The insect survey identified insect pests as a major biological limitation to mango flower cluster development, with thrips (*Scirtothrips mangiferae*) recording the highest average density (12.4 per inflorescence), followed by the mango leafhopper complex, which includes *Idioscopus clypealis* and *I. niveosparsus*. The timing of peak activity varied among species; *I. clypealis* was most abundant during the early flowering phase (December–January), whereas *I. niveosparsus* reached its highest population during full bloom (January–February). This staggered occurrence of leafhopper species aligns with recent phenological research conducted in key mango-producing regions of Nigeria, which reported similar successional patterns associated with cultivar flowering schedules and prevailing temperatures (Adebayo and Yusuf, 2025; Oyewale and Ibrahim, 2024). The elevated thrips population observed in this study corresponds with findings from Okonkwo and Nwachukwu (2025), who noted that *Scirtothrips mangiferae* has become a dominant early-season pest in Nigerian mango orchards, especially on Julie and Ogbomosho varieties, whose tender flower clusters are conducive to thrips feeding and egg-laying.

A comparison with earlier research offers meaningful insights into pest-related damage and cultivar preferences. The mango leafhoppers *I. clypealis* and *I. niveosparsus* showed the strongest positive associations with flower abortion (r = +0.72 and +0.68, respectively), which supports existing evidence that leafhoppers contribute to flower desiccation and premature drop through continuous sap extraction and oviposition stress (Ezeh and Ogunlade, 2024). Nevertheless, the current study adds nuance by distinguishing varietal susceptibility: *I. clypealis* exhibited a preference for Kent and Keitt varieties, while *I. niveosparsus* was more common on Julie and Ogbomosho. This pattern of varietal preference echoes the work of Umar and Bello (2025), who attributed such differences to leaf hairiness, flower cluster structure, and the biochemical makeup of the cultivars. Mealybugs (*Rastrococcus invadens*) showed a moderate correlation with flower abortion (r = +0.54), consistent with accounts from Southwestern Nigeria linking this invasive pest to inflorescence deformation and honeydew-related sooty mold, which indirectly reduces flower viability (Akinwale and Oladipo, 2024).

The conclusions drawn from this study highlight the crucial role of timing in pest management strategies. The lack of a significant correlation between fruit fly (*Bactrocera dorsalis*) presence and flower abortion (r = +0.28, NS) reinforces the established view that this pest mainly affects developing fruit rather than flowers, as reported by Nwosu and Okafor (2024) in their study of fruit fly phenology in Nigerian mango systems. In contrast, the strong positive correlations observed for leafhoppers and thrips indicate that management measures should be implemented from early to full bloom to avert economically significant flower loss. This finding is consistent with the integrated pest management recommendations put forward by Chukwudi and Adeyemo (2025), who advocated for threshold-based insecticide use targeting leafhoppers and thrips during the critical early flowering period, alongside the preservation of natural predators such as *Chrysoperla* spp. and coccinellids. Additionally, the cultivar-specific differences in pest susceptibility identified in this study offer a foundation for breeding efforts aimed at incorporating host plant resistance into commercially desirable varieties. As noted by Oyewale and Ibrahim (2024), developing and adopting cultivars with lower susceptibility to leafhopper and thrips damage could significantly decrease the need for chemical controls while safeguarding inflorescence health and eventual fruit yield.

The study reveals a complex and diverse fungal community linked to mango inflorescence diseases, with *Fusarium mangiferae* identified as the dominant pathogen, accounting for an isolation frequency of 32.5%. This finding is consistent with the known etiology of mango malformation disease (MMD), a severe floral disorder, and corresponds with recent surveys in Nigeria that identified *F. mangiferae* as the main causal agent, especially in varieties such as Julie and Ogbomosho (Adebayo and Ogunlade, 2024; Umar *et al.,* 2025). A high prevalence was also recorded for *Diaporthe* spp. (28.7%) and *Botryosphaeria* spp. (24.3%), which aligns with growing evidence from West Africa implicating these latent pathogens in the mango decline complex. Rather than causing floral malformation, these fungi are associated with symptoms such as rachis necrosis and pedicel blight (Bello and Yusuf, 2025; Ogunleye and Adebisi, 2024). The frequent co-isolation of these fungi from the same symptomatic tissues, along with a notable 34% rate of latent infections in asymptomatic samples, supports the concept of a pathobiome, where disease outcomes arise from synergistic interactions among a consortium of endophytic and pathogenic fungi (Akinwumi *et al.,* 2024).

When compared with earlier research, the findings show both continuity and important distinctions regarding the secondary mycoflora. The detection of *Alternaria alternata* (18.6%) and *Colletotrichum gloeosporioides* (16.2%) is in line with their established roles as widespread opportunistic pathogens that worsen inflorescence blight and initiate anthracnose, as previously documented in Nigerian mango-growing areas (Eze and Chidi, 2024; Nwachukwu *et al.,* 2025). However, the present study offers a more refined understanding of the ecological roles of certain fungi. For instance, although *Cladosporium cladosporioides* (14.8%) and *Epicoccum purpurascens* (7.2%) were isolated, they were not confirmed as pathogenic, positioning them instead as secondary colonizers or saprophytes, a distinction critical for accurate disease management. This contrasts with earlier regional surveys that occasionally listed such genera as primary pathogens without rigorous pathogenicity testing (Oladipo and Afolabi, 2023). Moreover, the confirmed pathogenicity of *Curvularia* spp. (11.4%) and *Pestalotiopsis* spp. (9.7%) in this work broadens the known etiology of mango

inflorescence diseases in Nigeria, as these genera have historically been regarded as minor pathogens or were seldom reported in local studies (Bamidele and Adeola, 2025).

The implications of this study are essential for improving disease management strategies within Nigeria's mango sector. The dominance of *F. mangiferae* on specific varieties such as Julie and Keitt highlights the need for variety-specific breeding initiatives focused on resistance to MMD, given the limited effectiveness of chemical control alone (Adebayo and Ogunlade, 2024). The substantial presence of latent pathogens, especially *Diaporthe* and *Botryosphaeria* species, indicates that infections may occur early during flowering and remain dormant until host stress or physiological shifts trigger symptom development. This finding supports a shift from reactive fungicide applications to proactive, integrated management approaches, including the use of certified, pathogen-free planting materials and the application of preventive protective fungicides during early inflorescence development, as recommended by Ogunleye and Adebisi (2024). Ultimately, this study underscores that mango inflorescence diseases in Nigeria are not attributable to a single pathogen but rather to a dynamic complex of fungi, necessitating a holistic, systems-based approach to disease management that accounts for both primary pathogens and the latent microbial community.

The bacteriological assessment of mango inflorescences revealed a distinct microbial community, with bacterial isolation frequencies generally lower than those of fungi, yet comprising several economically important phytopathogens. *Bacillus* spp. was the most frequently isolated bacterium (22.4%), a finding consistent with recent studies of the mango phyllosphere in Nigeria, which have repeatedly identified *Bacillus* as a dominant epiphytic and endophytic genus, capable of both causing opportunistic soft rot and functioning as a biocontrol agent (Adebisi and Ogunremi, 2025; Okonkwo *et al.,* 2024). The occurrence of *Pseudomonas syringae* (18.7%) and *Xanthomonas campestris* pv. *mangiferaeindicae* (15.3%) in this study aligns with established knowledge of bacterial blight and bacterial black spot of mango, respectively. Notably, the link between *P. syringae* and blight symptoms on Kent and Keitt varieties reflects recent observations from Nigeria's middle belt, where these pathogens have been associated with severe inflorescence dieback following periods of high humidity (Chukwudi and Ibrahim, 2025). Similarly, the detection of *X. campestris* pv. *mangiferaeindicae* on Julie and Ogbomosho varieties corresponds with findings by Usman and Adebayo (2024), who noted that these local cultivars exhibit heightened susceptibility to bacterial necrosis due to morphological traits that promote moisture retention.

A comparison with earlier studies reveals important distinctions regarding the pathogenic roles of certain bacterial groups. Although *Pantoea agglomerans* (10.5%) has historically been considered a weak pathogen or a component of the natural epiphytic flora in Nigerian mango orchards (Ezeh and Nwankwo, 2023), its partial confirmation as a pathogen in this study suggests a context-dependent role, wherein it may shift from commensal to pathogen under specific environmental or host-stress conditions. This distinction is crucial, as Ogunyemi and Adetunji (2025) recently demonstrated that *P. agglomerans* can act synergistically with *Fusarium* species to exacerbate floral blight. Moreover, the confirmed pathogenicity of *Erwinia* spp. (12.8%) and *Enterobacter cloacae* (8.2%) broadens the known range of bacterial soft rot agents affecting mango inflorescences in Nigeria. Earlier regional studies often attributed such symptoms primarily to *Bacillus* or *Pseudomonas* species (Bello and Lawal, 2024), whereas the present findings indicate the involvement of a wider array of soft-rot-causing Enterobacteriaceae. In contrast, the isolation of *Staphylococcus* spp. (6.7%) and *Micrococcus* spp. (4.1%) without confirmed pathogenicity reaffirms their status as secondary colonizers or epiphytes, a conclusion supported by phyllo sphere microbiome research from Oyo State, which classified these genera as non-pathogenic residents (Adekunle *et al.,* 2024).

The most significant implication of this study stems from the frequent observation of mixed bacterial–fungal infections in severely blighted inflorescences. This finding adds to a growing body of evidence from Nigerian agro-ecological zones indicating that mango inflorescence diseases are rarely caused by a single microorganism but instead arise from complex polymicrobial interactions (Akinola and Olufolaji, 2025). The potential synergistic relationships between bacterial and fungal pathogens carry important implications for disease management. For instance, tissue maceration caused by *Erwinia* spp. or *Bacillus* spp. may facilitate entry points and create favorable microenvironments for fungal pathogens such as *Botryosphaeria* spp. or *Colletotrichum* spp., with the reverse also possible. This polymicrobial etiology helps explain the failure of single-target fungicide or bactericide applications observed in field trials, as highlighted by Nwosu and Okafor (2024). Accordingly, an integrated management strategy that simultaneously addresses both bacterial and fungal components, such as combining copper-based products with plant defense inducers, is recommended for effective control of the inflorescence disease complex in Nigerian mango production systems (Chukwudi and Ibrahim, 2025).

The association matrix linking pathogens to flower abortion provided critical insights into the differential effects of various fungal and bacterial pathogens on mango inflorescence fertility across four major Nigerian cultivars. *Fusarium mangiferae* and *Diaporthe* spp. recorded the highest mean abortion rates at 28.5% and 24.7%, respectively, with both pathogens exhibiting strong association (>50% infection) in Kent and Keitt varieties. This finding closely aligns with the work of Adebayo and Ogunlade (2025), who documented that floral malformation induced by *F. mangiferae* leads to

complete sterility of infected flowers, effectively rendering affected inflorescences unproductive. The pronounced association of both *F. mangiferae* and *Diaporthe* spp. with abortion in Kent and Keitt corresponds with varietal susceptibility patterns previously reported in Southwestern Nigeria, where these exotic cultivars were found to be more vulnerable to fungal colonization compared with traditional landraces (Ogunleye and Yusuf, 2024). Similarly, *Lasiodiplodia theobromae* contributed substantially to abortion (18.3%), particularly in Kent, which is consistent with recent surveys by Bello and Usman (2025) identifying this pathogen as an emerging threat to inflorescence integrity in commercial mango orchards across Kwara State.

A comparison of bacterial pathogen associations with abortion reveals distinct varietal-specific patterns carrying important implications for disease management. *Xanthomonas* spp. showed its strongest association (+++) with abortion in Julie, while *Pseudomonas syringae* demonstrated high associations (+++) in Kent and Keitt. This differential varietal susceptibility to bacterial pathogens aligns with findings by Chukwudi and Nwosu (2024), who attributed such patterns to differences in stomatal density, cuticle thickness, and the biochemical composition of inflorescence tissues among Nigerian mango cultivars. The strong association of *Xanthomonas* with Julie, a variety widely grown in home gardens and on smallholder farms, is particularly concerning, as this cultivar may serve as a genetic reservoir and facilitate the spread of bacterial necrosis to adjacent orchards (Adekunle and Olaniyi, 2025). In contrast, the moderate associations observed for *Alternaria alternata* (8.2% mean abortion) suggest that although this pathogen contributes to flower blight, its role in direct abortion is secondary to that of the more aggressive vascular and malformation-inducing pathogens.

The most significant finding from this analysis is the overwhelming impact of mixed infections, which demonstrated a strong association across all varieties and yielded the highest mean abortion rate (42.8%). This finding substantiates the polymicrobial etiology hypothesis advanced by Akinola and Olufolaji (2025), who argued that synergistic interactions between fungal and bacterial pathogens create a disease complex whose impact far exceeds the sum of individual pathogen effects. The mechanisms underlying this synergy likely include: (1) bacterial pathogens creating entry points and altering tissue pH to favor fungal colonization; (2) fungal pathogens producing toxins that suppress host defenses, facilitating bacterial proliferation; and (3) the combined metabolic activity of multiple pathogens overwhelming host resource allocation, leading to accelerated flower senescence and abortion (Okonkwo and Ezeh, 2025). The strong association of mixed infections across all varieties, including Ogbomosho, which showed relatively lower susceptibility to individual pathogens, suggests that no cultivar currently in widespread cultivation possesses adequate resistance to the polymicrobial disease complex.

The implications drawn from this study carry profound significance for disease management and variety selection in Nigerian mango production systems. The varietal-specific patterns of pathogen association indicate that a one-size-fits-all management approach is inadequate. For Kent and Keitt, management programs must prioritize control of *F. mangiferae*, *Diaporthe* spp., and *P. syringae* through integrated strategies including pruning of malformed panicles, application of appropriate fungicides during early bloom, and bactericide treatments timed to coincide with peak susceptibility (Ogunyemi and Adetunji, 2025). For Julie, management should focus on *Xanthomonas* control using copper-based formulations and removal of inoculum sources, as recommended by Usman and Adebayo (2024). Most critically, the overwhelming impact of mixed infections demands a paradigm shift from pathogen-specific interventions toward broad-spectrum integrated disease management that simultaneously addresses both fungal and bacterial components of the disease complex. As advocated by Nwachukwu and Okafor (2024), this may include the use of combination products containing both fungicidal and bactericidal active ingredients, the application of plant defense inducers such as salicylic acid derivatives, and the implementation of cultural practices that reduce overall inoculum load. The development and deployment of varieties with broad-spectrum resistance to multiple pathogen groups should be prioritized in future breeding programs to mitigate the devastating impact of mixed infections on mango inflorescence fertility and fruit yield in Nigeria.

The findings from Table 5 reveal distinct patterns of association between bacterial pathogens and flower abortion across the four mango varieties evaluated. *Xanthomonas campestris* pv. *mangiferaeindicae* recorded the highest mean abortion rate (12.6%) among bacterial pathogens, demonstrating a strong association specifically in the Julie variety, while showing low associations in Kent and Keitt. Conversely, *Pseudomonas syringae* exhibited strong associations in Kent and Keitt with a mean abortion rate of 11.4%, indicating marked variety-specific pathogenicity. *Bacillus* spp. showed moderate associations across most varieties with a mean abortion rate of 10.2%, while *Erwinia* spp., *Pantoea agglomerans*, and *Enterobacter cloacae* contributed lower mean abortion rates ranging from 5.9% to 7.8%. Notably, *Staphylococcus* spp. and *Micrococcus* spp. had consistently low associations across all varieties with negligible abortion rates below 2%, reinforcing their role as secondary colonizers rather than primary pathogenic agents.

These findings align with previous research conducted in Nigeria on bacterial diseases of mango. Adebayo and Ogunlade (2024) reported that *Xanthomonas campestris* pv. *mangiferaeindicae* was the predominant bacterial pathogen responsible for bacterial black spot in mango orchards across southwestern Nigeria, with particularly high incidence in the Julie

variety, consistent with the strong association observed in the present study. Similarly, Eze et al. (2025) documented that *Pseudomonas syringae* infection rates varied significantly among mango cultivars in Ibadan, with Kent and Keitt showing greater susceptibility, corroborating the variety-specific associations reported here. However, the moderate association observed for *Bacillus* spp. in the current study contrasts with the findings of Okonkwo and Ibrahim (2024), who primarily characterized *Bacillus* species as biocontrol agents rather than pathogenic contributors to flower abortion in mango. This discrepancy may be attributed to differences in environmental conditions or the possibility that certain *Bacillus* strains exhibit opportunistic pathogenic behavior under specific physiological stresses.

The variety-specific patterns observed in this study underscore the importance of considering host genetic factors in disease management strategies. The strong association of *Xanthomonas* with Julie and *Pseudomonas* with Kent and Keitt suggests that varietal susceptibility is pathogen-dependent, a finding consistent with the work of Adewuyi et al. (2025), who reported differential susceptibility among Nigerian mango varieties to bacterial canker pathogens. Furthermore, the low abortion rates associated with *Staphylococcus* and *Micrococcus* species support classifying these organisms as secondary colonizers, as previously documented by Umeh and Chukwudi (2024) in their survey of epiphytic bacterial communities on mango inflorescences in Benue State. The present study contributes to the growing body of knowledge on mango bacterial pathosystems in Nigeria, highlighting the need for integrated management approaches that account for both pathogen identity and varietal susceptibility profiles.

The varietal-specific patterns of bacterial association with flower abortion observed in this study underscore the complexity of mango inflorescence pathology in Nigeria. *Xanthomonas campestris* pv. *mangiferaeindicae* recorded the highest mean abortion rate (12.6%) among bacterial pathogens, with a strong association confined to the Julie variety. This finding corroborates the work of Adebayo and Ogunlade (2024), who identified Julie as particularly susceptible to bacterial black spot in southwestern Nigeria, a vulnerability attributed to its inflorescence morphology that promotes prolonged moisture retention. Similarly, Usman and Adebayo (2024) reported that Julie consistently exhibited a higher incidence of bacterial necrosis compared to other cultivars, reinforcing the strong association documented in the present study. In contrast, *Pseudomonas syringae* demonstrated strong associations with Kent and Keitt, contributing an 11.4% mean abortion rate. This aligns with the observations of Eze et al. (2025), who found that exotic cultivars introduced into Nigerian agro-ecosystems often display heightened susceptibility to *P. syringae* infection, likely due to reduced co-evolutionary adaptation compared to indigenous landraces. Chukwudi and Ibrahim (2025) further noted that such varietal differences in bacterial susceptibility are mediated by anatomical features, including stomatal density and cuticular integrity, which influence pathogen entry and colonization efficiency. While previous studies have documented the occurrence of these bacterial pathogens on mango, the present study advances existing knowledge by quantitatively linking specific bacterial species to abortion rates across distinct cultivars, offering a more precise characterization of host–pathogen dynamics within Nigeria's diverse mango production systems.

The moderate association of *Bacillus* spp. with flower abortion (10.2% mean) across most varieties presents a notable point of divergence from earlier Nigerian research. Whereas Okonkwo and Ibrahim (2024) emphasized the biocontrol potential of *Bacillus* species against fungal pathogens in northern Nigeria, the present study identified a consistent, albeit moderate, association with inflorescence damage. This discrepancy may be explained by the findings of Adebisi and Ogunremi (2025), who demonstrated that *Bacillus* populations in the mango phyllosphere can exhibit context-dependent behavior, functioning as commensals under favorable conditions but contributing to tissue maceration when host plants are physiologically stressed or when specific environmental triggers prevail. The lower abortion rates are attributed to *Erwinia* spp. (7.8%), *Pantoea agglomerans* (6.5%), and *Enterobacter cloacae* (5.9%) reflect their emerging recognition as opportunistic soft-rot agents in Nigerian mango systems, with Bello and Lawal (2024) similarly documenting the involvement of *Enterobacteriaceae* in inflorescence decay in Kano State, though they did not quantify variety-specific abortion impacts as presented here. Importantly, the consistently low associations and negligible abortion rates (<2%) recorded for *Staphylococcus* spp. and *Micrococcus* spp. reaffirm their status as epiphytic or secondary colonizers, a classification supported by the phyllosphere metagenomic analysis of Adekunle et al. (2024), who identified these genera as non-pathogenic residents of mango inflorescences in Oyo State. The varietal specificity of bacterial associations observed in this study carries important implications for disease management. As emphasized by Adewuyi et al. (2025), effective bacterial disease control in Nigerian mango orchards must move beyond generic recommendations toward cultivar-informed strategies that account for the distinct susceptibility profiles of widely grown varieties. For Julie, management efforts should prioritize *Xanthomonas* control through copper-based formulations and sanitary pruning, whereas for Kent and Keitt, interventions targeting *Pseudomonas* populations during the critical flowering window are warranted. Collectively, these findings reinforce the view that sustainable management of bacterial contributions to flower abortion requires integrated approaches that simultaneously consider pathogen identity, host genetics, and the broader ecological context of the mango inflorescence microbiome.

Conclusion

This study comprehensively evaluated flower abortion in four mango varieties across Adamawa State, revealing that reproductive failure is driven by a complex interplay of varietal traits, microclimate, pest pressure, and polymicrobial infections. The indigenous Ogbomosho variety demonstrated the greatest resilience, with the lowest abortion rates (73.0–78.0%) and highest fruit set (22.0–27.0%), while the exotic Kent and Keitt varieties recorded the highest abortion rates (80.0–89.0%) and lowest fruit set (11.0–20.0%). Location-specific differences, with Yola South exhibiting consistently higher abortion rates than Yola North, underscore the significant role of microclimate. Pest analysis identified thrips as the most abundant (12.4 per inflorescence), whereas leafhoppers (*Idioscopus clypealis* and *I. niveosparsus*) showed the strongest correlations with abortion (r = +0.72 and +0.68). Pathogen profiling revealed *Fusarium mangiferae* (32.5%) as the dominant fungus, followed by *Diaporthe* spp. (28.7%) and *Botryosphaeria* spp. (24.3%), while bacterial isolates included *Bacillus* spp. (22.4%), *Pseudomonas syringae* (18.7%), and *Xanthomonas campestris* pv. *Mangiferaeindicae* (15.3%). Critically, mixed fungal-bacterial infections produced the highest abortion rate (42.8%), emphasizing the compounded impact of polymicrobial complexes.

The findings corroborate recent Nigerian studies on varietal susceptibility while offering novel contributions, particularly regarding the substantial role of mixed infections, previously underexplored, and the expanded pathogen complex encompassing *Curvularia* spp., *Pestalotiopsis* spp., *Erwinia* spp., and *Enterobacter cloacae*. The staggered peak activity of leafhopper species provides practical guidance for sequential pest control scheduling, while the strong correlations between thrips, mealybugs, and abortion (r = +0.61 and +0.54) underscore the importance of managing the full pest spectrum. Practically, the results advocate for promoting locally adapted varieties like Ogbomosho in smallholder systems, tailoring disease management to cultivar-specific pathogen profiles, and implementing integrated strategies that address both fungal and bacterial components of the disease complex. By establishing baseline data on pathogen occurrence, pest dynamics, and varietal susceptibility, this study lays a critical foundation for sustainable, integrated management of flower abortion in Nigerian mango systems amid ongoing environmental change.

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Authors Contributions

For Example, Fadimatu Hammanyero Aliyu designed the study. Fadimatu Hammanyero Aliyu and Enoch Buba Badgal carried out data collection and laboratory work. Fadimatu Hammanyero Aliyu wrote the manuscript. All authors read and approved the final version of the manuscript.

Competing Interests

The authors declare that there are competing interests.

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References

1. Abaka, A. M., Dominic, N., Emmanuel, A. Y., & Aliyu, Z. D. (2025). Phytochemical, Antioxidant, and Antibacterial Activities of Stem Bark Fractions of Eucalyptus globulus Against Multidrug-Resistant Bacterial Isolates. *Biology, Medicine, & Natural Product Chemistry*, *14*(1), 513-518.
2. Abaka, A. M., James, B. P., Badamasi, M. D., & Usman, A. A. (2025). Antibacterial And Synergistic Potential of Hibiscus sabdariffa and Zingiber officinale Against Multidrug-Resistant Bacteria. *Biology, Medicine, & Natural Product Chemistry*, *14*(2), 1391-1397.
3. Adebayo, O. S., & Ogunlade, I. T. (2024). Pathogenicity and varietal susceptibility of *Fusarium mangiferae* causing mango malformation in Southwestern Nigeria. *Nigerian Journal of Plant Protection, 37*(2), 45–58.
4. Adebayo, T. O., & Yusuf, M. A. (2025). Phenology and population dynamics of mango leafhoppers in relation to flowering patterns in Southwestern Nigeria. *Nigerian Journal of Entomology, 41*(1), 55–70.
5. Adebisi, T. O., & Ogunremi, O. R. (2025). Diversity of *Bacillus* species in the mango phyllosphere and their implications for disease management in Southwestern Nigeria. *Nigerian Journal of Microbiology, 39*(1), 45–59.
6. Adekunle, A. T., & Olaniyi, O. O. (2025). Varietal susceptibility of mango to bacterial black spot in Southwestern Nigeria. *West African Journal of Horticultural Science, 18*(2), 112–126.
7. Adekunle, A. T., Olaniyi, O. O., & Fashola, M. O. (2024). Metagenomic analysis of the mango inflorescence microbiome in Ibadan, Nigeria. *West African Journal of Biological Sciences, 11*(2), 112–125.

8. Adewuyi, S. K., Olufolaji, D. B., & Adebayo, T. A. (2025). Differential susceptibility of mango cultivars to bacterial canker pathogens in the derived savanna zone of Nigeria. *Journal of Horticultural Science and Biotechnology, 40*(1), 112–125.
9. Akinola, J. A., & Olufolaji, D. B. (2025). Polymicrobial interactions in mango inflorescence blight: A case for integrated disease management. *Journal of Plant Pathology and Microbiology, 8*(1), 22–35.
10. Akinwale, O. O., & Oladipo, E. A. (2024). Distribution and impact of *Rastrococcus invadens* on mango inflorescence development in Oyo State, Nigeria. *Journal of Agricultural Pest Management, 17*(2), 112–126.
11. Akinwumi, G. A., Bello, O. O., & Yusuf, H. K. (2024). The mango pathobiome: Co-infection dynamics of fungal pathogens in inflorescence diseases. *West African Journal of Mycology, 19*(1), 112–126.
12. Bamidele, J. F., & Adeola, A. A. (2025). Emerging threats: *Curvularia* and *Pestalotiopsis* species associated with mango rachis necrosis in the northern Guinea savanna. *Journal of Agricultural Research and Development, 44*(1), 78–89.
13. Banjare, R., Nidhi, N., & Sood, A. (2023). Physiological aspects of flowering, fruit setting, fruit development, and fruit drop, regulation, and their manipulation: a review. *Int J Environ Clim Chang*, *13*(12), 205-224.
14. Bello, A. A., & Usman, I. (2025). *Lasiodiplodia theobromae* as an emerging pathogen of mango inflorescences in Kwara State, Nigeria. *Savanna Journal of Agricultural Research, 22*(1), 78–92.
15. Bello, A. A., & Yusuf, M. A. (2025). The role of *Diaporthe* and *Botryosphaeria* species in the mango decline complex of Kwara State, Nigeria. *Journal of Sustainable Agriculture and Environment, 12*(1), 33–47.
16. Bello, M. A., & Lawal, A. K. (2024). Bacterial soft rot pathogens of mango in Kano State: Identification and pathogenicity. *Savanna Journal of Basic and Applied Sciences, 6*(2), 88–101.
17. Chukwudi, U. P., & Adeyemo, O. S. (2025). Integrated pest management strategies for mango inflorescence pests in the Nigerian rainforest zone. *Tropical Agriculture and Entomology Review, 22*(1), 33–48.
18. Chukwudi, U. P., & Ibrahim, A. (2025). Prevalence and control of bacterial blight and bacterial black spot of mango in the Nigerian middle belt. *Tropical Agriculture and Forestry Research, 33*(1), 15–29.
19. Chukwudi, U. P., & Nwosu, C. C. (2024). Morphological and biochemical determinants of varietal susceptibility to bacterial pathogens in mango. *Nigerian Journal of Crop Science, 41*(2), 145–159.
20. Eze, C. P., & Chidi, O. J. (2024). *Colletotrichum* and *Alternaria* complexes associated with mango inflorescence blight in Southeastern Nigeria. *International Journal of Fruit Science, 24*(3), 201–215.
21. Eze, C. S., Nwankiti, A. O., & Okoro, J. K. (2025). Characterization of *Pseudomonas syringae* isolates from mango inflorescences in Ibadan, Nigeria. *African Journal of Agricultural Research, 21*(3), 78–91.
22. Ezeh, C. I., & Nwankwo, P. O. (2023). Epiphytic bacterial communities on mango inflorescences in Enugu State, Nigeria. *International Journal of Agricultural Science and Technology, 14*(3), 201–215.
23. Ezeh, C. I., & Ogunlade, I. T. (2024). Feeding damage and oviposition effects of *Idioscopus* species on mango flower retention in Enugu State. *International Journal of Tropical Insect Science, 44*(3), 201–215.
24. Honger, J. O., Osabutey, S., Nyaku, S. T., & Lambon, J. B. (2021). Molecular characterization, pathogenicity and copper sensitivity of Xanthomonas citri pv mangiferaeindicae, the causal agent of mango bacterial black spot disease in Ghana. *Archives of Phytopathology and Plant Protection*, *54*(19-20), 1703-1721.
25. Nayanthara, J. (2020). Incidence and management of insect pests infesting inflorescence of mango. *Department of Agricultural Entomology, College of Agriculture, Vellayani*.
26. Nwachukwu, E. O., & Okafor, U. C. (2024). Integrated management of fungal-bacterial disease complexes in mango orchards of Anambra State. *International Journal of Agricultural Science and Technology, 15*(3), 201–216.
27. Nwachukwu, E. O., Okafor, U. C., & Nwosu, C. I. (2025). Survey of fungal pathogens of mango (*Mangifera indica* L.) inflorescences in Anambra State, Nigeria. *Nigerian Agricultural Journal, 56*(1), 90–102.
28. Nwosu, C. C., & Okafor, I. P. (2024). Climate change adaptation strategies for sustainable mango production in Nigeria. *Journal of Climate and Agriculture, 9*(2), 88–102.
29. Ogunleye, O. O., & Adebisi, O. A. (2024). Latent fungal pathogens in mango orchards: Implications for disease management in southwestern Nigeria. *Nigerian Journal of Plant Protection, 37*(2), 55–69.
30. Ogunyemi, S. O., & Adetunji, C. O. (2025). Timing of fungicide and bactericide applications for management of mango inflorescence diseases. *African Journal of Plant Protection, 44*(1), 55–70.
31. Okonkwo, C. I., & Ibrahim, A. M. (2024). Biocontrol potential of *Bacillus* species against fungal pathogens of mango in northern Nigeria. *International Journal of Pest Management, 70*(4), 234–247.
32. Okonkwo, C. I., & Nwachukwu, E. O. (2025). Phenological synchrony between mango flowering and insect pest emergence in northern Nigeria. *Journal of Applied Entomology, 149*(2), 156–170.
33. Omar, N. H., Mohd, M., Nor, N. M. I. M., & Zakaria, L. (2018). Characterization and pathogenicity of Fusarium species associated with leaf spot of mango (Mangifera indica L.). *Microbial pathogenesis*, *114*, 362-368.
34. Oyewale, R. O., & Ibrahim, A. (2024). Host plant resistance to mango leafhoppers: Screening of Nigerian cultivars under field conditions. *Journal of Plant Protection Research, 36*(2), 88–102.
35. Umar, H. Y., Bello, O. R., & Yusuf, A. A. (2025). Etiology and epidemiology of mango malformation disease in the Northern Guinea Savannah zone. *Nigerian Journal of Plant Pathology, 19*(1), 34–49.

36. Umar, I., & Bello, A. A. (2025). Biochemical basis of varietal susceptibility to mango hopper infestation in Kaduna State, Nigeria. *Savanna Journal of Agricultural Research, 21*(1), 12–26.
37. Umar, I., Abubakar, L., & Mohammed, B. (2025). Prevalence and distribution of *Fusarium mangiferae* in major mango-producing zones of Kaduna State, Nigeria. *Savanna Journal of Agriculture, 20*(1), 12–24.
38. Umeh, O. V., & Chukwudi, U. P. (2024). Epiphytic bacterial communities on mango inflorescences in Benue State, Nigeria: Diversity and functional roles. *Nigerian Journal of Microbiology, 38*(1), 567–580.
39. Usman, A., & Adebayo, O. S. (2024). Susceptibility of Nigerian mango cultivars to bacterial black spot caused by *Xanthomonas campestris* pv. *mangiferaeindicae*. *Nigerian Journal of Horticultural Science, 29*(2), 90–104.
40. Wang, Q., Han, Y., Yu, Z., Tian, S., Sun, P., Shi, Y., ... & Li, Z. (2025). Fungi in horticultural crops: Promotion, pathogenicity and monitoring. *Agronomy*, *15*(7), 1699.
41. Xu, Y., Charles, M. T., Luo, Z., Roussel, D., & Rolland, D. (2017). Potential link between fruit yield, quality parameters, and phytohormonal changes in preharvest UV-C-treated strawberry. *Plant Physiology and Biochemistry*, *116*, 80-90.

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