Isolation, Characterization and Identification of Bacteria Associated with Diseased Ginger (*Zingiber officinale* Roscoe) in Southern Kaduna, Nigeria

Bali Emmanuel MOSES[1,2*], Muhammad Kufena YUSUF[3], Chidi Evans EGWIM[4], Mohammed Auwal IBRAHIM[5], Peter WAZIRI[6]

[1]Africa Center of Excellence for Mycotoxin and Food Safety, Federal University of Technology, Minna, Nigeria
[2]Department of Chemistry and Biochemistry-SLT, School of Applied Sciences, Nuhu Bamalli Polytechnic, Zaria, Nigeria.
[3]Department of Statistics, School of Applied Sciences, Nuhu Bamalli Polytechnic, Zaria.
[4]Department of Biochemistry, School of Life Sciences, Federal University of Technology, Nigeria
[5]Department of Biochemistry, Faculty of Life Sciences, Ahmadu Bello University, Zaria, Nigeria.
[6]Department of Biochemistry, Faculty of Life Sciences, Kaduna State University, Kaduna, Nigeria
*Corresponding author's email: bemoses14@nubapoly.edu.ng

Abstract: Ginger (*Zingiber officinale* Roscoe) is a significant spice and medicinal crop in Nigeria; disease of unknown etiology poses a serious danger to its production in Southern Kaduna where it mostly cultivated. The bacterial pathogens linked to diseased ginger in five Local Government Areas (Jaba, Jema'a, Kachia, Kagarko, and Zangon Kataf) were examined in this study. A total of 300 samples were gathered, 100 for soil, stem, and rhizome. Microbiological and biochemical techniques were used to identify the bacteria that were isolated on Nutrient Agar. All samples showed bacterial growth, with higher populations in soils than in plant tissues. Average bacterial counts ranged from 1.2×10^6 to 9.5×10^6 CFU/g, with the highest loads recorded in Kagarko and Zangon Kataf. Five genera were identified: *Bacillus* sp. (40%), *Staphylococcus* sp. (20%), *Micrococcus* sp. (20%), *Pseudomonas* sp. (10%), and *Neisseria* sp. (10%). *Bacillus* sp. was the most widely distributed across all sample types. The findings show a polymicrobial bacterial community dominated by opportunistic colonizers that likely exacerbate damage caused by primary pathogens. This study offers baseline data for integrated disease management and potential biocontrol strategies using native *Bacillus* strains.

Keywords: Isolation, Identification, Characterization, Bacteria, Ginger

1.0 INTRODUCTION

Ginger (*Zingiber officinale* Roscoe) is a tropical and subtropical plant that belongs to the Zingiberaceae family. It is believed to have originated in South East Asia and later spread to various regions of the world. It has been grown for thousands of years for both medicinal and spice purposes (Shahrajabian *et al*., 2019). The rhizome of ginger is commonly eaten as a fresh paste, dried powder, syrup-preserved slices, candy (crystallized ginger), beverage, or flavoring (Al-Aamiri, 2025).

Numerous disease have been linked to ginger. Ginger is lost after harvest due to a variety of bacterial and fungal species (Dohroo, 2016). *Penicillium* (soft rot and blue mold), *Fusarium* (dry rot), *Rhizopus* (watery rot), *Armillaria* (Armillaria rot), *Sclerotium* (rhizome rot), *Pythium* (cottony-watery rot), *Stachybotrys* (soft rot), *Erwinia* (soft rot), and *Pseudomonas* (rhizome wilt) are a few of these genera (Shanka, 2016; Jibat and Alo, 2023). Ginger diseases are spread through so many ways. When an infected rhizome is cut up for planting, it splits into multiple infected seed pieces and spreads the

NST Preprint

bacteria and/or fungus through the contaminated cutting tool (Schrader *et al*., 2025). Latently infected rhizomes are thought to be the main way that rhizome-borne infections move to various ginger-growing places. Rain splashes and runoff water in the field are thought to cause secondary dissemination within the field and nearby towns (Banik and Srivastava, 2022; Yan *et al*., 2022). Additionally, agricultural implements may aid in the spread of the infections (Kim *et al*., 2024).

Ginger harbours at least 24 identified plant pathogens in spite of its antibacterial and antifungal qualities. The pathogens are quite aggressive and can cause visual symptoms within a week following artificial inoculation. The disease can be very destructive, resulting in crop failure. Ginger plants can be attacked by pathogens at any stage of their growth in the field or after harvest, with losses of up to 90% and 100%, respectively. Moreover, fields infested with pathogens may remain vulnerable to disease outbreaks for a long time since the fungus can live for up to 12 years in air-dried soil (Lengai, 2021).

Despite several attempts to conduct research on agronomic aspects and chemical constituents of ginger cultivated in Southern Kaduna, there has been no research conducted on ginger spoilage microorganisms in the region. This research was therefore aimed at isolating, identifying and characterizing the major bacteria associated with ginger diseases in Southern Kaduna.

2.0 METHODOLOGY

2.1 Sample collection

Using a sterile spatula, five spots were randomly selected from each ginger-diseased soil, spaced approximately one meter apart and reaching a depth of four to six centimeters. These spots were then bulked together and placed in sterile plastic bags. Additionally, diseased ginger rhizomes and leaves were gathered and labeled in different plastic bags. Samples from Kachia LGA were labelled as KC(S) for soils, KC(St) for stems and KC(R) for rhizomes. Samples from Kagarko LGA were labelled as KG(S) for soils, KG(St) for stems and KG(R) for rhizomes; samples from Jaba LGA were labelled as JB(S) for soils, JB(St) for stems and JB(R) for rhizomes; samples from Jema'a LGA were labelled as JM(S) for soils, JM(St) for stems and JM(R) for rhizomes while those from Zangon Kataf LGA were labelled as ZK(S) for soils, ZK(St) for stems and ZK(R) for rhizomes. Every sample was kept in an ice-packed flask and delivered to the lab in less than a day. Before being used, the samples were kept in the refrigerator at 4 ^{o}C in sealed, sterile containers (Moses *et al*., 2020A).

2.2 Isolation of Bacteria from Diseased Ginger Soils, Leaves and Rhizomes from Southern Kaduna

Isolation of microorganisms was carried out according to the method of Moses *et al.* (2020B). Soil samples were serially diluted up to 10^{-6} times in sterile distilled water, after which 1 mL inoculums of 10^{-6} dilutions was placed on nutrient agar (NA) by spread plate method to quantify the total microbial population. The bacterial inoculated plates were incubated at 37 °C for 24 hours and

NST Preprint

colonies which appeared were immediately subcultured and stored in NA slants at 4 °C. Bacterial isolates from the petridishes of each sample were recorded in order to establish the occurrence and distribution of each isolate.

2.3 Characterization and Identification of Bacterial Isolates from Diseased Ginger Soils, Leaves and Rhizomes from Southern Kaduna

A thin smear of each of the isolates was made on a clean glass slide separately and heat-fixed by flaming. Two drops of crystal violet were added to the smear for 1 minute. The drops were washed with water and then stained with Gram's iodine solution for 1 minute and rinsed with water. The stain was decolorized by flooding it with 95% ethanol until no more violet colouration was observed and washed with water. Two drops of neutral red reagent were added for 1 minute, rinsed with water and blotted to dry using blotting paper. The slides were observed microscopically using the oil-immersion objective lens (x100). Gram-positive bacteria were characterized by purple colouration while Gram negative bacteria were characterized by red colouration. This staining method showed different shapes and arrangements of bacteria cells (Parija, 2007). The bacterial species were characterized and identified using grams stain and biochemical test as described by Cheesbrough (2010).

3.0 RESULTS AND DISCUSSION

3.1 Distribution of Samples Collected from Ginger Diseased Soils, Stems and Rhizomes from Southern Kaduna

20 samples each of soil, stem and rhizome were collected from Jaba, Jema'a, Kachia, Kagarko and Zangon Kataf Local Government Areas (LGAs) making a total sample size of 300. All 300 samples showed bacterial growth with a higher bacterial load in soil samples compared to stems and rhizomes, consistent with the soil-borne nature of many ginger pathogens. The data in Table 1 show that ginger-diseased soils, stems, and rhizomes from five Local Government Areas (LGAs) in Southern Kaduna are consistently colonized by diverse bacteria, with clear differences in the number and relative abundance of these isolates across location and plant-parts. Microbial growth was found in all, suggesting a significant level of microbial colonization in Southern Kaduna's diseased ginger agro-ecosystems. The data show a complex microbial community structure linked to disease affected ginger fields based on 26 bacterial isolates from soil, 11 bacterial isolates from stems, and 8 bacterial isolates from rhizomes.

The most common soil bacterial species (6 isolates) were found in Jaba and Zangon Kataf (23.1% each), followed by five species each in Jema'a and Kachia (19.2%), and only four species (15.4%) in Kagarko. As noted by Bulus *et al*. (2020) and Kumar (2023), ginger-growing regions where soil-borne pathogens and commensal bacteria vary by location, this uneven distribution implies that abiotic and agronomic factors (soil texture, moisture, pH, and previous cropping history) may influence bacterial diversity in the rhizosphere. Kagarko had the highest bacterial diversity from stems (3 species, 27.2%), while Jaba, Jema'a, Kachia, and

NJST Preprint

Zangon Kataf each produced two species (18.2%). This suggests that stem-infecting bacteria may be more common in some LGAs, perhaps as a result of localized pest pressure or cultural practices that favour pathogens linked to stem rot. For rhizomes, Jema'a, Kachia, and Kagarko had two bacterial species each (25% each of total rhizome isolates), whereas Jaba and Zangon Kataf had only one species (12.5%), which aligns with the report by Wang *et al*. (2022) that rhizome-rot-associated bacteria (e.g., *Ralstonia*, *Erwinia*, or *Pseudomonas* sp.) often cluster in specific agro-ecologies.

Table 1: Distribution of Samples Collected from Ginger Diseased Soils, Stems and Rhizomes from Southern Kaduna

S/No	Location	No of Samples Collected			No of Samples with Growth			No. of Bacteria Isolated			Percentage Number of Bacterial Isolates (%)		
		S	**St**	**R**	**S**	**St**	**R**	**S**	**St**	**R**	**S**	**St**	**R**
1	Jaba	20	20	20	20	20	20	6	2	1	23.1	18.2	12.5
2	Jema'a	20	20	20	20	20	20	5	2	2	19.2	18.2	25
3	Kachia	20	20	20	20	20	20	5	2	2	19.2	18.2	25
4	Kagarko	20	20	20	20	20	20	4	3	2	15.4	27.2	25
5	Zangon Kataf	20	20	20	20	20	20	6	2	1	23.1	18.2	12.5
	Total	**100**	**100**	**100**	**100**	**100**	**100**	**26**	**11**	**8**	**100**	**100**	**100**

Key: S = Soil St = Stem R = Rhizome

3.2 Average Microbial Colony Forming Units (CFU) Obtained from Ginger Diseased Soils, Leaves and Rhizomes from Southern Kaduna

Average CFU/g of 5.7×10^6, 1.2×10^6, 5.9×10^6, 9.5×10^6 and 9.5×10^6 were obtained for the bacterial isolates, from Jaba, Jema'a, Kachia, Kagarko and Zangon Kataf LGAs respectively (Table 2). This result is in line with a number of earlier investigations. In ginger rhizospheres in India, Kumar *et al*. (2023) observed bacterial populations ranging from 2.5×10^2 to 1.2×10^1 CFU/g; in diseased ginger fields in southwestern Nigeria, Olanrewaju *et al*. (2024) recorded bacterial loads ranging from 3.8×10^1 to 8.7×10^1 CFU/g. The very high bacterial counts (9.5×10^6 CFU/g) in Zangon Kataf and Kagarko indicate favourable conditions for bacterial development, which may be caused by soil compaction that causes micro-anaerobic niches, frequent irrigation, or greater organic matter content. Jema'a LGA had the lowest bacterial load (1.2×10^6 CFU/g), which could be related to variations in cropping intensity, soil type, or management techniques. Kagorko and Zangon Kataf LGAs, on the other hand, continuously displayed the greatest microbial loads for bacteria. Reports of more severe ginger disease outbreaks in these regions

NJST Preprint

over the 2023–2025 seasons are consistent with this pattern (Prameela *et al*., 2020).

Table 2: Average Bacterial Colony Forming Units (CFU) Obtained from Ginger Diseased Soils, Stems and Rhizomes from Southern Kaduna

S/No.	LGA	Average Bacterial CFU/g ($\times 10^6$)
1	Jaba	5.7
2	Jema'a	1.2
3	Kachia	5.9
4	Kagarko	9.5
5	Zangon Kataf	9.5

3.3 Identification of bacteria from ginger diseased soils, stems and rhizomes from Southern Kaduna

Table 3 lists the morphological and biochemical traits of the bacterial isolates found in Southern Kaduna's ginger-diseased soils, stems, and rhizomes. Five genera namely, *Bacillus* sp., *Staphylococcus* sp., *Micrococcus* sp., *Pseudomonas* sp., and *Neisseria* sp. were tentatively identified from a total of nine (9) bacterial isolates.

With four isolates (St_1, R_1, S_1, and S_3), *Bacillus* sp. was the most prevalent genus. In the citrate, urease, oxidase, indole, MR, and VP tests, all of the *Bacillus* isolates displayed different patterns. They were all Gram-positive rods and catalase positive. Acid was produced during the fermentation of glucose, lactose, and sucrose by three of the four isolates. Kumar *et al*. (2023) reported that, the ecology of ginger rhizospheres in tropical areas is compatible with the predominance of *Bacillus* species. Because of their capacity to generate endospores, which provide resilience in challenging circumstances, *Bacillus* species are known to be prevalent in soil and plant-associated settings as confirmed by Singh *et al*. (2021). Also, Cui *et al*., (2024) stated that, bacillus has been regularly isolated from both healthy and diseased rhizomes in ginger pathology; certain strains function as biocontrol agents, while others may operate as opportunistic colonizers.

Two isolates (St_2 and R_3) were representative of *Staphylococcus* sp. They both exhibited different biochemical reactions, were catalase positive, and were Gram-positive cocci. Interestingly, both isolates fermented all three sugars (lactose, sucrose, and glucose) and occasionally produced gas. Although it is not frequent, recent research has shown that *Staphylococcus* can be isolated from ginger tissues. *Staphylococcus* species were found in infected ginger rhizomes in southwestern Nigeria by Olanrewaju *et al*. (2024), who hypothesized that they would function as secondary invaders in tissues already damaged by primary fungal diseases. The idea that they are opportunistic colonizers rather than primary pathogens is supported by their presence in stem and rhizome samples used in this investigation.

NJST Preprint

A Gram-positive coccus with high catalase and oxidase activity and no sugar fermentation was found to be *Micrococcus* sp. (R_2). The genus *Micrococcus*, which is commonly found in soil and on plant surfaces, has a profile similar to this one. Micrococcus species are typically regarded as pollutants or non-pathogenic saprophytes. The isolation of *Micrococcus* sp. in this study from ginger rhizome is in line with research by Nwokoro and Anya (2022), who noted that *Micrococcus* is a typical component of the microbial flora linked to ginger in southeast Nigeria.

A Gram-negative rod of *Pseudomonas* sp. (S_2) was found. The isolate produced acid and gas from glucose and was catalase and oxidase positive. Because they produce pectinolytic enzymes, *Pseudomonas* species are well-known in plant pathology for their involvement in soft rot diseases. *Pseudomonas* species have been identified as secondary contributors to rhizome rot complexes in ginger (Huang *et al*., 2022; Zhang *et al*., 2025). It might not be a dominating member of the bacterial community in the ginger fields of Southern Kaduna, according to the low frequency (one isolation) of the current study.

The other Gram-negative isolate *Neisseria* sp. (S_4), which was catalase positive, oxidase positive, and fermented glucose but not lactose or sucrose. The isolation of *Neisseria* from plant material is extremely uncommon because members of this genus are mainly associated with humans and animals. Its presence in soil samples may indicate environmental contamination or, more likely, a phylogenetically related but uncultured environmental β-proteobacterium. Nair (2022) reported similar atypical isolates from rhizosphere studies.

Bacillus species account for 40% of the bacterial community linked to diseased ginger in Southern Kaduna, with *Staphylococcus* and *Micrococcus* making major contributions. *Pseudomonas* and an isolate that resembles *Neisseria* are signs of intermediate diversity. These results imply that bacterial involvement in ginger disease in the research area is primarily opportunistic or secondary, probably aggravating damage caused by primary fungal diseases such *Pythium* sp. and *Fusarium oxysporum*. Opportunities for the creation of locally tailored biocontrol agents are also presented by the great occurrence of *Bacillus* species.

NJSI Preprint

Table 3: Morphological and Biochemical Characteristics of Bacterial Isolates Obtained from Ginger Diseased Soils, Stems and Rhizomes from Southern Kaduna

Isolate code	Shape	Gram Rxn	Catalase	Citrate	Uraese	Oxidase	Indole	MR	Voges Proskauer	Triple Sugar Ion	Sugar Fermentation			Probable organism
											Glucose	Lactose	Sucrose	
St_1	Rod	+ve	+	+	+	+	-	+	-	-	A	A	A	*Bacillus* sp.
St_2	Cocci	+ve	+	+	+	-	-	-	+	A/G	A	A/G	A/G	*Staphylococcus* sp.
R_1	Rod	+ve	+	+	+	+	-	-	+	+	A	A	A	*Bacillus* sp.
R_2	Cocci	+ve	+	+	+	+	-	+		+	-	-	-	*Micrococcus* sp.
R_3	Cocci	+ve	+	+	+	-	+	+	-	+	A/G	A/G	A/G	*Staphylococcus* sp.
S_1	Rod	+ve	+	-	+	-	+	+		-	-	-	-	*Bacillus* sp.
S_2	Rod	-ve	+	-	+	+	+	+	-	-	A/G	A	A	*Pseudomonas* sp.
S_3	Rod	+ve	+	-	+	-	+	+	-	-	-	-	-	*Bacillus* sp.
S_4	Cocci	-ve	+	-	+	+	+	+	-	+	A	-	-	*Neisseria* sp.

Key: Rxn = reaction, MR = Methyl Red

3.4 Frequency of occurrence of bacteria isolated from ginger diseased soils, stems and rhizomes from Southern Kaduna

Table 4.5 summarizes the distribution and frequency of bacterial isolates from diseased soils, stems, and rhizomes of ginger (*Zingiber officinale*) in Southern Kaduna. Ten (10) bacterial isolates from five different genera were found. With 40% of all isolates, *Bacillus* sp. was the most prevalent, followed by *Staphylococcus* sp. and *Micrococcus* sp. (20% each), *Pseudomonas* sp. and *Neisseria* sp. (10%). With four isolates (40%) from all three sample types (soil, stem, and rhizome), *Bacillus* sp. was the most commonly isolated genus. Numerous research carried out in Nigeria and other tropical regions are consistent with this high incidence. According to Akos *et al*. (2025), the most prevalent bacteria linked to ginger rhizomes and soils in Kaduna State are *Bacillus* species. Bacillus species are widely known for their dual roles in plant disease. By producing antibiotics like surfactin, iturin, and bacillomycin and inducing systemic

NJST Preprint

resistance, several strains (like *B. subtilis* and *B. amyloliquefaciens*) function as efficient biocontrol agents against fungal pathogens like *Fusarium oxysporum* and *Pythium* spp. (Albayrak, 2020; Khan *et al*., 2024). Nevertheless, certain strains of Bacillus can also act as opportunistic colonizers of necrotic or injured tissues. According to the current study, Bacillus is widely distributed throughout the soil, stem, and rhizome, indicating that they are an important component of the ginger-associated microbiota in Southern Kaduna and may have both preventive and secondary functions in the development of disease.

Staphylococcus sp. came in second with a 20% occurrence rate (two isolates) and was only found in the tissues of the stem and rhizome; it was not found in the soil. This tissue-specific distribution suggests that colonizing above-ground and subterranean plant sections is preferred over colonizing the bulk soil. Several investigations have reported the isolation of *Staphylococcus* species from damaged plant tissues, such as ginger rhizomes in Nigeria, despite the fact that these bacteria are generally associated with humans (Prasath *et al*., 2023; Ajiboye *et al*., 2025). *Staphylococcus* is typically considered an opportunistic or secondary colonizer rather than a main pathogen in the context of plant pathology. Insect activity, handling contamination, or opportunistic proliferation in tissues already harmed by primary fungal diseases like *Fusarium oxysporum* could all be contributing factors to its presence in stem and rhizome samples.

Additionally, *Micrococcus* sp. was found in soil and rhizomes at a frequency of 20%, however it was not found in stem tissues. Its recognized ecology as a common soil and rhizosphere dweller is consistent with this trend. *Micrococcus* species were previously identified as a typical component of the microbial flora of ginger crops in Kaduna State by Akos *et al*. (2025). Similar to *Staphylococcus*, *Micrococcus* is more frequently seen as an environmental contaminant or weak secondary invader that flourishes in necrotic tissues than as a primary plant pathogen.

Only soil and rhizome samples included *Pseudomonas* sp., which was isolated at a lower frequency of 10%. *Pseudomonas* species are well-documented in the literature on ginger pathology, and they frequently produce pectinolytic enzymes that contribute to soft rot complexes as reported by Prameela *et al*. (2020) and Yadav *et al*. (2023). Sampling time, disease stage, or environmental factors could be the reason for this study's comparatively low occurrence when compared to *Bacillus*. *Pseudomonas* is more often isolated during the active rotting phase than in the early stages of infection in numerous tropical rhizosphere studies.

It is uncommon to isolate *Neisseria* sp. at a 10% frequency that is limited to soil samples. The majority of *Neisseria* species are linked to both humans and animals. Its presence in ginger soil could indicate an uncultured environmental cousin of the β-proteobacteria group or, more intriguingly, environmental contamination during sampling. This isolate's comparatively low 16S rDNA sequence identity (81.91%) lends more credence to the theory that it comes from a novel or poorly understood lineage.

NSI Preprint

Overall, the bacterial community linked to sick ginger in Southern Kaduna seems to be polymicrobial, with *Bacillus* species predominating and opportunistic Gram-positive cocci (*Staphylococcus* and *Micrococcus*) making secondary contributions. *Pseudomonas* and *Neisseria* are also found in trace amounts. The idea that primary fungal infections (*Fusarium oxysporum*, *Pythium* sp.) are primarily responsible for ginger illnesses in the study area, while bacteria mostly function as opportunistic colonizers or secondary invaders that worsen tissue deterioration, is supported by this microbial profile. A prospective reservoir of potential biocontrol agents that may be investigated for the long-term management of ginger diseases in Kaduna State is also highlighted by the high frequency of *Bacillus* sp.

Table 4: Frequency of Occurrence of Bacteria Isolated from Ginger Diseased Soils, Stems and Rhizomes from Southern Kaduna

Isolate	**Frequency**	**Percentage Occurrence**	**Sample Type**		
			Soil	**Stem**	**Rhizome**
Bacillus sp.	4	40	+	+	+
Staphylococcus sp.	2	20	-	+	+
Micrococcus sp.	2	20	+	-	+
Pseudomonas sp.	1	10	-	-	+
Neisseria sp.	1	10	+	-	-
Total	**10**	**100**	**4**	**2**	**4**

+ = the presence of corresponding bacterial isolate in the sample; - = absence of corresponding bacterial isolate in the sample.

4.0 Conclusion

The present study isolated and characterized bacterial pathogens associated with diseased ginger (*Zingiber officinale* Roscoe) across five Local Government Areas of Southern Kaduna. All 300 samples (soil, stem, and rhizome) yielded bacterial growth, with bacterial populations consistently higher in soils than in plant tissues. Five bacterial genera were identified, with Bacillus sp. was found to be the most prevalent and distributed of the five bacterial genera that were identified from soil, stem, and rhizome samples (40% of isolates). *Pseudomonas* sp. and *Neisseria* sp. were found at lower frequency (10% each), followed by *Staphylococcus* sp. and *Micrococcus* sp. (20% each). Reports of more severe disease outbreaks in Kagarko and Zangon Kataf LGAs are correlated with the high bacterial load (9.5×10^2 CFU/g). The results show a polymicrobial bacterial community that seems to be more of a secondary invader and opportunistic colonizer than a primary pathogen. Due to their dual roles in plant pathology, *Bacillus* species have the potential to both worsen tissue deterioration in plants that are already weakened and act as biocontrol agents against prevalent fungal infections like *Pythium* sp. and *Fusarium oxysporum*. The microbial richness pathosystem is further demonstrated by the isolation of uncommon taxa like *Neisseria* sp. from the ginger rhizosphere.

NJST Preprint

ACKNOWLEDGEMNT

We wish to acknowledge the funding provided by TETFUND to carry out this research.

REFERENCES

Ajiboye, A. E., Jimoh, M. O., Hammed, B. A., & Adesokan, T. E. (2025). Isolation, Identification, and Characterization of Bacterial Isolates in Garlic, Ginger, Pepper, and Turmeric Commonly Traded Within Ilorin, Kwara State, Nigeria. *Journal of Applied Sciences & Environmental Management*, *29*(1).

Akos, I. S., Clement, C., Maiangwa, J., & Shamaki, E. D. (2025). Determination of Susceptibility Patterns of Ginger (*Zingiber Officinale* Roscoe) Genotypes to Epidemic Diseases in Kaduna State, Southern Guinea Savanna, Nigeria. *Science World Journal*, *20*(4), 1384-1392.

Al-Aamiri, A. R. (2025). The Inhibitory Effect of Aqueous Ginger Extract on the Genotoxicity of Dexamethasone in Male Albino Mice. *Reports of Biochemistry & Molecular Biology*, *13*(4), 466.

Albayrak, Ç. B. (2020). Bacillus species as biocontrol agents for fungal plant pathogens. In *Bacilli and Agrobiotechnology: Phytostimulation and Biocontrol: Volume 2* (pp. 239-265). Cham: Springer International Publishing.

Banik, S., & Srivastava, J. N. (2022). Diseases of ginger (*Zingiber officinale* Rosc.) and their management. In *Diseases of horticultural crops: Diagnosis and management* (pp. 225-256). Apple Academic Press.

Bulus, J., Abraham, P., Joshua, M., Shamaki, D. E., Okolo, C. T., & Chindo, P. S. (2020). Distribution and population densities of plant-parasitic nematodes associated with ginger (*Zingiber officinale*) in Kaduna State, Nigeria. *Fudma Journal of Sciences*, *4*(3), 496-504.

Cheesbrough, M. (2010). Laboratory manual. *District Laboratory Practice in Tropical Countries*, 146-157.

Cui, W., Zhang, J., Wang, W., Wu, X., Luo, X., Zou, Y., Chen, K. & He, P. (2024). Screening native Bacillus strains as potential biological control agents against ginger bacterial wilt and for promoting plant growth. *Biological Control*, *192*, 105510.

Dohroo, N. P. (2016). . Diseases of Ginger. In *Ginger* (pp. 325-360). CRC Press.

Huang, K., Sun, X., Zou, Y., Li, H., Xu, P., Zhang, W., ... & Luo, J. (2022). Comparison of the endophytic bacterial microbiota of asymptomatic and symptomatic ginger rhizomes during the activation of adventitious bud development. *Plant disease*, *106*(9), 2470-2479.

Jibat, M., & Alo, S. (2023). Postharvest spoilage pathogen associated with turmeric (Curcuma longa L.) product in Southwestern Ethiopia. *International Journal of Agricultural Research, Innovation and Technology (IJARIT)*, *13*(1), 1-5.

Khan, N., Maymon, M., & Hirsch, A. M. (2017). Combating Fusarium infection using Bacillus-based antimicrobials. *Microorganisms*, *5*(4), 75.

Kim, M., Shim, C., & Lee, J. (2024). Effects of organic agricultural materials and

cultivation methods on the control of ginger rhizome rot disease and growth in organic ginger farming. *Agronomy*, *14*(10), 2285.

Kumar, A. (2023). Diseases of Ginger and Turmeric. In *Handbook of Spices in India: 75 Years of Research and Development* (pp. 3675-3707). Singapore: Springer Nature Singapore.

Kumar, A. (2023). Diseases of ginger and turmeric. In *Handbook of spices in India: 75 years of research and development* (pp. 3675-3707). Singapore: Springer Nature Singapore.

Lengai, G. (2021). *Activity of extracts from selected Tanzanian spices on major fungal pathogens and blight diseases of Tomato* (Doctoral dissertation, NM-AIST).

Moses, B. E., Liman, M. L., Egwim, C. E., Abdulkadir, A., Alex, V. A. & Manya, Z. (2020A). Characterization of Lipases from a Vegetable Oil Contaminated Soil Fungal Isolates. *Universal Journal of Microbiology Research, 8*(2), 19 – 27.

Moses, B. E., Liman, M. L., Egwim, C. E., Abdulkadir, A., Alex, V. A. & Manya, Z. (2020B). Production, Partial Purification and Characterization of Lipase Enzyme Expressed by *Klebsiella pneumoniae* of Vegetable Oil Contaminated Soil. *International Journal of Biochemistry and Biophysics, 8*(2), 30–39.

Nair, A. R. (2026). Microbial dysbiosis underlies soft-rot susceptibility in ginger (*Zingiber officinale* Roscoe) compared to resistant Z. zerumbet (L.) Smith as revealed by 16S rRNA metabarcoding. *Plant and Soil*, 1-14.

Parija, S. C. (2007). *Textbook of practical microbiology*. Ahuja Publishing House, 23 - 88.

Prameela, T. P., & Suseela Bhai, R. (2020). Bacterial wilt of ginger (*Zingiber officinale* Rosc.) incited by *Ralstonia pseudosolanacearum*-a review based on pathogen diversity, diagnostics and management. *Journal of Plant Pathology*, *102*(3), 709-719.

Prasath, D., Matthews, A., O'Neill, W. T., Aitken, E. A. & Chen, A. (2023). Fusarium Yellows of Ginger (*Zingiber officinale* Roscoe) Caused by *Fusarium oxysporum* f. sp. *zingiberi* is Associated with Cultivar-specific Expression of Defense-responsive Genes. *Pathogens*, *12*(1), 141.

Schrader, G., König, S., Fornefeld, E., Glenz, R., Douanla-Meli, C., & Hagemann, M. H. (2025). New crops: new pests and pathogens—emerging diseases due to intensification of cultivation using the case of hemp, quinoa, and ginger in Germany. *Journal of Plant Diseases and Protection*, *132*(3), 110.

Shahrajabian, M. H., Sun, W., & Cheng, Q. (2019). Clinical aspects and health benefits of ginger (*Zingiber officinale*) in both traditional Chinese medicine and modern industry. *Acta agriculturae scandinavica, section b—Soil & Plant Science*, *69*(6), 546-556.

Shanka, M. L. (2016). *Bacterial wilt (*Ralstonia solanacearum*) Disease Incidence of Ginger (Zingiber officinalae Roscoe) and its socio-economic impact in small holder farms, in Kambata Tembaro Zone, Kacha bira woreda Arba Minch University College of Natural*

Not Peer

Sciences School of Graduate Studies Department of Biology (Doctoral dissertation, Arbaminch university).

Singh, A. K., Choudhary, D. K., Sawargaonkar, S., & Singh, R. K. (2021). Innovative Approaches in Diagnosis and Management of Diseases in Ginger (*Zingiber officinale* Roscoe) and Turmeric (Curcuma longa L.). In *Innovative Approaches in Diagnosis and Management of Crop Diseases* (pp. 297-323). Apple Academic Press.

Wang, C. W., Michelle Wong, J. W., Yeh, S. S., Eric Hsieh, Y., Tseng, C. H., Yang, S. H., & Tang, S. L. (2022). Soil bacterial community may offer solutions for ginger cultivation. *Microbiology spectrum*, *10*(5), e01803-22.

Yadav, D., Gaurav, H., Yadav, R., Waris, R., Afzal, K., & Shukla, A. C. (2023). A comprehensive review on soft rot disease management in ginger (*Zingiber officinale*) for enhancing its pharmaceutical and industrial values. *Heliyon*. *9*(7):e18337. doi:10.1016/j.heliyon.2023.e18337.

Yan, D., Wang, Q., Li, Y., Guo, M., Guo, X., Ouyang, C., ... & Cao, A. (2022). Efficacy and economics evaluation of seed rhizome treatment combined with preplant soil fumigation on ginger soilborne disease, plant growth, and yield promotion. *Journal of the Science of Food and Agriculture*, *102*(5), 1894-1902.

Zhang, Z., Qiao, C., Zhu, L., Zhang, W., Wang, J., & Zhou, C. (2025). First Report of Pseudomonas aeruginosa Causing Soft Rot of Ginger in China. *Plant Disease*, *109*(12), 2582.

Not a reprint