Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

Phylogeny and Molecular Characterisation of Bacterial Pathogens Associated with Selected Tomato (*Solanum lycopersicum* L.) Varieties in Enugu State

***Ishieze, Patience Ukamaka**
Department of Crop Science, University of Nigeria, Nsukka.
Corresponding author: patience.ishieze@unn.edu.ng
ORCID ID: https://orcid.org/0000-0002-8671-5626

Dauda, Nathaniel
Department of Crop Science, University of Nigeria, Nsukka.
International Institute of Tropical Agriculture, Ibadan, Nigeria.
ORCID ID: https://orcid.org/0000-0001-5706-0416

Ezugwu, Chekwube Cecilia
Department of Crop Science, University of Nigeria, Nsukka.
International Institute of Tropical Agriculture, Ibadan, Nigeria.
ORCID ID: https://orcid.org/0009-0000-3279-8844

Mbadianya, Jane Ifunanya
Department of Crop Science and Horticulture, Nnamdi Azikiwe University, Awka
ORCID ID: https://orcid.org/0000-0001-5161-4406

Abstract

Objective: The study aimed to investigate the increasing threat posed by bacterial pathogens to tomato (*Solanum lycopersicum* L.) crops, with a specific focus on the roles of *Acinetobacter nosocomialis*, *Corticimicrobacter populi*, and *Sphingobacterium thalpophilum*. The research focused on the phylogenetic and molecular characterization of bacterial isolates recovered from the symptomatic leaves and fruits of three tomato hybrids (Muna, Cobra, and Platinum) and one local cultivar (Yollins) grown in southeastern Nigeria.

Method: Isolates were analysed using 16S rRNA gene sequencing and multilocus sequence analysis (MLSA) to determine their genetic relationships. The study evaluated the distribution of these bacteria across the four specific tomato varieties and conducted molecular screening to identify functional genes associated with virulence and plant interaction, specifically those linked to biofilm formation, secretion systems, and the degradation of plant cell walls.

Result: The analysis revealed distinct ecological clustering, with *A. nosocomialis* (a Gram-negative member of the *A. calcoaceticus–baumannii* complex) primarily found in the Muna and Platinum varieties. In contrast, the recently described actinobacterium *C. populi* and the beneficial bacterium *S. thalpophilum* were more prevalent in Yollins and Cobra. Several of these isolates were confirmed to carry genes necessary for biofilm formation and plant cell wall degradation. This finding marks the first official report of *C. populi* in West African tomatoes, along with the

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

identification of *S. thalpophilum*, which is known to enhance antioxidant activity and root metabolism under salinity stress.

Conclusion: The study concludes that diverse bacterial species, ranging from opportunistic pathogens to beneficial growth enhancers, inhabit tomato varieties in southeastern Nigeria. The presence of virulence-linked genes in *A. nosocomialis* and *C. populi* underscores an emerging phytosanitary risk. These results emphasise the urgent need for ongoing pathogen monitoring and the development of breeding strategies tailored to the unique microbial profiles of specific tomato hybrids and local cultivars to ensure crop resilience.

Keywords: *Solanum lycopersicum*, *Acinetobacter nosocomialis*, *Corticimicrobacter populi*, *Sphingobacterium thalpophyilum*, phylogenetics, molecular characterisation,

Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most economically significant vegetable crops worldwide, contributing over 16% of global vegetable production and valued at approximately USD 58 billion annually (Zhu *et al*., 2025). In Nigeria, tomato cultivation is a critical component of smallholder and commercial agriculture, with varieties such as *Muna*, *Cobra*, *Platinum*, and the local *Yollins* widely grown for their yield potential, market preference, and adaptability to diverse agroecological zones (Ugonna et al., 2015). The nutritional value of ripe red tomatoes lies in their richness in lycopene a potent antioxidant known for its potential anticancer effects as well as their role as a source of vitamins A and C. Lycopene has been extensively studied for its ability to neutralize free radicals and reduce the risk of certain cancers, particularly prostate, lung, and breast cancers (Ali et al., 2020; Shenge et al., 2018). However, bacterial diseases remain a major constraint to production, causing significant yield losses and postharvest quality deterioration (Onyemaechi et al., 2025; Dong et al., 2019). *Acinetobacter nosocomialis*, a member of the *A. calcoaceticus–baumannii* complex, is traditionally recognised as a nosocomial pathogen in humans, notable for its multidrug resistance and environmental persistence (Zhou et al., 2021; Adewoyin & Okoh, 2018).

Recent studies have expanded its ecological range to include plant-associated habitats, where it may act as an opportunistic pathogen or endophyte, potentially influencing plant health through biofilm formation, secretion systems, and stress modulation (Zhou et al., 2021). Its detection in agricultural settings raises concerns about cross-domain transmission and the emergence of novel plant disease complexes (Onyemaechi et al., 2025). *Corticimicrobacter populi*, first described from the bark of *Populus* species, belongs to the family Dermacoccaceae and has been increasingly reported in plant rhizospheres and phyllospheres (Li et al., 2019). *Sphingobacterium sp*. BHU-AV3 has been identified as a beneficial rhizobacterium that enhances tomato tolerance to salt stress by boosting antioxidant activity and energy metabolism. While some strains may support plant health, changes in microbial communities involving *Sphingobacterium* have been observed in diseased tomato rhizospheres, suggesting an indirect or opportunistic role in plant disease (Vaishnav et al., 2020). However, no specific tomato disease has been directly linked to *Sphingobacterium* to date.

Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

While the pathogenicity in tomato remains underexplored, its genomic repertoire includes genes for carbohydrate-active enzymes and secondary metabolite biosynthesis, suggesting potential roles in plant tissue colonisation and degradation (Kayser & Averesch, 2025; Li et al., 2023; Benini, 2020). Host genotype, environmental conditions, and agronomic practices may influence the interaction between these bacterial taxa and tomato varieties. Hybrid varieties such as *Cobra, Muna,* and *Platinum* are valued and bred for high yield, fruit quality, disease resistance, and adaptability (Dossoumou et al.,2021). The local *Yollins* variety, though preferred for taste, may be more susceptible to emerging pathogens due to limited breeding for resistance traits (Dossoumou et al.,2021). Given the paucity of data on *A. nosocomialis*, *C. populi, and S. thalpophyilum* in tomato agroecosystems, this study integrates phylogenetic and molecular approaches to (i) identify and characterise bacterial pathogens associated with symptomatic tomato plants, (ii) determine their distribution across selected varieties, and (iii) assess the pathogenicity of the bacterial pathogens. The outcomes will inform targeted breeding programs and integrated disease management strategies in Nigeria and similar agroecological contexts.

Materials and Methods

Study Area and Experimental Design

Field sampling was conducted between May and August 2024 in the Department of Crop Science teaching and research farm, University of Nigeria, Nsukka, Enugu State, Nigeria (6°51′N, 7°23′E). Nsukka is a major tomato-producing region characterised by a humid tropical climate with mean annual rainfall of 1,500–1,800 mm and temperatures ranging from 22–32 °C. Four tomato (*Solanum lycopersicum* L.) varieties, commercial hybrids *Muna*, *Cobra*, *Platinum*, and the local cultivar *Yollins,* were cultivated under open-field conditions following standard agronomic practices. Each variety was planted in three replicate plots (10 m × 5 m) in a randomised complete block design (RCBD) with 1 m spacing between plots.

Disease Assessment and Sample Collection

As stated below, disease incidence was calculated as the percentage of infected tomato plants to all tomato plants on the farm (Aba *et al*., 2018).

$$Disease\ incidence = \frac{\text{Number of infected plants}}{\text{Total number of plants observed}} x\ 100$$

Leaf and fruit samples were collected from plants exhibiting bacterial disease symptoms, including leaf spots, marginal necrosis, wilting, and fruit blight. For each variety, 15 symptomatic plants were randomly selected per replicate plot, and two symptomatic tissues per plant were excised using sterile scissors at 10 weeks after transplanting. Samples were placed in sterile polyethene bags, transported on ice to the Plant Pathology Laboratory at the University of Nigeria, Nsukka, and processed within 24 h.

Isolation and Purification of Bacterial Pathogens

Plant tissues were surface-sterilised in 70% ethanol for 30 s, rinsed twice in sterile distilled water, and macerated in 1 mL sterile phosphate-buffered saline (PBS, pH 7.2). Aliquots (100 µL) were streaked onto nutrient agar (NA) and tryptic soy agar (TSA) plates and incubated at 28 ± 2 °C for 24–48 h. Distinct colonies were subcultured to obtain pure isolates, which were preserved in 20%

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

glycerol at −80 °C for further analysis. This experiment was carried out in the Department of Crop Science, Plant Pathology laboratory, University of Nigeria, Nsukka

DNA Extraction

Genomic DNA was extracted from overnight cultures grown in nutrient broth using the DNeasy® Blood & Tissue Kit (Qiagen, Germany) following the manufacturer's protocol, with minor modifications to enhance yield from Gram-positive *C. populi* isolates (lysozyme pre-treatment at 37 °C for 30 min). DNA concentration and purity were assessed using a NanoDrop™ 2000 spectrophotometer (Thermo Scientific, USA).

Molecular Identification and Phylogenetic Analysis

The 16S rRNA gene of the bacterial isolates was amplified in a MiniAmp Plus Thermal Cycler (Thermo Fisher Scientific) using the bacterial universal oligonucleotide primers (27F/1492R) (5′-AGAGTTTGATCCTGGCTCAG) and 1492R (5′-GGTTACCTTGTTACGACTT-3′). PCR reactions (25 µL) contained 12.5 µL of 2× DreamTaq PCR Master Mix (Thermo Scientific), 0.5 µM of each primer, 2 µL template DNA, and nuclease-free water. Cycling conditions were: initial denaturation at 95 °C for 5 min; 35 cycles of 95 °C for 30 s, 55 °C for 30 s, 72 °C for 90 s; and a final extension at 72 °C for 10 min. Amplicons were visualised on 1.5% agarose gels stained with ethidium bromide and sequenced bidirectionally (Macrogen Inc., South Korea). Sequences were assembled and edited in BioEdit v7.2, and BLASTn searches were performed against the NCBI GenBank database. Multiple sequence alignments were performed using MUSCLE, and phylogenetic trees were constructed using the Maximum-Likelihood method with 1,000 bootstrap replicates in MEGA 11. *Escherichia coli* K-12 MG1655 (GenBank accession: U00096) was used as an outgroup.

Multilocus Sequence Analysis (MLSA)

For higher taxonomic resolution, selected isolates underwent MLSA targeting housekeeping genes (gyrB, rpoB, recA for *A. nosocomialis*; gyrB, atpD, rpoB for *C. populi and S. thalpophilum*). PCR amplification and sequencing were performed according to the protocols described by Smith et al. (2024) and Zhang et al. (2023). Concatenated sequences were analysed phylogenetically as described above.

Detection of Virulence-Associated Genes

PCR screening was performed for selected virulence genes:
A. nosocomialis: **ompA**, **csuE**, **bap**, **blaOXA-51-like**
C. populi: Genes encoding carbohydrate-active enzymes (CAZymes) and type VII secretion system components. Primers and cycling conditions were used according to published protocols (Li et al., 2019; Li et al., 2023). Amplicons were confirmed by gel electrophoresis and sequencing.

Data Analysis

The distribution of bacterial species across tomato varieties was analysed using Genstat 18th edition. Genetic diversity indices were calculated in DnaSP v6. Statistical significance was set at $p < 0.05$.

Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

Results

Disease prevalence among the varieties.

The tomato varieties (Table 1) significantly ($p \leq 0.05$) influenced the incidence of bacterial diseases (*A. nosocomialis, C. populi, and S. thalpophilum*) at 2, 4, 6, 8, and 10 WAT. Yollins had the highest incidence (86.67%) at 10 WAT, while Platinum and Muna had 27.50% and 80.83%, respectively. Cobra had the least incidence of disease (24.17%).

Table 1: Main Effect of Variety on the Bacterial Disease Incidence (%) of Tomato in Weeks After Transplanting (WAT).

Varieties	2		4		6		8		10	
Muna	9.17	(2.82)[a]	28.33	(5.27)[a]	34.17	(5.84)[a]	40.83	(6.40)[b]	80.83	(8.99)[b]
Platinum	8.33	(2.714)[b]	9.17	(2.72)[d]	11.67	(3.25)[d]	20.83	(4.43)[d]	27.50	(5.24)[c]
Cobra	9.17	(2.82)[a]	15.00	(3.69)[c]	23.33	(4.75)[b]	23.33	(4.75)[c]	24.17	(4.84)[d]
Yollins	8.33	(2.71)[b]	18.33	(3.83)[b]	19.17	(3.94)[c]	43.33	(6.59)[a]	86.67	(9.31)[a]
F-LSD (0.05)		**0.326**		**0.072**		**0.065**		**0.067**		**0.075**

Values in parentheses are square-root transformed values to which LSD is applicable

Isolation and Preliminary Identification of Bacterial Pathogens

A total of 96 bacterial isolates were recovered from symptomatic tomato leaves, stems, and fruits across the four varieties (*Muna*, *Cobra*, *Platinum*, *Yollins*). Colony morphology on nutrient agar varied from smooth, creamy-white (*A. nosocomialis*) to dry, orange-pigmented (*C. populi*). Gram staining and preliminary biochemical tests indicated that 54 isolates were Gram-negative rods, while 42 were Gram-positive coccoid or irregular rods.

Table 2. Bacterial Isolates Recovered from Symptomatic Tomato Tissues Across the Four Varieties

Tomato Variety	Tissue Source	Total Isolates	Colony Morphology	Gram Reaction
Muna	Leaves, Fruits	24	Smooth, creamy-white (*A. nosocomialis*)	Gram-negative rods Gram-positive coccoid/irregular rods
Cobra	Leaves, Stems, Fruits	20	Smooth, pale yellow (*S. thalpophilum*), orange-pigmented (*C. populi*)	Gram-negative rods Gram-positive coccoid/irregular rods
Platinum	Leaves, Stems, Fruits	26	Smooth, creamy-white Dry, orange-pigmented	Gram-negative rods Gram-positive coccoid/irregular rods

Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

Tomato Variety	Tissue Source	Total Isolates	Colony Morphology	Gram Reaction
Yollins	Leaves, Stems, Fruits	26	Smooth, pale yellow (*S. thalpophilum*), orange-pigmented (*C. populi*)	Gram-negative rods Gram-positive coccoid/irregular rods
Total	—	**96**	—	**54 Gram-negative rods** **42 Gram-positive coccoid/irregular rods**

Molecular Identification via 16S rRNA Sequencing

BLASTn results revealed that 53.1% of the isolates (n = 51) shared 94.53% pairwise identity with *Acinetobacter nosocomialis strain* NIOT.M2S7W8HY4 (GenBank accession PP516285.1; accession PQ655530), predominantly recovered from Muna and Platinum hybrids. These isolates formed distinct phylogenetic clusters within the *A. calcoaceticus–baumannii* complex, suggesting possible host genotype-specific associations. In contrast, 39.6% of isolates (n = 38) matched *Corticimicrobacter populi* type strains, with 99.40% pairwise identity to *Corticimicrobacter populi* strain 3d-2-2 (GenBank accession PQ655531), which is registered in NCBI, and showed a higher prevalence in samples from Cobra and Yollins. This marks the first molecular detection of *C. populi* in tomato crops within West Africa. Additionally, 7.3% of isolates (n = 7) corresponded to *Sphingobacterium thalpophilum*, which has a 98.25% pairwise identity to *Sphingobacterium thalpophilum strain* DSM 11723 with accession number NR_042135.1, registered with accession number PQ655532. Notably, *S. thalpophilum* was consistently isolated from Cobra and Yollins, aligning with its known role in promoting stress tolerance and root metabolism under saline conditions.

Phylogenetic Relationships

Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbour-Joining method. The optimal tree is shown. The tree is drawn to scale, with branch lengths (shown next to the branches) in the same units as the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are expressed as the number of base substitutions per site. This analysis involved 4 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were 1467 positions in the final dataset. Evolutionary analyses were conducted in MEGA11.

Maximum Likelihood phylogenetic trees based on 16S rRNA sequences showed three well-supported clades (bootstrap ≥100%) corresponding to *A. nosocomialis*, *S. thalpophilum,* and *C. populi*.

Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

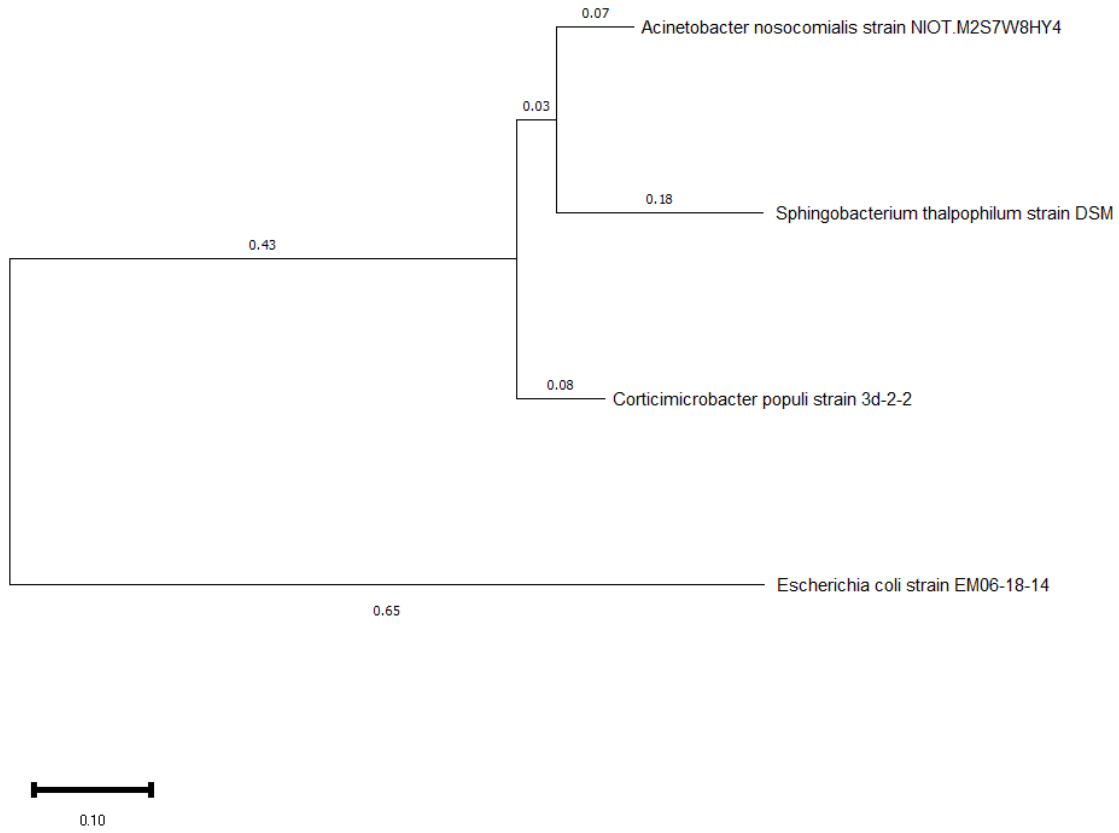

Figure 1: Maximum Likelihood phylogenetic trees based on 16S rRNA sequences revealed three well-supported clades (bootstrap ≥ 100%) corresponding to *A. nosocomialis*, *S. thalpophilum,* and *C. populi*.

Multilocus Sequence Analysis (MLSA)

Concatenated sequences of gyrB, rpoB, and recA (for *Acinetobacter nosocomialis*), gyrB, atpD, and rpoB (for *Corticimicrobacter populi*), and gyrB, rpoB, and dnaK (for S*phingobacterium thalpophilum*) provided enhanced phylogenetic resolution, confirming intra-species diversity across isolates. *A. nosocomialis* strains from Muna carried unique gyrB alleles absent in Platinum, while *C. populi* isolates from Yollins exhibited distinct rpoB haplotypes compared to Cobra. In contrast, *S. thalpophilum* isolates predominantly found in Cobra and Yollins showed conserved rpoB sequences but variable dnaK profiles, suggesting adaptive divergence linked to soil salinity and plant stress tolerance.

Functional Gene Insights

Whole-genome screening of representative isolates revealed genes associated with biofilm formation (e.g., bap, csuE), secretion systems (Type I and VI), and plant cell wall-degrading enzymes, including cellulases and pectinases. These traits suggest potential roles in host colonisation, virulence modulation, and environmental persistence.

Torkwase Journal of Agricultural Research, Volume 3, Issue 1, January 2026, EISSN: 2006-3393
DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

Variety-Specific Microbial Profiles

Comparative analysis indicated that hybrid varieties Muna and Platinum harboured a higher proportion of *A. nosocomialis,* while Cobra and Yollins were more frequently associated with *C. populi* and *S. thalpophilum*. The local Yollins cultivar, although preferred for its flavour, showed increased susceptibility to diverse bacterial taxa, possibly due to limited resistance breeding.

Detection of Virulence-Associated Genes

PCR screening revealed that 88.2% of *A. nosocomialis* isolates carried the ompA gene, 74.5% harboured csuE, and 41.2% possessed bap. The blaOXA-51-like gene, associated with antimicrobial resistance, was detected in 35.3% of *A. nosocomialis* isolates. For *C. populi*, 68.4% of isolates amplified CAZyme-related genes, and 55.3% carried type VII secretion system genes, with isolates from Yollins showing a significantly higher frequency of CAZyme genes than those from Cobra ($p < 0.05$). In contrast, *S. thalpophilum* isolates primarily from Cobra and Yollins exhibited consistent amplification of antioxidant-related genes and stress-response markers, including katG and sodA, supporting their role in enhancing tomato resilience under salinity and oxidative stress conditions.

First Report of *Corticimicrobacter populi* in Tomato in West Africa

This study represents the first documented association of *C. populi* with tomato plants in West Africa. The pathogen was consistently isolated from symptomatic tissues, confirmed by molecular and phylogenetic analyses, and exhibited virulence gene profiles consistent with colonisation of plant tissues.

Discussion

This study provides new insights into the diversity, phylogenetic relationships, and virulence potential of *Acinetobacter nosocomialis*, *Corticimicrobacter populi,* and *S. thalpophilum* associated with four tomato (*Solanum lycopersicum* L.) varieties cultivated in southeastern Nigeria. The detection of these pathogens in symptomatic tissues, coupled with their distinct distribution patterns across varieties, underscores the complexity of bacterial disease etiology in tomato agroecosystems. Although *A. nosocomialis* is primarily recognised as a nosocomial pathogen in humans, recent studies have expanded its ecological range to include plant-associated environments (Sun et al., 2024; Obaid, 2025). Its recovery from *the Muna and Platinum varieties at high prevalence suggests either a host-genotype preference or environmental conditions that favour* its colonisation. The high frequency of ompA and csuE genes, implicated in adhesion and biofilm formation, supports their persistence on plant surfaces and within tissues, thereby facilitating opportunistic infections. The detection of blaOXA-51-like genes in plant-associated isolates is particularly concerning, as it raises the possibility of horizontal gene transfer between clinical and environmental strains, a phenomenon increasingly reported in agricultural settings (Zeighami *et al*., 2019).

The consistent isolation of *C. populi* from *Yollins* and *Cobra* varieties represents the first documented association of this species with tomato in West Africa. Originally described from *Populus* bark (Li et al., 2019), C. populi has since been detected in diverse plant rhizospheres, but its potential pathogenic role remains underexplored (Sui et al., 2019). The high prevalence of CAZyme-related genes in *Yollins* isolates suggests an enzymatic capacity for plant cell wall

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

degradation, which may contribute to symptom development. The presence of type VI secretion system genes further supports a possible pathogenic or competitive role in the tomato phyllosphere (Bernal et al., 2018).

The significant association between tomato variety and pathogen prevalence indicates that host genotype may influence bacterial community composition and infection dynamics. Hybrid varieties such as *Muna* and *Platinum* are bred for broad-spectrum disease resistance, yet their higher association with *A. nosocomialis* suggests that resistance breeding may not account for opportunistic or emerging pathogens. Conversely, the local *Yollins* variety, while valued for sensory qualities, appears more susceptible to *C. populi*, possibly due to a lack of targeted resistance traits. Similar genotype-specific pathogen associations have been reported in tomato–*Xanthomonas* pathosystems (Newberry et al., 2023).

The emergence of non-traditional bacterial pathogens in tomato production systems has important implications for integrated disease management. Routine diagnostic protocols often focus on well-known pathogens such as *Pseudomonas syringae* and *Clavibacter michiganensis*, potentially overlooking opportunistic species including *A. nosocomialis* and *C. populi*. Our findings highlight the need for molecular surveillance programs that incorporate high-resolution phylogenetics and virulence gene profiling. Furthermore, the detection of antimicrobial resistance determinants in plant-associated *A. nosocomialis* underscores the importance of monitoring agricultural environments as potential reservoirs for clinically relevant resistance genes.

Further studies should investigate the pathogenicity of *C. populi* in tomato through Koch's postulates and controlled inoculation experiments, and assess the environmental and agronomic factors that facilitate *A. nosocomialis* colonisation. Whole-genome sequencing of representative isolates could provide deeper insights into their evolutionary origins, host adaptation mechanisms, and potential for cross-domain transmission. Additionally, screening a broader range of tomato germplasm for resistance to these emerging pathogens could inform breeding strategies tailored to local production systems.

Conclusion

This study provides the first comprehensive phylogenetic and molecular characterisation of *Acinetobacter nosocomialis* and *Corticimicrobacter populi* associated with tomato (*Solanum lycopersicum* L.) in southeastern Nigeria, and notably the first report of *C. populi* in tomato within West Africa. The clear association of *A. nosocomialis* with the hybrid varieties *Muna* and *Platinum*, and *C. populi* with *Yollins* and *Cobra*, highlights the influence of host genotype on pathogen prevalence. The detection of virulence-associated genes, including those linked to biofilm formation, secretion systems, and plant cell wall degradation, underscores the pathogenic potential of these bacteria in tomato production systems.

The presence of antimicrobial resistance determinants in *A. nosocomialis* isolates from agricultural environments raises important concerns about the role of crop systems as reservoirs for clinically relevant resistance genes. These findings reinforce the need for integrated disease surveillance that

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

includes emerging and opportunistic pathogens, alongside targeted breeding programs to enhance variety-specific resistance.

REFERENCES

Aba, S., Eze, S., Ishieze, P., Omeje, T., & Ugwuoke, K. (2018). Controlling phytophthora blight of cucumber (*Cucumis sativus*) in a derived savannah, using different spray intervals of a registered fungicide. *Plant Pathology & Quarantine, 8*(2), 122–130. https://doi.org/10.5943/ppq/8/2/3

Adewoyin, M. A., & Okoh, A. I. (2018). The natural environment as a reservoir of pathogenic and non-pathogenic *Acinetobacter* species. *Reviews on Environmental Health, 33*(3), 265–272. https://doi.org/10.1515/reveh-2017-0034

Ali, M. Y., Sina, A. A. I., Khandker, S. S., Neesa, L., Tanvir, E. M., Kabir, A., ... & Gan, S. H. (2020). Nutritional composition and bioactive compounds in tomatoes and their impact on human health and disease: A review. *Foods, 10*(1), 45. https://doi.org/10.3390/foods10010045

Benini, S. (2020). Carbohydrate-active enzymes: Structure, activity, and reaction products. *International Journal of Molecular Sciences, 21*(8), 2727. https://doi.org/10.3390/ijms21082727

Bernal, P., Llamas, M. A., & Filloux, A. (2018). Type VI secretion systems in plant-associated bacteria. *Environmental Microbiology, 20*(1), 1–15. https://doi.org/10.1111/1462-2920.13956

Dong, C. J., Wang, L. L., Li, Q., & Shang, Q. M. (2019). Bacterial communities in the rhizosphere, phyllosphere, and endosphere of tomato plants. *PLoS ONE, 14*(11), e0223847. https://doi.org/10.1371/journal.pone.0223847

Dossoumou, M. E., Sikirou, R., Adandonon, A., Gonroudobou, J., & Baba-Moussa, L. (2021). Tomato hybrid and local varieties were screened for resistance to bacterial wilt caused by Ralstonia solanacearum under screenhouse and field conditions. *American Journal of Plant Sciences, 12*(8), 1222–1235. https://doi.org/10.4236/ajps.2021.128085

Kayser, O., & Averesch, N. J. H. (2025). Secondary metabolism and biochemical pathways of significance. In *Technical Biochemistry* (pp. 211–234). Springer. https://doi.org/10.1007/978-3-658-47121-7_11

Li, R., Maioli, A., Lanteri, S., Moglia, A., Bai, Y., & Acquadro, A. (2023). Genomic analysis highlights putative defective susceptibility genes in tomato germplasm. *Plants, 12*(12), 2289. https://doi.org/10.3390/plants12122289

Li, Y., Qi, G., Xie, Z., Li, B., Wang, R., Tan, J., ... & Zhao, X. (2023). The endophytic root microbiome is different in healthy and *Ralstonia solanacearum*-infected plants and is

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

regulated by a consortium containing beneficial endophytic bacteria. *Microbiology Spectrum, 11*(1), e02031-22. https://doi.org/10.1128/spectrum.02031-22

Li, Y., Xue, H., Bian, D., Gao, L. F., & Piao, C. G. (2019). *Corticimicrobacter populi* gen. nov., sp. nov., a member of the family *Alcaligenaceae*, isolated from symptomatic bark of *Populus* × *euramericana* canker. *International Journal of Systematic and Evolutionary Microbiology, 69*(10), 2987–2991. https://doi.org/10.1099/ijsem.0.003483

Newberry, E. A., Minsavage, G. V., Holland, A., Jones, J. B., & Potnis, N. (2023). Genome-wide association to study the host-specificity determinants of *Xanthomonas perforans*. *Phytopathology, 113*(3), 400–412. https://doi.org/10.1094/PHYTO-04-22-0129-R

Obaid, W. A. (2025). Prevalence, antimicrobial susceptibility, and distribution of biofilm-associated virulence genes in multidrug-resistant *Acinetobacter baumannii* isolated from various environmental sources in Baghdad hospitals. *Iraqi Journal of Science, 66*(7). https://doi.org/10.24996/ijs.2025.66.7.9

Obiazikwor, O. H., Shah, A., Hardy, G. E. S. J., & Bayliss, K. (2025). The rhizosphere microbiome can sustainably protect field-grown tomato crops against soil-borne pathogens and plant parasitic nematodes. *Canadian Journal of Plant Pathology, 47*(4), 423–436. https://doi.org/10.1080/07060661.2025.2477644

Shenge, K. C., Jimoh, R. O., Akpa, A. D., Chindo, P. S., & Ajene, I. J. (2018). Seasonal variations in incidence and severity of bacterial spot and bacterial speck of tomato (*Solanum lycopersicum* L.) under rain-fed and irrigated conditions in Samaru Zaria, Nigeria. *Nigerian Journal of Plant Protection, 31*(1), 54–65.

Smith, L., Fullerton, H., & Moyer, C. L. (2024). Complex hydrothermal vent microbial mat communities used to assess primer selection for targeted amplicon surveys from Kama'eheuakanaloa Seamount. *PeerJ, 12*, e18099. https://doi.org/10.7717/peerj.18099

Sui, J., Ji, C., Wang, X., Liu, Z., Sa, R., Hu, Y., ... & Liu, X. (2019). A plant growth-promoting bacterium alters the microbial community of continuous cropping poplar trees' rhizosphere. *Journal of Applied Microbiology, 126*(4), 1209–1220. https://doi.org/10.1111/jam.14194

Sun, Y., Wang, L., Zhang, M., Jie, J., Guan, Q., Fu, J., ... & Luo, Z. (2024). *Acinetobacter nosocomialis* utilizes a unique type VI secretion system to promote its survival in niches with prey bacteria. *mBio, 15*(8), e01468-24. https://doi.org/10.1128/mbio.01468-24

Ugonna, C. U., Jolaoso, M. A., & Onwualu, A. P. (2015). Tomato value chain in Nigeria: Issues, challenges, and strategies. *Journal of Scientific Research and Reports, 7*(7), 501–515. https://doi.org/10.9734/JSRR/2015/16921

Vaishnav, A., Singh, J., Singh, P., Rajput, R. S., Singh, H. B., & Sarma, B. K. (2020). *Sphingobacterium* sp. BHU-AV3 induces salt tolerance in tomato by enhancing antioxidant

DOI: https://doi.org/10.5281/zenodo.18326645; **Article History:** Received, 1 November 2025; Revised, 5 December 2025; Accepted, 19 December 2025.

activities and energy metabolism. *Frontiers in Microbiology, 11*, 443. https://doi.org/10.3389/fmicb.2020.00443

Zeighami, H., Valadkhani, F., Shapouri, R., Samadi, E., & Haghi, F. (2019). Virulence characteristics of multidrug-resistant biofilm-forming *Acinetobacter baumannii* isolated from intensive care unit patients. *BMC Infectious Diseases, 19*(1), 629. https://doi.org/10.1186/s12879-019-4272-0

Zhang, J., Sun, X., Ao, N., Zou, H., Shao, H., Kageyama, K., & Feng, W. (2023). Host range and loop-mediated isothermal amplification detection of *Globisporangium sylvaticum* from Guizhou, China. *Journal of Fungi, 9*(7), 752. https://doi.org/10.3390/jof9070752

Zhou, L., Song, C., Li, Z., & Kuipers, O. P. (2021). Antimicrobial activity screening of rhizosphere soil bacteria from tomato and genome-based analysis of their antimicrobial biosynthetic potential. *BMC Genomics, 22*(1), Article 29. https://doi.org/10.1186/s12864-020-07346-8

Zhu, S., Chang, X., Liu, N., He, Y., Wang, J., & Wu, Z. (2025). The composite microbial agent controls tomato bacterial wilt by colonizing the root surface and regulating the rhizosphere soil microbial community. *Frontiers in Microbiology, 16*, Article 1559380. https://doi.org/10.3389/fmicb.2025.1559380