Original Article

Capsicum annuum PHYTOCHEMICALS AS POTENTIAL NATURAL ANTIMICROBIALS AGAINST SWEET POTATO POSTHARVEST ROT PATHOGENS

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ABSTRACT

Postharvest microbial spoilage is a major constraint to the storage stability of sweet potato (Ipomoea batatas), leading to significant economic losses, especially in tropical agricultural systems. Increasing concerns about food safety, environmental persistence, and resistance associated with synthetic preservatives have intensified the search for plant-derived antimicrobial alternatives. This study evaluated the phytochemical composition and antimicrobial activity of Capsicum annuum fruit extract against microorganisms associated with sweet potato rot. Ethyl acetate and methanolic extracts of C. annuum fruits were prepared by cold maceration and subjected to qualitative and quantitative phytochemical analysis. Rot-associated microorganisms were isolated from infected tubers and identified using morphological and biochemical methods, while antimicrobial activity was assessed using disc diffusion assays. Phytochemical screening revealed the presence of alkaloids, flavonoids, phenols, terpenoids, saponins, phytosterols, and cardiac glycosides, with higher concentrations of most compounds in the methanolic extract, particularly flavonoids, while eleven microorganisms were identified., Pathogenicity tests confirmed B. theobromae as the most aggressive rot pathogen. The extracts exhibited inhibitory activity against ten of the eleven isolates, with pronounced antifungal effects against R. arrhizus, A. niger, and B. theobromae, whereas A. flavus showed resistance. These results demonstrate that C. annuum possesses significant broad-spectrum antimicrobial potential to support its application as a natural bio-preservative for postharvest disease management in sweet potato storage systems.

KEYWORDS: **Capsicum Annuum; Sweet Potato Rot; Post-Harvest Pathogens; Phytochemical Composition; Natural Antimicrobial Agents**

INTRODUCTION

Postharvest losses remain a major global challenge, particularly in tropical regions such as sub-Saharan Africa and South Asia, where poor storage conditions and microbial spoilage can cause losses of 30–50% of root and tuber crops, with major economic and food-security consequences (Affognon et al., 2015; Shankar et al., 2024; Papoutsis et al., 2025).

Sweet potato (*Ipomoea batatas*) is important for rural livelihoods and nutrition because it adapts well to low-input, rain-fed systems and supplies calories, vitamins, minerals, and health-promoting phytonutrients. However, its roots are highly susceptible to mechanical injury and microbial invasion, resulting in substantial economic and nutrient losses (Paul et al., 2021). Synthetic fungicides such as carbendazim, imazalil, and thiabendazole are commonly used to control postharvest spoilage, but concerns about human health, environmental effects, resistant microbial strains, and consumer demand for residue-free produce limit their acceptability (Shankar et al., 2024). Advanced options such as controlled-atmosphere storage and irradiation are often unaffordable for smallholders (Kitinoja and Kader, 2015). Plant-based antimicrobials, therefore, offer a promising eco-friendly alternative. Secondary metabolites, including phenolics, flavonoids, alkaloids, and terpenoids, can disrupt microbial membranes and inhibit metabolic enzymes, and plant extracts have shown potential to suppress postharvest pathogens and extend produce shelf life (Papoutsis et al., 2025; Oke and Workneh, 2019; Oke and Workneh, 2013; Cowan, 1999).

Capsicum annuum contains capsaicinoids, flavonoids, and phenolic acids with documented antimicrobial properties and potential applications in natural food preservation (Materska and Perucka, 2005; Othman et al., 2011; Wahyuni et al., 2011; Olatunji and Afolayan, 2018). However, evidence on its activity against sweet potato rot inducing microorganisms and the relationship between its phytochemical composition and antimicrobial effects remains limited, particularly in tropical systems such as Nigeria. Therefore, this study aimed to evaluate the phytochemical composition of *C. annuum* fruit extracts and assess their antimicrobial activity against bacterial and fungal pathogens associated with sweet potato rot.

MATERIALS AND METHODS

Study Area and Sample Collection

Rotten sweet potato (*Ipomoea batatas*) samples were collected from major sweet potato producing Local Government Areas (LGAs) in Benue State, Nigeria. All laboratory procedures were conducted at the Microbiology and Plant Biochemistry Laboratories of the Rev. Fr. Moses Orshio Adasu University, Makurdi, Nigeria, following standard ethical and biosafety protocols.

Plant Extraction and Phytochemical Screening

Air-dried *Capsicum annuum* fruits were pulverized to powder using a clean kitchen blender. A 1000 g portion of the powdered sample was separately extracted with 2000 mL of ethyl acetate and methanol (1:2 w/v), a solvent-to-sample ratio selected to facilitate the extraction of polar and semi-polar phytochemicals (Do et al., 2015; Sultana et al., 2009). Cold maceration was carried out for 24 h at 25–28°C with agitation at 2 h intervals. Each extraction was performed in triplicate under identical conditions, and the resulting extracts were processed independently to ensure experimental reproducibility.

Mixtures were filtered through Whatman No. 1 paper, concentrated under

reduced pressure at 40°C using a rotary evaporator, and dried to constant weight. The percentage yield of each extract was calculated using the formula given by equation (1).

$$\text{Extract yield (\%)} = \frac{\text{Weight of dried extract}}{\text{Weight of plant material)}} \times 100 \text{ (Igoli et al., 2016; Sultana } \textit{et al.}\text{, 2009)} \quad (1)$$

Extraction yields from the three replicates were expressed as mean ± standard deviation, with variation maintained below 5%.

Preliminary Phytochemical Screening

Ethyl acetate and methanolic extracts were qualitatively screened for alkaloids, flavonoids, saponins, tannins, phenols, terpenoids, phytosterols, and cardiac glycosides using standard procedures (Harborne, 1998; Trease and Evans, 2002).

Alkaloids were tested for using the Dragendorff's reagent; flavonoids by the alkaline reagent test; saponins by persistent frothing; and tannins and phenolic compounds with ferric chloride. Positive reactions were identified by the characteristic precipitates, colour changes, or foam specified in the standard protocols. Terpenoids were assessed by the Salkowski test, phytosterols by the Liebermann–Burchard reaction, and cardiac glycosides by Keller–Killiani's test.

Quantitative Phytochemical Analysis

Selected phytochemicals in both extracts were quantified using established spectrophotometric or gravimetric procedures.

Total phenolics were determined by the Folin–Ciocalteu method at 765 nm using gallic acid as standard and expressed as mg GAE/g (Molole et al., 2022).

Total flavonoids were determined by the aluminium chloride colorimetric method at 415 nm using quercetin as a standard and expressed as mg QE/g (Aryal et al., 2019).

Saponins were quantified gravimetrically after aqueous-ethanol extraction and partitioning with diethyl ether and n-butanol; the final residue was expressed as percentage saponin content (Fang et al., 2026).

Alkaloids were determined by the acid–base gravimetric method using acidic ethanol and ammonium hydroxide precipitation (Sodimu et al., 2024).

Terpenoids and phytosterols were quantified spectrophotometrically from calibration curves prepared with appropriate reference compounds (Saptarini et al., 2016).

Microbial Isolation and Identification

A total of 180 rot-infected sweet potato (*Ipomoea batatas*) tubers were collected from three farmers in each of four major sweet potato producing LGAs—Konshisha, Kwande, Makurdi, and Vandeikya—over three sampling periods, with five tubers collected per farmer per period. Samples were transported in sterile polyethylene bags and processed within 24 h.

Approximately 5 × 5 mm tissue sections were aseptically excised from advancing rot margins, surface-sterilized in 5% sodium hypochlorite for 3 min, rinsed with sterile distilled water, and blotted dry (Krieg and Holt, 1984).

Sterilized tissues were plated on nutrient agar for bacteria and streptomycin-supplemented potato dextrose agar for fungi. Plates were incubated at 28 ± 2°C for 24–48 h (bacteria) or 3–5 days (fungi), and distinct colonies were repeatedly sub-cultured to purity (Krieg and Holt, 1984).

Bacteria were identified from colony morphology, Gram reaction, and catalase, oxidase, citrate, and sugar-fermentation tests following Bergey's Manual. Fungi were identified from colony features and microscopic spore morphology using lactophenol cotton blue staining (Barnett and Hunter, 1972).

Pathogenicity was evaluated on fresh, healthy sweet potato tubers. Tubers were washed, surface-sterilized with 70% ethanol, air-dried under sterile conditions, and wounded to approximately 5 mm depth with a sterile cork borer.

Each wound received 0.1 mL of a microbial suspension adjusted to approximately 10^6 CFU/mL for bacteria or an equivalent fungal spore suspension; controls received sterile distilled water.

Inoculated tubers were incubated at 28 ± 2°C under high humidity for 5–7 days. Rot development was monitored, lesion dimensions measured, and organisms re-isolated to satisfy Koch's postulates (Ross and Woodward, 2016; Krieg and Holt, 1984).

Antimicrobial Assay

The antimicrobial activity of ethyl acetate and methanolic extracts of *C. annuum* fruits was evaluated using the agar disc diffusion method against bacterial and fungal isolates obtained from infected sweet potato tubers. Bacterial assays used nutrient agar and fungal assays potato dextrose agar. Fresh inocula were suspended in sterile saline and adjusted to 0.5 McFarland standard (≈10^8 CFU/mL for bacteria) (Sanders, 2012). Sterile 6 mm filter-paper discs were impregnated with about 20 µL of extract at 25, 50, 75, and 100 mg/mL, dried under sterile conditions, and placed on inoculated agar (Sharifi-Rad et al., 2015; Seleshe and Kang, 2019).

Crude extracts were reconstituted in their respective solvents and standardized to defined concentrations before application to ensure treatment comparability. Plates were incubated at 37°C for 24 h for bacteria and 28°C for 72 h for fungi. Inhibition zones were measured in millimetres with a digital caliper; all assays were performed in triplicate. Ciprofloxacin (10 µg/disc) and fluconazole (10 µg/disc) were used as positive controls for bacterial and fungal isolates, respectively, while discs containing only the extraction solvents served as negative controls.

Statistical Analysis

All experiments were performed in triplicate, and results were expressed as mean ± standard deviation. Statistical analysis was conducted using one-way analysis of variance (ANOVA), and differences between means were considered significant at $p < 0.05$.

RESULTS

Plant Extracts and Phytochemical Profile

The percent yield of ethyl acetate (EA) and methanol (MeOH) crude extracts of *C. annuum* fruit and the phytochemical composition are presented in Tables 1. The ethyl acetate extract yielded 3.87 ± 0.12%, while the methanolic extract yielded 3.08 ± 0.10% from 1000 g of dried plant material.

Qualitative phytochemical screening revealed the presence of alkaloids, cardiac glycosides, flavonoids, phenols, phytosterols, saponins, and terpenoids in both extracts. Tannins were absent in both the ethyl acetate and methanol extracts. Flavonoids and saponins appeared more pronounced in the methanol extract (denoted as "++") compared to the ethyl acetate extract (denoted as "+"), suggesting that *C. annuum* is particularly rich in these compounds (Table 1).

Table 1: Extract Yield and Qualitative Phytochemical Composition of Capsicum annuum Fruit Extracts

Phytochemical	Ethyl acetate extract	Methanol extract
Yield (%)	3.87 ± 0.12	3.08 ± 0.10
Alkaloids	+	+
Flavonoids	+	++
Phenolic compounds	+	+
Terpenoids	+	+
Saponins	+	++
Phytosterols	+	+
Cardiac glycosides	+	+
Tannins	–	–

+ = present; – = absent

Quantitative phytochemical analysis

Quantitative analysis showed solvent-dependent differences in phytochemical concentrations (Table 2). Calibration plots were highly linear (R^2 > 0.99), supporting the reliability of the spectrophotometric determinations.

Methanol yielded slightly more alkaloids (1.13 ± 0.02 mg g^{-1}) than ethyl acetate (1.02 ± 0.03 mg g^{-1}), whereas flavonoids were higher in ethyl acetate (0.76 ± 0.03 mg g^{-1}) than methanol (0.57 ± 0.01 mg g^{-1}). Methanol extracted higher levels of cardiac glycosides (1.35 ± 0.02 vs 0.75 ± 0.01 mg g^{-1}) and phenolic compounds (1.05 ± 0.01 vs 0.76 ± 0.01 mg g^{-1}) than ethyl acetate. Methanol also gave higher phytosterols (1.46 ± 0.03 vs 1.20 ± 0.06 mg g^{-1}), saponins (1.25 ± 0.08 vs 1.14 ± 0.02 mg g^{-1}), and terpenoids (1.17 ± 0.13 vs 0.64 ± 0.01 mg g^{-1}). Tannins were absent from both extracts. Overall, methanol recovered higher concentrations of most quantified phytochemicals, while the results also showed compound-specific solvent effects (Table 2).

Table 2: Quantitative Phytochemical Composition of Capsicum annuum Fruit Extracts

Phytochemical	Ethyl acetate extract (mg g^{-1})	R^2	Methanol extract (mg g^{-1})	R^2
Alkaloids	1.02 ± 0.03		1.13 ± 0.02	
Flavonoids	0.76 ± 0.03	0.9943	0.57 ± 0.01	0.9928
Cardiac glycosides	0.75 ± 0.01	0.9978	1.35 ± 0.02	0.9965
Phenolic compounds	0.76 ± 0.01	0.9960	1.05 ± 0.01	0.9940
Phytosterols	1.20 ± 0.06	0.9936	1.46 ± 0.03	0.9952
Saponins	1.14 ± 0.02		1.25 ± 0.08	

Phytochemical	Ethyl acetate extract (mg g^{-1})	R^2	Methanol extract (mg g^{-1})	R^2
Terpenoids	0.64 ± 0.01	0.9951	1.17 ± 0.13	0.9939

Values represent mean ± standard deviation of three replicates.

Microbial Isolates from Sweet Potato Tubers

Descriptions of colony and morphological characteristics of the isolated microorganisms are presented in Table 3. Organisms with similar features were grouped together and allocated codes for onward identification tests. Three bacteria and eight fungi groups were coded, resulting in a total of eleven (11) organism types.

Biochemical analysis of the bacterial isolates (Table 3) revealed that all three were Gram-positive. Isolate MdSc was identified as Gram-positive tiny cocci in chains, Z as clustered cocci, and CDC as sarcina cocci. Isolate Z was positive to catalase test, whereas CDC and MdSc were negative. Based on colony characteristics, Gram staining reactions, and biochemical test results, the bacterial isolates were identified as *Sarcina spp.*, *Staphylococcus aureus*, and *Streptococcus spp*. Fungal identification confirmed the coded isolates as *Penicillium notatum*, *Rhizopus arrhizus*, *Aspergillus wentii*, *Absidia corymbifera*, *Penicillium frequentans*, *Aspergillus flavus*, *Botryodiplodia theobromae*, and *Aspergillus Niger*.

Table 3: Microorganisms Isolated from Infected Sweet Potato Tubers

Isolate Code	Microorganism	Classification	Identification Basis
Z	*Staphylococcus aureus*	Bacteria	Morphology and biochemical tests
MdSc	*Streptococcus* spp.	Bacteria	Morphology and biochemical tests
CDC	*Sarcina* spp.	Bacteria	Morphology and biochemical tests
Noni	*Botryodiplodia theobromae*	Fungus	Microscopic morphology
VDW	*Rhizopus arrhizus*	Fungus	Microscopic morphology
AN	*Aspergillus niger*	Fungus	Microscopic morphology
GM	*Aspergillus flavus*	Fungus	Microscopic morphology
PN	*Penicillium notatum*	Fungus	Microscopic morphology
BLM	*Penicillium frequentans*	Fungus	Microscopic morphology
WA	*Aspergillus wentii*	Fungus	Microscopic morphology
WHITE	*Absidia corymbifera*	Fungus	Microscopic morphology

Pathogenicity Test

Among bacteria, *Staphylococcus aureus* produced the greatest lesions (1.5 cm depth; 0.8 cm width), followed by *Sarcina spp.* (0.7; 0.5 cm) and *Streptococcus spp.* (0.5; 0.2 cm), while in the fungi family, *B. theobromae* was the most aggressive pathogen (2.2 cm depth; 1.9 cm width), followed by *A. corymbifera* (1.0; 0.9 cm). *P. notatum* and *A. flavus* produced the smallest lesions. Combined fungal inoculation produced 1.5 cm width and 0.8 cm depth, while combined bacteria produced 0.6 and 0.5 cm, respectively (Table 4).

Table 4: Pathogenicity of Microbial Isolates on Healthy Sweet Potato Tubers

Microorganism	Rot width (cm)	Rot depth (cm)	Pathogenicity level
Bacteria			
Staphylococcus aureus	0.80 ± 0.06	1.50 ± 0.10	High
Sarcina spp.	0.50 ± 0.04	0.70 ± 0.05	Moderate
Streptococcus spp.	0.20 ± 0.02	0.50 ± 0.04	Low
All bacteria (combined)	0.60 ± 0.05	0.50 ± 0.04	Moderate
Fungi			
Absidia corymbifera	0.90 ± 0.07	1.00 ± 0.08	High
Penicillium frequentans	0.40 ± 0.03	0.70 ± 0.05	Moderate
Aspergillus niger	0.40 ± 0.03	0.50 ± 0.04	Moderate
Aspergillus wentii	0.50 ± 0.04	0.40 ± 0.03	Moderate
Penicillium notatum	0.50 ± 0.04	0.30 ± 0.02	Moderate
Aspergillus flavus	0.20 ± 0.02	0.50 ± 0.04	Low
Botryodiplodia theobromae	1.90 ± 0.12	2.20 ± 0.15	High
All fungi (combined)	1.50 ± 0.10	0.80 ± 0.06	High

Values represent mean lesion dimensions measured after incubation**.**

Antimicrobial Activity

The antimicrobial activity of *C. annuum* extracts against eleven sweet potato pathogenic microorganisms showed variable inhibition patterns across species and extract dilutions (Table 5). Results were presented as mean ± SEM, and differences between groups were determined using One-Way ANOVA with Tukey post hoc test ($p < 0.05$). Generally, the control antibiotics (Ciprofloxacin for bacteria and Fluconazole for fungi) produced higher inhibition zones compared to the extracts. However, certain pathogens responded strongly to the plant extract.

Rhizopus arrhizus demonstrated the highest sensitivity, with the extract stock showing excellent inhibition (6.50 ± 0.22 mm), achieving 134.24% of the control zone, effectively surpassing the standard antifungal agent. *A. niger* also showed excellent inhibition with the extract stock (5.10 ± 0.17 mm, 94.00% of control), which was comparable to the control (5.50 ± 0.00 mm). *A. orymbifera* recorded 93.25% inhibition relative to control, though its response pattern was unusual, showing 2.50 ± 1.12 mm at stock concentration but increasing to 5.67 ± 0.21 mm at the 10^2 dilution. *P. notatum* exhibited good inhibition (6.33 ± 0.21 mm, 89.91% of control), while *P. frequentans* (5.83 ± 0.17 mm, 79.10%) and *B. theobromae* (5.00 ± 0.00 mm, 85.64%) displayed good to moderate inhibition. *A. wentii* showed moderate inhibition (3.33 ± 1.05 mm, 58.13% of control).

Bacterial pathogens showed only mild inhibition relative to controls. *Sarcina spp.* exhibited inhibition zones of 6.17 ± 0.17 mm at stock concentration, representing 39.78% of the control (24.71 ± 0.21 mm). *S. aureus* showed 6.67 ± 0.21 mm inhibition (25.95% of control). *Streptococcus spp*. showed no inhibition at stock concentration (0.00 ± 0.00 mm, 32.79% of control), though inhibition appeared at higher dilutions (75 mg/mL: 6.00 ± 0.26 mm; 100 mg/mL: 7.50 ± 0.22 mm).

Aspergillus flavus was completely resistant to the extract and all its dilutions, showing no zone of inhibition at any concentration tested (0.00 ± 0.00 mm),

though it was sensitive to the control antifungal agent (6.12 ± 0.17 mm).

Statistical analysis revealed significant differences ($p < 0.05$) among the inhibition zones produced by *C. annuum* extracts across different microbial species and extract concentrations. The variation in susceptibility among isolates was significant, indicating species-specific responses to the phytochemical constituents of the extract. Dose-dependent relationships were observed for several susceptible organisms, with decreasing inhibition zones corresponding to increasing dilution factors.

Table 5: Inhibitory Activity (mm) and MIC (mg/mL) of Capsicum annuum extracts against Sweet Potato Rot Microorganisms

Microorganism	Stock (SK)	25 mg/mL	50 mg/mL	75 mg/mL	100 mg/mL	MIC (mg/mL)	Positive control
Staphylococcus aureus	6.67 ± 0.21[a]	6.33 ± 0.21[a]	6.17 ± 0.17[a]	5.17 ± 0.17[a]	5.00 ± 0.00[a]	25	25.70 ± 0.22
Streptococcus spp.	0.00 ± 0.00[b]	–	5.33 ± 0.21[c]	6.00 ± 0.26[c]	7.50 ± 0.22[c]	50	22.87 ± 0.76
Sarcina spp.	6.17 ± 0.17[a]	6.33 ± 0.21[a]	6.33 ± 0.21[a]	8.17 ± 0.48[b]	9.83 ± 0.60[c]	25	24.71 ± 0.21
Botryodiplodia theobromae	5.00 ± 0.00[a]	5.17 ± 0.17[a]	5.67 ± 0.21[a]	4.50 ± 0.92[a]	5.17 ± 0.17[a]	25	6.62 ± 0.17
Rhizopus arrhizus	6.50 ± 0.22[a]	–	–	0.83 ± 0.83[b]	–	75	5.46 ± 0.21
Aspergillus niger	5.17 ± 0.17[a]	4.17 ± 0.83[a]	1.67 ± 1.05[b]	1.67 ± 1.05[b]	1.67 ± 1.05[b]	25	5.50 ± 0.00
Aspergillus flavus	–	–	–	–	–	Resistant	6.12 ± 0.17
Penicillium notatum	6.33 ± 0.21[a]	6.17 ± 0.31[a]	5.83 ± 0.17[a]	5.33 ± 0.21[a]	5.00 ± 0.00[a]	25	7.04 ± 0.22
Penicillium frequentans	5.83 ± 0.17[a]	5.50 ± 0.22[a]	5.50 ± 0.22[a]	4.17 ± 0.83[a]	5.50 ± 0.22[a]	25	7.37 ± 0.22
Aspergillus wentii	3.33 ± 1.05[a]	5.33 ± 0.21[a]	5.50 ± 0.22[a]	5.17 ± 0.17[a]	5.33 ± 0.21[a]	25	9.46 ± 0.22
Absidia corymbifera	2.50 ± 1.12[a]	5.00 ± 0.00[a]	5.67 ± 0.21[a]	2.50 ± 1.12[b]	3.33 ± 1.05[b]	25	6.08 ± 0.17

Values represent Inhibition zone diameter (mm). – = no inhibition observed.
Positive Control: ciprofloxacin (bacteria) or fluconazole (fungi).
Values represent mean inhibition zone diameter ± SEM (mm).
Values with different superscript letters (a–c) within rows differ significantly ($p < 0.05$, ANOVA with Tukey post-hoc test).

DISCUSSION

Phytochemical Composition of C. annuum Extracts

The phytochemical screening of *C. annuum* fruit extracts confirmed presence of diverse array of bioactive secondary metabolites, including alkaloids, flavonoids, phenolic compounds, terpenoids, saponins, phytosterols, and cardiac glycosides. Quantitative analysis further revealed that the methanolic extract contained relatively higher concentrations of most phytochemicals compared to the ethyl acetate extract, particularly flavonoids and phytosterols, indicating that solvent polarity plays a critical role in extraction efficiency.

The enhanced recovery observed with methanol can be attributed to its ability to solubilize polar and semi-polar compounds such as phenolics, glycosides, and flavonoids. This observation is consistent with established phytochemical extraction principles, where polar solvents typically yield higher concentrations of

biologically active compounds (Do et al., 2015; Sasidharan et al., 2011). The relatively high abundance of these compounds suggests that *C. annuum* possesses a chemically rich profile capable of supporting multiple biological activities.

From a mechanistic perspective, phenolic compounds and flavonoids are known to exert antimicrobial effects through membrane destabilization, inhibition of nucleic acid synthesis, and interference with key metabolic enzymes (Cushnie and Lamb, 2005; Górniak et al., 2019; Liu et al., 2025). In addition, terpenoids and alkaloids may disrupt membrane permeability and cellular homeostasis, while saponins can interact with membrane sterols, leading to increased permeability and eventual cell lysis (Cowan, 1999; Masyita et al., 2022; Huang *et al*., 2022). The coexistence of these compounds suggests that the antimicrobial activity of *C. annuum* extracts is likely mediated through multiple complementary mechanisms rather than a single pathway.

Importantly, beyond general phytochemical classes, *C. annuum* is known to contain capsaicinoids, particularly capsaicin, which represents a major bioactive compound responsible for its antimicrobial activity. Capsaicin has been reported to disrupt microbial membrane integrity, alter ion transport, and interfere with energy metabolism, thereby contributing significantly to microbial inhibition (Shan et al., 2007; Periferakis et al., 2023; Ekom et al., 2021). The presence of capsaicinoids alongside phenolic compounds may therefore enhance the overall antimicrobial potency of the extract through synergistic interactions.

Antimicrobial Activity of C. annuum Extracts

The antimicrobial assays demonstrated that *C. annuum* extract exhibited inhibitory activity against the majority of the isolated microorganisms, with a clear pattern of stronger antifungal activity compared to antibacterial effects. Fungal pathogens such as *Rhizopus arrhizus*, *Aspergillus niger*, and *Botryodiplodia theobromae* showed pronounced susceptibility, whereas bacterial isolates exhibited relatively mild inhibition.

This differential susceptibility can be explained by structural and physiological differences between fungal and bacterial cells. Fungal organisms possess ergosterol-rich cell membranes and filamentous growth structures that are more susceptible to disruption by phytochemicals such as phenolics, terpenoids, and saponins (Cowan, 1999; Pinto et al., 2009; Khan et al., 2010). In contrast, bacterial cells may exhibit greater resistance due to differences in cell wall architecture and intrinsic defense mechanisms, including efflux systems and permeability barriers (Nikaido, 2003; Cox and Wright, 2013).

The observed antimicrobial activity can be directly linked to the phytochemical composition of the extracts. Phenolic compounds and flavonoids may inhibit microbial enzymes involved in energy metabolism and cellular replication (Cushnie and Lamb, 2005; Liu et al., 2025), while alkaloids and capsaicinoids can interfere with membrane integrity and intracellular processes (Shan et al., 2007; Periferakis et al., 2023). Tannins, where present, may further contribute by forming complexes with microbial proteins and enzymes, thereby inhibiting growth and metabolic activity (Cowan, 1999; Tajkarimi et al., 2010). The combined presence of these compounds supports a multi-target mode of action.

Notably, the resistance observed in *Aspergillus flavus* may be attributed to

intrinsic resistance mechanisms, including the production of detoxifying enzymes and protective metabolic systems capable of neutralizing plant-derived antimicrobial compounds (Westrick et al., 2021; Shishodia et al., 2019). Such resistance highlights the importance of understanding species-specific responses when developing plant-based antimicrobial strategies.

Implications for Postharvest Disease Management

The findings in this research support the potential of *C. annuum* extracts as natural agents for postharvest disease management. Their diverse bioactive constituents may act through multiple targets, potentially reducing the likelihood of resistance (Cowan, 1999; Burt, 2004).

The stronger antifungal activity is particularly relevant because fungi are major drivers of sweet potato spoilage during storage; suppression of these pathogens could delay rot progression and extend tuber storage life. Plant-derived antimicrobials may also offer lower environmental impact, reduced toxicity, and greater consumer acceptance than synthetic preservatives (Burt, 2004). *C. annuum*, a locally available bio-material, could therefore be useful where advanced storage technologies are inaccessible. However, these results derive from in vitro assays and may not fully predict performance under storage conditions; the specific active compounds were also not isolated or individually characterized.

For scalable postharvest use the extract, further research is neeeded to isolate and characterize active constituents, clarify mechanisms of action, test effectiveness under practical storage conditions, and optimize formulations and application strategies.

CONCLUSION

This study has demonstrated that *C. annuum* extract possesses significant antimicrobial potential against key microorganisms implicated in postharvest sweet potato rot. The isolation and pathogenicity assessment of bacterial and fungal species confirmed the complexity of microbial involvement in tuber deterioration and highlight the importance of effective control strategies in postharvest systems.

Phytochemical analysis revealed that *C. annuum* fruit extracts contain a diverse range of bioactive compounds, including alkaloids, flavonoids, phenolic compounds, terpenoids, saponins, cardiac glycosides, and phytosterols, with higher concentrations generally observed in the methanolic extract. These compounds are known to exert antimicrobial effects through multiple mechanisms, which likely contributed to the inhibitory activity observed in this study.

The extracts exhibited measurable antimicrobial activity against most of the isolated pathogens, with stronger effects observed against fungal species than bacterial isolates. This selective antifungal activity, supported by statistically significant differences ($p < 0.05$) and observable concentration-dependent responses, underscores the potential effectiveness and reproducibility of *C. annuum* as a natural antimicrobial agent.

Overall, the findings highlight *C. annuum* as a promising, low-cost, and environmentally friendly candidate for the development of plant-based preservatives for postharvest disease management, especially against sweet potato rot. However, further studies are required to isolate and characterize the active compounds, elucidate their mechanisms of action, and evaluate their performance under practical storage conditions. Such efforts will be essential for translating these findings into scalable solutions for reducing postharvest losses and enhancing food security.

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