



## Prevalence and Molecular Characterization of Fungal Uropathogens among Young Female Adults in Ikorodu, Lagos State, Nigeria: An Unexpected Predominance of *Aspergillus* Species

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### ABSTRACT

Urinary tract infections (UTIs) represent a significant health concern among young female adults globally. While bacterial pathogens dominate UTI etiology, fungal organisms have become increasingly important uropathogens, particularly in specific patient populations. This study investigated the prevalence of UTI among young female adults in Ikorodu, Lagos State, Nigeria, and characterized isolated fungal organisms using molecular techniques. A cross-sectional study was conducted involving 87 young female adults aged 15-30 years between February and April 2023. Mid-stream urine samples were collected and processed using standard microbiological techniques. Fungal isolates were identified through conventional methods and confirmed using PCR-RFLP and DNA sequencing of the ITS region. The overall UTI prevalence was 58.62% (51/87 cases), with the highest prevalence in women aged 21-25 years (31.03%) and married participants (34.48%). Seven distinct fungal species were isolated and molecularly characterized, with *Aspergillus niger* being the most prevalent (21.57%), followed by *A. welwitschiae* (19.61%), *Aspergillus tubingensis* (15.69%), *A. aculeatus* (13.73%), *A. tamarii* (11.77%), *A. sclerotiorum* (9.8%), and *Penicillium citrinum* (7.84%). *Aspergillus* species comprised 88.24% of all isolates. This study reveals an alarmingly high prevalence of fungal presence in urine samples among young female adults, with an unprecedented predominance of *Aspergillus* species rather than the typically expected *Candida* species. These findings raise important questions about environmental contamination, opportunistic infections, and regional epidemiological patterns requiring further investigation.

**Keywords:** Urinary tract infection, fungal pathogens, *Aspergillus* species, molecular characterization, epidemiology

### Introduction

Despite the global burden of UTIs, there remains limited data on the epidemiology and mycological characteristics of fungal uropathogens in tropical African settings, particularly Nigeria. Urinary tract infections (UTIs) constitute one of the most prevalent infectious diseases worldwide, affecting millions of individuals annually and representing a significant burden on global healthcare systems (Yang *et al.*, 2022; He *et al.*, 2025).

These infections are particularly common among women, with anatomical, physiological, and behavioural factors contributing to their increased susceptibility (Medina and Castillo-Pino, 2019). The economic impact of UTIs is substantial, with healthcare costs in the United States alone exceeding \$1.6 billion annually, making them one of the most expensive medical conditions across all age groups (Foxman, 2014; Stamm & Norrby, 2001).

The pathophysiology of UTIs involves the invasion and multiplication of microorganisms within the urinary tract, typically ascending from the periurethral area to the bladder and potentially to the upper urinary tract (Flores-Mireles *et al.*, 2015; Nielubowicz & Mobley, 2010). The epidemiology of UTIs varies significantly across different populations and geographical regions (Medina & Castillo-Pino, 2019; Tandogdu & Wagenlehner, 2016). In young, healthy women, the incidence of uncomplicated cystitis averages 0.5 episodes per person per year, with the highest rates occurring in sexually active women aged 18-39 years (Gupta *et al.*, 2011; Scholes *et al.*, 2000).

Risk factors for UTI development in women include female anatomy with the short urethra facilitating bacterial ascension, sexual activity which can introduce bacteria into the urinary tract, use of spermicides and diaphragms which alter vaginal flora, menopause leading to decreased oestrogen levels and changes in the urogenital environment, and poor personal hygiene practices (Hooton, 2012; Foxman, 2010). Additional risk factors include diabetes mellitus, urinary tract abnormalities, immunosuppression, catheterization and other urological procedures, and a previous history of UTIs (Grigoryan *et al.*, 2014; Nicolle, 1987; Zhai *et al.*, 2021; Walker *et al.*, 2016).

While bacteria remain the predominant cause of UTIs, fungal organisms have gained recognition as significant uropathogens, particularly in specific patient populations (Achkar & Fries, 2010; Lundstrom & Sobel, 2001). *Candida* species are the most commonly isolated fungal uropathogens, with *C. albicans* being the most frequent.

However, non-*Candida* species of fungi including various *Aspergillus* species, have been increasingly reported as causes of urinary tract infections, particularly in immunocompromised patients and those with structural urinary tract abnormalities (Weinberger *et al.*, 2003; Rivett *et al.*, 1986). The pathogenesis of fungal UTIs differs from bacterial infections in several important ways (Paul *et al.*, 2003; Bounoux *et al.*, 2010). Fungal organisms typically have different virulence factors, including the ability to form biofilms on medical devices and mucosal surfaces, which contribute to treatment resistance and recurrent infections (Costa *et al.*, 2022). The host immune response to fungal pathogens also differs, often requiring both innate and adaptive immune mechanisms for effective clearance (Pfaller & Diekema, 2007; Wisplinghoff *et al.*, 2004).

*Aspergillus* species are primarily recognized as environmental saprophytes and opportunistic pathogens causing respiratory infections in immunocompromised hosts. However, isolated renal and urinary tract aspergillosis, while rare, has been documented in the literature (Bongomin *et al.*, 2023). Recent research has highlighted the complex biology, immunopathogenicity, and drug resistance patterns of *Aspergillus fumigatus* and related species (van de Veerdonk *et al.*, 2025). The clinical significance of *Aspergillus* species isolated from urine samples remains controversial, as these organisms may represent environmental contamination, colonization, or true infection depending on clinical context.

Understanding regional variations in UTI etiology is crucial for developing appropriate diagnostic and therapeutic strategies. This study aims to address this knowledge gap by investigating the prevalence and molecular characterization of fungal organisms isolated from urine samples of young female adults in Ikorodu, Lagos State, Nigeria.

## Materials and Methods

### Study Design and Ethical Considerations

This comprehensive cross-sectional study was conducted between February and April 2023 in Ikorodu, Lagos State, Nigeria. The study protocol was reviewed and approved by the Biological Sciences Ethics Committee at Crescent University's College of Natural and Applied Sciences (Ethics approval number: CUNAS-BSC-2023-001). All participants provided written informed consent after receiving detailed information about the study objectives, procedures, and potential risks. The study was conducted in accordance with the Declaration of Helsinki (World Medical Association, 2013) and local ethical guidelines for human subject research (Council for International Organizations of Medical Sciences, 2016).

### Study Population and Sampling

The target population consisted of young female adults aged 15-30 years residing in Ikorodu, Lagos State. A total of 100 participants were initially recruited using systematic random sampling from the community. Inclusion criteria included female gender, age between 15-30 years, willingness to participate and provide informed consent, and ability to provide a clean-catch urine sample. Exclusion criteria included current pregnancy, menstruation at the time of sample collection, current use of antibiotics or antifungal medications within the previous two weeks, and inability to provide informed consent.

Sample size calculation was based on previous studies reporting UTI prevalence rates of 30-50% in similar populations, with a desired precision of 5% and 95% confidence level. The calculated minimum sample size was 81 participants, with 100 participants recruited to account for potential dropouts and non-responses (Kass, 1956; Stamm *et al.*, 1982).

### Data Collection

A structured questionnaire was administered to all participants to collect demographic information, medical history, and potential risk factors for UTI. The questionnaire included sections on age, marital status, educational level, occupation, sexual activity, contraceptive use, personal hygiene practices, previous UTI history, and current symptoms. The questionnaire was pretested on a small group of participants and modified based on feedback to ensure clarity and cultural appropriateness (Juntunen & Heiskanen, 2004; Lifshitz & Kramer, 2000).

### Sample Collection and Processing

Mid-stream urine samples were collected from 87 participants who successfully completed the study protocol. Participants received detailed instructions on proper collection techniques to minimize contamination. Samples were collected in sterile, wide-mouth containers and transported to the laboratory within two hours of collection. Visual examination was performed to assess colour, clarity, and the presence of sediment or other abnormalities (Kunin *et al.*, 1993; Lipsky, 1989).

Urinalysis was conducted using Health Mate DUS 10 urinalysis test strips (Hannover, Germany) to assess various parameters, including specific gravity, pH, protein, glucose, ketones, bilirubin, urobilinogen, nitrites, leukocyte esterase, and blood. Microscopic examination of urine sediment was performed to identify cells, bacteria, fungi, and other microscopic elements. State clear the other microscopic elements examined in this study

### Microbiological Analysis

Urine samples were cultured on Potato Dextrose Agar (PDA) plates supplemented with chloramphenicol (50 µg/mL) to inhibit bacterial growth. Plates were incubated at 25°C for 5-7 days and examined daily for fungal growth. Isolated colonies were subcultured on fresh PDA plates to obtain pure cultures.

Preliminary identification was based on colony morphology, including colour, texture, size, and growth pattern. Microscopic examination was performed using lactophenol cotton blue staining to observe hyphal structures, conidiation patterns, and spore morphology. Photomicrographs were taken using a digital camera attached to the microscope for documentation (Trease & Evans, 2002; Harborne, 1998).

### Molecular Identification

Genomic DNA extraction was performed using a modified protocol of Makimura *et al.* (1994). Fresh fungal colonies were harvested and suspended in 300 µL of lysis buffer containing 200 mM Tris-HCl (pH 7.5), 25 mM EDTA, 0.5% SDS, and 250 mM NaCl. The suspension was heated at 100°C for 30 minutes and was vortexed for 5 minutes. After cooling, 150 µL of 3.0 M sodium acetate was added, and the mixture was incubated at -20°C for 60 minutes. The solution was centrifuged at 12,000 g for 10 minutes, and the supernatant was transferred to a fresh tube. DNA precipitation was performed using an equal volume of cold isopropanol, followed by washing with 70% ethanol and resuspension in 50 µL of TE buffer.

PCR amplification of the ITS region was performed using universal primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (White *et al.*, 1990). The PCR reaction mixture contained 2 µL of template DNA, 25 µL of 2X PCR master mix, 1 µL each of forward and reverse primers (10 µM), and sterile water to a final volume of 50 µL. PCR conditions included initial denaturation at 94°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 55°C for 30 seconds, and extension at 72°C for 1 minute, with a final extension at 72°C for 7 minutes.

PCR products were analysed by electrophoresis on 1% agarose gel stained with ethidium bromide and visualized under UV light. PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length

Polymorphism) analysis was performed using MvaI Fast digest enzyme (Fermentas Life Sciences, Lithuania) according to the manufacturer's instructions (Kordalewska *et al.*, 2019). Restriction fragments were separated on 2% agarose gel and compared with standard profiles for species identification.

DNA sequencing was performed using the same ITS1 and ITS4 primers on both strands by MWG Biotech (Ebersberg, Germany). Sequence quality was assessed, and consensus sequences were assembled using sequence analysis software. Species identification was performed using the nucleotide BLAST algorithm against the NCBI GenBank database, with sequences showing  $\geq 97\%$  similarity considered for species assignment (Schoch *et al.*, 2012; Nilsson *et al.*, 2008).

### Quality Control and Data Management

All laboratory procedures included appropriate positive and negative controls. Sterility of media and reagents was verified through incubation of uninoculated plates and solutions. Standard reference strains were used for molecular identification validation when available. All data were recorded in duplicate, and discrepancies were resolved through repeat testing.

Data were entered into Microsoft Excel spreadsheets and subsequently transferred to SPSS version 25.0 for statistical analysis. Double data entry was performed to minimize transcription errors, and range and consistency checks were conducted to identify potential errors.

### Statistical Analysis

Descriptive statistics were calculated for all variables, including frequencies and percentages for categorical variables and means with standard deviations for continuous variables. Chi-square tests were used to assess associations between categorical variables, while t-tests and ANOVA were used for continuous variables. Statistical significance was set at  $P < 0.05$ .

**Results**

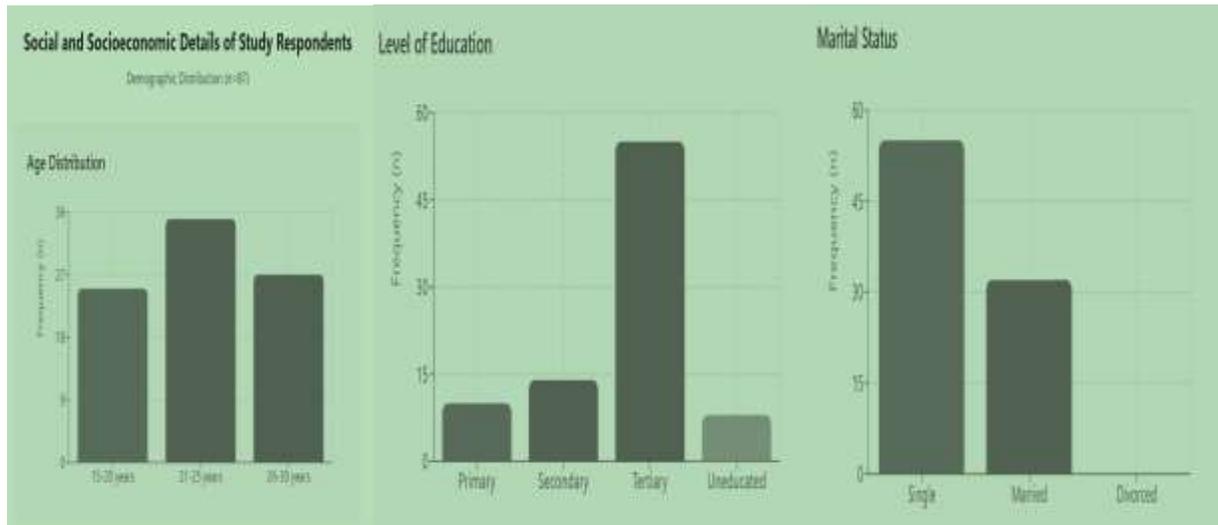
**Demographic Characteristics and Response Rate**

The study achieved an excellent response rate of 87% (87/100 participants), which exceeded the minimum threshold for adequate statistical analysis. The demographic distribution of participants showed that the majority were in the 21-25 age group (35 participants, 40.23%), followed by the 26-30 age group (27 participants, 31.03%) and the 15-20 age group (25 participants, 28.74%). Regarding marital status, 55 participants (63.22%) were single, while 32 (36.78%) were married, with no divorced participants in the study population.

**Table 1: The percentages of the participants' responses**

Response Status	Frequency (n)	Percentage (%)
Responded	87	87.0
Not Responded	13	13.0
<b>Total</b>	<b>100</b>	<b>100.0</b>

Educational attainment varied across the study population, with the majority having a tertiary education (55 participants, 63.22%), followed by secondary education (14 participants, 16.09%), primary education (10 participants, 11.49%), and 8 participants (9.2%) having no formal education. This distribution reflects the urban setting of the study and the emphasis on education in the region.



**Fig. 1a, 1b, and 1c showing the Socioeconomic demographics of the respondents**

### UTI Prevalence and Associated Factors

The overall prevalence of fungal presence in urine samples was 58.62% (51 positive cultures out of 87 participants). When analysed by age groups, the 21-25 age group showed the highest prevalence with 31.03% of all positive cases, followed by the 15-20 age group (16.09%) and the 26-30 age group (11.49%). Marital status emerged as a significant factor, with married women showing a higher rate

of fungal isolation (34.48% of positive cases) compared to single women (24.14% of positive cases). Educational level also showed interesting associations with fungal isolation rates. Participants with tertiary education had the highest number of positive cases (34.48%), followed by those with secondary education (11.49%), primary education (5.75%), and those without formal education (6.89%).



Fig 2: UTI Prevalence in Relation to Demographic Variables

### Fungal Characterization

A total of 51 fungal isolates were recovered from the positive urine cultures, representing seven distinct species. *Aspergillus niger* was the most prevalent organism, accounting for 11 isolates (21.57%). The next most abundant species was *Aspergillus welwitschiae*, which had 10 isolates, accounting for 19.61% of the total.

Following that was *Aspergillus* sp. with 8 isolates, representing 15.69%. *Aspergillus aculeatus* had 7 isolates, making up 13.73%, while *Aspergillus tamarii* contributed 6 isolates, or 11.77%. *Aspergillus sclerotiorum* was represented by 5 isolates, corresponding to 9.8%. Lastly, *Penicillium citrinum* was the least common organism, with 4 isolates, which is 7.84%.

**Table 2: Percentage occurrence of isolated fungal strains in patients' urine samples**

Organisms	No. of Occurrence	Percentage of Occurrence (%)
<i>Aspergillus welwitschiae</i>	10	19.61
<i>Aspergillus sp.</i>	8	15.69
<i>Aspergillus tamaritii</i>	6	11.77
<i>Aspergillus sclerotiorum</i>	5	9.8
<i>Penicillium citrinum</i>	4	7.84
<i>Aspergillus niger</i>	11	21.57
<i>Aspergillus aculeatus</i>	7	13.73

### Cultural and Microscopic Characteristics

Detailed morphological characterization revealed distinct features for each isolate. *Aspergillus niger* colonies appeared cream-coloured initially, developing black colouration with maturation, showing raised elevation and entire margins. Microscopically, they displayed non-septate hyphae, radiate conidial heads, and globose vesicles with round conidia.

*Aspergillus welwitschiae* presented as cream-coloured colonies with very rapid growth, unraised elevation, and irregular margins. The microscopic examination revealed unbranched hyphae, bi-seriate conidial heads, and spherical conidia. *Aspergillus aculeatus* showed brownish colonies with white edges, rapid growth, and similar microscopic features to other *Aspergillus* species but with distinct conidial arrangement patterns.

*Penicillium citrinum* differed morphologically from the *Aspergillus* species, presenting as whitish colonies with rapid growth and characteristic *Penicillium*-type conidiation patterns under microscopic examination.

### Molecular Identification Results

PCR amplification of the ITS region was successful for all isolates, producing amplicons of approximately 500-600 base pairs. PCR-RFLP analysis using *MvaI* enzyme generated distinct restriction patterns that allowed preliminary species-level identification. DNA sequencing confirmed the morphological and PCR-RFLP identifications, with all sequences showing  $\geq 97\%$  similarity to reference sequences in the GenBank database.

The molecular analysis confirmed the identification of two isolates of *Aspergillus welwitschiae* (accession numbers OR073681 and OR073682), along with one isolate each of *Aspergillus tubingensis* (OR073683), *Aspergillus tamaritii* (OR073684), *Aspergillus sclerotiorum* (OR073685), and *Penicillium citrinum* (OR073686). Additionally, two isolates of *Aspergillus niger* were identified (OR073687 and OR073688), as well as *Aspergillus aculeatus* (OR073689). All sequences have been deposited in GenBank and assigned unique accession numbers for future reference.

The phylogenetic analysis confirmed that all *Aspergillus* isolates belonged to the expected taxonomic groups within the genus, with appropriate clustering patterns consistent with their species assignments. The *Penicillium citrinum* isolate clustered appropriately within the *Penicillium* genus, confirming its distinct taxonomic position.

## Discussion

### Epidemiological Significance of High Prevalence

The fungal isolation rate of 58.62% observed in this study is remarkably high compared to rates reported from other regions of Nigeria and sub-Saharan Africa. Previous studies from Nigeria have reported prevalence rates ranging from 31.6% in Kano (Northern Nigeria) to 46.5% in Ebonyi state (Eastern Nigeria), suggesting significant regional variations. (Nworie & Eze, 2010).

The elevated prevalence in our study population may reflect several factors, including urbanization patterns, socioeconomic conditions, hygiene practices, healthcare accessibility in the Ikorodu area of Lagos State, or methodological differences in sample collection and processing.

The demographic patterns observed in our study align partially with global epidemiological trends while revealing some unique characteristics. The highest prevalence in the 21-25 age group (31.03%) corresponds with the period of peak sexual activity, which is a well-established risk factor for UTI development in young women (Scholes *et al.*, 2000). However, the substantial prevalence across all age groups suggests that factors beyond sexual activity may be contributing to fungal presence in urine samples. The association between marital status and fungal isolation rates, with married women showing higher rates (34.48%), requires careful interpretation. This finding may reflect increased sexual activity, pregnancy history, contraceptive use patterns, or other factors associated with marriage in this cultural context. The relationship between educational level and fungal isolation presents an interesting pattern, with higher-educated participants showing increased rates. This may reflect increased healthcare-seeking behaviour and recognition among educated women, occupational factors, or reporting bias.

### The *Aspergillus* Predominance: A Departure from Expected Patterns

The prevalence of *Aspergillus* species (88.24% of isolates) in our study represents a significant departure from *Candida albicans*, which is the most prevalent fungus in UTI in medical mycology literature.

Studies by Kauffman *et al.* (2000) and Sobel *et al.* (2011) have documented that *Candida* species account for over 95% of fungal uropathogens in most clinical settings. *Aspergillus* species, when detected in urine, typically represent less than 1% of fungal isolates and usually occur in severely immunocompromised patients with disseminated infection (Bongomin *et al.*, 2023).

*Aspergillus niger*, the most prevalent isolate in our study, is primarily recognized as an environmental saprophyte commonly found in soil, decaying organic matter, and indoor environments. Its isolation from urine samples may indicate several possibilities: environmental contamination during sample collection or processing, opportunistic colonization in individuals with local factors favouring fungal growth, or true pathogenic infection in the presence of predisposing factors such as diabetes, catheterization, or anatomical abnormalities. *Aspergillus welwitschiae*, the second most prevalent isolate (19.61%), is a black *Aspergillus* species that has been increasingly recognized as an emerging pathogen in certain geographical regions. This species has been associated with respiratory infections and occasional invasive disease in immunocompromised patients. Its consistent isolation from multiple urine samples in this study warrants attention and further investigation (Agarwal *et al.*, 2013).

The presence of *Penicillium citrinum* (7.84% of isolates) adds another dimension to the mycological profile. This species is known for producing mycotoxins, particularly citrinin, which has nephrotoxic properties. The isolation of this organism from urine samples raises concerns about potential mycotoxin exposure and its implications for renal health (Ali & Degen, (2019).

The diversity of *Aspergillus* species isolated, including *A. aculeatus*, *A. tamaris*, and *A. sclerotiorum*, suggests a complex environmental reservoir and possible multiple exposure sources. These species are typically associated with food spoilage, indoor air quality issues, and agricultural environments, which may reflect the socioeconomic and environmental conditions of the study population.

### Contamination Versus True Infection: Critical Considerations

The clinical significance of *Aspergillus* species in urine requires careful evaluation and represents the central challenge in interpreting our findings. Several factors must be considered when distinguishing between contamination and true infection.

Evidence suggesting possible contamination includes: (1) *Aspergillus* species are ubiquitous environmental organisms, (2) single mid-stream urine samples were collected without repeat cultures, (3) no clinical symptoms or immune status data were systematically collected, and (4) the organisms isolated are not typical uropathogens. Evidence suggesting possible true infection or colonization includes: (1) consistent isolation across multiple independent samples, (2) successful culture and growth on selective media, (3) the high prevalence suggests a pattern beyond random contamination, and (4) some *Aspergillus* species can cause opportunistic urinary tract infections (Bongomin *et al.*, 2023).

The literature on *Aspergillus* urinary tract infections indicates that while rare, these infections do occur, particularly in immunocompromised patients, those with structural urinary abnormalities, or following urological procedures. Recent research has highlighted the complex biology and pathogenicity of *Aspergillus* species (van de Veerdonk *et al.*, 2025). However, our study was not designed to definitively distinguish between contamination, colonization, and infection.

The pattern we observed could reflect several scenarios: (1) environmental contamination during sample collection or processing, possibly related to housing conditions, occupational exposures, or ambient environmental factors in the tropical climate, (2) true colonization of the urinary tract or periurethral area without symptomatic infection, (3) unrecognized opportunistic infections in individuals with subtle immune deficiencies or local predisposing factors, or (4) a unique epidemiological pattern specific to this population and region.

### Molecular Identification and Taxonomic Contributions

The successful molecular identification of all isolates using ITS sequencing demonstrates the power of molecular taxonomy in clinical mycology. The ITS region has proven to be an excellent molecular barcode for fungal species identification, providing resolution that is often superior to morphological methods alone (Schoch *et al.*, 2012; Kõljalg *et al.*, 2013). The high similarity scores ( $\geq 97\%$ ) obtained for all sequences confirm the reliability of the identifications.

The deposition of sequences in GenBank (accession numbers OR073681-OR073689) contributes to the growing database of fungal sequences from clinical sources in West Africa, an understudied region in terms of medical mycology. These sequences will serve as valuable references for future studies and contribute to our understanding of fungal diversity and epidemiological patterns in tropical Africa (Begerow *et al.*, 2010).

Molecular techniques, including PCR-based methods and DNA sequencing, have revolutionized fungal identification by providing rapid, accurate, and reproducible results (Hoang *et al.*, 2019; Bellemain *et al.*, 2010). Traditional identification methods based on morphological characteristics are often time-consuming and may lack specificity, particularly for closely related species. Our use of combined morphological and molecular approaches provided robust species-level identification that would not have been possible with either method alone.

## Clinical and Public Health Implications

These findings necessitate mycological surveillance beyond *Candida sp.*, rigorous sampling protocols to minimize contamination, and demographic-targeted health interventions.

**Critical Public Health Concerns:** *Penicillium citrinum* produces citrinin, a nephrotoxic mycotoxin that can cause renal tubular damage and compromise kidney function through direct exposure or systemic absorption (Oestreicher *et al.*, 2019). *Aspergillus* species are potent allergen producers whose spores and metabolites can trigger IgE-mediated hypersensitivity reactions (Denning *et al.*, 2006). These allergic responses manifest as vulvovaginal pruritus (itching), irritation, mucous membrane inflammation, and allergic dermatitis in the female genital tract. Such reactions may mimic or exacerbate urogenital symptoms, complicating clinical diagnosis and potentially being misattributed to bacterial or other etiologies. Chronic exposure to *Aspergillus* allergens can cause systemic allergic responses, including respiratory sensitization, allergic bronchopulmonary aspergillosis, and immune system dysregulation (Agarwal *et al.*, 2013).

From a clinical perspective, these findings highlight several important considerations. The possibility of *Aspergillus* species as potential uropathogens in this region suggests that routine mycological surveillance should extend beyond *Candida* species. Sample collection procedures must be rigorous to minimize environmental contamination, particularly in tropical settings with high ambient fungal loads. Understanding demographic patterns could inform targeted health education and intervention programs.

From a public health perspective, whether these isolates represent contamination or true infection, the high prevalence raises concerns about environmental health, sanitation infrastructure, and potential occupational or residential exposures to high fungal loads. This suggests further critical investigation of environmental sources, housing conditions, and occupational factors in this population, as to the main possible sources of the *Aspergilli* contamination.

The high prevalence of fungal UTIs in this population, combined with the unusual mycological profile, has important implications for clinical practice and public health interventions. The predominance of environmental fungi raises questions about appropriate treatment approaches, as conventional antifungal protocols are primarily designed for *Candida* infections (Pappas *et al.*, 2016; Kullberg & Arendrup, 2015).

## Conclusion

This study reveals 58.62% fungal isolation from urine samples among young females in Ikorodu, with unprecedented *Aspergillus* predominance (88.24%) over typical *Candida sp.* Molecular characterization identified seven species, contributing valuable taxonomic data to public databases (GenBank OR073681-OR073689). These findings may posit that environmental contamination, urinary colonization, or opportunistic infections underscore complexities in tropical settings with high ambient fungal loads. Clinically, findings mandate expanded mycological surveillance and rigorous sampling protocols. Public health concerns include environmental exposures, sanitation infrastructure, nephrotoxic mycotoxin risks from *Penicillium citrinum*, and allergen-mediated vulvovaginal symptoms from *Aspergillus* species.

Future research priorities have to include prospective studies with repeat cultures, clinical correlation, immune status assessment, environmental reservoir identification, and optimized collection methods. This study contributes essential data to the limited tropical African fungal uropathogen literature, raising important questions warranting further comprehensive investigation. This study contributes valuable data to the limited literature on fungal uropathogens in tropical Africa and raises important questions that warrant further investigation through more comprehensive, hypothesis-driven research.

## Acknowledgments

The authors express gratitude to the participants who volunteered for this study and to the staff of Lagos State Polytechnic for providing plant identification services. We acknowledge the technical support provided by the laboratory staff at Crescent University and the sequencing services provided by MWG Biotech.

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