

Epidemiological and Molecular Identification of Trichophyton Species Associated With Dermatophytoses in Northeast Nigeria

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Abstract

Background

Dermatophytoses are superficial fungal infections that affect skin, hair, and nails. *Trichophyton* species are the primary causative agents of these infections. Despite their burden, diagnosis in many settings remains limited to conventional methods, often leading to misidentification and inadequate treatment. This study investigated the prevalence, and risk factors associated with *Trichophyton*-related dermatophytosis among patients in the selected health facility in Bauchi State Northeastern Nigeria.

Methods

This hospital-based cross-sectional study was conducted between May 2024 and November 2025. It involved 385 patients with clinical signs of dermatophytoses at the Infectious Disease Hospital, Bayara Bauchi State Nigeria. Samples were analyzed using conventional microscopy and culture. Molecular identification was performed via PCR amplification of the 18S rRNA gene using ITS primers. Epidemiological data were collected using structured questionnaires and analyzed statistically using SPSS version 23.0.

Results

The overall prevalence of *Trichophyton*-related infections was 24.94%, with *T. rubrum* (21.82%) more common than *T. soudanense* (3.12%). Molecular analysis confirmed two strains of *T. rubrum* and one strain of *T. soudanense*. Significant risk factors included regular contact with animals, low socioeconomic status, irregular bathing, communal living, and outdoor labor. ($p < 0.05$).

Conclusion

This hospital-based study underscored the public health importance of *Trichophyton* infections in Northeastern Nigeria, with *T. rubrum* being the predominant species. Effective control measures should focus on hygiene education, environmental sanitation, and targeted public health interventions in high-risk populations.

Clinical trial number: Not applicable.

INTRODUCTION

Superficial fungal infections affecting the skin, hair, and nails, collectively referred to as superficial mycoses, represent some of the most common dermatological conditions worldwide, particularly in tropical and subtropical regions where warm and humid environmental conditions favor fungal proliferation [1, 2]. Among the diverse fungal pathogens implicated in these infections, dermatophytes remain the most important etiological agents, with species of the genus *Trichophyton* being frequently associated with human and animal infections [3].

Dermatophytes are traditionally classified into three genera; *Trichophyton*, *Microsporum*, and *Epidermophyton*, based on morphological characteristics and host preference. Among these genera, *Trichophyton* is the most diverse and clinically significant, comprising numerous pathogenic species such as *T. rubrum*, *T. mentagrophytes*, *T. tonsurans*, *T. schoenleinii*, and *T. verrucosum* [1, 3]. These species are further categorized into anthropophilic, zoophilic, and geophilic groups depending on their ecological niche and primary host. Anthropophilic species predominantly infect humans and are commonly associated with chronic infections with minimal inflammation, whereas zoophilic and geophilic species often induce more inflammatory responses due to their animal or environmental origin [4].

These keratinophilic fungi possess the ability to degrade keratinized tissues, enabling colonization of the stratum corneum, hair shafts, and nails, leading to clinical manifestations collectively known as dermatophytoses, including tinea capitis, tinea corporis, tinea pedis, tinea unguium, and tinea cruris [4, 5]. Transmission of dermatophytes generally occurs through direct contact with infected individuals or animals, or indirectly through contaminated fomites and environmental surfaces [5, 6].

Globally, dermatophytoses affect approximately 20–25% of the population, making them a significant public health concern [2, 7]. The burden is particularly high in developing countries where socioeconomic conditions, overcrowding, limited access to healthcare, and poor hygiene practices facilitate transmission. In children, especially those with tinea capitis, reported prevalence rates range from 21% to 87% in many developing regions, with peak occurrence in individuals younger than 12 years [8, 9]. In Nigeria, the reported prevalence of dermatophytosis varies widely across different geographical regions, ranging from 3.4% to 55.1%, reflecting variations in environmental conditions, population behavior, hygiene practices, and socioeconomic factors [8].

The identification of dermatophytes has traditionally relied on conventional diagnostic approaches such as direct microscopic examination and culture. While these methods remain widely used due to their accessibility and cost-effectiveness, they have several limitations, including long incubation periods, subjective interpretation of morphological characteristics, and difficulty distinguishing closely related species [10]. In recent years, molecular techniques have increasingly been employed to enhance diagnostic accuracy. Polymerase chain reaction (PCR) amplification and sequencing of the internal transcribed spacer (ITS) region of ribosomal DNA have emerged as reliable tools for the precise identification and phylogenetic characterization of dermatophytes [11]. These molecular approaches have improved species-level identification and facilitated the discovery of cryptic species within the *T. mentagrophytes* complex, including the recently recognized *T. indotineae*, which has been associated with aggressive infections and resistance to terbinafine therapy [6].

Despite the substantial burden of dermatophyte infections, laboratory confirmation is often lacking in many resource-limited settings where empirical treatment remains common practice. The absence of accurate laboratory diagnosis may lead to inappropriate therapy, delayed treatment, and potential emergence of antifungal resistance. Additionally, several environmental, behavioral, and socioeconomic factors contribute to the persistence and transmission of dermatophyte infections. These include close

contact with infected animals, communal living conditions, poor personal hygiene, and sharing of personal grooming tools such as combs, clippers, and towels [8, 12].

Given the clinical and public health significance of *Trichophyton* species in dermatophytosis, there is a need for improved epidemiological understanding and accurate identification of circulating species in endemic regions. Therefore, this study investigated the prevalence of *Trichophyton*-related dermatophytosis among patients presenting with suspected skin and scalp infections at a referral health facility in Northeast Nigeria. In addition, the study assessed associated risk factors and applied both conventional mycological methods and molecular techniques to identify and characterize the dermatophyte isolates. Integrating epidemiological data with molecular identification may provide valuable insights into the distribution and diversity of *Trichophyton* species and support improved diagnostic and control strategies in the region.

MATERIALS AND METHODS

Study Area

This study at the Infectious Disease Hospital (IDH), Bayara, a referral health facility for infectious diseases in Bauchi State, Northeastern Nigeria. The hospital is located in Birshi, Bauchi Local Government Area (LGA), and serves patients from Bauchi State and neighboring northeastern states of Nigeria. The area lies at coordinates 10.2820° N latitude and 9.8120° E longitude (Figure 1) [13].

Study Design and Population

A hospital-based cross-sectional study was conducted between May 2024 and November 2025, among patients presenting with clinical signs suggestive of dermatophytosis at the Infectious Disease Hospital Bayara.

The study population consisted of patients of all age groups and both sexes who presented with clinical features suggestive of dermatophytosis affecting the skin, scalp, or nails during the study period.

Inclusion criteria

Participants presented with clinical symptoms suggestive of dermatophytosis (e.g., scaly lesions, pruritus, hair loss, or nail discoloration), who provided informed consent to participate in the study (or assent with parental/guardian consent for minors) were included in the study.

Exclusion criteria

Participants who were unwilling to participate in the study, those who had received systemic antifungal therapy prior to sample collection, and those who did not present clinical features suggestive of superficial fungal infection

Participants were recruited using consecutive sampling, whereby all eligible patients presenting during the study period were invited to participate until the required sample size was reached.

Ethical Considerations

Ethical approval for this study was obtained from the Research and Ethics Committee of the Infectious Disease Hospital Bayara, Bauchi State, Nigeria, a recognized secondary healthcare institution under the Bauchi State Ministry of Health (Approval reference number: IDH/2024/5V1; dated 4th, May 2024). Written informed consent was obtained from all adult participants prior to enrollment. For participants below seven years of age, consent was obtained from parents or legal guardians, while assent was obtained from children aged seven years and above. Participation was voluntary, and confidentiality of all participant information was strictly maintained. All study procedures were conducted in accordance with the Declaration of Helsinki (2013).

Sample Size Determination

Sample size was calculated using Cochran's formula for estimating a proportion as shown below:

$$n = \frac{Z^2 \times P(1 - P)}{d^2}$$

Where:

(Z) = standard normal deviate at 95% confidence level (1.96)

(p) = assumed prevalence = 0.50 (50%).

(d) = desired precision (margin of error) = 0.05

$$\text{Hence, } n = \frac{(1.96)^2 \times 0.50(1 - 0.50)}{0.05^2}$$

$$n = 384.16$$

Therefore, the approximate sample size for this study was 385 pregnant women.

Data Collection

Data on demographic characteristics and potential risk factors were collected using a structured questionnaire administered at the time of sample collection.

The questionnaires were developed after reviewing previously published studies assessing prevalence and risk factors of dermatophytosis among Nigerian populations. The questionnaires consisted of sections covering socio-demographic characteristics, and risk factors of the infection. To ensure clarity

and contextual relevance, the questionnaires were pretested among 20 individuals in a health facility outside the study area. Feedbacks from the pretests were used to modify ambiguous or unclear questions. The internal consistency of the items was assessed using Cronbach's alpha reliability analysis, which yielded an acceptable reliability coefficient of ≥ 0.73 , indicating adequate internal consistency of the instrument. In addition, the questionnaires were reviewed by a group of experts in epidemiology and public health from Federal University of Health Sciences Azare, to assess their content validity, ensuring that the items adequately captured the study variables.

Sample Collection

Clinical samples, including skin scrapings, infected hair, and nail or lesion materials, were collected from 385 patients presenting with signs and symptoms consistent with dermatophytosis. All samples were collected by trained laboratory personnel following a standardized aseptic protocol to ensure consistency and minimize contamination.

Prior to sample collection, the affected area was cleansed using a sterile cotton swab soaked in 70% ethanol to remove surface contaminants. Specimens were then obtained by gently scraping the active margins of lesions using sterile scalpels or forceps, depending on the site of infection.

Each sample was placed in a sterile, labeled disposable container and transported to the Microbiology Laboratory of Sa'adu Zungur University, Gadau, within 2–4 hours of collection. During transportation, samples were maintained at ambient temperature and processed immediately upon arrival. Where immediate processing was not possible, samples were stored at 4°C for a maximum of 24 hours before analysis.

At the time of sample collection, structured questionnaires were administered to participants to obtain relevant socio-demographic and risk factor information.

Isolation of Fungal Pathogens

Clinical specimens were inoculated onto Sabouraud Dextrose Agar (SDA) supplemented with chloramphenicol to inhibit bacterial growth. The medium was prepared by dissolving 39 g of SDA in 1000 mL of distilled water and sterilized at 121°C for 15 minutes.

The inoculated plates were incubated at 28–30°C and monitored for fungal growth for up to 21 days, to allow adequate recovery of slow-growing dermatophytes. Plates with no visible growth after 21 days were considered negative [14].

Identification of Fungal Pathogens

Direct microscopic examination of clinical specimens was performed prior to culture using 10% potassium hydroxide (KOH) preparation to detect fungal elements such as hyphae and arthroconidia [14].

Following incubation, fungal isolates were identified based on their macroscopic and microscopic characteristics. Colony morphology, including color (surface and reverse), texture, and growth rate, was assessed. Microscopic identification was carried out using lactophenol cotton blue (LPCB) staining to examine characteristic fungal structures such as septate hyphae and conidia, consistent with dermatophyte species, particularly *Trichophyton* spp [14].

Molecular Identification

Fungal isolates were subcultured on Sabouraud Dextrose Agar and preserved at 4°C prior to molecular analysis. For DNA extraction, isolates were grown in Sabouraud Dextrose Broth and incubated at 28°C for 10–14 days.

Fungal mycelia were harvested and processed for genomic DNA extraction following the method described by Rezaie et al. [15], with slight modifications. Briefly, approximately 300 mg of fungal mycelia was ground into a fine powder using liquid nitrogen. The powder was suspended in extraction buffer (50 mM Tris-HCl, pH 8.0; 50 mM EDTA; 1% SDS) with proteinase K and incubated at 65°C for 60 minutes. The mixture was then centrifuged, and the supernatant treated with RNase before purification using phenol:chloroform:isoamyl alcohol (25:24:1). DNA was precipitated using isopropanol and sodium acetate, washed with 70% ethanol, air-dried, and stored at –20°C until use.

Molecular identification was performed by amplification of the internal transcribed spacer (ITS) region of ribosomal DNA, which is the standard genetic marker for fungal identification. PCR amplification was carried out using universal fungal primers ITS1 (5'-TCC GTA GGT GAA CCT GCGG-3') and ITS4 (5'-TCC TCC GCT TAT TGA TAT GC-3') [16, 17].

Each 25 µL PCR reaction mixture contained 2.5 µL of 10× reaction buffer, 0.5 µL of dNTPs, 1.5 µL of MgCl₂, 0.5 µL each of forward and reverse primers, 0.5 µL of Taq DNA polymerase, 2 µL of template DNA, and nuclease-free water to volume.

PCR amplification was performed under the following conditions: initial denaturation at 94°C for 5 minutes, followed by 30 cycles of denaturation at 94°C for 30 seconds, annealing at 55°C for 40 seconds, and extension at 72°C for 40 seconds, with a final extension at 72°C for 10 minutes.

Amplified PCR products were resolved on 1% agarose gel stained with ethidium bromide and visualized under UV illumination. A 100 bp DNA ladder was used as a molecular size marker. The expected amplicon size for the ITS region was approximately 500–600 base pairs.

PCR amplification products were verified by agarose gel electrophoresis prior to sequencing. The products were then purified and sequenced. The obtained sequences were analyzed using the Basic Local Alignment Search Tool (BLAST) on the NCBI database to determine species identity based on sequence similarity. Phylogenetic analysis was performed using MEGA version 11 software to assess the genetic relationships between the isolates and reference sequences.

Data Handling Procedure

All completed questionnaires were checked for consistency and completeness before being entered in to SPSS v25.0 for analysis. Data cleaning was performed to identify missing information and inconsistencies before the statistical analysis. Questionnaires with large number of missing information were excluded from the analysis. Analyses were done using complete case analysis, where only observations with available data for the variables of interest were included. The proportion of missing data was minimal and therefore unlikely to significantly influence the study findings.

Data Analysis

Data obtained from questionnaires and laboratory findings were entered into Microsoft Excel and analyzed using Statistical Package for the Social Sciences (SPSS) version 23. Descriptive statistics, including frequencies and percentages, were used to summarize sociodemographic characteristics, prevalence of *Trichophyton* species, and distribution of risk factors.

The association between categorical variables and the occurrence of *Trichophyton*-related dermatophytosis was assessed using the Chi-square (χ^2) test. Variables with p-values less than 0.05 were considered statistically significant.

To evaluate factors associated with *Trichophyton*-related dermatophytosis, logistic regression analysis was performed. Crude odds ratios (ORs) with 95% confidence intervals (CIs) were calculated to estimate the strength of associations between independent variables and the outcome variable.

All statistical tests were two-tailed, and a p-value of less than 0.05 was considered statistically significant.

The outcome variable in the logistic regression model was coded as 1 = absence of infection and 0 = presence of infection; therefore, odds ratios less than 1 indicate increased likelihood of infection.

RESULTS

Based on phenotypic characterization, two *Trichophyton* species were identified among the isolates obtained from patients with dermatophytosis. Macroscopic and microscopic examination suggested the presence of *Trichophyton rubrum* and *Trichophyton soudanense* as the predominant species.

Molecular identification using PCR amplification of the ITS region was successfully performed, yielding amplicons of the expected size (approximately 500–600 bp). The amplified products were subsequently sequenced, and species identity was confirmed through sequence analysis using the Basic Local Alignment Search Tool (BLAST) against the National Center for Biotechnology Information database.

Phylogenetic analysis further supported these findings, with the isolates clustering closely with corresponding reference strains retrieved from the NCBI database. The *T. rubrum* isolates formed a

distinct cluster with known *T. rubrum* sequences, while the *T. soudanense* isolate grouped with reference *T. soudanense* strains (Figures 2 and 3).

The study also revealed that, out of the 385 participants tested, 96 were positive of *Trichophyton*-related dermatophytosis yielding an overall prevalence of 24.94%. The specie-based prevalence indicated high prevalence of *Tricophyton rubrum* (21.82%) than *Trichophyton soudanense* (3.12%) (Figure 4).

Further, the study indicated that, out of the study participants, the overall prevalence of *Trichophyton*-related dermatophytosis was higher among males (15.32%) compared to females (9.61%), though the association was not statistically significant ($\chi^2 = 1.65, p = 0.20$).

On the age basis, the study pointed that, age group was significantly associated with high prevalence of the infection ($p = 0.002$). The highest prevalence was recorded in participants aged 65 years and above (9.61%), while 10–19 year age group accounted for the lowest prevalence of the infections (0.52%).

In terms of residence, a significant association was observed ($p < 0.001$). Individuals living in rural areas had the highest prevalence (16.62%) compared to those in urban (5.19%) and semi-urban (3.12%) settings.

There was a strong association between regular contact with animals and prevalence of the infection, where a prevalence of 20.78% was recorded among those with animal contact compared to 4.16% for those without contact ($p < 0.001$).

Socioeconomic status was significantly associated with infection prevalence ($p < 0.001$). Those with low income had the highest prevalence (14.03%) followed by middle income class (7.27%) while those from high income class had lowest prevalence of the infection (3.64%).

Bathing habits were also significant ($p < 0.001$), where the infection was more common among those who did not bathe regularly (15.58%) compared to those who did (9.35%).

Sharing of personal grooming tools showed no significant association ($p = 0.071$), though higher prevalence was observed among those who shared tools (15.32%) compared to those who did not (9.61%).

Interestingly, individuals living in communal settings had a higher prevalence (15.84%) than those who did not (9.09%) ($p < 0.001$), and those involved in farming or outdoor labor had a higher infection rate (15.58%) than those who were not (9.35%) ($p = 0.009$) (Table 1).

Table 1: Prevalence of *Trichophyton*-related Dermatophytosis in the Study Area

Variables	Prevalence (%)	χ^2	<i>p-value</i>
Gender			
Males	15.32	1.65	0.20
Females	9.61		
Age			
0-9years	2.86	19.49	0.002*
10-19years	0.52		
20-24years	4.16		
25-64years	7.79		
65years and above	9.61		
Residence			
Urban	5.19	18.337	0.000*
Semi Urban	3.12		
Rural	16.62		
Regular contact with animals			
Yes	20.78	132.818	0.000*
No	4.16		
Socioeconomic status			
Low income	14.03	92.776	0.000*
Middle income	7.27		
High income	3.64		
Bathing frequency			
Regularly	9.35	66.444	0.000*
Not regularly	15.58		
Sharing personal grooming tools (clippers, combs, towels)			
Yes	15.32	3.264	0.071
No	9.61		
Living in a communal setting (e.g., boarding school, barracks)			

Yes	15.84	28.717	0.000*
No	9.09		
Involvement in farming or outdoor labor			
Yes	15.58	6.744	0.009*
No	9.35		

"*" = Significant at $p < 0.05$, " χ^2 " = Chi-square

Logistic regression analysis identified several factors significantly associated with *Trichophyton*-related dermatophytosis. Regular contact with animals was significantly associated with the occurrence of infection ($p < 0.001$; OR = 0.045; 95% CI: 0.024–0.083), indicating that individuals with animal contact had markedly higher odds of infection compared to those without contact.

Similarly, participants from low-income households were significantly more likely to be infected ($p < 0.001$; OR = 0.092; 95% CI: 0.048–0.175). Irregular bathing was also significantly associated with increased likelihood of infection ($p < 0.001$; OR = 0.138; 95% CI: 0.083–0.229).

Living in communal settings showed a strong association with infection ($p < 0.001$; OR = 0.240; 95% CI: 0.139–0.414), while involvement in farming or outdoor labor was also a significant predictor ($p = 0.010$; OR = 0.523; 95% CI: 0.319–0.857).

Other variables such as gender, age, and sharing of personal grooming tools were not statistically significant predictors ($p > 0.05$) (Table 2).

Table 2: Bivariate Logistics Regression Analyses for the Risk Factors Associated with *Trichophyton*-related Dermatophytoses

Variables	Infected	Not infected	Tot	<i>P</i>	OR	95% CI	
Gender							
Males	59	159	218	0.200	0.734	0.457	1.179
Females	37	130	167		1	-	
Age							
0-9years	11	37	48	0.186	0.514	0.226	1.167
10-19years	2	28	30		6.509	0.842	50.323
20-24years	16	51	67		1.092	0.556	2.143
25-64years	30	65	95		0.742	0.419	1.314
65years and above	37	108	145		1	-	
Residence							
Urban	20	53	73	0.000*	1.187	0.659	2.135
Semi Urban	12	162	174		3.996	2.047	7.801
Rural	64	74	138		1	-	
Regular contact with animals							
Yes	80	56	136	0.000*	0.045	0.024	0.083
No	16	233	249		1	-	
Socioeconomic status							
Low income	54	72	126	0.000*	0.092	0.048	0.175
Middle income	28	17	45		0.044	0.020	0.099
High income	14	200	214		1	-	
Bathing frequency							
Regularly	36	233	269	0.000*	0.138	0.083	0.229

Not regularly	60	56	116	1			
Sharing personal grooming tools (clippers, combs, towels)							
Yes	59	150	209	0.072	1.544	0.962	2.479
No	37	139	176	1			
Living in a communal setting (e.g., boarding school, barracks)							
Yes	35	36	71	0.000*	0.240	0.139	0.414
No	61	132	193	1			
Involvement in farming or outdoor labor							
Yes	36	69	105	0.010*	0.523	0.319	0.857
No	60	220	280	1			

The outcome variable in the logistic regression model was coded as 1 = absence of infection and 0 = presence of infection; therefore, odds ratios less than 1 indicate increased likelihood of infection.

“*” = Significant at $p < 0.05$, “OR” = odds ratio

DISCUSSION

The findings of this study identified *Trichophyton soudanense* and *Trichophyton rubrum* as significant contributors to the overall burden of dermatophytoses in the study population. These results aligned with previous research conducted in Nigeria and elsewhere, which have identified these fungal species as common causative agents of dermatophytoses. The predominance of *Trichophyton rubrum* in this study is consistent with findings from Kano State, as reported by Adeleke *et al.* [18], The consistent of *T. rubrum* across different regions may reflect its adaptability and widespread distribution in Nigeria [18].

However, the study contrasted the findings of Nweze, [19] who documented *T. schoenleinii* as the primary causative agent of dermatophytosis in Borno State. These regional differences may be influenced by environmental factors, population demographics, and healthcare practices that affect fungal pathogen transmission dynamics.

In contrast to this study, *T. mentagrophytes* was reported as the predominant species in southwestern Nigeria by Ayanlowo *et al.* [20]. In this study, *T. rubrum* was a significant contributor not *T*

mentagrophytes. This discrepancy could be due to environmental differences such as climate, humidity and socio-economic conditions that favor the growth and spread of some fungal species over others. Furthermore, *T tonsurans* was identified as the most common etiological agent in Anambra State [21].

The findings of this study also suggest that the infection may be more prevalent among males, although this association is not statistically significant. However, age, residence, regular contact with animals, socioeconomic status, bathing habits, and living in communal settings are associated with the high prevalence of the infection.

The study revealed that age is significantly associated with the prevalence of *Trichophyton*-related dermatophytosis, with the highest prevalence observed in participants aged 65 years and above. This finding contrasted the previous studies that have reported a high burden of the infections among children than older adults [8, 9]. The increased prevalence among older adults as observed in this study may be attributed to declining immune function, poor hygiene practices and increased exposure to risk factors.

The study also found that residence was associated with the prevalence of *Trichophyton*-related dermatophytosis. *Trichophyton*-related dermatophytosis. Individuals living in rural areas had a higher prevalence of the infection compared to those in urban and semi-urban settings. This finding is consistent with previous studies that have reported a higher incidence of fungal infections in rural areas, likely due to close proximity to livestock, contaminated soil and limited access to healthcare services [22, 23, 24].

The study also identified several factors associated with *Trichophyton*-related dermatophytosis, including regular contact with animals, low socioeconomic status, irregular bathing habits, living in communal settings, and involvement in farming or outdoor labor. These findings are consistent with previous studies that have reported the importance of environmental and behavioral factors in the transmission of the infections [5, 6, 12, 24].

Public health implications and Clinical Implications

The relatively high prevalence of *Trichophyton*-related dermatophytosis highlights the need for targeted community-level interventions in Northeastern Nigeria. Risk factors such as poor hygiene, low socioeconomic status, and communal living conditions suggest that infection control requires not only clinical management but also improvements in environmental sanitation and health education. Public health programs should focus on awareness campaigns, early diagnosis, and prevention strategies, particularly in rural and underserved communities where the burden is highest.

From a clinical perspective, the predominance of *Trichophyton rubrum* and the confirmation of species through molecular techniques underscore the importance of accurate laboratory diagnosis in guiding appropriate antifungal therapy. Reliance on empirical treatment without laboratory confirmation may lead to misdiagnosis and inappropriate drug use, potentially contributing to antifungal resistance.

Strengthening diagnostic capacity in routine clinical settings is therefore essential for improved patient outcomes.

Strengths and Limitations of the Study

One of the major strengths of the study is that, the study combined both conventional and molecular methods for the identification of *Trichophyton* species, thereby improving diagnostic accuracy. In addition, the inclusion of epidemiological and risk factor analysis provides a comprehensive understanding of the burden and determinants of dermatophytosis in the study area. The relatively large sample size further enhances the reliability of the findings.

However, several limitations should be acknowledged. Selection bias may have influenced the findings of this study. Participants were recruited from a single referral health facility and limited to individuals presenting with clinical symptoms suggestive of dermatophytosis. This approach may exclude asymptomatic individuals or those with mild infections who did not seek healthcare, thereby potentially overestimating the prevalence of *Trichophyton*-related infections. In addition, the use of consecutive sampling rather than probability-based sampling limits the representativeness of the study population.

Furthermore, the molecular characterization was performed on a limited number of representative isolates, which may not fully capture the genetic diversity of circulating *Trichophyton* species in the study area. The cross-sectional design also limits the ability to establish temporal or causal relationships between identified risk factors and infection.

Although efforts were made to ensure complete data collection, there is a possibility of missing or incomplete data, particularly in questionnaire-based variables such as hygiene practices and socioeconomic status. Such missing data may introduce bias and affect the accuracy of estimated associations. However, data quality checks were performed to minimize inconsistencies during entry and analysis.

Also, the observed associations between risk factors and *Trichophyton*-related dermatophytosis may be influenced by residual confounding. Although logistic regression analysis was performed, some potential confounders such as underlying comorbidities (e.g., diabetes, immunosuppression), nutritional status, and prior antifungal use were not fully controlled for in this study. These factors may independently affect susceptibility to infection and could have influenced the strength of the reported associations.

CONCLUSION

This study demonstrated the presence of *Trichophyton*-related dermatophytosis among patients attending a referral facility in Northeast Nigeria, *T. rubrum* emerging as the dominant species confirmed through molecular identification. The findings highlighted important socio-demographic and behavioral risk factors, particularly among individuals with regular animal contact, low socioeconomic status, poor hygiene and communal living conditions. These factors were associated with infection in this study and should be prioritized in public health strategies.

The integration of molecular techniques appears to have improved accuracy of fungal identification and demonstrated the limitations of conventional methods alone. This emphasized the need for improved diagnostic capacity in endemic areas. To help reduce the spread of dermatophytoses, there is a pressing need for community-based health education, better hygiene practices, and improved access to dermatological care. Further research is warranted to better characterize the epidemiology of these infections and strengthen prevention and treatment approaches.

Recommendations

Based on the findings of this study, the following recommendations are proposed:

1. Strengthening of laboratory diagnostic capacity, including integration of molecular techniques, for accurate identification of dermatophytes.
2. Implementation of community-based health education programs focusing on personal hygiene, avoidance of sharing personal items, and proper management of infected individuals and animals.
3. Improvement of environmental sanitation and living conditions, particularly in rural and communal settings.
4. Routine screening and early treatment of high-risk populations such as farmers and individuals with frequent animal contact.
5. Further large-scale, multicenter studies to better understand the epidemiology and genetic diversity of dermatophytes in Nigeria.

Abbreviations

1. 18S rRNA: 18S Ribosomal Ribonucleic Acid
2. BLAST: Basic Local Alignment Search Tool
3. DNA: Deoxyribonucleic Acid
4. dNTPs: Deoxynucleoside Triphosphates
5. EDTA: Ethylenediaminetetraacetic Acid
6. IDH: Infectious Disease Hospital
7. ITS: Internal Transcribed Spacer
8. KOH: Potassium Hydroxide
9. LGA: Local Government Area
10. MEGA: Molecular Evolutionary Genetics Analysis
11. NCBI: National Center for Biotechnology Information
12. OR: Odds Ratio
13. PCR: Polymerase Chain Reaction
14. SDA: Sabouraud Dextrose Agar
15. SDS: Sodium Dodecyl Sulfate

16. SPSS: Statistical Package for the Social Sciences

17. UV: Ultraviolet

Declarations

Ethical Approval and Consent to Participate

Prior to the commencement of the data collection, the study received approval from the Ethical Research and Review Committee of the Infectious Disease Hospital Bayara, Bauchi State Nigeria, a recognized secondary healthcare institution under the Bauchi State Ministry of Health, in a letter dated 4th May, 2024 with reference number IDH/2024/5V1. Duly signed informed consent was obtained from adult patients and from the guardians of children below seven years prior to the sample collection. Assent was obtained from children aged seven years and above. Participation in the study was voluntary, and participants were free to withdraw at any stage without any consequence. Confidentiality of patients' information was maintained, and all data were anonymized prior to analysis. All procedures were conducted in accordance with Helsinki's (2013 revision) Declaration.

Consent for Publication: Not applicable

Availability of Data and Materials

The nucleotide sequences generated in this study have been deposited in the GenBank database of the National Center for Biotechnology Information and are publicly available under accession numbers PZ163101, PZ163102 and PZ163103.

Competing Interests

The authors declare that, there is no competing interest

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Author Contributions

AM designed the work, collected samples and did laboratory analysis, IMM prepared the manuscript, BAM and HAG performed data analysis, while MA proofread the entire work.

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Figures

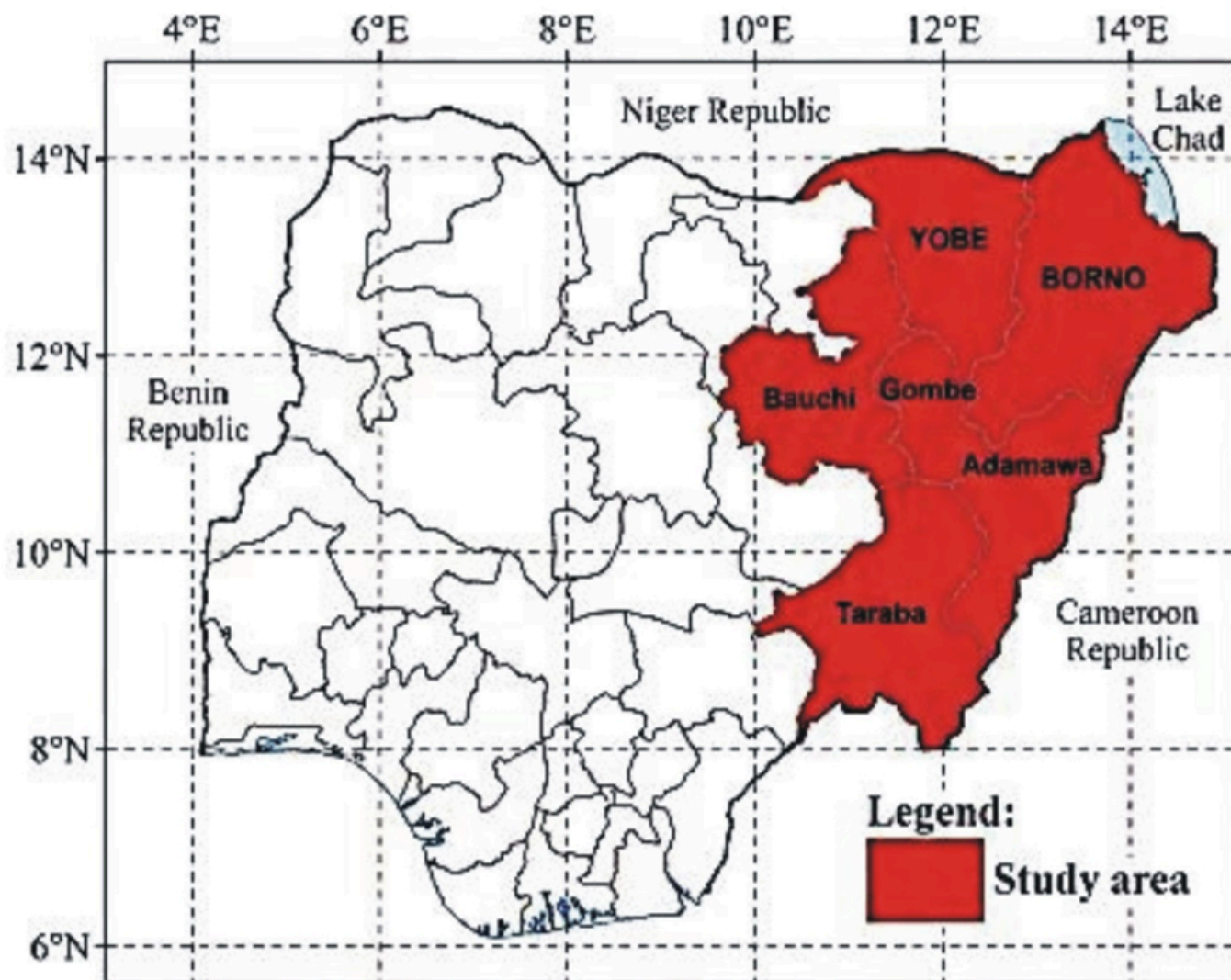


Figure 1

Legend not included with this version.

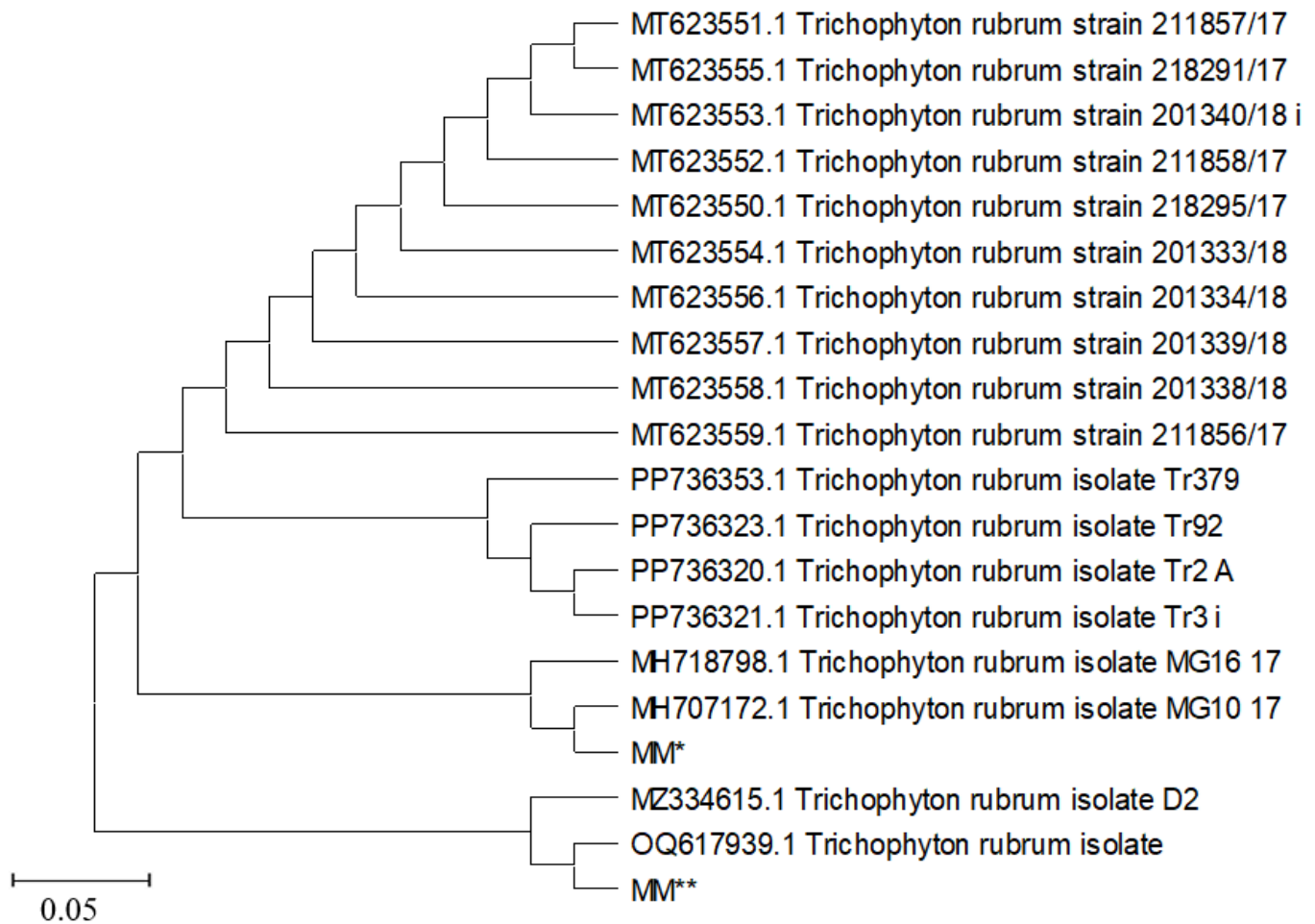


Figure 2

Phylogenetic tree showing the relationship between ITS sequences of the *Trichophyton rubrum* isolates and reference sequences retrieved from the NCBI database. The tree was constructed using the maximum likelihood method in MEGA version 11. The scale bar represents substitutions per site.

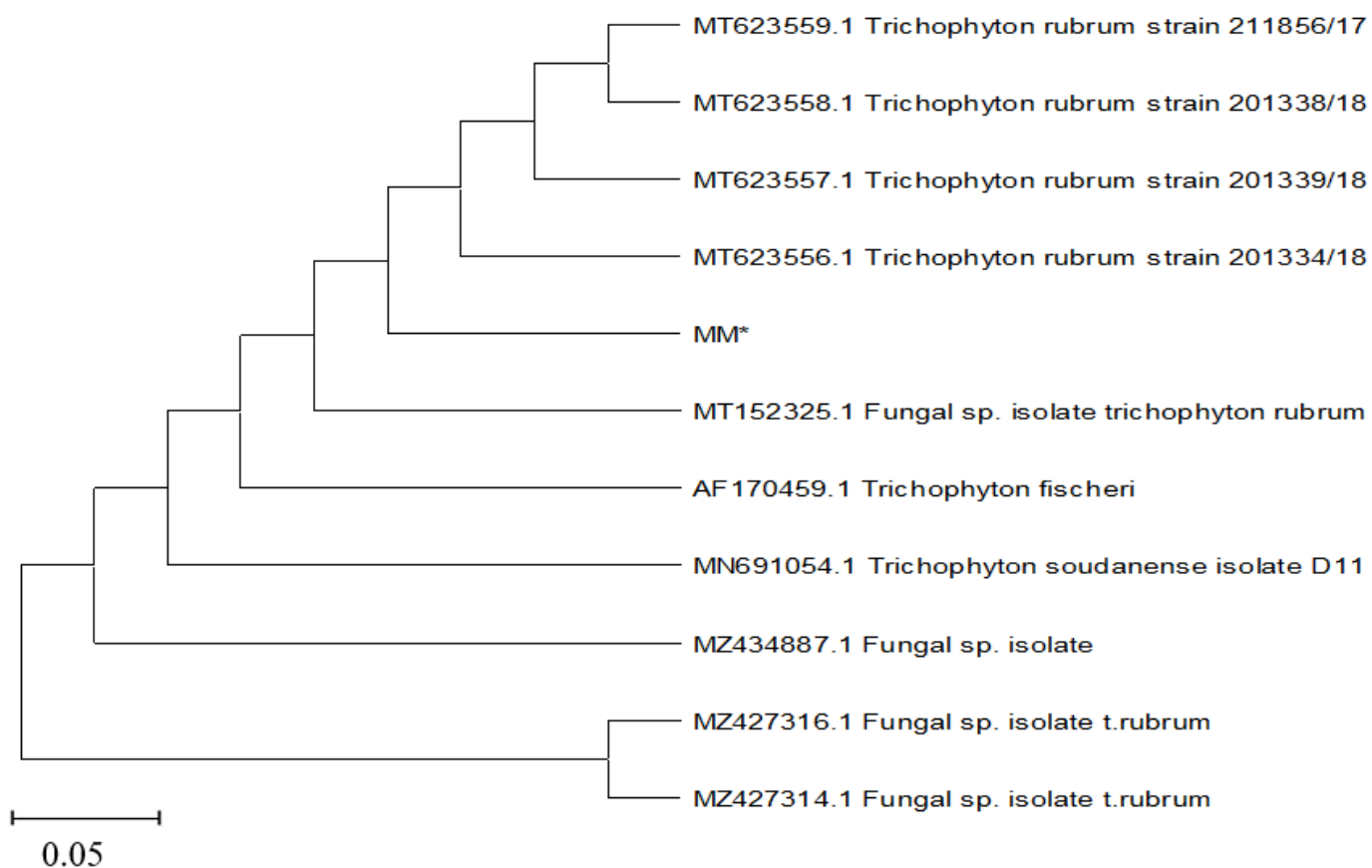


Figure 3

Phylogenetic tree showing the relationship between the ITS sequence of the *Trichophyton soudanense* isolate and reference sequences from the NCBI database. The tree was constructed using the neighbor-joining method. The scale bar represents substitutions per site.

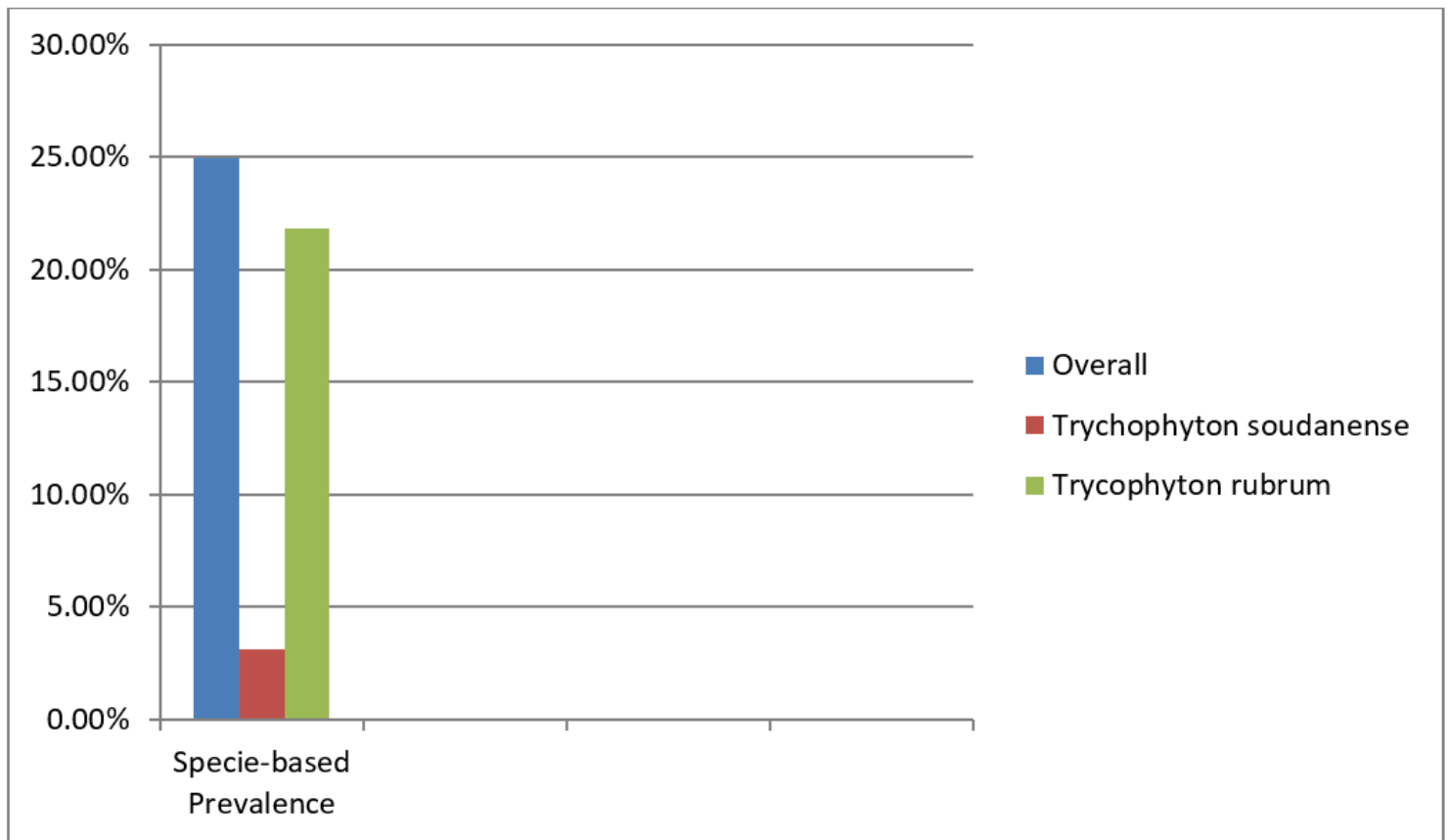


Figure 4

Specie-based prevalence of the Pathogens