

Epidemiological and Molecular Characterization of Trichophyton Species Associated with Dermatophytoses in Northeast Nigeria

Auwal Magaji

auwalmagaji@outlook.com

Federal University of Health Sciences, Azare, Bauchi State, Nigeria.

Ibrahim Musa Moi

Sa'adu Zungur University

Muhammad Abdullahi

National Open University of Nigeria

Bashir Abubakar Muhammad

Sa'adu Zungur University

Haladu Ali Gagman

Sa'adu Zungur University

Research Article

Keywords: Dermatophytosis, Trichophyton, Conventional, Prevalence, Epidemiology Molecular

Posted Date: March 20th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-8985440/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Additional Declarations: No competing interests reported.

Abstract

Background

Dermatophytoses are superficial fungal infections affecting 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, molecular characteristics, and risk factors associated with *Trichophyton*-related dermatophytosis among patients in the selected health facility in northeast Nigeria.

Methods

A cross-sectional study involving 385 patients with clinical signs of dermatophytoses was conducted at the Infectious Disease Hospital, Bayara. 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.

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. Logistic regression identified these as strong predictors of infection ($p < 0.05$).

Conclusion

The study underscored the public health importance of *Trichophyton* infections in northeast Nigeria, with *T. rubrum* being the predominant species. Molecular techniques improved species identification accuracy. 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

Fungal infections of the skin, hair, and nails are known as superficial mycoses. They are among the most common dermatological problems worldwide particularly in tropical and subtropical regions where warmth and humidity promote fungal proliferation [1, 2]. Of the fungi implicated in these infections, dermatophytes especially members of the genus *Trichophyton* are the most frequently encountered pathogens in both humans and animals [3]. *Trichophyton* species are keratinophilic fungi that digest

keratin and colonize the outer layers of the skin, nails, and hair causing dermatophytoses such as tinea capitis, tinea corporis, tinea pedis, tinea unguium, and tinea cruris [4, 5].

Dermatophytes are traditionally classified into three genera *Trichophyton*, *Microsporum* and *Epidermophyton* based on their microscopic morphology and host specificity. Of these, *Trichophyton* is the most diverse and clinically important, comprising numerous pathogenic species such as *T. rubrum*, *T. mentagrophytes*, *T. tonsurans*, *T. schoenleinii* and *T. verrucosum* [1, 3]. These species are further categorized ecologically into anthropophilic (human-associated), zoophilic (animal-associated) and geophilic (soil-associated) groups, each differing in pathogenicity and host interaction [5].

Transmission occurs through direct contact with infected individuals or animals, or indirectly via contaminated fomites or the environment [4, 6].

Trichophyton species are responsible for various clinical conditions depending on the site of infection. For instance, *T. rubrum* commonly causes tinea corporis and tinea pedis, while *T. tonsurans* is a leading cause of tinea capitis in children [7]. The infections often manifest as circular, scaly and itchy lesions with characteristic borders. Inflammatory reactions tend to be more severe with zoophilic and geophilic species, while anthropophilic species tend to cause more chronic and less inflammatory conditions [6, 8].

Globally, dermatophytoses affect an estimated 20–25% of the population, with infections caused by *Trichophyton* species accounting for the majority [2, 9]. The prevalence in children, especially tinea capitis, ranges between 21% and 87% in developing countries, with peak occurrence in those under 12 years [10, 11]. In Nigeria, prevalence estimates vary significantly by region, ranging from 3.4% to 55.1%, and are influenced by factors such as age, sex, hygiene practices, and socioeconomic conditions [10].

Several studies across Nigeria have demonstrated regional variations in the prevalence of *Trichophyton* species causing tinea capitis. For example *T. schoenleinii* was predominant in Borno State, *T. rubrum* in Kano, *T. mentagrophytes* in southwestern states and *T. tonsurans* in Anambra State [12, 13]. These findings underscored the need for continuous mycological surveillance and localized management strategies.

The identification of *Trichophyton* species traditionally relies on direct microscopy and culture, which provide preliminary morphological characterization. However, these methods are limited by their time requirements, subjectivity and difficulty distinguishing between closely related species [14]. In recent years, molecular techniques such as polymerase chain reaction (PCR) and sequencing of the internal transcribed spacer (ITS) region of ribosomal DNA have emerged as powerful tools for the precise identification and phylogenetic classification of dermatophytes [15]. Molecular characterization has not only increased diagnostic accuracy but also uncovered cryptic species within the *T. mentagrophytes* complex, including the recently identified *T. indotineae*, known for its aggressive clinical course and resistance to terbinafine [6].

Despite the clinical burden of *Trichophyton*-related infections, many patients in endemic regions continue to receive empirical treatment without laboratory confirmation. This not only promotes resistance but also delays appropriate therapy. Poor awareness, limited access to diagnostic laboratories and cultural practices further contribute to the underreporting and persistence of infections. In addition, environmental and behavioral risk factors such as close contact with animals, communal living, inadequate personal hygiene, and shared grooming tools (eg clippers, combs, towels etc) are key contributors to the transmission of *Trichophyton* species [10, 16].

Given the medical and public health significance of *Trichophyton* species in superficial fungal infections, the current study was designed to investigate the prevalence of dermatophytoses caused by *Trichophyton* spp. among patients presenting with skin and scalp infections at the selected health facility in northeast Nigeria. The study further aimed to identify associated risk factors and utilize both conventional and molecular techniques to accurately characterize the isolates. By integrating epidemiological data with molecular identification, this study could provide valuable insights into the distribution, diversity and control of *Trichophyton* species in endemic settings.

MATERIALS AND METHODS

Study Area

This study was conducted at the Infectious Disease Hospital (IDH) Bayara one of the referral centers in northeastern Nigeria (Fig. 1) for infectious diseases especially those affecting skin. It is located in Birshi, Bauchi Local Government Area (LGA), Bauchi State, Nigeria. It was established on March 11, 1982, and licensed under the Federal Ministry of Health with facility code 05/02/1/2/1/0002. Bauchi LGA covers approximately 3,219 km² with estimated population of 881,600, with 51.1% males and 48.9% females. It is located on the coordinates: 10.2820° N latitude and 9.8120° E longitude (Fig. 1) [17].

Study Design and Population

The study was cross-sectional, and involved collecting data from patients at IDH Bayara at a single point in time.

The study population comprised patients of all genders and ages with clinical signs and symptoms of superficial mycoses. Patients unwilling to participate in the study and those without clinical symptoms of superficial mycoses were excluded.

Sample Size Determination

The sample size was calculated using Cochran's formula. Prevalence of 50% as reported by Idris *et al.* [18], and precision of 5% were taken at 95% confidence level.

$$n = \frac{(z/2)^2 pq}{d^2}$$

Where:

P = previous prevalence (50%)

q = 1-p

d = precision (5%)

9Z/2) = 1.96 for 95% confidence level

n = sample size

Therefore,

$$n = \frac{(1.96)^2 \times 0.5 (1 - 0.5)}{0.05^2}$$

Therefore, 385 patients with clinical presentations of the infections were enrolled in the study.

Ethical Considerations

Ethical approval

was obtained from the Research and Ethics Committees of the Infectious Disease Hospital Bayara in a letter dated 4th May, 2024 with reference number IDH/2024/5V1. Dual 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. Confidentiality of patients' information was maintained, and all procedures were conducted in accordance with Helsinki's (2013) Declaration.

Sample Collection

Skin scrapings, hair, or lesion samples were collected from 385 patients exhibiting signs and symptoms of dermatophytoses. Before the sample collection, the affected site of the patient's body was cleaned using a sterile cotton swab soaked in 70% ethanol. The samples were placed in sterile disposable dishes and transported to the Microbiology Laboratory, Sa'adu Zungur University Gadau, for further analysis. Meanwhile, 385 structured questionnaires were administered to the patients at the time of sample collection to obtain sociodemographic and risk factor data from the patients

Isolation of Fungal Pathogens

Fungal pathogens were isolated using Sabouraud Dextrose Agar (SDA), prepared by dissolving 39 g of SDA in 1000 mL of distilled water, followed by sterilization at 121°C for 15 minutes. After cooling, the medium was inoculated with patients' samples and incubated at 35°C for up to 7 days [19].

Identification of Fungal Pathogens

Prior to the isolation, direct microscopic examination was conducted. The samples were treated with 10% Potassium Hydroxide (KOH) to dissolve keratin, and observed for the fungal spores, under 10X and 40X objectives. Upon isolation, the colonies were assessed for color, texture, and topography [19, 20].

Molecular Identification

The isolates were maintained on Sabouraud dextrose agar and kept at 4°C. The isolates were cultured in Sabouraud dextrose broth, and incubated for 14 days at 28°C. Small portion of the isolate's mycelia was reaped and centrifuged at 1600×g for ten minutes, and then washed with ice-cold phosphate buffered saline and then stored at – 70°C.

The genomic DNA from the isolates was isolated as stated by Rezaie *et al.*, [21]. About three hundred milligram (300mg) of the mycelia was grounded to powder with liquid nitrogen. 500µL of extraction buffer (50mM Tris-HCl pH 8.0), 50mM EDTA, 25µL of 20% SDS, and 10µL of proteinase-K, were added and gently mixed. This was followed by incubation at 65°C for 60min and centrifugation at 3000×g for 15min. 25µL of Rnase was added to the supernatant and incubated at 37°C for 30 in. This was then mixed with 500µL of phenol:chloroform:isoamyl alcohol (25:24:1) and centrifuged at 10000×g for 10min. The supernatant were collected and transferred to a new steriled eppendorff tube. This was then mixed with 500µL of chloroform:isoamyl alcohol (24:1) and centrifuged at 10000×g for 10min. The supernatant were collected and transferred to another eppendorff tubes. The DNA was precipitated by the addition of 500µL of isopropanol and 30µL of 3M Sodium acetate. This was then followed by centrifugation at 15000×g for 30min. The supernatants were then discarded. The DNA pellet was rinsed with 200µl of 70% cold ethanol and centrifuged at 10000×g for 10min. The pellet was then air dried and stored at -20°C [21].

ITS1 (5'-TCC GTA GGT GAA CCT GC-3') and the ITS4 (5'-TCC TCC GCT TAT TGA TAT G-3') were used as forward and reverse primers respectively [22, 23]. A 25µL PCR reaction mixture was prepared comprising of 2.5µL of 10× reaction buffer, 0.5µL of 10mM dNTPs, 1.5µL of 25mM MgCl₂, 0.5µL of 0.2mM of each of the ITS1 and ITS4 primers, 0.5µL of Taq DNA polymerase (Promega Coporation, USA), 0.5µL of genomic DNA and 18.5µL of distilled water. The PCR reactions were carried out on a thermal cycler (MJ Research Inc. USA), with the following conditions: 1 cycle in an initial step for 5min at 94°C, then 30 cycles consisting of denaturation at 94°C for 30s, then annealing for 40s at 55°C, and then extension at 72°C for 40s. This was followed by a final extension at 72°C for 10min. 5µl of PCR product was loaded on 1% agarose in 1X Tris–Acetic Acid– EDTA buffer and stained with 0.5mg/ml ethidium bromide for

40min at 80V, and visualized with UV trans-illuminator (Alpha Innotech, USA). This was then compared with a standard DNA size marker (100bp DNA ladder), and photographed in UV light [22, 23]. The PCR products were sent for sequencing. The sequence result was processed by using the web-based blasting program- basic local alignment search tool (BLAST), at the NCBI website, and the data were compared with the NCBI/Genbank database. The phylogenic tree was constructed using MEGA 11.

Data Analysis

In presenting the results of this research, a multifaceted approach was employed, integrating tables and charts to effectively communicate key findings visually. The interpretation of these results was underpinned by robust statistical analyses, leveraging a diverse set of tools including Chi-square test where applicable. All of these were computed using SPSS version 23.

RESULTS

Phenotypically, the current study reported two species of *trychophyton* to be associated with dermatophytoses among patients from northeastern states of Nigeria, at the infectious disease hospital Bayara. However, the molecular identification confirmed two *Trichophyton* species (two different strains of *Trichophyton rubrum* and one strain of *Trichophyton soudanense*) based on 18S rRNA homology. The 18S rRNA gene sequences of the pathogens were compared using BLAST with reference sequences from the NCBI database. Phylogenetic trees for the isolates were constructed using MEGA 11 (Figs. 3 and 4).

The study also revealed that, the overall prevalence of *Trichophyton* species among patients with dermatophytoses in northeastern Nigeria was 24.94%. The specie-based prevalence indicated high prevalence of *Tricophyton rubrum* (21.82%) than *Trichophyton soudanense* (3.12%) (Fig. 2).

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 ($p = 0.000$). Individuals living in rural areas had the highest prevalence (16.62%) compared to those in urban (5.19%) and semi-urban (3.12%) settings.

The participants, who currently had skin, nail or scalp infections were more likely to have higher prevalence of the infection (18.18%) than those who had not (6.75%) ($p = 0.045$).

There was a strong association between regular contact with animals and high prevalence of the infection, where a prevalence of 20.78% among those with animal contact compared to 4.16% among those without ($p = 0.000$).

Socioeconomic status significantly influenced infection prevalence ($p = 0.000$). 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 (3.64%).

Bathing habits were also significant ($p = 0.000$), with infection 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%) versus 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%) ($p = 0.000$), 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	p-value
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		
Do you currently have a skin, nail, or scalp infection?			
Yes	18.18	4.032	0.045*
No	6.75		
Do you have 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		
How often do you bathe?			
Regularly	9.35	66.444	0.000*
*" = Significant at $p < 0.05$, " χ^2 " = Chi-square			

Variables	Prevalence (%)	χ^2	<i>p</i> -value
Not regularly	15.58		
Do you share personal grooming tools (clippers, combs, towels)?			
Yes	15.32	3.264	0.071
No	9.61		
Do you live in a communal setting (e.g., boarding school, barracks)?			
Yes	15.84	28.717	0.000*
No	9.09		
Are you involved 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 revealed several significant predictors of Trichophyton-related dermatophytosis. Regular contact with animals significantly increased the odds of infection ($p = 0.000$, OR = 0.045, 95% CI: 0.024–0.083).

Also, participants from low-income households were significantly more likely to be infected ($p = 0.000$, OR = 0.092, 95% CI: 0.048–0.175). Similarly, irregular bathing was associated with significantly higher odds of infection ($p = 0.000$, OR = 0.138, 95% CI: 0.083–0.229).

Living in communal settings significantly increased the odds of infection ($p = 0.000$, OR = 0.240, 95% CI: 0.139–0.414), as the involvement in farming or outdoor labor was a significant predisposing factor ($p = 0.010$, OR = 0.523, 95% CI: 0.319–0.857). Also, presence of current skin, nail or scalp infection was significantly associated ($p = 0.046$, OR = 0.596, 95% CI: 0.358–0.991).

Other variables like gender, age, and sharing grooming tools were not statistically significant predictors of the infection among the patients (Table 2).

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

Dermatophytoses							
Variables	+	-	Tot	P	OR	Confidence Interval	
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		
Do you currently have a skin, nail, or scalp infection?							
Yes	70	178	248	0.046*	0.596	0.358 -	0.991
No	26	111	137		1		
Do you have regular contact with animals?							
Yes	80	56	136	0.000*	0.045	0.024 -	0.083
No	16	233	249		1		
“*” = Significant at p < 0.05, “OR” = odds ratio							

Variables	+	-	Tot	<i>P</i>	OR	Confidence Interval	
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		
How often do you bathe?							
Regularly	36	233	269	0.000*	0.138	0.083 -	0.229
Not regularly	60	56	116		1		
Do you share personal grooming tools (clippers, combs, towels)?							
Yes	59	150	209	0.072	1.544	0.962 -	2.479
No	37	139	176		1		
Do you live 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		
Are you involved in farming or outdoor labor?							
Yes	36	69	105	0.010*	0.523	0.319 -	0.857
No	60	220	280		1		
“*” = Significant at p < 0.05, “OR” = odds ratio							

DISCUSSION

The findings of this study highlighted *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 globally, which have identified these fungal species as common causative agents of dermatophytoses. The predominance of *Trichophyton rubrum* in this study corresponded with findings from Kano State, as reported by Adeleke *et al.* [24]. The consistent

occurrence of *T. rubrum* across different regions suggests its adaptability and widespread distribution in Nigeria.

However, the study contrasted the findings of Nweze, [25] 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.* [26]. 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 [27].

The findings of this study also suggest that the infection is more prevalent among males, although the association is not statistically significant. However, age, residence, regular contact with animals, socioeconomic status, bathing habits, and living in communal settings are significant predictors 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 [10, 11]. The increased susceptibility among older adults as reported in this study may be attributed to declining immune function, poor hygiene practices and increased exposure to risk factors.

The study also highlighted the importance of residence in determining the prevalence of Trichophyton-related dermatophytosis. Individuals living in rural areas had 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 [28, 29, 30].

The study also identified several significant risk 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 [4, 6, 16, 30].

CONCLUSION

This study revealed a high burden of *Trichophyton*-related dermatophytosis in bortheastern Nigeria with *T. rubrum* emerging as the dominant species confirmed through molecular characterization. The findings

highlighted critical sociodemographic and behavioral risk factors particularly among individuals with regular animal contact, low socioeconomic status, poor hygiene and communal living conditions. These factors significantly influence infection prevalence and should be prioritized in public health strategies.

The integration of molecular techniques enhanced the accuracy of fungal identification and demonstrated the limitations of conventional methods alone. This emphasized the need for improved diagnostic capacity in endemic areas. To curb 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 monitor antifungal resistance patterns and develop effective prevention and treatment protocols.

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, 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. Confidentiality of patients' information was maintained, and all procedures were conducted in accordance with Helsinki's (2013) Declaration.

Consent for Publication: Not applicable

Availability of Data and Materials

All data for this research are contained in the manuscript. Additional information and materials can be obtained from NCBI website, and the corresponding author on a serious request.

Competing Interests

The authors declare that, there is no competing interest

Funding

No funding was obtained from any institution. The study was funded by the authors throughout.

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.

Acknowledgments

We sincerely thank the entire staff of the Infectious Disease Hospital Bayara especially those in the Department of Microbiology for providing necessary supports during this study.

References

1. Husain AE, Abdel Fattah NS, Afify AA, Mostafa NS. Epidemiology and risk factors of superficial fungal infections in Toukh Primary Health Care Centre. Egypt J Hosp Med. 2018;72(7):4898–902. 10.21608/ejhm.2018.10171.
2. Feng W, Chen C, Mo S, Qi C, Gong J, Li XN, et al. Highly oxygenated meroterpenoids from the Antarctic fungus *Aspergillus terreus*. Phytochemistry. 2019;164:184–91.
3. Roderick J, Hay A. Hunter's Tropical Medicine and Emerging Infectious Diseases. 10th ed. London: Elsevier; 2020. pp. 646–7.
4. Gupta N, Shukla V, Shukla P. Clinical pattern of superficial mycosis in rural type 2 diabetes mellitus patients. Int J Res Med Sci. 2018;6:2295–8.
5. Moriello KA. Decontamination of 70 foster family homes exposed to *Microsporum canis* infected cats: A retrospective study. Vet Dermatol. 2019;30:178–e55.

6. Kassem R, Shemesh Y, Nitzan O, Azrad M, Peretz A. Tinea capitis in an immigrant pediatric community: a clinical signs-based treatment approach. *BMC Pediatr.* 2021;21:36.
7. Getso MI, Hashemi SJ, Ghazvini RD, Yusuf SM, Khodavaissy S, Gerami-Shoar M, et al. Determination of dermatophytes isolated from tinea capitis using conventional and ITS-based sequencing methods in Kano, Nigeria. *J Mycol Med.* 2021;31(3):101157.
8. Tan CW, Foong AY, Liew HM, Koh MJ. A review of tinea capitis in a cohort of Asian children. *Ann Acad Med Singap.* 2018;47(4):156–8.
9. Lao M, Wang X, Ding M, Yang Z, Chen H, Liang L, et al. Invasive fungal disease in patients with systemic lupus erythematosus from Southern China: A retrospective study. *Lupus.* 2019;28:77–85.
10. Leung AKC, Leong KF, Lam JM. Tinea imbricata: An overview. *Curr Pediatr Rev.* 2019;15(3):170–4.
11. Sharma B, Nonzom S. Superficial mycoses, a matter of concern: Global and Indian scenario: an updated analysis. *Mycoses.* 2021;64(8):890–908. 10.1111/myc.13264.
12. Adebayo AM, Adelodun AA, Olabumuyi OO, Adelabu AM. Prevalence and distribution of tinea infections among primary school children in a rural setting of South-West Nigeria. *Afr J Med Med Sci.* 2020;49:271–80.
13. Birhanu MY, Temesgen H, Ketema DB, Desta M, Getaneh T, Bekele GM. Tinea capitis among schoolchildren in Ethiopia: A systematic review and meta-analysis. *PLoS ONE.* 2023;18(2):e0280948. 10.1371/journal.pone.0280948.
14. Rajagopalan M, Inamadar A, Mittal A, Miskeen AK, Srinivas CR, Sardana K, et al. Expert Consensus on The Management of Dermatophytosis in India (ECTODERM India). *BMC Dermatol.* 2018;18(1):6.
15. Farokhipor S, Ghiasian SA, Nazeri H, Kord M, Didehdar M. Characterizing the clinical isolates of dermatophytes in Hamadan city, Central west of Iran, using PCR-RLFP method. *J Mycol Med.* 2018;28(1):101–5.
16. John AM, Schwartz RA, Janniger CK. The kerion: An angry tinea capitis. *Int J Dermatol.* 2018;57(1):3–9.
17. Klein GK, Beusen A, Deilman J, Stehfest E. Anthropogenic Land Use Estimates for the Holocene-HYD 2,3. *Earth Syst Sci Data.* 2017;9:927–53.
18. Idris A, Ramadan T, Auwal K, Akande A, Rogo L, Abbas M. Dermatormycoses Among People Living with Diabetes Mellitus in Kano, Nigeria. *Alqalam J Med App Sci.* 2023;6(2):883–9.
19. Larone DH. Medically important fungi: A guide to identification. 5th ed. Washington, D.C.: American Society for Microbiology; 2011.
20. UK Standard for Microbiology Investigation (UK SMI). *Five year strategy 2020–2025.* 2020.
21. Rezaie S, Ban J, Mildner M, Poitschek C, Brna C. Characterization of a cDNA clone, encoding a 70 kDa heat shock protein from the dermatophyte pathogen *Trichophyton rubrum*. *Gene.* 2000;241:27–33.
22. Shehata AS, Mukherjee PK, Aboulatta HN, El Akhras AI, Abbadi SH, Ghannoum MA. Single-step PCR using (GACA)₄ primer: utility for rapid identification of dermatophyte species and strains. *J Clin*

- Microbiol. 2008;46(8):2641–5.
23. Yang G, Zhang M, Li W, An L. Direct species identification of common pathogenic dermatophyte fungi in clinical specimens by semi-nested PCR and restriction fragment length polymorphism. *Mycopathologia*. 2008;166:203–8.
 24. Adeleke S, Usman B, Ihesiulor G. Dermatophytosis among itinerant quranic scholars in Kano (Northwest) Nigeria. *Niger Med Pract*. 2008;53(3):33–5.
 25. Nweze EI. Etiology of dermatophytoses amongst children in northeastern Nigeria. *Med Mycol*. 2001;39(2):181–4.
 26. Ayanlowo O, Akinkugbe A, Oladele R, Balogun M. Prevalence of *Tinea capitis* infection among primary school children in a rural setting in south-west Nigeria. *J Public Health Afr*. 2014;5(1).
 27. Nweze EI, Okafor JI. Prevalence of dermatophytic fungal infections in children: a recent study in Anambra State, Nigeria. *Mycopathologia*. 2005;160(3):239–43.
 28. Moto JN, Maingi JM, Nyamache AK. Prevalence of *Tinea capitis* in school going children from Mathare, informal settlement in Nairobi, Kenya. *BMC Res Notes*. 2015;8:274.
 29. Pérez-Tanoira R, Marín I, Berbegal L. Mycological profile of *tinea capitis* in schoolchildren in rural southern Ethiopia. *Med Mycol*. 2017;55(3):262–8.
 30. Magaji A, Yakubu A, Mahmud Z, Aminu S, Salihu MR, Sambo H. The Role of Socioeconomic and Environmental Determinants in the Prevalence and Distribution of Superficial Mycoses in Bauchi State Nigeria. *Dujopas*. 2025;11(2b):352–63.

Figures

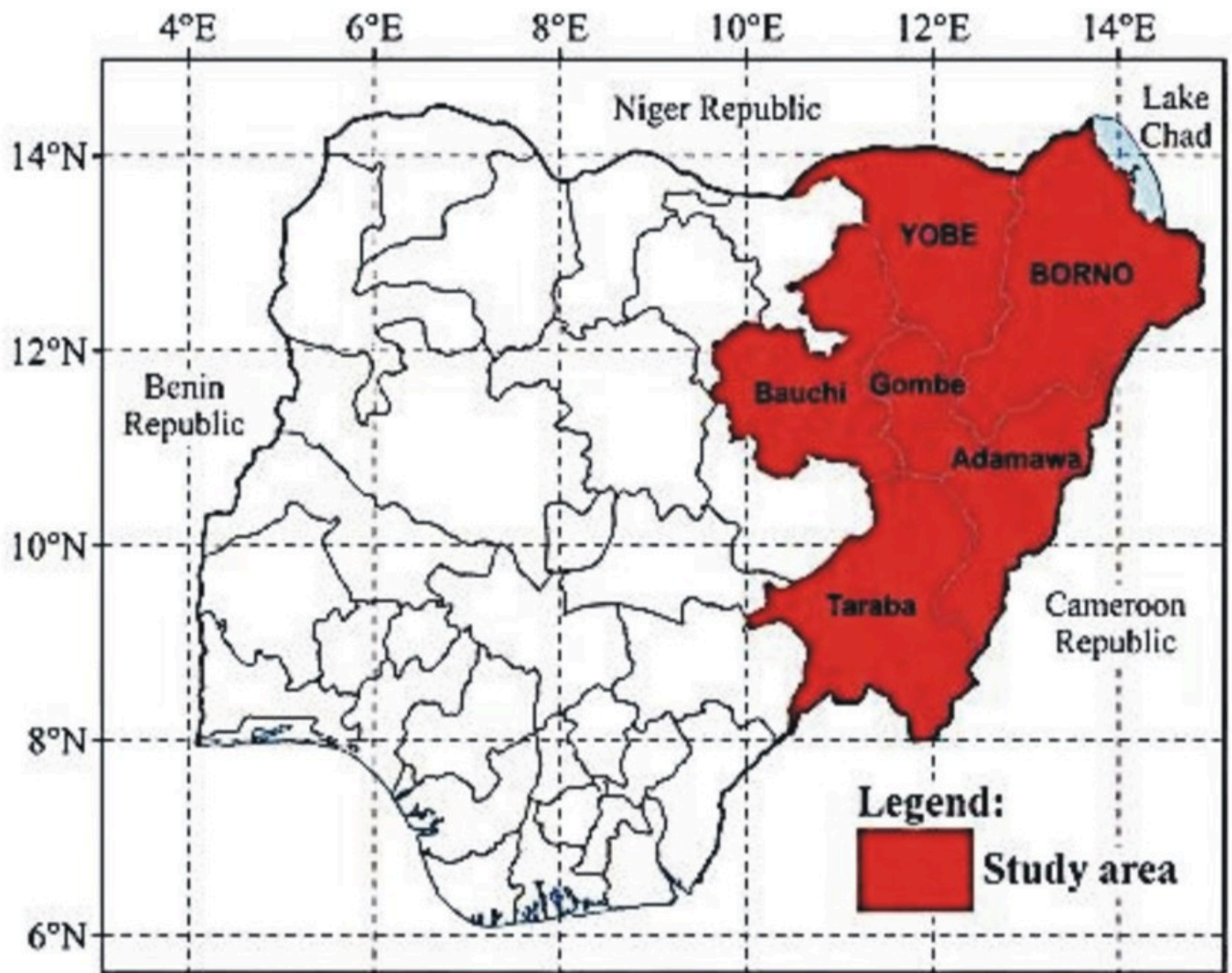


Figure 1

Map of Nigeria Showing the Study Area

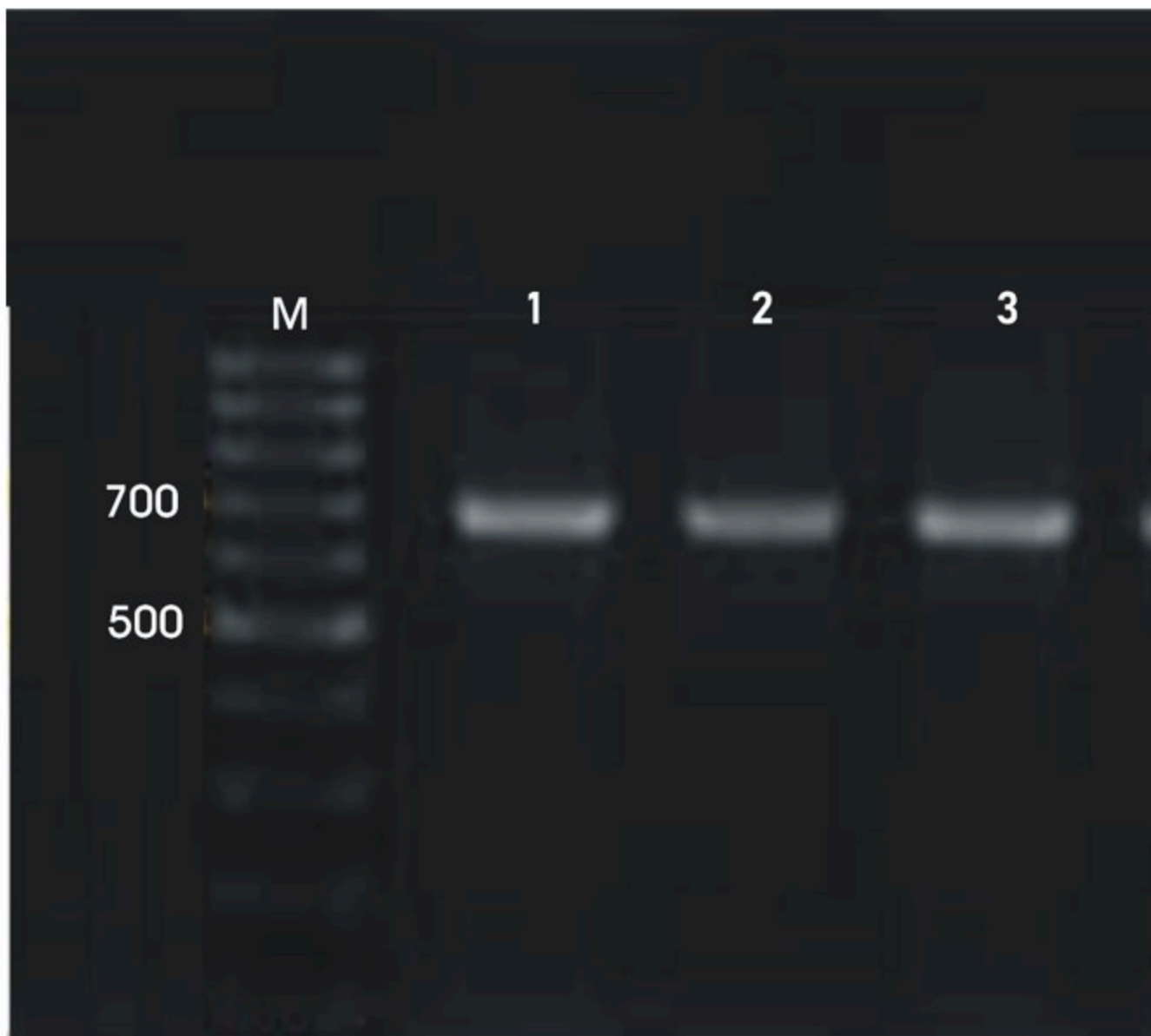


Figure 2

Agarose gel electrophoresis of amplified 18S rRNA gene using ITS primer.. Lane: M-represents marker, lanes 1-2 represent isolates of *T. rubrum* and 3 represents *T. soudanense* isolate

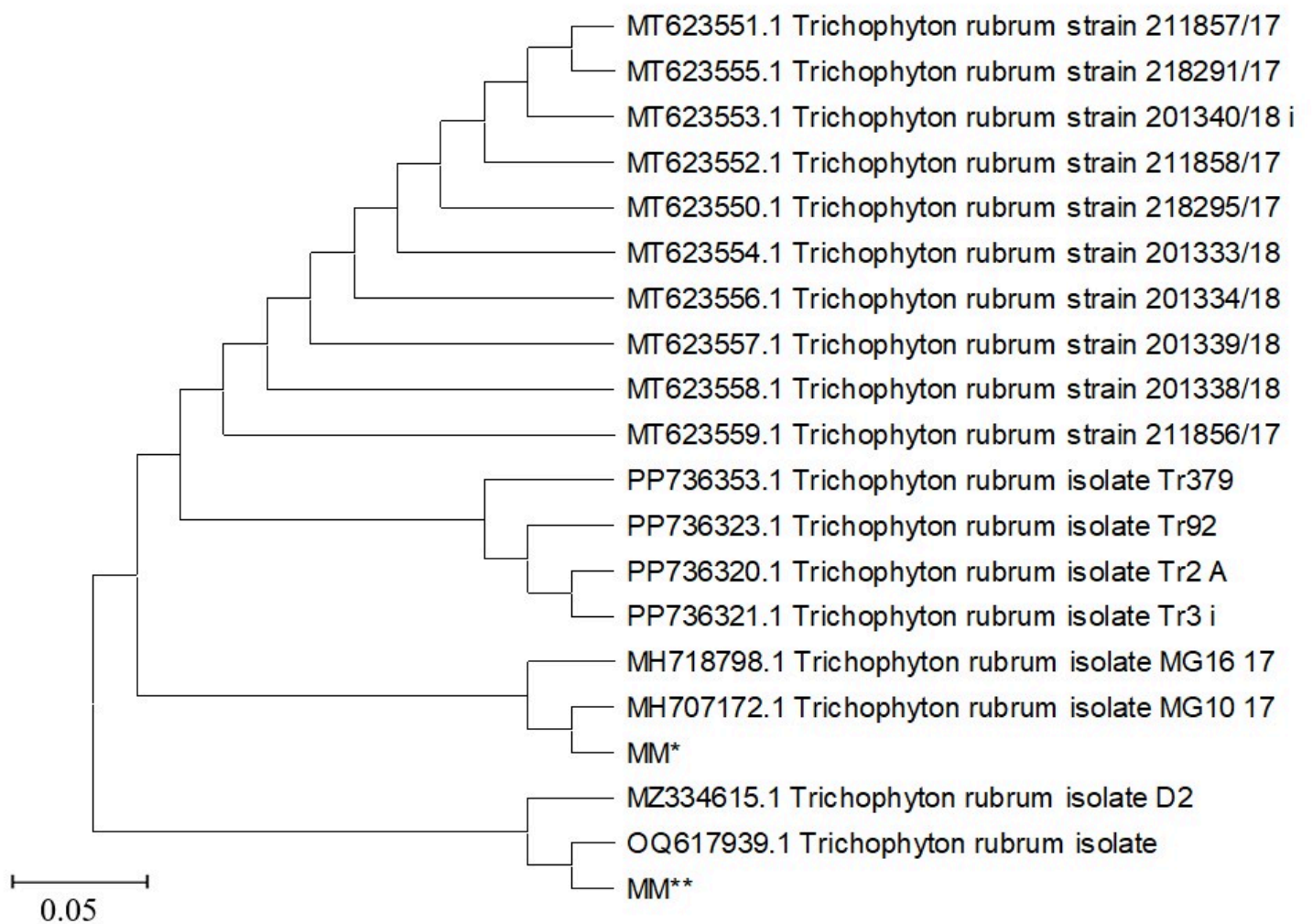


Figure 3

A phylogenetic tree showing the relationship between the 18S rRNA gene sequences of the Isolated *T. rubrum* and that of other *T. rubrum* species from NCBI. The *T. rubrum* strains isolated were designated as MM* and MM** strains. The maximum likelihood was inferred using the Neighbor-joining method. The horizontal bar indicates 0.05

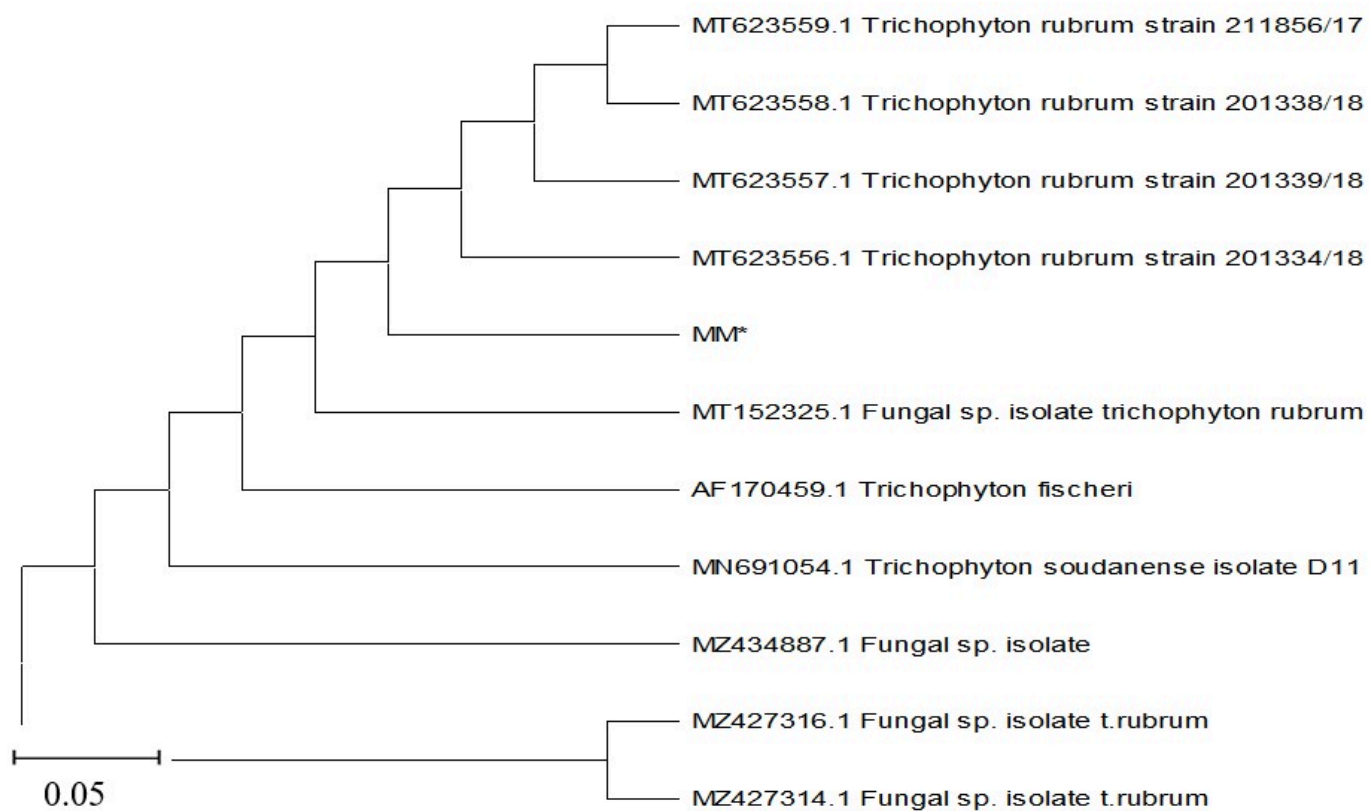


Figure 4

A phylogenetic tree showing the relationship between the 18S rRNA gene sequences of the Isolated *T. soudanense* and that of other *T. soudanense* species from NCBI. The *T. soudanense* strain isolated was designated as MM* strain. The maximum likelihood was inferred using the Neighbor-joining method. The horizontal bar indicates 0.05

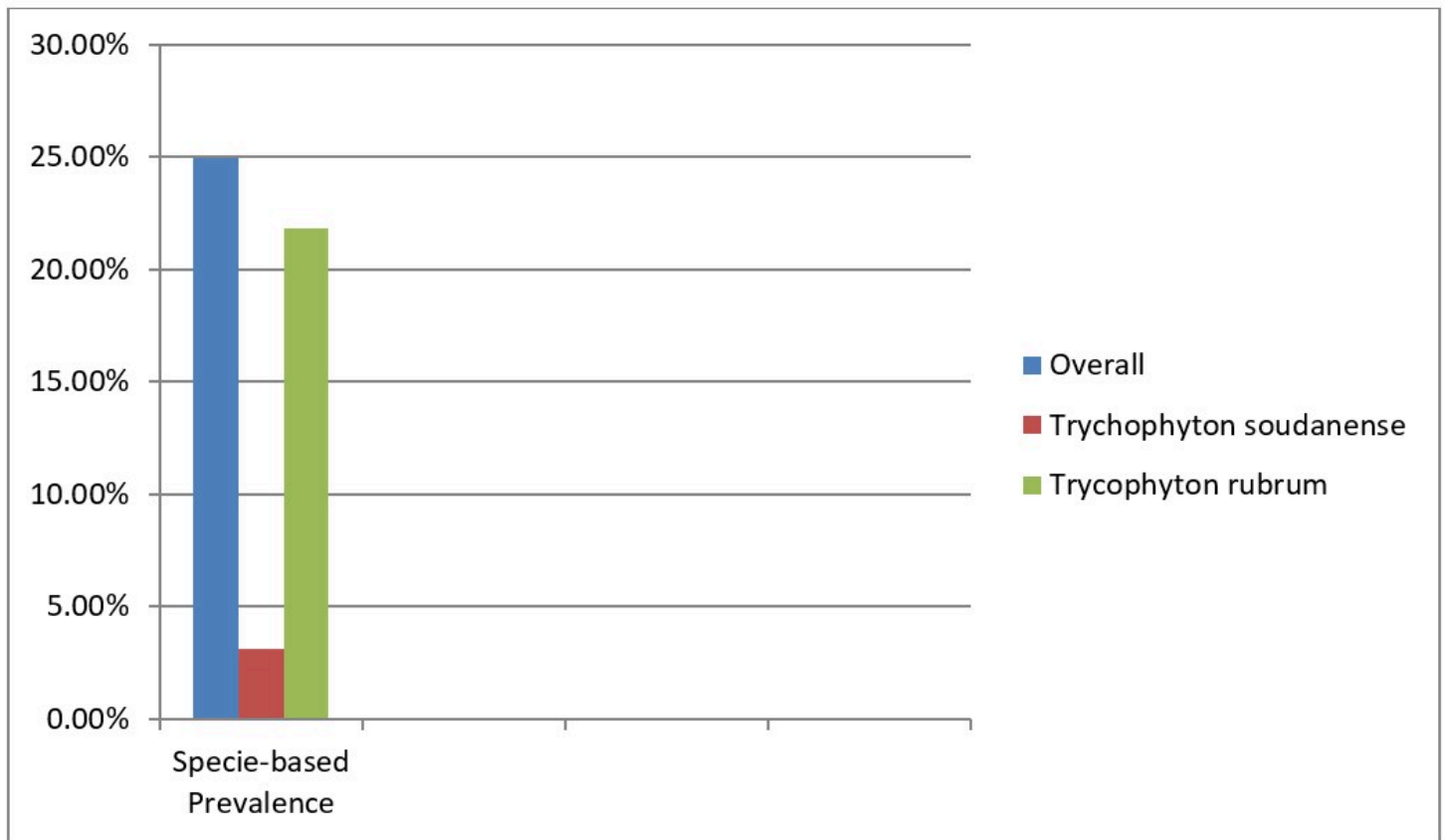


Figure 5

Figure 2: Specie-based prevalence of the Pathogens