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Evaluation of Dermatophytes Responsible for Dermatophyte Infection among Diabetes Patients in Lagos, Nigeria

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ABSTRACT

Dermatophytes are fungal pathogens that invade keratinised tissues, causing tinea infections named according to the site affected. Predominantly found in the genera *Trichophyton*, *Microsporum*, and *Epidermophyton* with *Trichophyton* being the most clinically significant. Diabetes mellitus, a chronic metabolic disorder with major public health implications, disrupts glucose, fat, and protein metabolism. Research on the association between glycemic status and dermatophytosis is limited. This study aimed to determine the prevalence of dermatophyte infections among diabetic patients in Lagos, Nigeria. In this cross-sectional study, 400 diabetic patients clinically diagnosed with dermatophytosis were recruited from two tertiary hospitals in Lagos State between August 2015 and February 2016. Microbial identification of dermatophytes involved conventional isolation, biochemical analysis, and polymerase chain reaction (PCR) targeting the internal transcribed spacer region, followed by gene sequencing. Results showed that, Tinea pedis was the most prevalent infection (89.75%), followed by tinea capitis (6.25%) and tinea unguium (3%). Culture results showed no growth in 14% of samples, single isolates occurred in 45.25%, and multiple isolates occurred in 54.75% of the patients. Sixty isolates were presumptively identified as dermatophytes based on culture, but only 31 were confirmed molecularly. The primary etiological agents were *Trichophyton interdigitale* (42%), *Trichophyton mentagrophytes* (19%), and *Arthroderma vespertilii* (13%), followed by other *Arthroderma* species. This study identifies *Trichophyton* and *Arthroderma* species as the major dermatophytes causing infections in diabetic patients. Significantly, it is the first study to implicate *Arthroderma* species in dermatophytosis in Nigeria

Keywords: Dermatophytes, Dermatophytosis, Diabetes, Keratinised Tissues, Tinea pedis, *Trichophyton, Arthroderma*, PCR.

Introduction

Dermatophytes are a group of closely related fungi possessing the ability to colonize keratinized tissues such as skin, hair and nails of humans and animals (Ramaraj *et al*., 2016a). They cause an infection called dermatophytosis and the organisms responsible are in the three main genera of *Trichophyton, Microsporum* and *Epidermophyton* (Tashmin *et al*., 2018a). These organisms possess, in varying quantities, enzymes such as proteinases, keratinase, elastase and lipolytical enzymes which aid their ability to invade these set of tissues (Martinez-Rossi *et al.,* 2017), and are, therefore, responsible for majority of fungal infections in man and animals worldwide making them a major public health concern (Sahoo & Mahajan, 2016; Phudang *et al.,* 2019).

Globally, studies show varying incidence rate, but it is generally agreed that between 20% and 25% of the world's population is affected (Razzaghi-Abyaneh & Shams-Ghahfarokhi, 2021; Girish et al., 2018). Recent studies reveal that dermatophyte infections, notably tinea capitis (scalp ringworm), are widespread among children worldwide and the incidence varies by area, socioeconomic status, and population category (Nguyen et al., 2020; Kruithoff *et al.,* 2023).

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In southern European countries, dermatophytes are responsible for 40 to 68% of cases, with yeast accounting for 21 to 55% of cases (Petrucelli et al., 2018) while it is much higher in Asia and Africa (Coulibaly *et al.,* 2018; Rajagopalan et al., 2018). Fungal diseases have become a major global economic burden. In 2018, the United States spent approximately USD 6.7 billion on fungal diseases (Kruithoff et al., 2023; Rayens & Norris, 2018). At least USD 500 million is spent on fungal infections caused by dermatophytes alone. Lack of effective therapy may play a major role in the high expenses associated with fungal infections (Kruithoff *et al*., 2023). Hair, skin, and nails can be affected by dermatophytes across all societal levels, causing significant changes in hair, skin, or nails. Although they are not life-threatening, they are challenging to treat and may negatively affect a person's appearance (Bristow & Joshi, 2023; Shukla *et al*., 2016).

In Nigeria**,** more than 11.8% of its population suffers from serious fungal infections every year, resulting in approximately 960,000 deaths with the incidence rate ranges from 2.1% to 41 (Adesiji *et al*., 2019). It was also reported that the incidence of tinea capitis among children was 62% in males and 38% in females, with higher rates in rural areas and most other tineas are also found in children (Ayanlowo et al., 2018; Rasheed *et al.,* 2024 & Om *et al.,* 2022). Although they are not life-threatening, they are challenging to treat and may negatively affect a person's appearance (Bristow & Joshi, 2023; Shukla *et al.,* 2016). Infections caused by dermatophytes have overtime shown wide variation in distribution, incidence, epidemiology, etiology and host range. Several factors such as geographical location, prevailing climatic condition, healthcare standards and socioeconomic condition of the citizenry like high poverty level, malnutrition, poor personal hygiene and environmental sanitation, overcrowding etc assist in the proliferation of these infections (Chanyachailert *et al*., 2023; Narain *et al*., 2018).

As a result of low antifungal susceptibility and the need for long-term management, dermatophyte infections can be challenging to treat, especially in patients with immunosuppression. For those intolerants of conventional antifungals, natural herbal remedies, lasers, and photodynamic therapies may be suggested (Durdu, & Ilkit, 2022)

Diabetes mellitus is defined by a relative or complete deficiency of insulin, resulting in disrupted metabolism of glucose, fat, and protein. This chronic metabolic disorder carries significant economic, social, and human implications, especially in developing countries, and is regarded as a critical public health issue (Parada *et al*., 2013). In 2007, over 246 million people suffered from diabetes mellitus, and it has become a pandemic disease worldwide (Dinesh & Saikumar, 2021). According to International Diabetes Federation, it is estimated that 853million people will suffer from diabetes by 2025 (IDF, 2025). A consensus among experts suggests that individuals with diabetes mellitus face an elevated risk of developing dermatophyte infections. However, some debate persists regarding the extent of this association (Dinesh & Saikumar, 2021). Research has demonstrated that individuals with diabetes are significantly more susceptible to skin infections, with reported incidence rates ranging from 20% to 50%., and this heightened risk is particularly evident among patients with type 2 diabetes mellitus and is frequently correlated with inadequate glycemic control (Dinesh & Saikumar, 2021). Individuals with concurrent conditions, such as diabetes mellitus, face an elevated risk of developing fungal infections of the nails, which can lead to serious complications. Diabetic patients frequently encounter foot problems, primarily as a result of neuropathy and compromised blood flow. Consequently, they are at a heightened risk of amputations due to ulcers, fissures, and secondary infections. Infections are a common issue for those living with diabetes (Vazheva *et al*., 2022). Timely intervention with antifungal agents is crucial for elderly diabetic patients presenting with dermatophyte infections, as these conditions can compromise the integrity of the skin and predispose individuals to subsequent bacterial infections. Topical antifungal therapies are typically effective and represent a more cost-efficient option compared to systemic oral treatments for the majority of dermatophyte infections affecting the foot (Dinesh & Saikumar, 2021).

There is limited research examining the link between an individual's glycemic status and the development of dermatophytosis. This study was therefore conducted in view of the above and the fact that there have been no recent studies on evaluating or tracking the circulating species or strains of dermatophytes responsible for causing dermatophytosis in Lagos, Nigeria.

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Materials and Methods

Clinical Sample Collection

The collection of clinical samples was carried out from the month of August 2015 to February 2016. Three hundred (300) clinical samples were collected from patients who were already being managed for diabetes and who presented with cases of skin infection at the skin clinic of the Lagos State University Teaching Hospital (LASUTH).

During the same period, one hundred (100) clinical samples were collected from patients not previously known to be diabetic but presenting with skin infections. In all these cases verbal and informed consent was obtained through administering patient information sheet, informed consent form and or assent form for minors and doctor's clinical diagnosis of dermatophyte infection (Gupta *et al.,* 2018).

The disease area of the skin, hair or nails was thoroughly cleaned with methylated spirit swab and using sterile scalpel or scissors, skin scale, nail or hair clippings were collected in sterile paper bags, labelled appropriately using codes and transported to the laboratory for analysis (Havlickova *et al.,* 2008). Samples were not collected from patients that did not fulfill the above inclusion criteria.

Cultivation and Isolation of Dermatophytes

The method described by (Ramaraj *et al.,* 2016) was adapted in isolating the dermatophytes. The skin, nail or nail clippings of the patients were sprinkled on Saboraud dextrose agar (SDA) (Oxoid, Basingstoke, UK) supplemented with dermasel selective supplement (SR0075E: Oxoid, Basingstoke, UK). SDA was prepared according to manufacturer's guide for 500ml of medium.

One vial of dermasel selective supplement reconstituted with sterile water was added to the medium and autoclaved at 121ºC for 15 minutes. After autoclaving and allowing medium to cool to about 45ºC, medium was poured aseptically into sterile disposable Petri dishes and allowed to set.

Thereafter clinical samples were sprinkled onto agar medium and incubated at room temperature of 25ºC for 2 weeks to obtain fungal growth.

Methylene Blue Mount

A fungal inoculum plug was prepared according to standardized methods (Lester *et al.,* 2022). Briefly, a sterile 5 mm cork borer was used to aseptically cut an agar plug from the active growing margin of the mature colony on the Sabouraud Dextrose Agar plate. This fungal tuft, containing both surface mycelium and underlying agar was placed on a clean glass slide using a sterile scalpel and flooded with drops of methylene blue. Then the filament was gently teased, covered with a clean cover slip ensuring no air bubbles are trapped and viewed under high power objective. The hyphae, spore structure and their arrangements were then observed.

DNA extraction

DELLAPORTA method as described by Dhingra & Sinclair (2018) was used. Pure fungal cells stored in ice at a temperature of -20ºC were first allowed to thaw and then centrifuged at 10,000rpm for 2 minutes. Supernatant was decanted leaving pure fungal cells which were then used for DNA extraction. The fungal cells were transferred into fresh 1.5ml micro centrifuge tube to which was added 750µl dellaporta extraction buffer. 50µl of 20% sodium dodecyl sulphate (SDS) was also added, mixed thoroughly using a vortex and the tube incubated at 65ºC for 10 minutes. After incubation, 250µl of 5M potassium acetate was added, mixed properly by vortexing and incubated on ice for about 20 minutes. After incubation on ice, the tube was centrifuged at 13,000rpm for 15 minutes, supernatant decanted into another 1.5ml micro centrifuge tube and 500µl isopropanol added. The content was mixed thoroughly by vortexing and then incubated at -20ºC for 35 minutes. The tube was then centrifuged at 13,000rpm for 10 minutes, supernatant was decanted off and the pellet allowed to dry at room temperature. The pellets were then redissolved in 0.7ml TE buffer and centrifuged at 13,000rpm for 10 minutes to pellet insoluble debris. From this, the supernatant was transferred into another 1.5ml Eppendorf tube to which was added an equal volume of 1:1 phenol/chloroform, mixed thoroughly by vortexing and centrifuged at 13,000rpm for 10 minutes. The upper aqueous phase of the centrifuged mixture was transferred into a fresh Eppendorf tube to which was added 75µl 3M sodium acetate and 500µl isopropanol.

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The content was mixed thoroughly by vortexing and DNA pellet was obtained by brief centrifugation at 8,000rpm for 1minute. Pellet was then washed with 1ml of ice cold 70% ethanol, dried and redissolved in 100µl 10mM Tris, 1mM EDTA, pH 8 or sterile water.

Polymerase Chain Reaction (PCR)

This was carried out according to Schoch et al., (2020) to amplify the ITS gene of the fungi using the primer pair ITS-1 (5'TCCGTAGGTGAACCTGCGG) and ITS-4 (5'TCCTCCGCTTATTGATATGC). The PCR reaction was carried out using the Solis Biodyne 5X HOT FIREPol Blend Master mix. In a 25 µl reaction mixture containing 1X Blend Master mix buffer (Solis Biodyne), 1.5 mM $MgCl_2$, 200µM of each deoxynucleoside triphosphates (dNTP)(Solis Biodyne), 20pMol of each primer (BIOMERS, Germany), 2 unit of Hot FIREPol*DNA* polymerase (Solis Biodyne), additional Taq DNA polymerase was incorporated into the reaction mixture to make a final concentration of 2.5 units of Taq *DNA* polymerase, Proofreading Enzyme, 5µl of the extracted DNA, and double distilled water was used to make up the reaction mixture. Thermal cycling was conducted in a Pieltier Thermal Cycler 100 (MJ Research series) for an initial denaturation of 95°C for 15 minutes followed by 35 amplification cycles of 30 seconds at 95°C; 1 minute at 61°C and 1 minute 30 Seconds at 72°C. This was followed by a final extension step of 10 minutes at 72°C.

PCR Product Purification

Standard ethanol purification protocol by Green & Sambrook (2020) was used. 20µl of absolute ethanol was added to the amplified DNA product from PCR and incubated at room temperature for about 15 minutes. This was then centrifuged at 10,000rpm for 15 minutes after which the supernatant was decanted, the pellets further centrifuged before adding 40µl of 70% ethanol. The supernatant from this was decanted, pellets air dried and 10µl of ultrapure water was added.

Agarose Gel Electrophoresis

The amplification product from PCR was separated using 1.5% agarose gel electrophoresis at a voltage of 100V for 1 hour 30 minutes; after preparing the electrophoresis tray in the casting apparatus.

Then 1.5 grams agarose powder was weighed and introduced into a 100mls 0.5X TBE buffer. The mixture was dissolved by boiling on a hot plate, allowed to cool to about 60°C and 50µl ethidium bromide was added. This was then gently mixed by swirling and poured into the electrophoresis tray with the combs in place to obtain a gel thickness of about 5mm. After about 20 minutes to allow gel solidify, the tray was removed from the casting apparatus and placed in the electrophoresis tank ensuring the buffer covers the top of the gel. The comb was then carefully removed from the gel and a mixture of 10µl sample and 2µl of loading dye was carefully loaded into the wells created by the combs. 5µl of DNA ladder and control was also loaded. Thereafter the electrodes were connected to the power pack such that the negative terminal was closest to the sample and the electrophoresis ran at 100V until the loading dye had migrated about three-quarters of the gel. The process was turned off, electrodes disconnected and gel observed under UV light (Lee et al., 2020)

Sequencing

The PCR amplified ITS1 and ITS4 of the 60 samples (20µl) were sequenced at Epoch Lifescience Texas, U.S.A using BigDye Terminator v3.1 cycle sequencing kit and ABI Prism 3100 genetic analyzer.

Results

A simple demographic analysis of the 400 participants of this study as depicted in Table 1 below showed that 379 participants representing 94.75% were adults and 21 (5.25%) were children. Also 268 of the participants representing 67% of the sample size were female while the number of males was 132 (33%).

Table 1: Demographic characteristics of study participants with dermatophyte infection

Characteristics	n (%)
Total Participants	400 (100.0)
Gendre	
Male	132 (33.0)
Female	268 (67.0)
Age Group (Years)	
< 18	21 (5.25)
≥ 18	379 (94.75)

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Table 2 presents the results of the distribution and summary of dermatophyte isolated per clinical sample based on cultural characteristics.

Table 2: Distribution and Summary of Dermatophyte Isolates per Clinical Sample based on Cultural Characteristics

Number of Isolate per Sample	Frequency (*n*)	Percentage (%)
0	56	14.0
1	181	45.3
2	115	28.8
3	36	9.0
4	8	2.0
5	3	0.8
6	1	0.3
Total Samples	400	100.0
Mean ± SD	1.41 ± 0.98	
Median (IQR)	1(1-2)	

The culture result varied from no growth (14%) to single (45.25%) and multiple isolates (54.75%). Of all the 400 plates, 56 plates had no growth, 181 plates had single growth while others had multiple fungal growth. A total of 60 isolates were presumptively identified as a dermatophyte using cultural characteristics. However, only 31 were confirmed as dermatophytes using molecular methods.

The results of the growth responses of dermatophyte from different clinical manifestations are as shown in Figure 1. The result revealed that, tinea pedis, a dermatophyte infection of the feet was most prominent representing 89.75% of the samples collected. Tinea unguium had 3.0%, tinea capitis (6.25%), tinea cruris (075%) and tinea corporis (0.25%).

The result of the frequency of dermatophyte species identified from 400 clinical samples presented in Figure 2. The results in Fig. 2 revealed that, there were 9 different dermatophytes based on the species and strain types. *Trichophyton interdigitale* appeared the most with 13 members comprising 3 different strains based on the accession numbers. *Trichophyton mentagrophyte* had 6 in all comprising 2 different strains. *Arthroderma vespertilii* had 4 members, all of a single strain, *Arthroderma quadrifidum* and *Epidermophyton floccosum* both had 2 members each and of the same strain while *Trichophyton rubrum*, *Arthroderma otae*, *Arthroderma multifidum* and *Microsporum ferrugineum* all have single members identified.

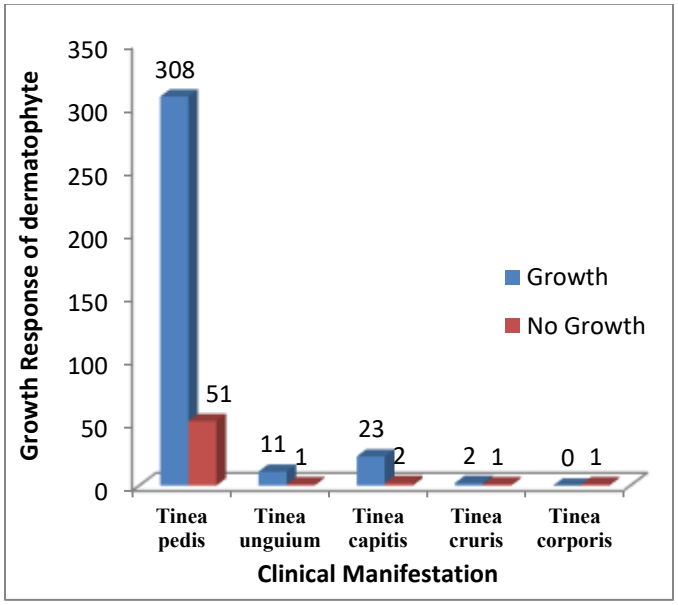

Fig. 1: Growth responses of dermatophyte samples from different clinical manifestations

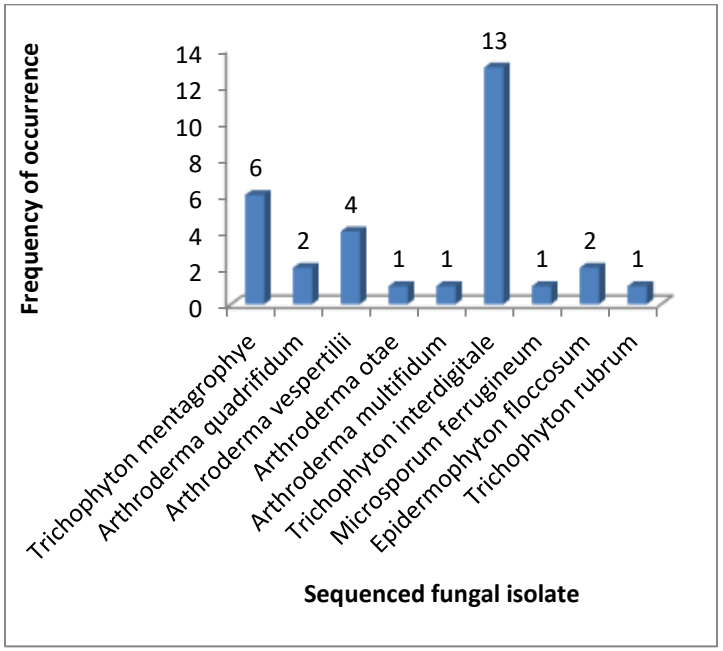

Fig. 2: Frequency of dermatophyte species identified from 400 clinical samples.
Note: Values represent the number of independent isolates (n) obtained for each species.

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As shown in Plate 1 below, in the agarose gel electrograph of PCR products obtained after running samples through agarose gel, amplicon size ranged from about 400 to 850bp for those visible. Samples 5 and 11 formed bands at approximately 800bp with samples 17, 19 and 28 forming bands at 850bp. Other samples also formed bands at corresponding base pairs even though not clearly visible.

The most prominent etiological agents identified were *Trichophyton interdigitale* (42%), *Trichophyton mentagrophyte* (19%), *Arthroderma vespertilii* (13%), followed by other *Arthroderma* species. *Tinea pedis* (89.75%) was the most prevalent dermatophyte infection of the samples collected, followed by tinea capitis (6.25%) and *tinea unguium* (3%).

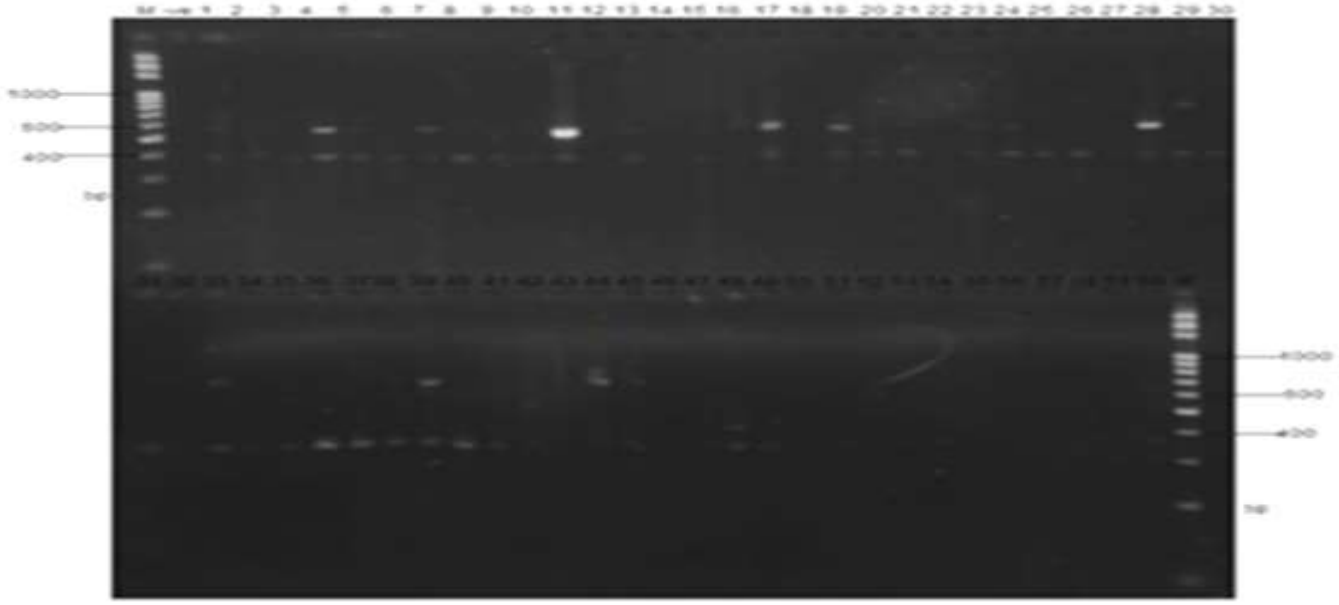

Plate 1: The agarose gel electrograph of PCR products obtained after running samples through agarose gel.

Discussion

From this study, the ratio of adult to children affected by this infection is approximately 20:1 (94.74%:5.25%). While it may be expected that the reverse should be the case because of the behavioural habits of children and therefore more children should attend hospitals for treatment, results of this study negate that of (Kromer *et al.*, 2021), their study had a ratio of 12:1 corroborating this result but clearly showing that the trend is skewed more against the children. Adult age which refers to the working population, often associated with increased physical activity in hot and humid climates that promote sweating (Sudha et al.,2016). Excessive sweating can reduce oil production, making the skin more susceptible to fungal infections (Sudha *et al*., 2016; Widhidewi *et al.,* 2023). Aging also affects the immune system, weakening the body's ability to fight illnesses. (Widhidewi *et al*., 2023)

Additionally, the skin becomes drier, thinner, and wrinkled, with fewer sweat and sebaceous glands, leading to a higher risk of infections and opportunistic organisms (Saxena *et al.,* 2020). Also, in line with other studies conducted such as that by (Kromer et al., 2021; Widhidewi et al., 2023, Nermeen et al., 2018) in which the percentage of females affected were 36.4%, 57%, and 62.8% respectively, this study also showed that a higher percentage of women (67%) were affected which may be indicative of the physical appearance of the woman generally in this part of the world in terms of their physiology. Many adult women upon marriage and child bearing generally become obese possessing skin folds in various parts of the body. This provides in conjunction with the hot humid tropical climate, conducive environment for the proliferation of these organisms. Owing to the self-conscious nature of women, they are likely to seek medical attention more than men (Sondakh *et al.,* 2016).

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Other studies however particularly in children gave a reverse result with many indicating that boys were more affected than girls (Haro et al., 2023; Gupta *et al.*, 2024). Boys are known to be generally more playful spending a lot more of their time outdoors. Also, a study on adult revealed that the incidence rate for Tinea corporis and Tinea cruris infection was more in males than female (Nagaral *et al.,* 2018).

This study also showed that most of the patients presented with tinea pedis (89.75%), an infection of the feet particularly of the toe web. Others that were significant are tinea unguium (3%) and tinea capitis (6.25%). Tinea pedis as an infection cause scaly rash, itchy, deep cracks between interdigital spaces of the feet and most times with foul odour which can be very uncomfortable and embarrassing for the patient (Ely & Rosenfeld, 2023).

While tinea unguium and tinea capitis may not cause as much discomfort as tinea pedis, the fact that they are exposed and present a negative cosmetic appearance may also be responsible for their slightly significant presence in this study (Gupta *et al*., 2021). For tinea cruris and corporis however, the very low percentage may be due to a subconscious feeling of unhygienic habits which may give rise to a sense of stigma as well as the fact that these are parts of the body usually not exposed to the public (Hay *et al*., 2020).

The study also showed the number of isolates per plate based on the cultural characteristics observed. 45.25% (181) of the samples analyzed presented with a single organism while 54.75% of samples had 2 or more isolates. This is an indication that more than one organism may be responsible for an infection and while it may be easy to manage an infection caused by a single etiological agent, it may not be so for multiple. The fact that multiple etiological agents are implicated may be responsible for the difficulty experienced in the management of these infections and why reoccurrence after treatment is rampant (Rajagopalan *et al.,* 2018).

Also, multiple concurrent dermatological diagnoses were documented in a 12-year skin disease pattern study at Lagos University Teaching Hospital's dermatology unit (Ayanlowo *et al.,* 2018). This result according to the study was similar to studies carried out in China and South Africa.

It is also important to note that 14% of the samples yielded no growth, a situation that can be ascribed to the absence of viable hyphal elements in the sample, an uneven colonization of sample collected by organism and prior antifungal therapy (Narain et al., 2018). While an error in clinical diagnosis is possible, other causes of changes in our skin structure and appearance such as drug reaction or immune response reactions leading to such conditions as atopic dermatitis, contact dermatitis, seborrhoeic dermatitis, psoriasis, eczema may be considered (Tashmin *et al.,* 2018).

Trichophyton sp. have been the most implicated of the three genera of dermatophytes in causing infection in man (Ramaraj *et al.,* 2016), this study agrees with this assertion. Of the 60 culturally different isolates subjected to molecular analysis, 31 samples gave significant relationship with documented databases. In line with the assertion above, *Trichophyton* had 20 (64.52%) divided into *Trichophyton mentagrophyte* (6), *Trichophyton rubrum* (1) and *Trichophyton interdigitale* (13). *Microsporum* had 1 (*Microsporum ferrugineum*), *Epidermophyton floccosum* was 2 and *Arthroderma* had 8 divided into *Arthroderma quadrifidum* (2), *Arthroderma otae* (1), *Arthroderma multifidum* (1) and *Arthroderma vespertilii* (4). An analysis of this based on their accession number shows that apart from organisms that were single isolates (*T. rubrum*, *M. ferrugineum*, *A. multifidum* and *A. otae*), *A. quadrifidum*, *E. floccosum* and *A. vespertilii* also had single strains isolated in this study. Two different strains of *T. mentagrophyte* was isolated and 3 for *T. interdigitale*. It was also observed that of the 13 isolates of *T. interdigitale*, 11 were of the same strain and the other 2 were single strains. This may be suggestive of new emerging strains of the organism which can be ascribed to migration and or mutation. It is important to note that none of the fungal isolates when queried against the genome bank library database was 100% homologous signifying that the organisms are all different strains.

Furthermore, in a study on Nucleotide Sequence Database Comparison for Routine Dermatophyte Identification by ITS2 Genetic Region DNA Barcoding, it was claimed that nucleotide databases often contain mislabelled sequences that impair sequence-based identification of organisms (Normand *et al*., 2018).

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Verification of reference databases was therefore advised in line with current revisions of fungal taxonomy. The study also showed that 4 of the 7 species of isolated and identified organisms are teleomophic forms of dermatophytes. At least more than 30 of the dermatophyte species are known to be human pathogens, although additional unidentified species are likely to exist (Dellière *et al.,* 2024). *Arthroderma otae* is recognised as the teleomorph of *Microsporum canis* which is quite common in this part of the world haven being reported in several journal publications (El-Damaty *et al*., 2017) and *Arthroderma quadrifidum* is the teleomorph of *Trichophyton terrestre* and is of geophilic origin (Sahoo & Mahajan, 2016). *Arthroderma multifidum* and *Arthroderma vespertilii* however do not have anamorphic forms but are said to be geophiic and zoophilic respectively (Gräser *et al*., 2018). The use of *Arthroderma multifidum* in the degradation of keratinous waste from poultry farms and barbers' shop in India has also been reported (Kumawat et al., 2016). According to the Amsterdam declaration on dermatophytes nomenclature which recognised the need for an orderly transition to a single-name nomenclatural system for all fungi, many of these sexual forms are now considered as normal genera with each species having a single binomial (Gräser *et al*., 2018; Borman & Johnson, 2023).

Conclusion

The isolation and identification of *Arthroderma multifidum*, *Arthroderma quadrifidum* and *Arthroderma vespertilii* from clinical samples of patients living within Lagos metropolis is an indication of new emerging species of dermatophytes causing dermatophytosis which can be ascribed to mutation and or migration since there is an ever increasing influx of people from other parts of the country and beyond seeking greener pasture in Lagos. Also important is the economic activity of the citizens which encourages import of used clothings, shoes and other materials from other nations in Europe and America.

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Ethical approval

The study was approved by the LUTH (ADM/DCST/HREC/098) and LASUTH (LREC/10/06/554) Health Research and Ethics Committees.

Conflict of interest

The authors have no conflicts of interest to declare.

Author's contribution

1. Abdul-Lateef Olanlege was involved in study design, data collection, statistical analysis, data interpretation, manuscript preparation, literature search, and fund collection
2. Temitope Popoola was involved in study design, statistical analysis and data interpretation
3. David Ojo was involved in study design, statistical analysis and data interpretation
4. Oluseyi Akinloye was involved in study design, statistical analysis and data interpretation
5. Muinah Fowora was involved in study design, data interpretation and manuscript preparation
6. Frances Ajose was in study design and data collection

Data Availability Statement: The raw data supporting the findings of this study cannot be shared publicly to protect patient privacy, in compliance with the ethical approvals granted for this research. However, anonymized datasets are available from the corresponding author upon reasonable request. All other relevant data are included in the article

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