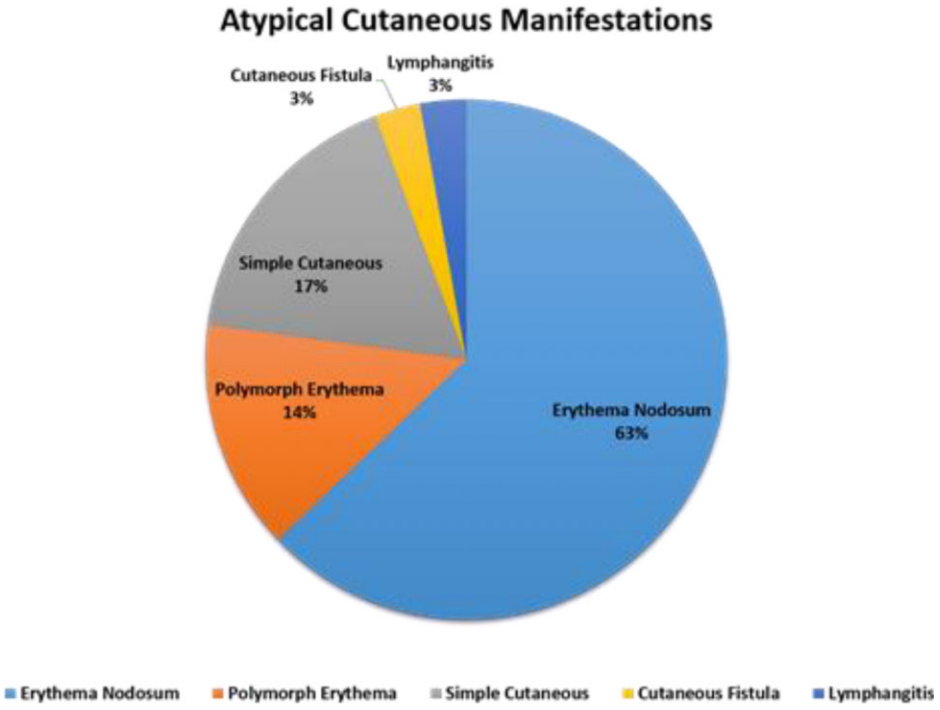

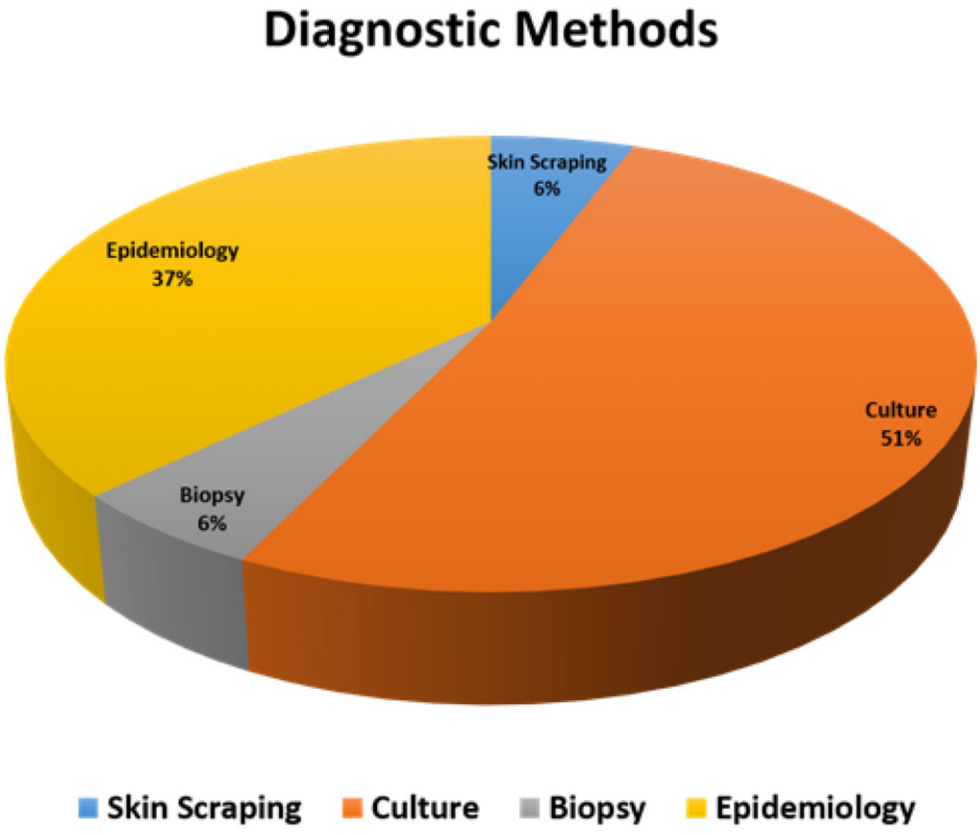

P096

Comprehensive analysis of *Trichophyton mentagrophytes*/interdigitale complex from human and animal origin

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Poster session 1, September 21, 2022, 12:30 PM - 1:30 PM

Objectives: Taxonomic delineation of etiologic agents responsible for recalcitrant dermatophytosis causing epidemic in India is still debated. The organism responsible for this epidemic was previously designated as *Trichophyton indotineae*, a clonal offshoot of *T. mentagrophytes*.

To evaluate the accurate identity of the agent causing the epidemic, we performed multigene sequence analysis of Trichophyton species isolated from human and animal origin.

Methods: The clinical isolates of *T. mentagrophytes*/interdigitale complex ($n = 213$) from PGIMER, and six isolates of animal origin (canine) from IVRI were included in the study. Seven genomic loci including internal transcribed spacer (ITS) region ($n = 219$), translational elongation factor (TEF 1-α) ($n = 40$), partial beta tubulin (BT) ($n = 40$), large ribosomal subunit (LSU) ($n = 34$), calmodulin (CAL) ($n = 29$), high mobility group transcription factor (HMG) ($n = 17$), and α-box ($n = 17$) were amplified by polymerase chain reaction (PCR). Phylogenetic tree was constructed by neighbor-joining method using ours and sequences retrieved from NCBI database. *Trichophyton quinckeanum* was used as the outgroup due to its high divergence. The identity labeling was validated as per the phylogenetic analysis of ITS gene in the present study [ITS gene ($n = 374$), TEF1-α ($n = 184$), BT ($n = 52$), LSU ($n = 50$), CAL ($n = 69$) and HMG transcription factor ($n = 102$)].

Results: Phylogenetic analysis of ITS, TEF 1-α, LSU gene revealed that except for one isolate (PGI-IVRI B24-A) of animal origin belonged to ITS genotype III and rest all isolates [human ($n = 213$) and animal origin ($n = 5$)] belonged to the same cluster, i.e., *T. mentagrophytes* ITS genotype VIII. The phylogenetic tree constructed based on the BT gene ($n = 39$) also clustered all our isolates together and isolates belonging to *T. mentagrophytes* ITS genotype IV, VIII, and *T. interdigitale* and one isolate (PGI-IVRI B24-A) formed a separate cluster and did not coalesce with other genotypes. Whereas CAL gene clustered all our isolates ($n = 28$) together except PGI-IVRI B24-A isolate which grouped with *T. mentagrophytes* type VII. Further HMG analysis reveals that all the isolated *Trichophyton* species from humans ($n = 11$) and animals ($n = 5$) contained HMG transcription factors but lacked α-box genes. One animal isolate (PGI-IVRI B24-A) consisted of both HMG transcription factor and α-box genes. The accurate identity of the isolates was based on our phylogenetic analysis (ITS gene). Based on the analysis of the 374 ITS sequences deposited in the GenBank database, 107 sequences were mislabeled, ie, T. mentagrophytes was named *T. interdigitale* or vice versa. Similarly, 184, 52, 50, 69, and 102 sequences of TEF1-α, BT, LSU, CAL, and HMG transcription factor deposited in the GenBank have 6, 23, 25, 3, and 7 sequences were mislabeled, respectively. Further, for the identical isolates ($n = 6$), we found multiple accession numbers with different labels.

Conclusion: In this study, for the first time we isolated 'Indian ITS genotype VIII' from animal. Isolation of *T. mentagrophytes* type III from animal but none among humans indicates its niche among animals. Adding to the confusion, outdated/inaccurate naming for these dermatophytes in the public database has created confusion in using appropriate species designation.

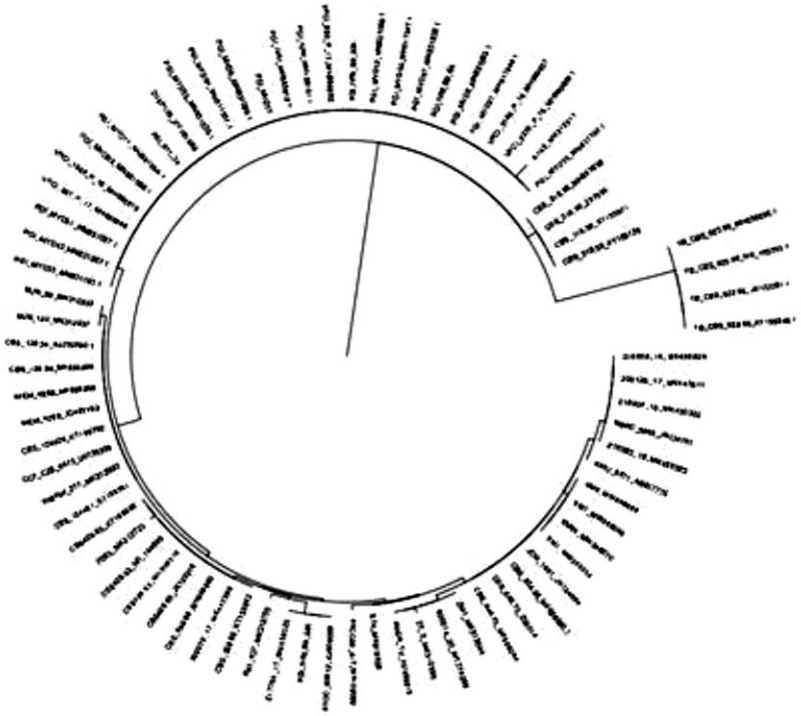

Figure 1. Phylogenetic tree based on ITS sequences (representative isolates) Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X.

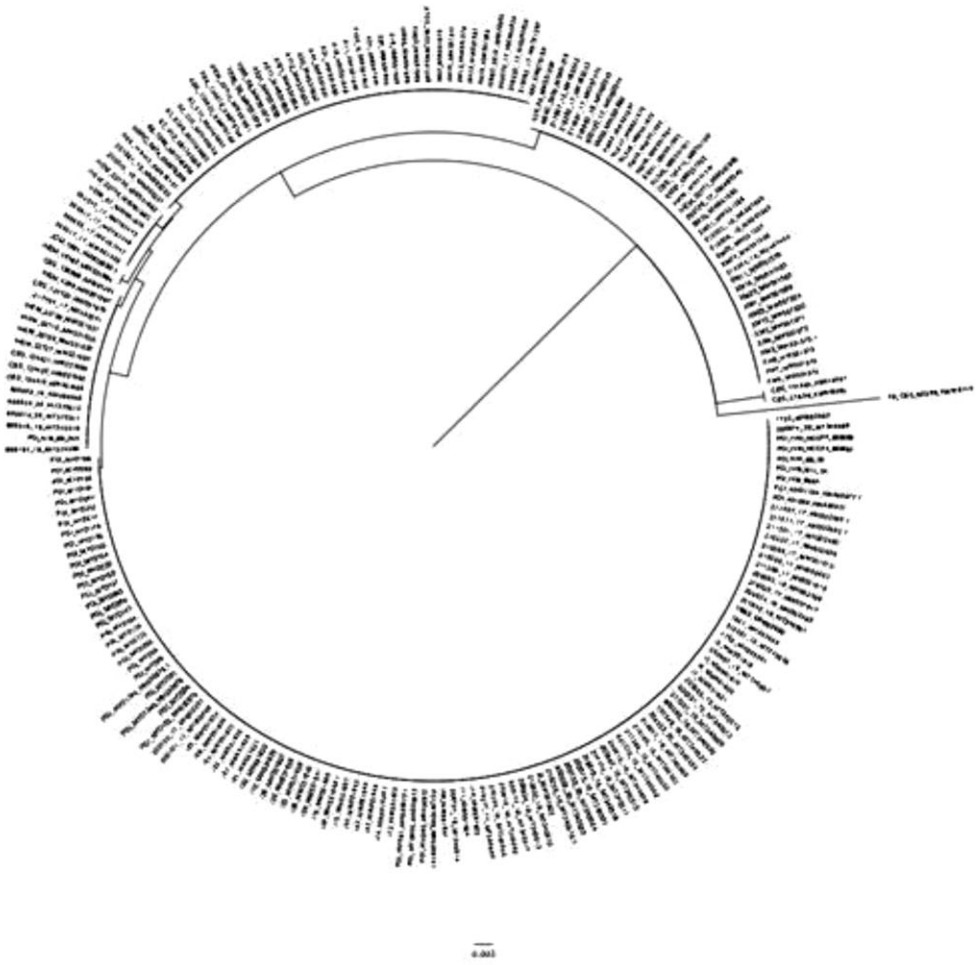

Figure 2. Phylogenetic tree based on *TEF 1-α* sequences Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates). The evolutionary distances were computed using the Kimura 2-parameter method. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X.

P097
Epidemiology of dermatophytes related infections in Kuwait: a retrospective study

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Poster session 1, September 21, 2022, 12:30 PM - 1:30 PM

Introduction and Objective: Dermatophytes are a common cause of cutaneous infections that affect a large number of healthy individuals throughout their lives. Although such infections are classically benign, they have a negative impact on patient's physical and psychological health. We aim to explore the epidemiology of dermatophytes infections at a national level.

Methods: The study was conducted retrospectively. Demographic and microbiological data were obtained from laboratory information system in the Mycology Reference Laboratory in the year 2021. Dermatophytes were either isolated from clinical samples in mycology reference laboratory or sent from other laboratories for species identification. The clinical samples were divided into two parts. The first half was examined microscopically, and the second half was inoculated on Sabouraud agar media with and without cycloheximide and then incubated at 30°C for at least 2 weeks. Dermatophytes were identified by colonial morphology and microscopic characteristics.

Results: During the year 2021, 60 dermatophytes were found. The male to female ratio was 2:1. A total of 60% of patients were children. Half of the cases were isolated from hair specimens and the second half were from the skin. Only one dermatophyte was isolated from nail cultures. Regarding dermatophytes distribution, *Microsporum* species were the commonest and involved mostly *M. canis* (26). Other less common species included two *M. audouinii* and two *M. praecox*. A total of seven other *Microsporum* species were not identified to species level. On the other hand, 23 *Trichophyton* species were found including 5 *T. tonsurans*, 4 *T. interdigitale*, 3 *T. rubrum*, 1 *T. simii*, and 1 *T. erinacei*. A total of 9 other *Trichophyton* species were not identified to species level.

Conclusions: Higher rates of infection were seen in males compared to females. Phenotypic identification has failed in identifying a significant number of isolates. As in other types of molds, the phenotypic examination may also result in inaccurate identification, especially among uncommon and evolving species. Hence, molecular testing is essential for accurate identification and better understanding of the epidemiology of dermatophytes-related infections. The following species were reported for the first time in Kuwait, namely: *T. erinacei*d, *T. simii*, and *M. praecox*.

P098
Human prototothecosis: Acase report in Northeastern Brazil

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Introduction: Prototothecosis is an emergent disease caused by members of the genus Prototheca. Most such infections probably occurred by traumática inoculation into subcutaneous tissues.

Objectives: It is to report a case of human cutaneous prototothecosis identified in the state of Maranhão, northeast Brazil. Case report: 75-year-old patient, Merchant, from the municipality of São Luís Island, Northeastern Brazil. He sought care referring to an erythematous and painful lesion on the left arm that started 6 months before the treatment. On examination, he presented an infiltrative, hyperemic lesion with burning pain throughout the upper limb (Fig. 1). The patient reported that a week before the onset of the condition, he suffered trauma on the arm, with a laceration in the skin, while cleaning a sewage system with clay pipes. During the healing process, he noticed a hyperemic, slightly pruritic lesion measuring 2 cm which did not improve. He sought medical assistance at the dermatological service, who suspected dermatophytosis, initiating treatment with terbinafine (250 mg, once a day), evolving with worsening of the lesion. A lesion biopsy was indicated, to histopathological examination, which showed circular, moniliform structures, diagnosed as prototothecosis (Fig. 2). Treatment with itraconazole (200 mg/day) was started, with no therapeutic response and the lesion spread throughout the patient's left upper limb. Submitted