In a country like India, we are faced with additional challenges in the form of certain infectious diseases whose burden is borne mainly by the socio-economically disadvantaged, mainly in the tropics. These diseases and strategies for their mitigation have been taken up by the World Health Organization (WHO) in a big way by means of the initiatives for Control of Neglected Tropical Diseases (NTDs). Besides bacterial and viral diseases, Eukaryotic organisms are also important entities as etiological agents of dermatophytosis.

Eukaryotic microorganisms (EMM) comprise many kinds of medical, mycological, medical protozoology, and medical entomology need greater attention in India. Except malaria which has been at the forefront owing to the huge disease burden and associated morbidity, several other parasitic infections have indeed been neglected—an issue which the WHO rightly highlighted as part of its NTDs initiative.

Though Mycetoma, chromoblastomycosis, and other deep mycoses are the only fungal diseases to find a place on the list of NTDs, many other fungal diseases continue to plague our communities. Mucormycotic candidiasis and dermatomycoses may neither be common in the tropics nor are they neglected (rather, dermatomycoses tend to be overlooked in many cases) but they merit utmost simple because of the discomfort and disfigurement to daily life that they cause.

We propose that a network of Medical eukaryotic microorganisms (MEM) Laboratories be set up with special emphasis on the NTDs on a regional and national scale in our country to effectively deal with these infections prevalent in our community.

The diagnostic services offered by these MEM-NTDLs can comprise:
- Microscopy, including fluorescent microscopy and special stains
- Multilaboratory MALDI-TOF
- Multiplex PCR
- NGS, including barcode DNA sequencing technologies exemplified by the nanopore MinION

For dealing with these eukaryotic diseases, we believe that we need to adopt advanced techniques like MALDI and NGS in a big way.

Culture, which continues to be the gold standard for bacteriological diagnosis, may now be termed to have historical significance at best in the case of fungal diseases because of the slow turnaround time and the ubiquitous presence of fungal spores acting as lab contaminants. Similarly, serological techniques may have a very limited role in the workup of eukaryotic infections owing to the complete antigenic profile of these organisms and the chemistry of the disease conditions. Microscopy can be retained for the relative prosaic simplicity and rapidity of results.

The ‘advanced’ diagnostic techniques mentioned above have been around for quite some time now and have been widely applied for the rapid diagnosis and presumptive training and provision of appropriate technical staff, a MEM-NTDL can be operated successfully at the district level in a planned manner. This would greatly enhance the quality of health services available to our population and enable our country to reach the goal of Health for All in the near future.

Following identification, comes the very important aspect of antimicrobial/chemotherapy susceptibility testing. Here, however, the growth-based, culture-dependent ventures should be sought—the role of Biomarker related to the growth and metabolism of eukaryotic organisms should be explored and incorporated in practical diagnostics as an aid to infectious disease therapy and patient management. This can be part of the scope of the MEM-NTDL of the future.

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**Molecular epidemiology of Trichophyton mentagrophytes infections among canines from Northern India**

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Objective: Dermatomycoses are anthropophilic fungi that cause skin infections among humans and animals. Recently, the incidence rates of fungal infections especially due to the Trichophyton spp. are being considered as endemic in many geographical locations. The cause of recent range of dermatomycoses due to this agent in humans is not known. It is assumed that pet may be one of the sources which are not elaborated till now. The present study was conducted to understand the molecular heterogeneity of Trichophyton spp. of canines and felines, and their phylogenetic relationship with human isolates.

Methods: The samples (skin/scrapings) were collected from 146 canines and 34 felines exhibiting clinical signs of dermatophytosis during the period of 2020-2021 from the veterinary hospitals and farms in the states of Uttar Pradesh and Kerala, India. All the samples were attempted for isolations on Sabouraud’s dextrose agar (with chloramphenicol and cycloheximide at 0.5 and 0.3 g per l, respectively). The antifungal susceptibility assay was performed by following the Clinical and Laboratory Standards Institute (CLSI) guidelines, document M38-A2 for Hanseniaspora (LCLS-Wayne, PA, USA, 2017). The isolates presumptively identified as Trichophyton spp. were characterized further based on PCR and sequencing of three genetic markers such as ITS, TEF-1α, and beta-tubulin genes. Phylogenetic analysis and taxonomic delineation of the Trichophyton isolates were performed. Three human isolates of T. mentagrophytes were used for comparative study.

Results: A total of 67 (45.53%) /7042) samples revealed the presence of fungal hyphae on direct microscopic examination. On culturing, 52 samples were found to be positive for dermatomycoses. Among these, 10 isolates were presumptively identified as T. mentagrophytes spp. based on morphological and microscopic examinations. Most of the strains were sensitive to all drugs tested except fluconazole, which showed a resistant pattern for most strains. Based on sequence homology and phylogenetic inferences, the Trichophyton isolates belonged to four different species/genotypes, such as T. mentagrophytes genotype VIII (3), T. mentagrophytes (2), T. verrucosum (2), and T. gregarium (1). Human isolates were represented as T. mentagrophytes genotype VIII (2) and T. hamatum (1).

Conclusion: To conclude, the study reports for the first time the prevalence, species distribution, and antifungal resistance among Trichophyton spp. from canines in India. Even though the Trichophyton prevalence was lower in canines, the presence of T. mentagrophytes genotype VIII/IIa is of great public health significance. This indicates the monastic chaining of strains especially T. mentagrophytes genotype VIII in both hosts and are also considered as the recently endemic pathogenic clone in India.

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**Screening of Belgian bats and hibernacula for the detection of related fungal microbes and the detection of Pseudogymnoascus dejectaneus**

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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Bats can be infected by fungal pathogens such as Pseudogymnoascus dejectaneus, the causative agent of the white-nose syndrome. Their body surface can also be colonized by fungal contaminants or carry transmittable fungal species and particulate in their droppings. The present study aimed to assess the presence of P. dejectaneus in Belgian hibernacula, to describe the skin mycoses of active bats during summer and autumn, and to analyze possible differences in fungal diversity among bats, sampling sites, and sex. In total, 154 bat specimens belonging to seven species were sampled from various locations. Culture-based methods revealed an important mycological diversity with 20 different taxa. Overall, a mean of 5.7 taxa per bat was recorded but significant differences were observed between sampling sites and seasons with a higher diversity in autumn as compared to summer. The mycoses were dominated by cosmopolites and plant-associated species, in particular from the genera Cladosporium, Pseudallescheria, and Aspergillus. Other species known to be related to bats or their environment, like Actinomycetes, were also recovered. Although P. dejectaneus was not detected, the samples of hibernacula harbored a fungal community dominated by soil, tree, or leaf mycohymic species, such as Trichoderma, Penicillium, and Alternaria. Some fungal populations were found also on the bat abrasion zones, which is consistent with the potential for fungal contamination and would be an important source of fungal infections in bats. The diversity of fungal species found in Belgian hibernacula was not linked to their geographic origin, age, sex, or species, but to the type of cave and the date of sampling. Given the threats to bat populations, these results can contribute to the development of mycological monitoring protocols for bats and hibernacula.