As the world enters the third decade of the 21st century, infectious diseases continue to pose major challenges to the survival and well-being of human kind. The COVID-19 pandemic demonstrated how indispensable technological advances and innovations are in our fight against the vast legions of bugs; also, it is a fascinating living proof of the adage ‘Necessity is the mother of invention’ to witness at what stupendous pace not only diagnostics but therapies and even vaccines were developed, approved, validated, distributed and utilized. All fueled by the overwhelming and unprecedented health emergency that was the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) pandemic. Many more infectious pathogens, presumably viral, are believed to be waiting in the wings. Monkeypox did not waste much time in proving as right!

In our country, India, the foresight of our best scientific brains and scientific policymakers led to the establishment of a network of Viral Research and Diagnostic Laboratories (VRDL) at the medical college, state, and regional levels with the premier institutes like National Institute of Virology (NIV), Pune, acting as an able mentor, under the aegis of the Indian Council of Medical Research (ICMR). The VRDL Network proved its worth and played an extremely important role in monitoring and
MANAGING THE PANDEMIC AS... 

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 their strategies for their mitigation have been taken up by the World Health Organization (WHO) in a big way by means of the Initiative for Control of Neglected Tropical Diseases (NTDs). Besides bacterial and viral diseases, Eukaryotic organisms are also important entities as etiological agents of these diseases. Eukaryotic medical microbiology (EMM) comprises medical microbiology, medical parasitology, medical mycology, and medical entomology, and medical entomology needs greater attention in India. Except malaria which has been the foremost one 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 NTD elimination initiative.

Though Mycoses, chromobacteriosis, 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. Micrococcaceae candidiasis and dermatomycoses may not be commoner in the tropics not as they neglected (rather, dermatomycoses tends to be overlooked in many cases!) but they merit attention simply because of the discomfort and disruption to daily life that they cause. We propose that a network of Medical eukaryotic microbiology (MEM) Laboratories be set up with special emphasis on the NTDs in a regional and national scale in our country to effectively deal with these infections prevalent in our communities.

The diagnostic services offered by these 'MEM-NTDIs' can comprise of:

- Microscopy, including fluorescent microscopy and special stains
- Molecular analysis
- Culture: using conventional and diagnostic media
- Antigen detection
- Serology
- Immunodiagnosis
- ND, PCR

While many of these services can be offered as a general diagnostic service, there is a need for a specific network of MEM Laboratories to provide services for the tropical NTDs. The network will facilitate the following:

- Development of standard guidelines for diagnosis and treatment of tropical mycoses
- Development of quality control mechanisms
- Enhancement of laboratory services in the public and private sector
- Training of laboratory personnel
- Surveillance and research
- Development of diagnostic kits
- Publication of diagnostic protocols
- Coordination with other organizations, e.g., national and international bodies

The network will be a valuable asset for the management of tropical mycoses and will help in the control of these diseases in India.

**PN03**

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

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**Objective:** Dermatomycoses are opportunistic fungal that cause skin infections among animals and humans. Recently, the incidence rates of fungal infections especially due to Trichophyton spp. are being considered as endemic in many geographical locations. The cause of recent range of dermatomycoses due to the agent in humans is not known. It is assumed that pets may be one of the sources which are not established 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/scraping) were collected from 146 canines and 54 felines exhibiting clinical signs of mycoses during the period 2009-2021 from the veterinary hospitals and farms in the states of Uttar Pradesh and Karnataka, India. All the samples were attempted for isolation on Sabouraud’s dextrose agar (with chloramphenicol and cycloheximide at 0.05 and 0.5 g/l, respectively). The antifungal susceptibility assay was performed by following the Clinical and Laboratory Standards Institute (CLSI, guidelines, document M2-A10 for Hazenomos fungi) (CLSI, Wayne, PA, USA). The isolates were preliminarily identified as Trichophyton spp. characterized further based on PCR and sequencing of three genomic markers such as ITS, TEF-L, and beta-tubulin genes. Phylogenetic analysis and taxonomic determination of the Trichophyton isolates were performed. Three human isolates of T. mentagrophytes were used for comparative study.

**Results:** A total of 67 (55.36%), 67(44%) 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 presumpatively identified as T. mentagrophytes spp. based on morphological and microscopic examination. 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 inference, the Trichophyton isolates belonged to four different species/geospecies, such as T. mentagrophytes geospecies VIII (3), T. mentagrophytes (2), T. verrucosum (1), and T. gypseum (1). Human isolates were represented as T. mentagrophytes geospecies VIII (2) and T. jenneri (1).

**Conclusion:** To the best of our knowledge, this is the first report 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 geospecies VIII is of great public health significance. This indicates the endemic clumping of strains especially T. mentagrophytes geospecies VIII that are both known as the commonly endemic pathogenic clone in India.