## Evaluation and genotyping of Cryptococcus neoformans in India

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## Abstract

Fungi, as pathogens, represent a small minority when compared to the other microbial agents. However, advances in the healthcare of patients with non-infectious diseases coupled with the rise of HIV/AIDS globally and continued outbreaks of primary fungal pathogens in otherwise healthy hosts have led to an overall increase of these etiologic agents. Presently, the etiologic agent of cryptococcosis is classified into two species, Crytpococcus neoformans with two varieties: C. neoformans var. grubii and C. neoformans var. neoformans and C. gattii. C. neoformans and C. gattii infections cause an estimated one million cases of cryptococcal meningitis per year among people with HIV/AIDS resulting in nearly 625000 deaths. The wide variety of presentations of the disease seen in India suggests the possibility of strain variation. The present study analyzed the burden of cryptococcal meningitis in India as the study cases involved individuals from different regions. The cerebrospinal fluid samples were subjected to cytology and cultural, biochemical and mass spectrometric identification, genotyped by Multiloci Sequence Typing (MLST) and phylogenetically analyzed. The demographics of the study population were also studied and analyzed. The genotyping of the clinical strains revealed the predominance of VNI molecular type. The C. gattii strains belonged to VGIV molecular type. C. gattii was not very prevalent in the area and majority of the infections observed were caused by C. neoformans var. grubii. The study group involved subjects from the different parts of India and therefore can be inferred to be a reflection of the country's cryptococcal meningitis burden.

## **Biography**

Jyothi E K has completed her PhD in Neuromicrobiology in the year 2015 from National Institute of Mental Health and Neurosciences (NIMHANS), Bangalore, India. Her doctoral thesis is on neurotuberculosis and cryptococcal meningitis.

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