

P0570

Paper Poster Session

Diagnostic parasitology

First report on genetic diversity of *Enterocytozoon bieneusi* among renal transplant recipients

Ujjala Ghoshal*¹, Sonali Khanduja¹, Raj K Sharma², Uday C Ghoshal³

¹Sanjay Gandhi Postgraduate Institute of Medical Sciences, Microbiology, Lucknow, India

²Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow, India, Lucknow, India

³Sanjay Gandhi Postgraduate Institute of Medical Sciences, Gastroenterology, Lucknow, India

Background: Microsporidia, commonly *Enterocytozoon bieneusi*, infecting immunocompromised hosts like renal transplant (RT) recipients are often transmitted from human (anthroponotic spread) and/or animal to human (zoonotic spread) in patients with HIV. However, there is no study on genetic diversity of *E. bieneusi* infecting RT recipients. Accordingly, we aimed to evaluate genotypes of *E. bieneusi* among RT recipients and compared them with already available sequences from animals and humans using phylogenetic analysis.

Methods: Stool samples of RT recipients infected with microsporidia (identified using modified trichrome stain) were subjected to species identification using PCR-RFLP. All samples positive for *E. bieneusi* were subjected to genotyping by amplifying internal transcribed spacer (ITS) sequences. The obtained ITS sequences were aligned with already reported sequences and phylogenetic tree was constructed using Mega 5 software.

Results: A total of 22 RT recipients had microsporidia using modified trichrome stain. 21/22 (95.5%) were positive by PCR_RFLP and all had *E. bieneusi*. ITS sequences of 21 *E. bieneusi* were classified into eight novel genotypes (Ind1 to Ind8). Genotypes Ind2, Ind3, Ind4 and Ind8 showed close sequence similarity to genotypes reported exclusively in humans. Phylogenetic analysis further supported anthroponotic transmission of these genotypes. Genotypes Ind1, Ind5, Ind6 and Ind7 showed close sequence similarity to genotypes reported among animals and humans. Phylogenetic analysis further supported zoonotic transmission of these genotypes.

Conclusions: This is the first study on genetic diversity of *E. bieneusi* infecting RT recipients. Eight novel genotypes of *E. bieneusi* were identified. *E. bieneusi* was presumed to be transmitted anthropologically as well as zoonotically among renal transplant recipients. Preventive measures should be employed to avoid *E. bieneusi* infection among renal transplant recipients.

