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**Genotyping of *Enterocytozoon bieneusi* infecting renal transplant recipients**

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**Background:** *Enterocytozoon bieneusi* (*E. bieneusi*), infecting renal transplant (RT) recipients may be transmitted anthropologically or zoologically. Accordingly, we aimed to a) evaluate genotypes of *E. bieneusi* among RT recipients, and b) infer phylogenetic interpretation on transmission of different genotypes among infected hosts.

**Material/methods:** Stool samples of 22 RT recipients infected with microsporidia (identified using modified trichrome staining) were subjected to species identification. All *E. bieneusi* positive samples were subjected to genotyping. The phylogenetic tree was constructed using Mega 5 software.

**Results:** Of 22 microsporidia infected RT recipients, 21/22 (95.5%) had *E. bieneusi*. ITS sequences of 21 *E. bieneusi* were classified into eight genotypes (Ind1 to Ind8). Among them, 4 (Ind5 to Ind8) were novel. Genotypes Ind2, Ind3, Ind4, Ind7 and Ind8 showed close sequence similarity to genotypes reported exclusively from humans. Phylogenetic analysis further supported their anthroponotic transmission. Genotypes Ind1, Ind5 and Ind6 showed close sequence similarity to genotypes reported from both animals and humans. Phylogenetic analysis further supported their zoonotic transmission. Anthroponotic transmission of *E. bieneusi* was more common among males (11, 100% vs. 7/10, 70%; P=0.05), presenting with diarrhea (11, 100% vs. 6/10, 60%; P=0.02) and watery stool (10/11, 91% vs. 5/10, 50%; P=0.03).

**Conclusions:** Eight genotypes (Ind1 to Ind8) of *E. bieneusi* infecting renal transplant recipients were identified. Among them, four genotypes (Ind5 to Ind8) are novel. *E. bieneusi* is presumed to be transmitted anthropologically as well as zoonotically among infected RT recipients.