



Molecular Detection And Genotyping Of *Enterocytozoon bieneusi* In Humans From Hainan, China: High Diversity And Unique Endemic Genetic Characteristics

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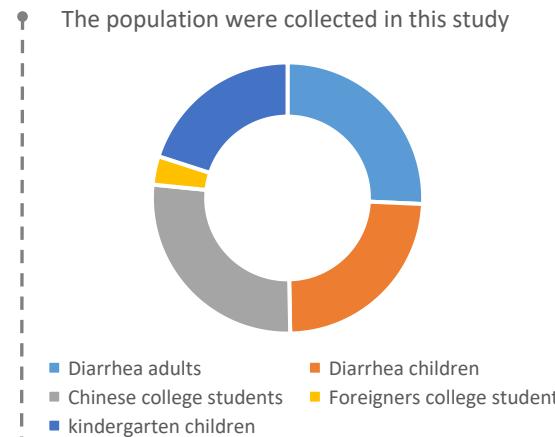
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Introduction

Enterocytozoon bieneusi (*E. bieneusi*) is a zoonotic potential pathogen which was found in humans and animals worldwide. We investigated the prevalence and the genetic characteristics of *E. bieneusi* in humans from Hainan, China.

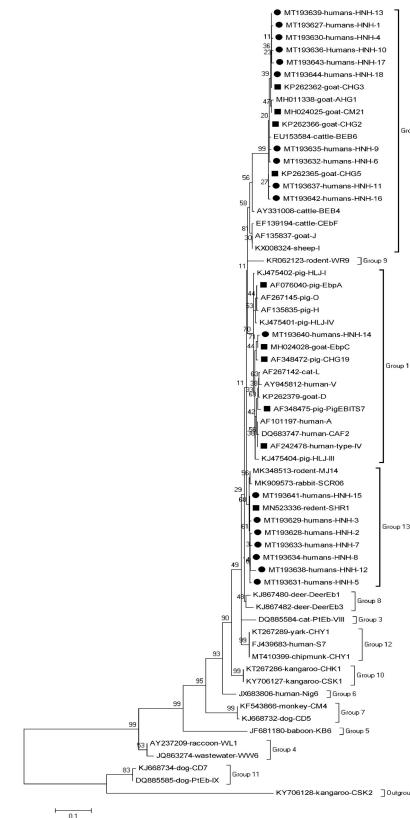
Methods

1264 fecal samples were collected from 628 patients with diarrhea (325 adults and 303 children), and 636 asymptomatic population including 383 college students (340 Chinese and 43 foreigners) and 253 kindergarten children. *E. bieneusi* was identified by nested PCR amplification the internal transcribed spacer (ITS) region. Phylogenetic tree was established by a neighbor-joining method.



Results

The overall prevalence of *E. bieneusi* was 3.7% (47/1264), with 5.6% in the patients with diarrhea (5.8% for adults and 5.3% for children) and 1.9% in the asymptomatic population (2.9% for Chinese, 2.3% for foreigners and 0.4% for kindergarten children). The prevalence of *E. bieneusi* in humans with diarrhea was significantly higher than that in



Phylogenetic relationship of the genotypes of *E. bieneusi* in humans. The square and circle filled in black indicate known and novel genotypes, respectively.

without diarrhea ($P < 0.05$). Twenty-eight genotypes were identified, including ten genotypes (CHG5, CHG3, SHR1, CHG2, Type IV, EbpC, EbpA, PigEBITS7, CHG19 and CM21) and 18 novel genotypes (HNH-1 to HNH-18). The genotypes above were clustered into group 1 ($n = 6$), group 2 ($n = 14$) and group 13 ($n = 8$).

Conclusions

This is the first report on the identification of *E. bieneusi* in humans from Hainan, China. The association between *E. bieneusi* infection and diarrhea was observed. High diversity and distinctive distribution of *E. bieneusi* genotypes found here reflect the unique epidemic genetic characteristics of *E. bieneusi* in humans living in Hainan.