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Occurrence of *Cryptosporidium*, *Enterocytozoon bienersi* and *Blastocystis* genotypes in *Rousettus leschenaultii* collected from an urban public park of Hainan Province, China

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Objective: To obtain information about the occurrence of *Blastocystis* spp., *Cryptosporidium* spp., and *Enterocytozoon (E.) bienersi* in fruit bats (*Rousettus leschenaultii*) collected from an urban public park Hainan Province, China and to analyze the genetic characteristics of the obtained parasites carried by those bats.

Methods: On 4th June 2019, ten piles of fresh faecal sample of fruit bats were collected from the Wanlv Yuan Gardens in central Haikou, Hainan of China. *Blastocystis* spp., *Cryptosporidium* spp., and *E. bienersi* were examined by sequencing analysis of the small subunit rRNA gene or internal transcribed spacer (*ITS*) gene.

Results: Among the 10 DNA specimens analyzed, seven (70.0%) were positive for *Cryptosporidium* spp. and two (20.0%) were positive for *E. bienersi* but none of them were positive for *Blastocystis*. For *Cryptosporidium*, two novel genotypes were identified which shared 98.2% and 94.4% homology with *Cryptosporidium (C.) andersoni* Type C, respectively, and were named as *C. andersoni* Type D (in 6 specimens) and E (in one specimens). The two *E. bienersi*-positive isolates were identified as a known zoonotic genotype (PigEbITS7) and a novel genotype (named HNB-I) respectively.

Conclusions: The finding of *C. andersoni* and *E. bienersi* genotype PigEbITS7 in fruit bats in Hainan, China suggests that these parasites carried by fruit bats can be transmitted to other animals and humans to cause zoonotic infections.

Keywords: *Cryptosporidium*; *Enterocytozoon bienersi*; *Blastocystis*; genetic characterization; bats

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