Genetic characterizations of *Cryptosporidium* spp. in wild rats, farmed bamboo rats and Asiatic brush-tailed porcupine from Hainan, China

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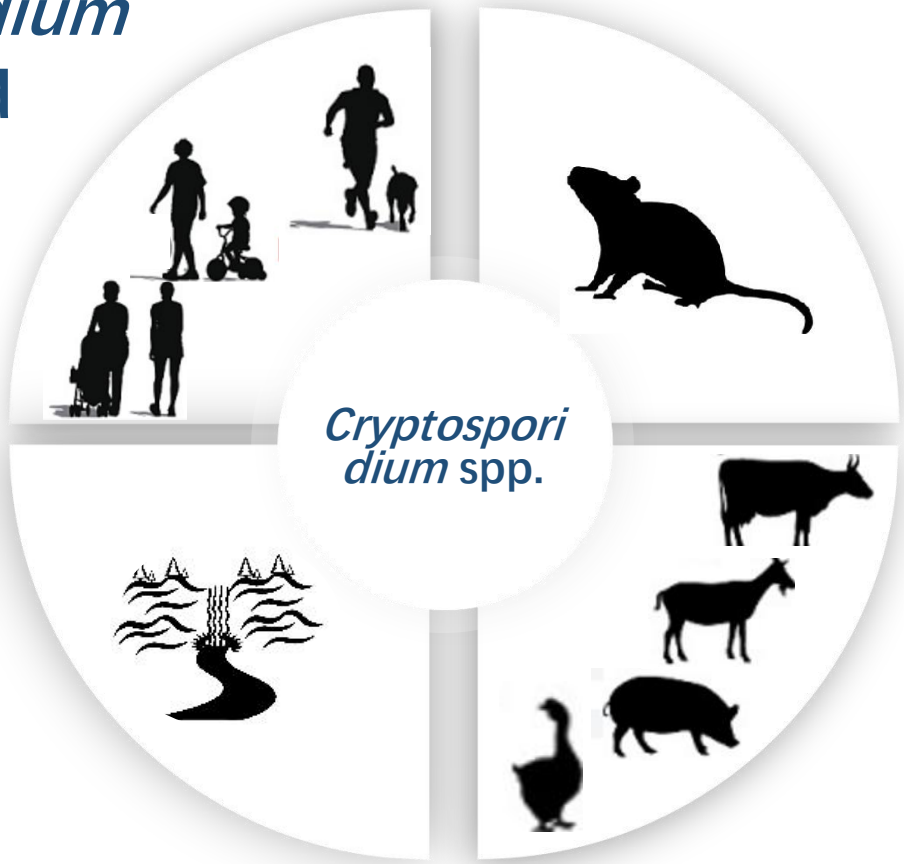

Keyword: *Cryptosporidium* sp.; Rodents; Hainan; Genotype

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Introduction

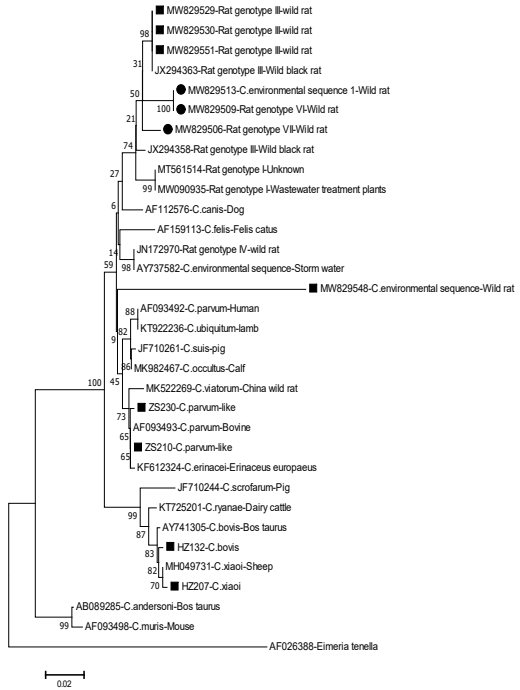
Cryptosporidium spp. are an important cause of diarrhea in both humans and animals. This study was to evaluate the prevalence, genotypic diversity of *Cryptosporidium* in various rodents in Hainan, China.

Methods

Cryptosporidium was detected from 219 wild rats, 360 farmed bamboo rats (*Rhizomyidae*) and 257 farmed Asiatic brush-tailed porcupine (*Atherurus macrourus*) by nest-PCR amplification of the partial SSU rDNA gene.

Results

The total prevalence of *Cryptosporidium* was 12.2% (102/836). The prevalence of *Cryptosporidium* in wild rats (53/219; 24.2%) was higher than that in farmed bamboo rats (37/360; 10.3%) and Asiatic brush-tailed porcupine (12/257; 4.7%). Seven species-*C. ubiquitum* (n = 15), *C. occultus* (n = 14), *C. parvum* (n = 6), *C. muris* (n = 3), *C. viatorum* (n = 2), *C. bovis* (n = 1) and *C. xiaoi* (n = 1)- and eleven genotypes (*C. parvum*-like, Bamboo rat genotype I and II, Civet genotype I, Rat genotype I to IV, Rat genotype VI and VII, *C.* environmental sequence) of *Cryptosporidium* were identified.



Phylogenetic relationship of the *Cryptosporidium*. The filled squares and circles represent the novel genotypes and sequences identified here, respectively.

Meanwhile, a novel genotype *C.* environmental sequence -like (similarity 95.39% with the sequence FJ205699) was found in a wild rat.

Conclusions

All the seven species identified here were found in humans previously highlights the possible cross-species transmission of *Cryptosporidium* between those rats and humans as well as other animals.