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Prevalence and genotyping of *Enterocytoen bieneusi* in farmed black goats from Hainan Province, the southernmost part of China

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Objective: To investigate the infection rate and genotype distribution of *Enterocytoen (E.) bieneusi* in farmed black goats from the Hainan Province, China.

Methods: A total of 341 fresh fecal samples were collected from black goats farmed in five different locations of the Hainan Province, China. *E. bieneusi* was examined and genotyped through PCR and sequencing analysis of the internal transcribed spacer (ITS) region of this pathogen.

Results: The average prevalence of *E. bieneusi* in black goats from the five locations was 24.0% (82/341) ranging from 6.3% (4/63) to 37.2% (32/86) ($\chi^2=17.252$, $P<0.01$). The detected 82 *E. bieneusi* isolates belonged to eight ITS genotypes including six known genotypes (AHG1, CHG2, CHG3, CHG5, CM21 and D) and two novel genotypes (HNG- I and HNG- II). Amongst the genotypes, CHG5 was the most prevalent with a prevalence of 57.3% (47/82), followed by CHG3 (28.0%, 23/82), CHG2 (4.9%, 4/82), CM21 (3.7%, 3/82), D (2.4%, 2/82), AHG1 (1.2%, 1/82), HNG- I (1.2%, 1/82) and HNG- II (1.2%, 1/82). In those genotypes, only genotype D was found in humans previously.

Conclusions: This represents the first report identifying *E. bieneusi* in black goats from Hainan Province of China. The results indicate that *E. bieneusi* has a high prevalence and a wide distribution in those animals from Hainan Province, but the risk of zoonotic transmission of *E. bieneusi* from them to human is low.

Keywords: *Enterocytozoon bieneusi*; Genotype; ITS region; Goats; Hainan

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