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# Molecular identification and subtype analysis of *Blastocystis* in pigs, cattle and goats in Hainan, China

Wei Zhao<sup>1,2,3</sup>, Tian-ming Ma<sup>1,2,3</sup>, Huan-huan Zhou<sup>1,2,3</sup>, Meng Qi<sup>4</sup>, Zong-xi Cao<sup>5</sup>, Zhe Chao<sup>5</sup>, Li-min Wei<sup>5</sup>, Quan-wei Liu<sup>5</sup>, Rui-ping Sun<sup>5</sup>, Feng Wang<sup>5</sup>, Yan Zhang<sup>5</sup>, Xin-li Zheng<sup>5</sup>✉, Gang Lu<sup>1,2,3</sup>✉

<sup>1</sup>Department of Pathogenic Biology, Hainan Medical University, Haikou, Hainan, China

<sup>2</sup>Hainan Medical University–The University of Hong Kong Joint Laboratory of Tropical Infectious Diseases, Hainan Medical University, Haikou, Hainan, China

<sup>3</sup>Key Laboratory of Tropical Translational Medicine of Ministry of Education, Hainan Medical University, Haikou, Hainan Province, China

<sup>4</sup>College of Animal Sciences, Tarim University, Alar, Xinjiang Province, China

<sup>5</sup>Institute of Animal Science and Veterinary Medicine, Hainan Academy of Agricultural Sciences, Haikou, Hainan Province, China

**Objective:** To determine the infection rates and subtype distributions of *Blastocystis* in pigs, cattle, and goats in Hainan Province, China.

**Methods:** From September 2018 to May 2019, a total of 659 fresh fecal samples were collected from 188 pigs, 341 goats, and 130 cattles farmed in cities of Hainan Province. All the samples were analyzed for the presence of *Blastocystis* by amplifying the SSU rRNA gene. Phylogenetic analysis was performed by constructing a neighbor-joining tree using the program Mega X.

**Results:** Thirty-one percent (204/659) of the animals were confirmed to be infected with *Blastocystis*, with 42.2% (144/341) of the goats, 30.8% (40/130) of the cattle, and 10.6% (20/188) of the pigs. Twelve subtypes of *Blastocystis* were identified, including ST10 ( $n=114$ ), ST5 ( $n=37$ ), ST26 ( $n=16$ ), ST24 ( $n=8$ ), ST14 ( $n=8$ ), ST21 ( $n=8$ ), ST23 ( $n=4$ ), ST25 ( $n=4$ ), ST1 ( $n=2$ ), ST2 ( $n=1$ ), ST4 ( $n=1$ ), and ST12 ( $n=1$ ). There were 11 (ST1, ST2, ST4, ST5, ST10, ST12, ST14, ST21, ST23, ST24, and ST26) and six subtypes (ST10, ST21, and STs23-ST26) in goats and cattle, respectively. All the pig-derived *Blastocystis* isolates belonged to ST5. A total of 37 representative sequences were obtained from the 12 subtypes of *Blastocystis*, including 14 sequences that have been described previously and 23 novel sequences were identified which were composed of ST10 ( $n=9$ ), ST5 ( $n=8$ ), ST21 ( $n=3$ ), ST26 ( $n=2$ ), and ST14 ( $n=1$ ).

**Conclusions:** This is the first study to identify the presence of *Blastocystis* in pigs, cattle, and goats from Hainan Province, China, and provides baseline data useful for controlling and preventing *Blastocystis* infection in farm communities. Pigs and goats appear to be the major reservoirs of potential zoonotic infections with ST1, ST2, ST4, ST5, and ST12 and zoonotic infections in pigs and goats with those subtypes should be considered potential public health threats. The new ST sequences of *Blastocystis* identified here provide novel insights into the genotypic variation in *Blastocystis*.

**Keywords:** *Blastocystis*; Pig; Goat; Cattle, Genotypic variation

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✉Corresponding author: Gang Lu, Department of Pathogenic Biology, Hainan Medical University, No. 3 Xueyuan Road, Haikou, Hainan Province, China.

E-mail: [luganghn@163.com](mailto:luganghn@163.com)

Xin-li Zheng, Institute of Animal Science and Veterinary Medicine, Hainan Academy of Agricultural Sciences, Haikou, Hainan Province, China.

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