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Distribution and molecular characterization of *Cryptosporidium* species or genotypes in four species of farmed animals from Hainan Island of China

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Objective: To assess the infection status of *Cryptosporidium* spp. in the four common species of farmed animal (pigs, cattle, goats and geese) in the Hainan Island of China, followed by molecular characterization of the parasite.

Methods: During March to July 2019, 864 DNA were extracted from the fecal samples of 188 pigs, 341 goats, 130 cattle, and 169 geese which were collected from four, five, six, and three cities of the Hainan Province, China, respectively. The species/genotypes and subtypes of *Cryptosporidium* were identified by employing nested-PCR amplification of the SSU rRNA and the 60 kDa glycoprotein (*gp60*) genes of the parasite, respectively.

Results: *Cryptosporidium* was identified in 68 (7.9%) out of 864 animals, with 45 (13.2%) goats, 13 (6.9%) pigs, 4 (3.1%) cattle, and 6 (3.6%) geese. *Cryptosporidium* (*C.*) *xiaoi* ($n=24$) and *C. ubiquitium* ($n=21$) were identified in goats; *C. suis* ($n=7$) and *C. scrofarum* ($n=6$) in pigs; *C. parvum* ($n=3$) and *C. occultus* ($n=1$) in cattle; and *C. baileyi* ($n=1$) and *Cryptosporidium* goose genotype I ($n=3$) in geese. The 21 *C. ubiquitium* isolates shared a same subtype III a, and the subtype of three *C. parvum* was II dA15G1.

Conclusions: We present for the prevalence of the *Cryptosporidium* in cattle, goats, pigs and geese from the Hainan Island of China for the first time. The molecular characterization of the *Cryptosporidium* isolates obtained here propose that the goats, cattle and pigs are potential sources of *C. ubiquitium*, *C. parvum*, and *C. suis* infections, in humans.

Keywords: *Cryptosporidium*; Farmed animals; Zoonotic; Hainan Island

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