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Prevalence and Molecular Characterization of *Cryptosporidium* in Domestic Animals in Central Vietnam

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Introduction

Cryptosporidiosis caused by *Cryptosporidium* parasite is a critical diarrheal disease in humans and livestock, and young and neonatal individuals sometimes show severe symptoms. In Vietnam, the government has recently promoted livestock production. However, the data of cryptosporidiosis have been still limited. Therefore, the aim of this study is prevalence and molecular characterization of *Cryptosporidium* in common domestic animals in central Vietnam.

Materials and Methods

Fecal samples were collected from cattle, pigs and ostriches in central Vietnam. *Cryptosporidium* oocysts were detected by modified Ziehl-Neelsen staining method, and species identification was conducted by using 18S rRNA, HSP70, and actin genes.

Results

In cattle, overall prevalence on samples and herd levels were 18.9% (44/232) and 50% (20/40), respectively. Genotyping based on 18S rRNA gene revealed the presence of the two non-zoonotic species *Cryptosporidium ryanae* and *C. bovis*, the former of which is a dominant species. In pigs, overall prevalence of 14.5% (28/193) was estimated. Genetic identification based on the 18S ribosomal RNA and 70 kDa heat shock protein genes revealed two species/genotypes *Cryptosporidium suis* and *Cryptosporidium* pig genotype II. In ostriches, overall prevalence was identified as 23.7% (110/464). Molecular analysis in the 18S rRNA, HSP70, and actin genes demonstrated the presence of only *Cryptosporidium* avian genotype II. The presence of these host-adapted species/genotypes suggests that domestic animal may not pose a significant public health risk in the study area.