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Prevalence and Molecular Identification of *Fasciola* in Cattle in Central Vietnam.

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Introduction

Fasciolosis is a critical parasitic disease of cattle, causing significant economic losses. Fasciolosis also occurs in humans, resulting in diseases of liver. In this study, we investigated prevalence and determined molecular characterization of *Fasciola* in central Vietnam, a hyper-endemic area of human fasciolosis.

Materials and Methods

Fecal samples from calves and adult cattle were examined for *Fasciola* eggs by sedimentation method. A subset of fecal samples and blood samples was examined by sedimentation method and ELISA technique. *L. viridis* and *L. swinhoei* from paddy fields, lake banks, water fern ponds, sewerages were examined for *Fasciola* larvae. Sixteen *Fasciola* flukes from naturally infected cattle were used for molecular analysis. Species identification was conducted by using nuclear ITS1 and ITS2 regions, NDI gene, and mitochondrial CO1 gene.

Results

Overall prevalence of *Fasciola* was 45.3% (487/1075). From the subset of the animals (235), 46.3% were shedding *Fasciola* eggs while 87.2% were *Fasciola* seropositive. Prevalence of *Fasciola* in calves (37.6%) was low compared to that in adult cattle (53.7%). The prevalence in the rainy season (50.8%) was significantly different to that in the dry season (38.1%). Prevalence of *Fasciola* in *L. viridis* and *L. swinhoei* were 0.95% (31/3.269) and 0.62% (7/1.128), respectively. Analyses of sequences from ITS1 and ITS2 of the ribosomal RNA revealed that 13 out of 16 isolates were *F. gigantica* type, whereas three isolates presented a hybrid sequence from *F. gigantica* and *F. hepatica*. All the mitochondrial sequences (COI and NDI) were of *F. gigantica* type, suggesting that the maternal lineage of the hybrid form is from *F. gigantica*.