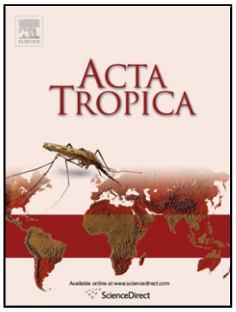

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Serological detection and molecular characterization of piroplasmids in equids in Brazil

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Highlights

- 18.9% and 5.55% of the horses were seroreactive for *T. equi* and *B. caballi*, respectively.
- Molecularly characterization the piroplasmid was studied.
- Nine different *T. equi* genotypes were identified for the first time in Equidae in south Brazil.

Abstract

Equine piroplasmosis is a disease caused by the hemoparasites *Babesia caballi* and *Theileria equi* and is considered to be the most important parasitic infection affecting Equidae. The objective of the present study was to carry out an epidemiological molecular and serological survey for the presence of these two protozoal organisms in equids from the northwestern region of the State of Rio Grande do Sul (RS), south Brazil. For this purpose, blood samples were collected from 90 equids in the city of Passo Fundo, RS, Brazil. Those were animals used for sport activities, outdoor recreational riding, and work including cattle herding and mounted patrol. Anti-*T. equi* and anti-*B. caballi* IgG antibodies were detected in the sera of those animals by commercial ELISA kits. The molecular diagnosis of equine piroplasmosis due to *T. equi* or *B. caballi* (or both) consisted in the amplification of the 18S rRNA gene by nested PCR followed by sequencing of the amplified PCR product and sequence comparison and phylogenetic analysis of the isolates; 17 (18.9%) and 5 (5.55%) out of the 90 serum samples tested in this study were positive for *T. equi* and *B. caballi*, respectively. Piroplasmid 18S rRNA gene fragments were detected by PCR in 24.4% (22/90) of the