Potentially Same Novel *Ehrlichia* Species in Horses in Nicaragua and Brazil

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**To the Editor:** In our previously published report, we found that blood samples from 4 naturally infected horses in Nicaragua were PCR positive for the 16S rDNA, *sodB*, and *groEL* genes of an *Ehrlichia* species (1). Similarly, Vieira and colleagues reported a potentially novel *Ehrlichia* sp. infecting horses in South America, with a high seroprevalence in carthorses; 1 horse blood sample was PCR positive for *Ehrlichia* 16S rDNA and *dsb* genes (2). Because these 2 studies sequenced different 16S rDNA regions, the *Ehrlichia* sp. found in Nicaragua could not be established as the same one infecting horses in Brazil.

We retrieved an *Ehrlichia* PCR-positive horse blood sample (2) from Brazil and performed partial PCR and sequencing of the 16S rDNA, *sodb*, and *groEL* genes (1). Phylogenetic analysis of the sequences (3–5) demonstrated a close relationship between the *Ehrlichia* spp. found in Brazil and Nicaragua, with posterior probability values of 100% for all 3 gene fragments (online Technical Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/24/5/17-2076-Techapp1.pdf). The 16S rDNA were 100% identical for all 3 gene fragments (online Technical Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/24/5/17-2076-Techapp1.pdf). The 16S rDNA were 100% identical for all 3 gene fragments (online Technical Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/24/5/17-2076-Techapp1.pdf).

These findings suggest that the novel *Ehrlichia* sp. found infecting horses in Nicaragua and Brazil are potentially the same species. Future studies are needed to determine cell culture practices, characterize potential clinical signs of infection, and establish the main vector of this novel equine *Ehrlichia* species.

**References**


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Human Infection with *Burkholderia thailandensis*, China, 2013

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**To the Editor:** We read with interest the research letter from Chang et al. (1). To have such severe clinical disease attributed to *Burkholderia thailandensis* infection...
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**Technical Appendix**

**Technical Appendix Figure 1.** Phylogenetic analysis of gene fragments of *Ehrlichia* isolates found in horses in Nicaragua and Brazil compared with reference strains. Trees were constructed by using 181 bp of 16S rDNA (A), 561 bp of groEL (B), and 579 bp of sodb (C) genes.
Technical Appendix Figure 2. Alignment of partial amino acid sequences of *Ehrlichia* isolates found in horses, Nicaragua and Brazil. *E. ruminantium* was used as the reference strain in sodB (A) and groEL (B) sequence alignments.