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

Thállitha S.W.J. Vieira, Barbara A. Qurollo, Anna C.B. Mongruel, Rafael A. Baggio, Odilon Vidotto, Edward B. Breitschwerdt, Rafael F.C. Vieira

Author affiliations: Universidade Federal do Paraná, Curitiba, Brazil (T.S.W.J. Vieira, A.C.B. Mongruel, R.A. Baggio, R.F.C. Vieira); North Carolina State University, Raleigh, North Carolina, USA (B.A. Qurollo, E.B. Breitschwerdt); Universidade Estadual de Londrina, Londrina, Brazil (O. Vidotto)

DOI: https://doi.org/10.3201/eid2405.172076

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 (100%) and *groEL* 99% identical (94.8%) alignments (online Technical Appendix Figure 2).

These findings suggest that the novel *Ehrlichia* spp. 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


Address for correspondence: Thállitha S.W.J. Vieira, Departamento de Medicina Veterinária, Campus Agrárias, Universidade Federal do Paraná, R. dos Funcionários, 1540, Juvevê, Curitiba, PR, 80035-050, Brazil; email: thallitha.vieira@ufpr.br

---

Human Infection with *Burkholderia thailandensis*, China, 2013

David A.B. Dance, Derek Sarovich, Erin P. Price, Direk Limmathurotsakul, Bart J. Currie

Author affiliations: Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Vientiane, Laos (D.A.B. Dance); Centre for Tropical Medicine and Global Health, University of Oxford, Oxford, UK (D.A.B. Dance); London School of Hygiene and Tropical Medicine, London, UK (D.A.B. Dance); University of the Sunshine Coast, Sippy Downs, Queensland, Australia (D. Sarovich, E.P. Price); Mahidol-Oxford Research Unit, Bangkok, Thailand (D. Limmathurotsakul); Royal Darwin Hospital and Menzies School of Health Research, Darwin, Northern Territory, Australia (B.J. Currie)

DOI: https://doi.org/10.3201/eid2405.180238

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

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.