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

Thállitha S.W.J. Vieira, Barbara A. Qurollo, Anna C.B. Mongrue, 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. Mongrue, 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 (181 bp/181 bp; GenBank accession no. KJ434178), *sodB* 99% identical (561 bp/567 bp; GenBank accession nos. MG385129, KJ434180), and *groEL* 99% identical (579 bp/584 bp; GenBank accession nos. MG385128, KJ434179). When we compared translated amino acid sequences of the *Ehrlichia* spp. from Brazil and Nicaragua, we observed high percent age identities with the *groEL* (100%) and *sodB* (97.8%) alignments (online Technical Appendix Figure 2). Furthermore, when compared with *E. ruminantium*, the most closely related *Ehrlichia* sp. on the basis of phylogenetic analyses, percent age identities from the *groEL* (94.8%) and *sodB* (78.8%) alignments were lower for both *Ehrlichia* spp.

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 from Chang et al. (1). To have such severe clinical disease attributed to *Burkholderia thailandensis* infection...