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 (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

- O'Nion VL, Montilla HJ, Qurollo BA, Maggi RG, Hegarty BC, Tornquist SJ, et al. Potentially novel *Ehrlichia* species in horses, Nicaragua. Emerg Infect Dis. 2015;21:335–8. http://dx.doi.org/ 10.3201/eid2102.140290
- Vieira TS, Vieira RF, Krawczak FS, Soares HS, Guimarães AM, Barros-Filho IR, et al. *Ehrlichia* sp. infection in carthorses of low-income owners, southern Brazil. Comp Immunol Microbiol Infect Dis. 2016;48:1–5. http://dx.doi.org/10.1016/j.cimid.2016.07.002
- Sela I, Ashkenazy H, Katoh K, Pupko T. GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. Nucleic Acids Res. 2015;43(W1):W7–14. http://dx.doi.org/10.1093/nar/gkv318
- Drummond AJ, Suchard MA, Xie D, Rambaut A. Bayesian phylogenetics with BEAUti and the BEAST 1.7. Mol Biol Evol. 2012;29:1969–73. http://dx.doi.org/10.1093/molbev/mss075
- Darriba D, Taboada GL, Doallo R, Posada D. jModelTest 2: more models, new heuristics and parallel computing. Nat Methods. 2012;9:772. http://dx.doi.org/10.1038/nmeth.2109

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

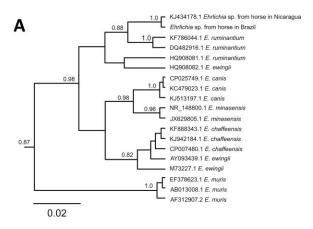
Author affiliations: Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Vientiane, Laos (D.A.B. Dance); Centre for Tropical Medicine and Global Health, University of Oxford, Oxford, UK (D.A.B. Dance); London School of Hygiene and Tropical Medicine, London, UK (D.A.B. Dance); University of the 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)

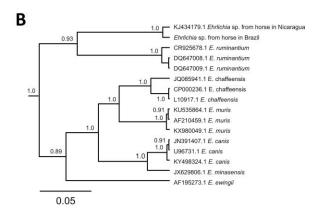
DOI: https://doi.org/10.3201/eid2405.180238

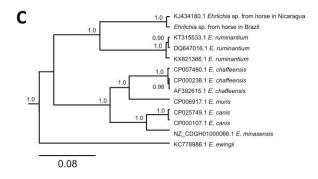
To the Editor: We read with interest the research letter from Chang et al. (1). To have such severe clinical disease attributed to *Burkholderia thailandensis* infection

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

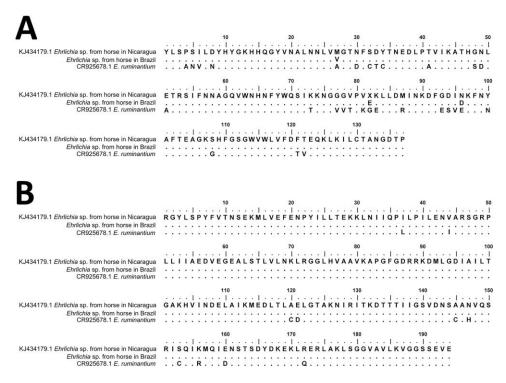
Technical Appendix







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.