

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 (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.

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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

published in peer-reviewed literature is of major significance to the research community, especially given the biosecurity aspects regarding melioidosis. We are writing, however, because we have serious doubts about the identity of the organism described.

The clinical features of the case are typical of septicemic melioidosis with pulmonary involvement. The pictures of the colonies in the technical appendix look very similar to *B. pseudomallei*, with which we have extensive experience in both Australia and Southeast Asia over the past 30 years. This identification was the most likely suggested by the phenotypic tests used. Furthermore, the virulence of the strain in mice bore more resemblance to that of *B. pseudomallei* than *B. thailandensis*, and the strain contained putative virulence determinants not normally found in *B. thailandensis*. Species identification thus appears to rest on arabinose assimilation and 16S rDNA sequence. Assimilation tests are notoriously difficult to read, and without knowledge of the 16S rDNA primers or sequence region of

comparison, it is plausible that a lack of resolution between *B. pseudomallei* and *B. thailandensis* has led to incorrect species attribution.

We therefore believe that there is insufficient evidence to prove that this case was caused by *B. thailandensis* and that the presented data suggest that this isolate was, in fact, *B. pseudomallei*. We are always happy to advise colleagues about the investigation and management of possible cases of melioidosis, but in these circumstances, we felt that it was necessary to place our concerns on record.

Reference

1. Chang K, Luo J, Xu H, Li M, Zhang F, Li J, et al. Human infection with *Burkholderia thailandensis*, China, 2013. *Emerg Infect Dis*. 2017;23:1416–8. <https://doi.org/10.3201/eid2308.170048>

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