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 (579 bp/584 bp; GenBank accession nos. MG385129, 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

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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...