for *N. helminthoeca* Maringá dog 1 (112 bp for *rrs*, 92 bp for *gro*ESL, 143 bp for *rpo*B) were short compared with those in GenBank (*rrs* 1,453 bp, *gro*ESL 1,914 bp, *rpo*B, 464 bp). Efficiency and sensitivity of targeting small DNA regions was necessary since storage and shipment of frozen samples were not optimal. Small DNA sequences are often suboptimal for delineation of phylogenetic relationships.

Bootstrapping analyses showed poor resolution (<380/1,000 iterations) below the genus level for the short rrs region examined. However, both the short rpoB and groESL regions examined had high bootstrap values (941/1,000 and 995/1,000 iterations, respectively). This finding differentiation allowed of Ν. helminthoeca and the Brazilian dog strain from N. sennetsu, N. risticii, and other related Anaplasmataceae and provided a high degree of confidence in the identification. More work is being implemented to obtain longer sequences to confirm and extend these genotypic comparisons. We propose further study to isolate the pathogen from other dogs for comparative biologic analyses.

Although SPD is caused by *N*. *helminthoeca*, infections by other *Neorickettsia* spp., including *N*. *risticii* (Potomac horse fever) and *N*. *sennetsu* (sennetsu fever), illustrate the potential of these widely distributed species to infect and cause disease in mammals and humans. Detection of *N. helminthoeca* in Brazilian dogs extends the range of this species and warrants a broad search for infections and spectrum of disease of *Neorickettsia* in animals and humans.

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References

 Dumler JS, Rikihisa Y, Dasch GA. Family II Anaplasmataceae. In: Garrity GM, editor. Bergey's manual of systemic bacteriology. 2nd ed. Vol. 2. New York: Springer; 2005. p. 117–43.

- Headley SA, Vidotto O, Scorpio D, Dumler JS, Mankowski J. Suspected cases of *Neorickettsia*-like organisms in Brazilian dogs. Ann N Y Acad Sci. 2004;1026:79–83.
- Taillardat-Bisch AV, Raoult D, Drancourt M. RNA polymerase β-subunit-based phylogeny of *Ehrlichia* spp., *Anaplasma* spp., *Neorickettsia* spp. and *Wolbachia pipientis*. Int J Syst Evol Microbiol. 2003;53:455–8.
- 4. Dumler JS, Barbet AF, Bekker CP, Dasch GA, Palmer GH, Ray SC, et al. Reorganization of genera in the families *Rickettsiaceae* and *Anaplasmataceae* in the order Rickettsiales: unification of some species of *Ehrlichia* with *Anaplasma*, *Cowdria* with *Ehrlichia* and *Ehrlichia* with *Neorickettsia*, descriptions of six new species combinations and designation of *Ehrlichia equi* and "HGE agent" as subjective synonyms of *Ehrlichia phagocytophila*. Int J Syst Evol Microbiol. 2001;51: 2145–65.
- Rikihisa Y, Zhang C, Kanter M, Cheng Z, Ohashi N, Fukuda T. Analysis of p51, groESL, and the major antigen P51 in various species of *Neorickettsia*, an obligatory intracellular bacterium that infects trematodes and mammals. J Clin Microbiol. 2004;42:3823–6.
- Inokuma H, Brouqui P, Drancourt M, Raoult D. Citrate synthase gene sequence: a new tool for phylogenetic analysis and identification of *Ehrlichia*. J Clin Microbiol. 2001;39:3031–9.
- Cordy DR, Gorham JR. The pathology and etiology of salmon disease. Am J Pathol. 1950;26:617–37.

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Correction: Vol. 12, No. 4

In "Potential Arbovirus Emergence and Implications for the United Kingdom" by Ernest A. Gould et al., an error occurred on page 549. The first paragraph of the article incorrectly states that African horse sickness virus is circulating in Europe. The sentence should read "Finally, the family *Reoviridae* contains a variety of animal arbovirus pathogens, including bluetongue virus, which is currently circulating in Europe, and African horse sickness virus, which has been found in Europe but is not currently circulating."

The corrected text appears in the online article at http://www.cdc.gov/ncidod/EID/vol12no04/05-1010.htm

We regret any confusion this error may have caused.