Rickettsiales in Ticks Removed from Outdoor Workers, Southwest Georgia and Northwest Florida, USA

Technical Appendix

Sample Acquisition

For tick collections, submissions were accepted from forestry and wildlife workers who worked throughout the region (Baker, Calhoun, Stewart, Thomas, Decatur, Dooly, Macon Counties in Georgia and Gladsden County in Florida). We notified participants about the project by emails and meetings. Workers were given tubes of 70% ethanol and asked to store and submit ticks in these tubes if they wished to participate in the project. Workers were instructed to separate ticks by date and location (if possible). The date(s) and location(s) where workers had obtained the tick(s) were recorded. No other information (e.g., time spent outdoors, past information on tick infestations or tick bites, etc.) was provided.

Tick Identification and Pathogen Testing

We morphologically identified nonlarval Dermacentor variabilis and Amblyomma spp. ticks. Amblyomma larvae and Ixodes spp. (all stages) were identified by using PCR targeting the 16S rRNA gene and sequencing (1). Ticks submitted in 2009 and 2010 were tested for Rickettsia spp., Ehrlichia chaffeensis, and E. ewingii by using a multiplex quantitative PCR targeting the 17-kDa gene of Rickettsia spp. and the 16S rRNA gene of Ehrlichia spp. (2).

Samples positive for Rickettsia spp. were analyzed by using a restriction fragment length polymorphism assay targeting the major outer membrane protein A gene by using primers RR190.70 and RR190.701R (3), followed by digestion with restriction enzymes RsaI and PstI (4). Ticks collected in 2011 were tested for Rickettsia spp., Ehrlichia chaffeensis, and E. ewingii by using nested PCRd specific for the 17-kDa (Rickettsia spp.) or 16S rRNA genes (Ehrlichia spp.) (4). Any samples positive for Rickettsia spp. that were not successfully identified by 17-kDa sequencing were then tested by using PCR and sequencing of the outer membrane protein A
gene (5). For all ticks, the gltA gene of Panola Mountain *Ehrlichia* sp., the *fla* gene of *Borrelia* spp., and the msp2 gene of *Anaplasma phagocytophilum* were targeted (1).

References


