Abstract

In the central area of Argentina, the epidemiological and molecular characteristics of Chlamydia pneumoniae infections in reptiles are still unknown. A nested polymerase chain reaction of the rpoB gene was used to detect C. pneumoniae in cloacal swab samples from 19 reptiles at a recreational area. Eleven (57.89%) reptiles were positive; the sequencing and phylogenetic analysis confirmed the presence of this bacterium. Neither C. pneumoniae DNA in the caregivers pharynges nor IgM antibodies anti-C. pneumoniae in their serum samples were detected; however, caregivers presented very high titers of IgG anti-C. pneumoniae. The detection of C. pneumoniae DNA in reptiles demonstrated the circulation of this agent in the recreational area and could be responsible for the exacerbated immune response of the personnel handling the reptiles, which suggests a potential zoonotic cycle. This is the first report of the detection of C. pneumoniae in reptiles in Argentina.

Keywords

Chlamydia pneumoniae, Reptiles, Phylogenetic Analysis, Immune Response, Argentina.