Abstract

Bacteria belonging to the family Chlamydiaceae cause a broad spectrum of diseases in a wide range of hosts, including humans, other mammals and birds. However, very little is known about chlamydial infections in birds in our region. In the present study, we examined 28 clinically normal birds in illegal captivity that were confiscated in the province of Córdoba, Argentina. The objective was to detect Chlamydia spp. in cloacal swabs by genetic analysis of the ompA gene. Nested-PCR of the ompA gene identified five samples as Chlamydophila pecorum and the sequence analysis demonstrated the presence of the ompA gene of C. pecorum in these birds. On the other hand, Chlamydophila psittaci was not detected. These birds could be either asymptomatic reservoirs or subclinical carriers of C. pecorum. This is the first report of the detection of C. pecorum in Argentina.

Keywords

Chlamydophila pecorum, birds in captivity, ompA gene, sequence analysis.