Abstract

Objective This study was aimed at investigating the frequency of infection by Cp. psittaci and determining its genotype in individuals at potential risk of exposure to the bacteria. Methodology The study involved 170 individuals: a risk group (n= 96) and a lowrisk control group (n=74). Cp. psittaci was detected and genotyped by single-tube nested PCR and ompA gene sequencing. Results Eight (8.3 %) positive cases were detected in the risk group and 1 (1.4 %) in the control group (p<0.04). Cp. psittaci was found in 16.7 % of pigeons’ fecal samples. Cp. psittaci infection with was more frequent in symptomatic (17.7 %) than asymptomatic (6.3 %) individuals in the risk group. Analysing the genomes isolated from human and bird specimens revealed the presence of genotype B. Conclusion The presence of Cp. psittaci genotype B in the population being evaluated could have been attributed to zoonotic transmission from pigeons to humans, an underestimated potential public health problem in Venezuela requiring the health authorities’ involvement.

Keywords
Chlamyphila psittaci, Columba livia, ompA, zoonotic transmission, nested PCR (source: MeSH, NLM).