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***Chlamydia psittaci* genotype B in a pigeon (*Columba livia*) inhabiting a public place in San José, Costa Rica**

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Abstract

Human chlamydiosis is a zoonotic disease of avian origin caused by *Chlamydia psittaci*. The highest infection rates have been detected in parrots (*Psittacidae*) and pigeons (*Columbiformes*), the latter most frequently carry the genotypes B and E. These genotypes have been shown to also infect humans. Because pigeons (*Columba livia*) cohabit with humans in urban areas, *C. psittaci* present in the dust from dry feces of infected pigeons may be transmitted by inhalation and represent a significant public health problem. Between 2012 and 2013 a total of 120 fecal samples were collected from pigeons at four public places (Plaza de la Cultura, Parque Morazán, Parque Central de Guadalupe, Plaza de las Garantías Sociales) in San José, Costa Rica. A nested polymerase chain reaction (PCR) was used to amplify a region of the outer membrane protein A gene of *C. psittaci*. Only one sample was positive in PCR and the positive sample was further subjected to sequencing and genotyping. Sequencing identified this sample as *C. psittaci* genotype B. This study is the first report to show the presence of this organism in pigeons of Costa Rica, and shows that the infected pigeons may represent a significant risk for humans who visit public places that are inhabited by pigeons.

Keywords: *Chlamydia psittaci*, Costa Rica, Genotype B, Pigeons, Zoonosis.

Introduction

Avian chlamydiosis is caused by *Chlamydia psittaci* (*C. psittaci*), a gram-negative and obligate intracellular bacterium, with nine (A to F, E/B, M56, and WC) known genotypes (Van Lent *et al.*, 2012). *C. psittaci* has been identified in 465 different bird species (Kaleta and Taday, 2003), but the highest rate of infection was found in parrots (*Psittacidae*) and pigeons (*Columbiformes*) (de Freitas *et al.*, 2002; Dovc *et al.*, 2005; Dovc *et al.*, 2007).

C. psittaci is shed regularly or intermittently in feces, lacrimal fluids, nasal discharges, oropharyngeal mucus and crop milk of the infected birds. Extreme environmental changes can trigger the onset of clinical disease in the infected birds; however prolonged subacute clinical forms of the disease are most common (Gerlach, 1986). Avian chlamydiosis presents in the form of nonspecific clinical signs to severe systemic disease, especially in young animals (Andersen and Vanrompay, 2003).

All genotypes of *C. psittaci* can be transmitted to humans and cause psittacosis or parrot fever (Andersen and Vanrompay, 2003); this transmission can occur either through inhalation, ingestion or via direct contact with the infected birds (Longbottom and Coulter, 2003). In humans, the disease can vary from nonspecific flu-like symptoms to severe pneumonia. Also, cases of endocarditis and encephalitis have been reported (Crosse, 1990).

C. psittaci is the most common pathogen found in domestic pigeons and mainly belong to the genotypes B and E (Vanrompay *et al.*, 1993; Andersen and Vanrompay, 2000; Magnino *et al.*, 2009). Because pigeons spread chlamydial infection and usually fly distances of about 5 km, these birds represent a major risk to public health as they cohabit with humans in urban and rural areas, in public places, parks and even gardens. It is believed that pigeons have been underestimated for a long time as an important source of human chlamydial infections (Heddema *et al.*, 2006a; Vázquez *et al.*, 2010).

A study carried out in Costa Rica in 2001 found antibodies against *C. psittaci* in 12.4% of 129 captive macaws (*Ara macao* and *Ara ambigua*) (Herrera *et al.*, 2001). Recently *C. psittaci* was detected in four (3.4%) out of 117 captive psittacine birds, which cohabited in human households and in two of those cases the organism was found to be of genotype A (Sheleby-Elias, 2010).

The objective of the present study was to determine the presence of *C. psittaci* in feces of pigeons of urban public places and parks that are frequently visited by children, elderly and tourists.

Materials and Methods

Size, type of sample and sampling method

Between October 2012 and May 2013 a total of 120 pigeons were tested in four different public parks (Plaza de la Cultura, Plaza de las Garantías Sociales,

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Parque Morazán and Parque Central Guadalupe) in San José, by cookie crumbs.

Feces were collected from the floor with sterile swabs from defecating birds, and transferred into tubes containing 0.5 ml Minimal Essential Medium. The swabs were stored at 4°C for 24 hours until further processing.

Polymerase chain reaction (PCR)

For DNA extraction DNeasy® Blood & Tissue Kit of QIAGEN (Venlo, Netherlands) was used and the extraction was performed according to the manufacturer's instructions. For the detection of *C. psittaci*, a nested PCR described by Sachse and Hotzel (2003) was used, which partially amplifies the gene outer membrane protein A (*ompA*) to identify the genus *Chlamydia*. The primers used were: 191CHOMP (5'-GCIYTITGGGARTGYGGITGYGCIAC-3') and CHOMP371 (5'-TTAGAAICKGAATTGIGCRTTIAYGTTGIGCIGC-3'). All amplification products were subjected to a second PCR to identify *C. psittaci*, using the primers CHOMP 336s (5'-CCRCAAGMTTCTTRGAYTTCAWYTTGTTRAT-3') and 218PSITT (5'-GTAATTTCIAGCCCAGCACAATTYGTG-3').

Samples with bands of 389-404 bp were considered positive for *C. psittaci*. DNA of *C. psittaci* was donated by the Clinic of Birds, Reptiles, Amphibians and Fish, Justus Liebig University, Giessen, Germany and was used as a positive control; nuclease free water (molecular biology grade, Thermo Scientific, Waltham, USA) was used as a negative control.

Sequencing, genotyping and construction of the phylogenetic tree

One positive sample identified during nested PCR was genotyped through analysis of *ompA* sequences (Heddema et al., 2006b).

The primers used were CPSittGenoFor (5'-GCTACGGGTTCCGCTCT-3') and CPSittGenoRev (5'-TTTGTGATYTTGAATCGAAGC-3'), which amplify conserved regions of the *ompA* gene covering four variable domains. The size of the amplified fragment was 1041bp. PCR product was purified using the QIAquick® kit (QIAGEN, Venlo, Netherlands), according to the manufacturer's instructions.

The DNA sample was sent to Macrogen (Seoul, Korea) for sequencing. Partial sequence was aligned with BioEdit Sequence Alignment Editor® (Hall, 1999) and compared using the BLASTn algorithm with the database of National Center for Biotechnology Information. Then the sequences were imported into MEGA 5 (Tamura et al., 2011), using the Jukes & Cantor algorithm (Jukes and Cantor, 1969) and the UPGMA method (Sneath and Sokal, 1973), for the design of the phylogenetic tree. A total of 10000

replicates were calculated (Felsenstein, 1985). The analysis included the reference sequences of the nine *C. psittaci* genotypes available in the database of GenBank, A (accession number AY762608), B (AF269265), C (L25436), D (AF269266), E (X12647), F (AF269259), E/B (AY762613), M56 (AF269268) and WC (AF269269) (Sachse et al., 2008), the phylogenetic tree was rooted with the *C. caviae* strain (GPIC, GenBank AF269282) (Zhang et al., 1989).

Results

Only one out of 120 samples yielded positive results during the first PCR (576-597pb), and the specific band (389-404pb) was subsequently amplified using the nested PCR (Fig. 1).

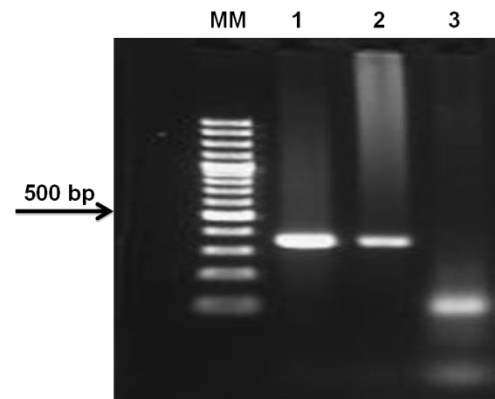


Fig. 1. Gel electrophoresis of the amplified PCR products of *ompA* gene of *C. psittaci* (MM: molecular marker; 1: positive control; 2: pigeon from Costa Rica; 3: negative control).

The sample that tested positive for *C. psittaci* was collected from a pigeon from the public park Plaza de la Cultura. Sequencing confirmed the results, and identified this sample as *C. psittaci* genotype B (Fig. 2).

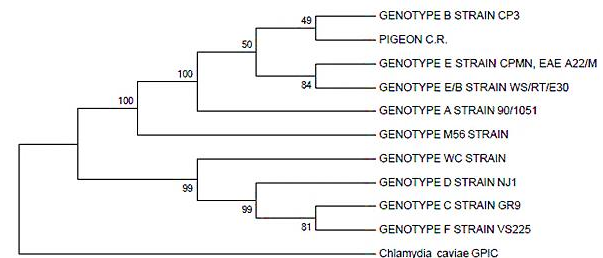


Fig. 2. Phylogenetic tree of gene *ompA* sequence of one pigeon sample (PIGEON C.R.) of Costa Rica that tested positive for *C. psittaci*.

The sequence analysis of the product of PCR using BLASTn, found 99.9% (1029/1030) nucleotide

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