ISSN: 2226-4485 (Print) ISSN: 2218-6050 (Online)

ISSN: 2218-6050 (Online) Original Article

Submitted: 17/09/2013 Accepted: 20/11/2013 Published: 02/12/2013

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.

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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,

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 was performed according extraction 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 Chlamydia. The primers used 191CHOMP (5'-GCIYTITGGGARTGYGGITGYGCI AC-3') and CHOMP371 (5'-TTAGAAICKGAATTGIGCRTTIAYGTGIGCIGC-3'). All amplification products were subjected to a second PCR to identify C. psittaci, using the primers 336s **CHOMP** CCRCAAGMTTTTCTRGAYTTCAWYTTGTTRAT 218PSITT -3') and 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'-TTTGTTGATYTGAATCGAAGC-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).

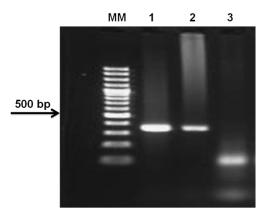


Fig. 1. Gel electrophoresis of the amplified PCR products of *omp*A gene of *C. psittaci* (MM: molecular marker; 1: positive control; 2: pigeon from Costa Rica; 3: negative control).

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).

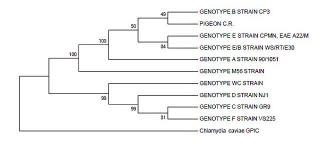


Fig. 2. Phylogenetic tree of gene *omp*A sequence of one pigeon sample (PIGEON C.R.) of Costa Rica that tested positive for *C. psittaci*.

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

identity with sequences of *C. psittaci* genotype B deposited in GenBank (CP003797.1, AY762609.1, AF269265.1). Comparison of the partial sequence of the fecal pigeon sample of Costa Rica with a *C. psittaci* sequence isolated in 1958 from air sacs of pigeons in California, USA by Bush and Everett (2001) is shown in Figure 3.

		$\cdots \cdots \cdots \cdots$		11	
	5	15	25	35	45
PIGEON C.R. AF269265.1	CGCTCTCTCC	TTACAAGCCT	TGCCTGTAGG TGCCTGTAGG	GAACCCAGCT	GAACCAAGTT
	55	 65		 85	 95
PIGEON C.R.	TATTAATCGA	TGGCACTATG	TGGGAAGGTG	CTTCAGGAGA	TCCTTGCGAT
AF269265.1	TATTAATCGA	TGGCACTATG	TGGGAAGGTG	CTTCAGGAGA	TCCTTGCGAT
	105	115	 125	135	145
PIGEON C.R. AF269265.1	CCTTGCGCTA	CTTGGTGTGA	CGCCATTAGC CGCCATTAGC	ATCCGCGCAG	GATACTACGG
AF205203.1					
PIGEON C.R.	166	165	175	105	105
AF269265.1	AGATTATGTT	TTCGATCGTG	TATTAAAAGT TATTAAAAGT 225	TGATGTGAAT	AAAACTTTTA
	205	215		235	245
PIGEON C.R.	GCGGCATGGC	TGCAACTCCT	ACGCAGGCTA ACGCAGGCTA	C-AGGTAACG	CAAGTAATAC
AF269265.1	GCGGCATGGC	TGCAACTCCT	ACGCAGGCTA	C-AGGTAACG	CAAGTAATAC
	255	265	 275	285	295
PIGEON C.R. AF269265.1	TAATCAGCCA	GAAGCAAATG	GCAGACCGAA GCAGACCGAA	CATCGCTTAC	GGAAGGCATA
A1203203.1			325		
PIGEON C.R.	305 TCCAACATCC	315	325	335	345
AF269265.1	TGCAAGATGC	AGAGTGGTTT	TCAAATGCAG TCAAATGCAG	CCTTCCTAGC	CTTAAACATT
	355	 365	375	385	395
PIGEON C.R.	TGGGATCGCT	TCGACATTTT	CTGCACCTTA CTGCACCTTA	GGGGCATCCA	ATGGATACTT
AF269265.1	TGGGATCGCT	TCGACATTTT	CTGCACCTTA	GGGGCATCCA	ATGGATACTT
	405	415	 425	435	445
PIGEON C.R. AF269265.1	CAAATCAAGT	TCGGCTGCAT	TCAACTTGGT TCAACTTGGT	TGGGTTAATA	GGGTTTTCAG
]		475		
PIGEON C.R.	455 CTACCAACTC	465 AACCTCTACC	475 GATCTTCCAA	485 TGCAACTTCC	495 TAACGTAGGC
AF269265.1	CTACCAACTC	AACCTCTACC	GATCTTCCAA GATCTTCCAA	TGCAACTTCC	TAACGTAGGC
	505	515	 525	535	545
PIGEON C.R. AF269265.1	ATTACCCAAG	GTGTTGTGGA	ATTTTATACA ATTTTATACA	GACACATCAT	TTTCTTGGAG
Ar209205.1			 575		
PIGEON C.R.	555 CGTAGGTGCA	565 CGTGGAGCTT	575 TATGGGAATG	585 TGGTTGTGCA	595 ACTITAGGAG
AF269265.1	CGTAGGTGCA	CGTGGAGCTT	TATGGGAATG	TGGTTGTGCA	ACTITAGGAG
	605	615	 625	635	645
PIGEON C.R.	CTGAGTTCCA	ATACGCTCAA	TCTAATCCTA TCTAATCCTA	AGATTGAAAT	ACTCAACGTC
AF269265.1		ATACGCTCAA	675	AGAITGAAAT	ACTCAACGIC
PIGEON C.R.	655	665	675	685	695
AF269265.1	ACTICAAGCC	CAGCACAATT	TGTGATTCAC TGTGATTCAC	AAACCAAGAG	GCTATAAAGG
	705	 715	 725		745
PIGEON C.R.	AGCTAGCTCG	AATTTTCCTT	TACCTATAAC TACCTATAAC	GGCTGGAACA	ACAGAAGCTA
AF269265.1	AGCTAGCTCG	AATTTTCCTT	TACCTATAAC	GGCTGGAACA	ACAGAAGCTA
	755	765	II 775	785	795
PIGEON C.R. AF269265.1	CAGACACCAA	ATCAGCTACA ATCAGCTACA	ATTAAATACC ATTAAATACC	ATGAATGGCA ATGAATGGCA	AGTAGGCCTC
]		 825		
PIGEON C.R.	GCCCTGTCTT	815 ACAGATTGAA	TATGCTTGTT	CCATATATTG	GCGTAAACTG
AF269265.1	GCCCTGTCTT	ACAGATTGAA	TATGCTTGTT TATGCTTGTT	CCATATATTG	GCGTAAACTG
	855	865	**************************************	885	895
PIGEON C.R. AF269265.1	GTCAAGAGCA	ACTITICATG	CTGATACTAT CTGATACTAT	CCGCATTGCT	CAACCTAAAT
A.E. 50 3E 03.1			925		
PIGEON C.R.	905 TAAAATCGGA	915 GATTCTTAAC	925 ATTACTACAT	935 GGAACCCAAG	945 CCTTCTAGGA
AF269265.1	TAAAATCGGA	GATTCTTAAC	ATTACTACAT	GGAACCCAAG	CCTTCTAGGA
	95.5	965	 975	985	 995
PIGEON C.R.	TCAACCACTG	CTTTGCCCAA	TAATAGTGGT TAATAGTGGT	AAGGATGTTC	TATCTGATGT
AF269265.1	TUAACCACTG		TAATAGTGGT	AAGGATGTTC	TATCTGATGT
DICEON C D	1005	1015	1025 AAATCAACAA		
PIGEON C.R. AF269265.1	CTTGCAAATT	GCTTCGATTC	AGATCAACAA	A	
	nment of				the own

Fig. 3. Alignment of the nucleotide sequences of the *omp*A gene sequence of *C. psittaci* obtained from a pigeon in Costa Rica (PIGEON C.R.) with that of *C. psittaci* genotype B (AF269265.1) isolated in 1958 from air sacs of pigeons in California, USA. The nucleotide difference between the sequences is underlined at the position.

Discussion

This is the first study in Costa Rica that reported the presence of *C. psittaci* genotype B in a pigeon of a public park in Costa Rica, and is consistent with the international literature which mentions that this genotype is found more frequently in domestic and feral pigeons (Vanrompay *et al.*, 1993; Andersen and Vanrompay, 2003; Magnino *et al.*, 2009).

Only one bird was found to be positive for the pathogen (3.3%), in contrast to studies carried out in Madrid (61/116, 52.6%), Zagreb (30/232, 12.9%) and Amsterdam (26/331, 7.8%) (Pruckner-Radovcic *et al.*, 2005; Heddema *et al.*, 2006a; Vázquez *et al.*, 2010), but our results are in accordance with studies carried out in Ghent (1/61, 1.6%) (Dickx *et al.*, 2010). The reasons could be due to several factors such as type of the study, sample size, or the sampling method.

In addition, false negative results could not be ruled out, due to polymerase inhibitors in the samples or because of intermittent shedding of *C. psittaci* from cloacal samples that could have resulted in an underestimation of the agent (Pruckner-Radovcic *et al.*, 2005).

Nevertheless, it may also indicate a low infection rate of *C. psittaci* in pigeons of Costa Rica, which would be consistent with studies carried out by Sheleby-Elias (2010), who detected a low infection rate (3.4%) of *C. psittaci* in captive psittacine birds inhabiting the households. The genotype present in captive parrots was determined as genotype A.

The finding of this zoonotic agent in the feces of a pigeon shows that *C. psittaci* is found in places that are regularly visited by human population, especially on weekends by families with young children, who feed the pigeons. This poses a significant risk of transmission of the agent by inhalation or direct contact with the infected birds (Longbottom and Coulter, 2003).

The low infection rate determined in the present study is beneficial to the public health (Pruckner-Radovcic et al., 2005), nevertheless it is recommended that more comprehensive and representative studies are required to determine the prevalence of *C. psittaci* in urban pigeons, establish the genotypes circulating in these birds, because certain genotypes (A and D) can cause serious infections in people, while others, such as genotype B, usually cause mild respiratory symptoms (Dickx et al., 2010).

Finally, we recommend implementation of control programs for decreasing the prevalence of this disease in pigeons, coupled with environmental educational programs, to prevent a possible spread of *C. psittaci* to people visiting public places of Costa Rica.

Acknowledgements

This research was conducted within the framework of the project titled "Detection of infectious agents in _____

wild birds of Costa Rica"; project number NFEG05 of the Universidad Nacional.

Special thanks to Prof. Dr. Michael Lierz, Clinic of Birds, Reptiles, Amphibians and Fish, Justus Liebig University, Giessen, Germany, who kindly donated DNA of *C. psittaci* that was used as a positive control in the PCR in our investigation. Ethical guidelines were followed during this investigation, as animals were used in our study.

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