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Genome Sequences of the Zoonotic Pathogens *Chlamydia psittaci* 6BC and Cal10[▽]

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Chlamydia psittaci **is a highly prevalent avian pathogen and the cause of a potentially lethal zoonosis, causing life-threatening pneumonia in humans. We report the genome sequences of *C. psittaci* 6BC, the prototype strain of the species, and *C. psittaci* Cal10, a widely used laboratory strain.**

The obligate intracellular pathogen *Chlamydia psittaci* causes zoonotic psittacosis or ornithosis, a severe and sometimes fatal respiratory disease of humans that is acquired from infected birds. *C. psittaci* is found in bird populations worldwide, with sporadic epidemic outbreaks (1). Infection in birds is often asymptomatic, with transmission to humans reported regularly, particularly in individuals with a high exposure risk, such as veterinarians and other animal handlers (4). *C. psittaci* is a U.S. CDC category B bioterrorism agent due to the ease of respiratory dissemination and associated morbidity and mortality rates (5). Notably, a 1930 Maryland outbreak of psittacosis, linked to the 1929-1930 psittacosis pandemic, directly led to the founding of the National Institutes of Health (7, 9).

We sequenced the type strain *C. psittaci* 6BC, isolated from a parrot during the 1929-1930 psittacosis pandemic (3). Isolates of *C. psittaci* 6BC have been shown to be genetically variable (10)—we sequenced a genetic variant of *C. psittaci* with lower virulence. We also sequenced *C. psittaci* Cal10, originally termed the meningopneumonitis virus, which was isolated from ferrets inoculated with throat washings from humans with an influenza-like respiratory infection (8).

The finished genome of *C. psittaci* 6BC was determined using the whole-genome shotgun method (11). Gaps were closed using a combination of primer walking, generation and sequencing of transposon-tagged libraries of large-insert clones, and multiplex PCR (11). Gene identification and annotation were performed as previously described (11). Functional assignment, identification of membrane-spanning domains, determination of paralogous gene families, and identification of regions of unusual nucleotide composition were performed as previously described (11). The *C. psittaci* Cal10 draft genome was determined using Titanium pyrosequencing on a 454 GS FLX and assembled using Celera Assembler with *C. psittaci* 6BC as the reference. The *C. psittaci* Cal10 draft genome consists of 3 ordered contigs (160-fold coverage). *C. psittaci* 6BC annotation was mapped to Cal10 using a pipeline based on the Mummer 3.1 package (6).

The *C. psittaci* 6BC genome is 1,171,667 bp, containing 1,016 putative coding sequences (CDSs). The *C. psittaci* Cal10 draft genome is 1,169,283 bp, containing 982 CDSs. Both strains possess the conserved *C. psittaci* plasmid (8 CDSs, 7,553 bp). *C. psittaci* 6BC and Cal10 both possess a single full-length copy of the cytotoxin ortholog within the chlamydial plasticity zone (PZ). The virulence-associated membrane attack complex/perforin gene, truncated in or absent from all other chlamydial genomes except koala strain *C. pneumoniae* LPCoLN (11), is also located in the PZ in two copies, one full length and one truncated.

The *C. psittaci* 6BC and Cal10 chromosomes are essentially identical, with 119 intragenic (48 nonsynonymous, 30 synonymous, and 41 insertion/deletion) single-nucleotide polymorphisms (SNPs) and 31 intergenic SNPs identified. SNP accumulation ("hot spots") occurs in four regions; one hot spot maps to the chlamydial PZ within the *C. psittaci* cytotoxin ortholog, two other hotspots are found within distinct *pmpG* clusters, and the fourth centers on a CDS predicted to encode phosphatidylinositol-4-phosphate 5-kinase, a lipid-modifying enzyme involved in actin remodeling that has been shown to be instrumental in chlamydial entry into the host cell (2).

Nucleotide sequence accession numbers. Genome and plasmid sequences have been deposited at GenBank under accession numbers CP002586 (*C. psittaci* 6BC chromosome), CP002587 (*C. psittaci* 6BC plasmid), and AEZD00000000 (*C. psittaci* Cal10 draft chromosome and plasmid).

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