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). 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). The *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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REFERENCES