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GENOME ANNOUNCEMENTS

Full-Length *De Novo* Sequence of the *Chlamydophila psittaci* Type Strain, 6BC▽

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***Chlamydophila psittaci* is an obligate intracellular zoonotic pathogen, mainly of birds. It is the causative agent of psittacosis in birds and humans. Here we report the full-length *de novo* genome sequence of the avian isolate 6BC, the type strain of the species *C. psittaci*.**

Chlamydophila psittaci, the pathogenic agent of psittacosis (parrot disease or ornithosis) (14), is an obligate intracellular Gram-negative bacterium reported to infect a wide range of primarily avian, but also other vertebrate hosts: e.g., cattle, goats, horses, or crocodiles (12, 17). Transmissions from birds to humans occur (7, 10, 18).

The avian isolate 6BC was the original type strain of the former species *Chlamydia psittaci* (16) and has been retained as the type strain of the emended species *Chlamydophila psittaci* (5).

Strain 6BC was isolated originally from a parakeet in California in 1941 (ATCC no. VR-125). This sample was donated to K.S. by D. Vanrompay (University of Ghent, Belgium) in 2004 and has been passaged in BGMK (Buffalo green monkey kidney) cells on a regular basis.

To facilitate discrimination between chlamydial DNA and contaminant host DNA, *C. psittaci* 6BC cells were proliferated in human HeLa cells (ATCC no. CCL-2) prior to DNA extraction. We used a combination of Roche 454 pyrosequencing, Illumina, and Sanger sequencing to determine the complete genomic sequence of *C. psittaci* 6BC. Approximately 28 million 40-bp reads were obtained on an Illumina Genome analyzer II, and 47,000 reads of an average length of 386 bp were obtained on a Roche Genome sequencer FLX.

A backbone sequence was constructed by assembling all reads with MIRA3 (2). Gaps were closed with Gap 4.10 (1), and contig order was verified by PCR and Sanger sequencing. To locate areas of low (<10-fold) coverage and potential ambiguities, all Illumina reads were remapped against the completed sequence backbone. On average, a 487-fold sequence coverage was achieved. Sections of low coverage were confirmed by subsequent Sanger sequencing.

The DNA sequence was annotated by using the ISGA pipeline (11), available at http://isga.cgb.indiana.edu/. Briefly, potential protein-, rRNA-, and tRNA-coding genes were predicted by Glimmer3 (3), RNAmmer (13), and tRNAscan-SE (15), respectively. The predicted protein sequences were searched against nonredundant protein databases (NCBI, SwissProt, and Protein Data Bank) with AB-BLASTp (8). The predicted proteins were compared against the PFAM (6) and TIGRFAM (9) databases with HMMPFAM (4). The results from these analyses were combined into a gene function prediction that informed a manual annotation of the sequence and predicted proteins.

The genome is composed of a circular 1,171,660-bp chromosome containing 967 predicted protein-coding genes and a 7,553-bp plasmid containing 8 protein-coding sequences.

Comparison of *C. psittaci* 6BC, *Chlamydophila abortus* S26/3 (accession no. NC_004552), *Chlamydophila felis* Fe/C-56 (NC_007899), and *Chlamydophila caviae* GPIC (NC_003361) revealed high colinearity. The *C. psittaci* genome contains 38 tRNA genes and one rRNA operon containing three (5S, 23S, and 16S) rRNAs. The bacterial chromosome has a GC content of 39.06%, similar to other *Chlamydiaceae*. A total of 89.39% of the *C. psittaci* genome is predicted to be coding sequences.

Nucleotide sequence accession numbers. The genome sequence of *C. psittaci* strain 6BC has been deposited in GenBank and assigned accession no. CP002549 (chromosome) and CP002550 (plasmid).

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