JOURNAL OF BACTERIOLOGY, Mar. 2011, p. 1282–1283 Vol. 193, No. 5
0021-9193/11/$12.00 doi:10.1128/JB.01435-10

Genome Sequence of the Zoonotic Pathogen *Chlamydophila psittaci*▽

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Received 29 November 2010/Accepted 13 December 2010

We present the first genome sequence of *Chlamydophila psittaci*, an intracellular pathogen of birds and a human zoonotic pathogen. A comparison with previously sequenced *Chlamydophila* genomes shows that, as in other chlamydiae, most of the genome diversity is restricted to the plasticity zone. The *C. psittaci* plasmid was also sequenced.

Avian *Chlamydophila psittaci* infections range from chronic and symptomless to acute, with various mortality rates (11, 12). Epidemic outbreaks of *C. psittaci* have been reported among wild birds and commercially farmed poultry, causing significant economic losses (11, 12). Although it primarily infects birds, *C. psittaci* is a human zoonotic pathogen causing pneumonia or fever following close contact with infected birds (12).

We sequenced *C. psittaci* strain RD1, which was isolated from a mixed culture with *Chlamydia trachomatis* serovar L2b. Although human mixed ocular infections with these two species have been reported (7), *C. psittaci* strain RD1 is thought to derive from a laboratory-based cross-contamination event from an undetermined source soon after *C. trachomatis* strain isolation. DNA was prepared (17), sequenced using 454 pyrosequencing on a GS20 machine with an average read length of 100 bp, and assembled using Newbler (Roche). The contigs were ordered using the *Chlamydophila abortus* genome as a reference (18) and manually finished to produce an improved high-quality draft genome sequence (6) of six contigs, with approximately 40.7× coverage. The five unspanned gaps are clearly marked in the genome annotation (size estimates based on comparison with *C. abortus*: 3,592 bp between *pmp11G* and *pmp13G* [*pmp12G* is absent], 116 bp at the 3′ end of *pmp16G*, and three gaps of 887, 797, and 1,481 bp within the rRNA operon). Annotation and comparative analysis with the closely related species *C. abortus*, *Chlamydophila caviae*, and *Chlamydophila felis* (1, 8, 14, 18) were performed using Artemis (16) and ACT (5).

The draft genome sequence of *C. psittaci* comprises 1,156,417 bp, showing average nucleotide identities of 91.3, 85.9, and 84.8% with *C. abortus*, *C. caviae*, and *C. felis*, respectively. The *C. psittaci* genome is predicted to encode 959 coding sequences (CDSs). Analysis of *ompA* indicates that *C. psittaci* strain RD1 belongs to genotype A (9, 13). Like other *Chlamydophila* genomes, that of *C. psittaci* carries 36 tRNA genes and one rRNA operon and shows high conservation of gene content and order with other members of its genus. A total of 16 pseudogenes were detected within the genome, including two polymorphic membrane protein (*pmp*) genes (*cpsi_2861* and *cpsi_2911*) (10) and one transmembrane head/inclusion membrane family (TMH/Inc) gene (*cpsi_7871*) (2, 15). The *C. psittaci* strain RD1 plasmid, designated pRD1, is 7,553 bp long, encodes 8 CDSs, and differs by only four single-nucleotide polymorphisms from *C. psittaci* plasmid pCpA1 (NC_002117).

Most of the *C. psittaci*-specific sequences are located in the plasticity zone (PZ), which carries an additional 18,139 bp of sequence compared to *C. abortus*, including a 9,762-bp CDS predicted to encode a cytotoxin (*cpsi_5561*) which shows 44% identity with cytotoxins found at the same locus in *C. felis* and *C. caviae*. The PZ also contains the intact *guaBA-add* operon (*cpsi_5591-5611*) encoding proteins thought to be involved in purine nucleotide interconversion (1, 14, 18). *C. psittaci* lacks the tryptophan biosynthesis operon (3, 4).

Nucleotide sequence accession numbers. The sequences determined in this study have been deposited in the EMBL database under accession numbers FQ482149 (chromosome) and FQ482150 (plasmid).

This work was supported by Wellcome Trust grant WT076964.

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▽ Published ahead of print on 23 December 2010.

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