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Complete Genome Sequence of *Chlamydia trachomatis* Ocular Serovar C Strain TW-3

Vítor Borges,[a,b] Miguel Pinheiro,[c] Luís Vieira,[d] Daniel A. Sampaio,[d] Alexandra Nunes,[a,b] Maria J. Borrego,[a] João P. Gomes[a,b]

Reference Laboratory of Bacterial Sexually Transmitted Infections[a] and Bioinformatics Unit,[b] Department of Infectious Diseases, National Institute of Health, Lisbon, Portugal; School of Medicine, University of St. Andrews, Fife, United Kingdom[c]; Innovation and Technology Unit, Human Genetics Department, National Institute of Health, Lisbon, Portugal[d]

***Chlamydia trachomatis* is the etiological agent of trachoma, the leading infectious cause of blindness worldwide. We report here the first complete and annotated genome of a *C. trachomatis* trachoma-causing serovar C strain (strain TW-3). The chromosome and plasmid are 1,043,554 bp and 7,501 bp in length, respectively.**

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Address correspondence to João P. Gomes, j.paulo.gomes@insa.min-saude.pt.

The obligate intracellular bacterium *Chlamydia trachomatis* is the major cause of bacterial sexually transmitted infections worldwide and is also responsible for trachoma, the leading infectious cause of blindness. Trachoma results from a conjunctival chronic inflammatory state leading to the formation of irreversible corneal opacities and blindness (1, 2). It is one of 17 neglected tropical diseases and is targeted for elimination by 2020 by the World Health Organization (WHO) through the implementation of the SAFE strategy: lid surgery (S), antibiotics to treat the infection (A), facial cleanliness (F), and environmental changes (E) (3). Trachoma affects about 2.2 million people and it is endemic in >50 countries, predominantly in sub-Saharan Africa, the Middle East, and Asia (2). This epidemiological pattern is essentially associated with *C. trachomatis* ocular serovars A and B (4) (from the existent 15 major serovars), whereas serovar C seems relatively common in indigenous Australian communities (5, 6). Of note, serovar C has been also associated with *Chlamydia*-related arthritis (7). There are already five and two annotated genomes from serovars A and B (8–10), respectively. We report here the first complete and annotated sequence of a trachoma-causing *C. trachomatis* serovar C strain, TW-3.

The C/TW-3 strain was isolated in Taiwan in 1959 from the human conjunctiva (11). We obtained this strain from the American Type Culture Collection (ATCC VR-1477) and propagated it in HeLa229 cell monolayers before proceeding with bacterial purification using discontinuous urographin density gradients (12). The whole-genome sequence was determined by using a paired-end strategy (2 × 250 bp) with the platform Illumina MiSeq. The reads were mapped to *C. trachomatis* chromosome and plasmid sequences (8–10) using both Bowtie 2 (version 2.1.0 [http://bowtie-bio.sourceforge.net/bowtie2/index.shtml]) (13) and the Burrows-Wheeler Aligner (BWA) software (version 0.7.5a [http://bio-bwa.sourceforge.net/]) (14). Globally, 5,233,958 reads (with a mean quality score >30 for >95% of the read bases) were mapped, which yielded a mean coverage of 1,117-fold and 6,717-fold for the chromosome and plasmid, respectively. Single-nucleotide polymorphisms (SNPs) and indels were identified using SAMtools, followed by variant calling using BCFtools (http://samtools.sourceforge.net/) (15), and were carefully inspected through the Integrative Genomics Viewer (version 2.3.12 [http://www.broadinstitute.org/igv/]) (16). Both the typing gene (*ompA*) and problematic regions (e.g., *tarP*) were confirmed by PCR, followed by Sanger sequencing. The sequence was annotated by the NCBI Prokaryotic Genomes Annotation Pipeline 2.3.

The genome sequence of C/TW-3 revealed a chromosome of 1,043,554 bp in length, with a G+C content of 41.30% and 922 predicted coding sequences (CDSs). Plasmid analysis revealed the existence of about six copies per chromosome (based on the ratio of mean coverage for plasmid/chromosome), which fits with previous data (17), and the plasmid was found to be 7,501 bp in length, comprising eight CDSs (G+C content of 36.25%).

The availability of a complete and annotated genome sequence of an additional trachoma-causing serovar may contribute to the elucidation of the genetic basis underlying the pathogenic differences between *C. trachomatis* ocular strains (7, 18, 19).

Nucleotide sequence accession numbers. The complete genome sequence of *C. trachomatis* serovar C (strain TW-3) has been assigned GenBank accession no. CP006945 (chromosome) and CP006946 (plasmid).

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