Genome Sequence of the Obligate Intracellular Animal Pathogen Chlamydia pecorum E58

Sergio Mojica, Heather Huot Creasy, Sean Daugherty, Timothy D. Read, Teayoun Kim, Bernhard Kaltenboeck, Patrik Bavoil and Garry S. A. Myers


Updated information and services can be found at:
http://jb.asm.org/content/193/14/3690

*These include:*

**REFERENCES**

This article cites 6 articles, 4 of which can be accessed free at:
http://jb.asm.org/content/193/14/3690#ref-list-1

**CONTENT ALERTS**

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: http://journals.asm.org/site/misc/reprints.xhtml
To subscribe to another ASM Journal go to: http://journals.asm.org/site/subscriptions/
The obligate intracellular bacterial pathogen *Chlamydia pecorum* is found in cattle and other ruminants, swine, and koalas and other marsupials, causing a wide diversity of disease with significant economic impact. Strains of *C. pecorum* were members of the *Chlamydia psittaci* species until separated in 1992 on the basis of DNA-DNA hybridization and immunological data (2). *C. pecorum*-associated diseases in sheep, goats, cattle, horses, and pigs include polyarthritis, pneumonia, urogenital tract infections, abortion, conjunctivitis, mastitis, encephalomyelitis, enteritis, pleuritis, and pericarditis; in koalas, *C. pecorum* causes conjunctivitis and infertility. Limited gene sequencing and serological studies have suggested that there is significant strain diversity within this chlamydial species (6), consistent with the observed diverse spectrum of hosts and diseases. We sequenced the type strain, *C. pecorum* E58, originally isolated from the brain of a calf with sporadic bovine encephalomyelitis (3).

The finished complete genome of *C. pecorum* E58 was determined using the whole-genome shotgun (WGS) method (4). Physical and sequencing gaps were closed using a combination of primer walking, generation and sequencing of transposon-tagged libraries of large-insert clones, and multiplex PCR (4). Identification of putative protein-coding genes and annotation of the genome were performed as previously described (4). An initial set of coding sequences (CDSs) predicted to encode proteins was identified with GLIMMER (1). CDSs consisting of fewer than 30 codons were eliminated. Frameshift and point mutations were corrected or designated “authentic,” as previously described (4). 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 (4).

* Corresponding author. Mailing address: Institute for Genome Sciences and Department of Microbiology and Immunology, University of Maryland School of Medicine, 801 West Baltimore Street, Baltimore, MD 21201. Phone: (410) 706-5678. Fax: (410) 706-1482. E-mail: gmyers@som.umaryland.edu.

\[^V\] Published ahead of print on 13 May 2011.