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Genome Sequence of the Obligate Intracellular Animal Pathogen *Chlamydia pecorum* E58[▽]

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***Chlamydia pecorum* is an obligate intracellular bacterial pathogen that causes diverse disease in a wide variety of economically important mammals. We report the finished complete genome sequence of *C. pecorum* E58, the type strain for the species.**

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).

The *C. pecorum* E58 genome is 1,106,197 bp, containing 1,073 putative coding sequences (CDSs), and is highly similar to other members of the genus in both gene content and genomic synteny. Most gene content variation in *Chlamydia* is found within the plasticity zone (PZ) at the replication terminus, including several putative chlamydial virulence factors. *C. pecorum* E58 possesses two full-length copies of the chlamydial cytotoxin arranged in tandem within the PZ. Three copies of phospholipase D, suggested to play a role in chlamydial lipid modification or metabolism, are also found in the *C. pecorum* PZ. Similarly, the virulence-associated membrane attack complex (MAC)/perforin gene, which is either truncated or absent in most chlamydial genomes, is present as a single full-length copy. Tryptophan metabolism plays a key role in chlamydial persistence and tissue tropism; the ability to biosynthesize tryptophan is variable across the *Chlamydiae*. Unlike most members of the *Chlamydiae*, *C. pecorum* E58 possesses a nearly complete biosynthetic pathway (*trpABFCDR*), similar to that observed in *Chlamydia caviae* (5).

This is the first genome sequence reported for this species; however, additional genome sequencing is required to explore the reported *C. pecorum* strain diversity.

Nucleotide sequence accession number. The genome sequence for *C. pecorum* E58 has been deposited at GenBank under accession number CP002608.

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