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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Bartonella quintana*, a Bacterium Isolated from Rhesus Macaques

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***Bartonella quintana* is a re-emerging pathogen and the causative agent of a broad spectrum of disease manifestations in humans. The present study reports the complete genome of *B. quintana* strain RM_11, which was isolated from rhesus macaques.**

Bartonella quintana is a fastidious Gram-negative bacterium that was originally recognized as the agent of trench fever in World War I. As a re-emerging pathogen, *B. quintana* now correlates with a widening spectrum of human diseases, including chronic bacteremia, endocarditis, and bacillary angiomatosis (2, 4, 6). Humans are the only confirmed reservoir host for *B. quintana*. Genome comparison reveals that *B. quintana* isolated from European patients is a genomic derivative of *B. henselae*, which infects a broad range of animals, suggesting that the accelerated genome degradation may be associated with host-restricted vectors (1). Recently, *B. quintana* was isolated from a cynomolgus macaque and two rhesus macaques (5, 12), indicating that nonhuman primates may serve as animal reservoir hosts for the bacterium. Phylogenetic analysis based on multiple loci shows that *B. quintana* isolates from monkeys differ from those from humans (5, 12), suggesting the existence of nonhuman primate-adapted genotypes within the species. To elucidate the genetic characteristics and evolutionary relationships of the *B. quintana* population, we sequenced the genome of *B. quintana* strain RM-11, which was isolated from the blood of a rhesus macaque in China in 2011.

Whole-genome sequencing of this organism was performed with a combined strategy involving Solexa and Roche 454. A total of 4,000,000 pair-end reads (3-kb insert) were generated with a depth of 131.4-fold genome coverage by using the Illumina HiSeq2000 system (10), and 229,139 sequencing reads were generated with a depth of 59.8-fold genome coverage by using the Roche Genome Sequencer FLX system. The Illumina sequencing reads were assembled by using SOAPdenovo version 1.05 (8). Forty-three contigs were generated using Newbler Assembler (454 Life Sciences, Branford, CT) and assembled into 6 scaffolds using paired-end reads. Based on this assembly, the interscaffold and intrascaffold gaps were closed by local assembly and by sequencing PCR products using an ABI 3730 sequencer. Protein coding genes were predicted by using Glimmer version 3.0 (3). The rRNA and tRNA were identified using RNAmmer (7) and tRNAscan-SE (9), respectively.

The complete genome of *B. quintana* strain RM-11 contains a single circular chromosome of 1,587,646 bp. The overall G+C content of the chromosome is 38.77%. A total of 1,204 predicted protein coding genes, 42 tRNA genes, and two copies each of the 5S, 16S, and 23S rRNA genes were identified. Other notable functional features were two type IV secretion system operons (VirB and Trw). Genomic islands or prophage sequences that are present in *B. henselae* were not found in *B. quintana* strain RM-11. Using a reciprocal best BLAST hit strategy (11), we identified a total of 1,096 common genes between strains RM-11 and Toulouse, a human *B. quintana* isolate whose genome has been sequenced (1).

Nucleotide sequence accession number. The genome sequence and annotation information are accessible in the GenBank database with accession number CP003784.

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