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GENOME ANNOUNCEMENT

Genomic Comparison of *Rickettsia honei* Strain RB^T and Other *Rickettsia* Species

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***Rickettsia honei* strain RB^T was isolated from a febrile patient on Flinders Island, Australia, in 1991 and has been demonstrated to be the agent of Flinders Island spotted fever, a disease transmitted to humans by ticks. The comparison of this 1.27-Mb genome with other *Rickettsia* genomes provides additional insight into the mechanisms of evolution in *Rickettsia* species.**

The *Rickettsia* genus is composed of small, Gram-negative, obligate intracellular bacteria (1). These microorganisms underwent a reductive genomic evolution during their specialization to their intracellular lifestyle (2). Recent studies demonstrated that genome reduction was associated with virulence in rickettsiae (3). *R. honei* strain RB^T was isolated from a febrile patient on Flinders Island, Australia, in 1991 and has been described as a Flinders Island spotted fever (FISF) agent which is pathogenic for humans (4). FISF is characterized by fever, headache, myalgia, transient arthralgia, maculopapular rash, and in some cases cough (6). *R. honei* strain RB^T is transmitted to human mainly by *Bothriocroton hydrosauri* (formerly *Aponomma hydrosauri*) tick bites (5). Most cases occur in summer.

The genome sequencing of *R. honei* strain RB^T was performed by 454 shotgun sequencing. Briefly, the shotgun sequencing was performed using a GS-FLX Titanium sequencer (Roche, Meylan, France) and assembled into 11 contigs. All 11 contigs were part of the chromosome, with a size of 1,268,758 bp and a G+C content of 32.4%, which is similar to other rickettsial genomes. No plasmid was detected. The chromosome was predicted to encode 1,284 genes (1,595 open reading frames [ORFs]). Among these genes, 1,046 (81%) were complete, 158 (12%) were split into two or more ORFs, and 80 (6%) were present as fragments. Of the 1,284 genes, 751 (58%) encoded proteins with putative functions, and 533 (42%) encoded hypothetical proteins and proteins of unknown function. The *R. honei* genome had 3 noncontiguous rRNA genes (5S, 16S, and 23S rRNA), 33 tRNAs, and 3 other RNAs.

Phylogenically, *R. honei* is closely related to *R. rickettsii*, *R. conorii*, and *R. slovaca* (4). The 11 *R. honei* contigs exhibited an almost perfect colinearity with these 3 genomes, with the exception of an inversion of 34,133 bp, 81,501bp and 32,367 bp, respectively. By comparison with the closest genome, that of *R. conorii*, *R. honei* missed 56 genes but had an additional 89 specific genes. Most of these differentially present genes encoded ankyrin repeat-containing proteins, leucine-rich repeats (LRRs), tetratricopeptide repeat-containing proteins, transposases, and proteins of unknown function. By comparison with *R. prowazekii*, the agent of epidemic typhus, the most pathogenic *Rickettsia* species with the smallest genome (834 genes only), *R. honei* missed only 37 genes. These genes encoded proteins of unknown function ($n = 17$), transposases ($n = 3$), ankyrin repeat-containing proteins ($n = 2$), transferases ($n = 6$), and synthetases ($n = 3$) and one from each of the following categories: cell surface antigens, BioY family proteins, multisubunit Na^+/H^+ antiporters, protein kinase C inhibitors, Sec7 domain-containing proteins, site-specific recombinases, and VirD4 proteins. Thus, none of these genes is likely to play a role in rickettsial virulence. In contrast, many genes involved in the biosynthesis and regulation of biosynthesis of amino acids and nucleotides present in *R. honei* were absent from *R. prowazekii*. Further studies will be conducted to investigate whether a reduced metabolism of amino acids and/or nucleotides plays a role in the pathogenesis of rickettsiae.

Nucleotide sequence accession number. The genome sequence has been deposited in the GenBank database under accession number AJTT00000000.

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