

Genomic Analysis of *Rickettsia japonica* Strain YH^T

Xin Dong, Khalid El Karkouri, Catherine Robert, Didier Raoult, and Pierre-Edouard Fournier

Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, InsermU1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de Médecine, Marseille, France

***Rickettsia japonica* strain YH, isolated in 1984 in Japan, is the type strain of *R. japonica*, the tick-borne agent of Japanese spotted fever. Here, we report the 1.33-Mb genome of this rickettsial species.**

Japanese spotted fever (JSF) was first reported in 1984 in the Tokushima prefecture in Japan (10). This disease, endemic in southwestern Japan, is caused by the spotted fever group bacterium *Rickettsia japonica* (13). JSF, transmitted by the *Dermacentor taiwanensis* and *Haemaphysalis flava* ticks, is an acute febrile spotted fever that may occasionally present as a severe disease (6, 7, 11). To date, the genomes from most rickettsial species have been sequenced. These strictly intracellular microorganisms underwent a reductive genomic evolution (2), and it was recently suggested that genome reduction was paradoxically associated with increased virulence (5). Here, we report the genome sequence of *R. japonica* strain YH^T.

Genomic DNA from *R. japonica* strain YH^T (deposited in the ATCC and CSUR collections under references VR-1336 and CSUR R128, respectively), isolated in 1985 from the blood of a patient in Japan (13) and grown in Vero cells, was pyrosequenced using the 454 GS-FLX titanium platform (Roche, Branford, CT). Paired-end sequencing resulted in 239,822 reads (mean length, 191 bases). These reads were assembled using the Newbler version 2.3 software (Roche). Potential coding sequences were predicted using AMIGene (3). Split or unpredicted genes were detected using Artemis (4) and BLASTN (1). Predicted gene functions were identified by searching against the RickBase, GenBank, and Pfam databases using BLASTP (1, 2, 12). rRNAs, tRNAs, and other RNAs were identified using BLASTN, tRNAscan-SE v.1.21 (9), and RNAmmer 1.2 (8).

The draft genome sequence of *R. japonica* strain YH^T consists of 29 contigs (ranging from 951 to 197,977 bp long, approximately 3- to 4-fold coverage) arranged into a single chromosomal scaffold, and one circularized plasmid, pRjap. The chromosome and plasmid sizes, G+C contents, and numbers of genes are 1,331,743 and 19,854 bases, 32.7 and 31.8%, and 1,239 (1,515 open reading frames [ORFs]) and 19 (21 ORFs) genes, respectively. Among the 1,239 chromosomal genes, 889 genes (71.8%) are complete, 183 (14.7%) are split, and 167 (13.5%) are present as fragments; 894 genes (72.2%) are assigned putative functions, and 345 (27.8%) encode hypothetical proteins or proteins of unknown function. *R. japonica* contains 1 rRNA operon with noncontiguous 16S and 23S rRNA genes, 33 tRNAs, and 3 other RNAs.

With the exception of 4 chromosomal inversions (13,405, 4,785, 65,590 and 38,431 bp), the *R. japonica* genome exhibited an almost perfect synteny with *R. rhipicephali*, its closest phylogenetic neighbor. *R. japonica* had 800 genes in common with *R. prowazekii*, the most pathogenic *Rickettsia* species. The *R. japonica* genome missed only 40 genes that were present in *R. prowazekii*, including 21 encoding proteins of unknown function, 3 transposases, 2 ankyrin repeat-containing proteins, 5 transferases, and one gene of each of the following categories: BioY family protein, cell surface antigen Sca6 protein, lipopolysaccharide (LPS) biosynthesis protein, Na⁺/proline symporter histidine kinase, poly-beta-hydroxybutyrate polymerase,

DNA invertase pin-like protein, twin-arginine translocation protein TatA, universal stress protein UspA, and VirD4 protein. However, no rickettsial virulence factor has been identified. In contrast, many genes involved in the biosynthesis and regulation of biosynthesis of amino acids and nucleotides present in *R. japonica* were absent from *R. prowazekii*.

Nucleotide sequence accession number. The genome sequence was deposited in GenBank under accession number [AMRT00000000](https://www.ncbi.nlm.nih.gov/nuccore/AMRT00000000).

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Address correspondence to Pierre-Edouard Fournier, pierre-edouard.fournier@univmed.fr.

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