

# First Draft Genome Sequences of Two Bartonella tribocorum Strains from Laos and Cambodia

Linda Hadjadj, Tawisa Jiyipong, Fadi Bittar, Serge Morand, Jean-Marc Rolain

▶ **To cite this version:**

Linda Hadjadj, Tawisa Jiyipong, Fadi Bittar, Serge Morand, Jean-Marc Rolain. First Draft Genome Sequences of Two Bartonella tribocorum Strains from Laos and Cambodia. Genome Announcements, 2018, 6 (2), 10.1128/genomeA.01435-17 . hal-02006202

**HAL Id: hal-02006202**
**https://amu.hal.science/hal-02006202**

Submitted on 20 Mar 2019

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

# First Draft Genome Sequences of Two *Bartonella tribocorum* Strains from Laos and Cambodia

**Linda Hadjadj,[a] Tawisa Jiyipong,[a,b] Fadi Bittar,[a] Serge Morand,[b,c] Jean-Marc Rolain[a]**

[a]Unité de Recherche sur les Maladies Infectieuses et Tropicales Émergentes (URMITE), UMR CNRS, IHU Méditerranée Infection, Faculté de Médecine et de Pharmacie, Aix-Marseille Université, Marseille, France
[b]Institut des Sciences de l'Evolution, UMR CNRS–IRD, Université Montpellier, Montpellier, France
[c]ASTRE, CIRAD, Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand

**ABSTRACT** *Bartonella tribocorum* is a Gram-negative bacterium known to infect animals, and rodents in particular, throughout the world. In this report, we present the draft genome sequences of two strains of *B. tribocorum* isolated from the blood of a rodent in Laos and a shrew in Cambodia.

*Bartonella* is a genus of Gram-negative bacteria. As facultative intracellular parasites, *Bartonella* species can infect humans and wild and domestic animals. *B. tribocorum* was first isolated from the blood of wild rats in France (1). Infections caused by this species in animals, and specifically in rodents, have been reported worldwide (2–5). Recently, it was also considered to be a zoonotic species that could cause undifferentiated chronic illness in humans following tick bites (6).

In 2011, a large series of blood samples ($n$ = 1,341) from rodents and shrews trapped in Cambodia, Laos, and Thailand was collected (2). The presence of *Bartonella* spp. was screened by quantitative PCR (qPCR) (7). Positive samples were also tested by a culture method on Columbia agar supplemented with 5% sheep's blood and incubated at 37°C in 5% $CO_2$ for up to 4 weeks. In this study, we sequenced the genome of two *B. tribocorum* strains, L103 (CSUR P2060) and C635 (CSUR P2059), suspected to be new species. Strains L103 and C635 exhibited similarities with *B. tribocorum* strain BM1374166 of 96% and 96.24%, respectively, according to the partial *rpoB* gene (locus tags CER18_05755 and CEV08_05060, respectively), and 96.75% and 96.16%, respectively, according to the partial *gltA* gene (locus tags CER18_05610 and CEV08_03755, respectively). This is just over the cutoffs of 95.4% for the partial *rpoB* gene and 96% for partial *gltA* gene used to discriminate species of *Bartonella* (8). Strain L103 was isolated from a rodent, *Mus cookii*, trapped in the province of Luang Prabang, Laos, while strain C635 was isolated from a shrew, *Suncus murinus*, trapped in the province of Sihanouk, Cambodia.

Genomic DNA (gDNA) of *B. tribocorum* strains L103 and C635 were sequenced on a MiSeq sequencer (Illumina, Inc., San Diego, CA, USA) using the paired-end strategy. Raw reads were assembled with A5-miseq software (9). Genome and subsystem-based annotations were performed by Rapid Annotation using Subsystem Technology (RAST) (10, 11). tRNA gene detection was performed using the tRNAscan-SE 2.0 tool (12), whereas rRNA genes were predicted using RNAmmer (13). Plasmid presence was checked by PlasmidFinder software (14).

After assembly, the two genomes were composed of 99 scaffolds. For strains L103 and C635, the total sizes were 2,193,610 bp, with G+C contents of 38.4%, and 2,098,038 bp, with G+C contents of 38.0%, respectively. The draft genomes of *B. tribocorum* strains L103 and C635 contained 2,160 and 2,113 coding sequences, respectively, with 3 rRNAs and 40 tRNAs each. The RAST annotation assigned these genes to 291 and 290 subsystems, respectively, for strains L103 and C635, with a maximum

**Received** 16 November 2017 **Accepted** 20 November 2017 **Published** 11 January 2018

**Citation** Hadjadj L, Jiyipong T, Bittar F, Morand S, Rolain J-M. 2018. First draft genome sequences of two *Bartonella tribocorum* strains from Laos and Cambodia. Genome Announc 6:e01435-17. https://doi.org/10.1128/genomeA.01435-17.

**Copyright** © 2018 Hadjadj et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Jean-Marc Rolain, jean-marc.rolain@univ-amu.fr.

number of genes associated with protein metabolism (17.66% and 17.53%, respectively), followed by amino acids and derivative metabolism (10.30% and 11.61%, respectively), and cofactors, vitamins, prosthetic groups, and pigment subsystems (8.50% and 9.09%, respectively). No studied strains carried a plasmid.

To our knowledge, these are the first draft genome sequences of *B. tribocorum* in Laos and also the first in Cambodia.

**Accession number(s).** These draft genome sequences have been deposited in NCBI GenBank under the sequence accession numbers NJGE00000000 and NJPP00000000 for strains L103 and C635, respectively.

## ACKNOWLEDGMENT

We thank TradOnline for proofreading the text.

## REFERENCES

1. Heller R, Riegel P, Hansmann Y, Delacour G, Bermond D, Dehio C, Lamarque F, Monteil H, Chomel B, Piémont Y. 1998. *Bartonella tribocorum* sp. nov., a new *Bartonella* species isolated from the blood of wild rats. Int J Syst Bacteriol 48:1333–1339. https://doi.org/10.1099/00207713-48-4-1333.
2. Jiyipong T, Jittapalapong S, Morand S, Raoult D, Rolain JM. 2012. Prevalence and genetic diversity of *Bartonella* spp. in small mammals from southeastern Asia. Appl Environ Microbiol 78:8463–8466. https://doi.org/10.1128/AEM.02008-12.
3. Martin-Alonso A, Houemenou G, Abreu-Yanes E, Valladares B, Feliu C, Foronda P. 2016. *Bartonella* spp. in small mammals, Benin. Vector Borne Zoonotic Dis 16:229–237. https://doi.org/10.1089/vbz.2015.1838.
4. Nasereddin A, Risheq A, Harrus S, Azmi K, Ereqat S, Baneth G, Salant H, Mumcuoglu KY, Abdeen Z. 2014. *Bartonella* species in fleas from Palestinian territories: prevalence and genetic diversity. J Vector Ecol 39:261–270. https://doi.org/10.1111/jvec.12100.
5. Malania L, Bai Y, Osikowicz LM, Tsertsvadze N, Katsitadze G, Imnadze P, Kosoy M. 2016. Prevalence and diversity of *Bartonella* species in rodents from Georgia (Caucasus). Am J Trop Med Hyg 95:466–471. https://doi.org/10.4269/ajtmh.16-0041.
6. Vayssier-Taussat M, Moutailler S, Féménia F, Raymond P, Croce O, La Scola B, Fournier PE, Raoult D. 2016. Identification of novel zoonotic activity of *Bartonella* spp., France. Emerg Infect Dis 22:457–462. https://doi.org/10.3201/eid2203.150269.
7. Raoult D, Roblot F, Rolain JM, Besnier JM, Loulergue J, Bastides F, Choutet P. 2006. First isolation of *Bartonella alsatica* from a valve of a patient with endocarditis. J Clin Microbiol 44:278–279. https://doi.org/10.1128/JCM.44.1.278-279.2006.
8. La Scola B, Zeaiter Z, Khamis A, Raoult D. 2003. Gene-sequence-based criteria for species definition in bacteriology: the *Bartonella* paradigm. Trends Microbiol 11:318–321. https://doi.org/10.1016/S0966-842X(03)00143-4.
9. Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics 31:587–589. https://doi.org/10.1093/bioinformatics/btu661.
10. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.
11. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res 42:D206–D214. https://doi.org/10.1093/nar/gkt1226.
12. Lowe TM, Chan PP. 2016. tRNAscan-SE on-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res 44:W54–W57. https://doi.org/10.1093/nar/gkw413.
13. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35:3100–3108. https://doi.org/10.1093/nar/gkm160.
14. Carattoli A, Zankari E, García-Fernández A, Voldby Larsen M, Lund O, Villa L, Møller Aarestrup F, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. Antimicrob Agents Chemother 58:3895–3903. https://doi.org/10.1128/AAC.02412-14.