genomeA
Journals.ASM.org

Draft Genome Sequence of the *Serratia rubidaea* CIP 103234^T Reference Strain, a Human-Opportunistic Pathogen

Rémy A. Bonnin,[a,b,c] Delphine Girlich,[a,b,c] Dilek Imanci,[d] Laurent Dortet,[a,b,c] Thierry Naas[a,b,c]

APHP, Bicêtre Hospital, Bactériologie-Hygiene Unit, Le-Kremlin Bicêtre, France[a]; EA7361 Structure, dynamic, function and expression of broad spectrum β-lactamases, Paris-Sud University, LabEx Lermit, Faculty of Medecine, Orsay, France[b]; French National Reference Center for Antibiotic Resistance, Carbapenemase-Producing *Enterobacteriaceae*, Le Kremlin-Bicêtre, France[c]; Molecular Genetics and Hormonology Department, Le Kremlin-Bicêtre, France[d]

We provide here the first genome sequence of a *Serratia rubidaea* isolate, a human-opportunistic pathogen. This reference sequence will permit a comparison of this species with others of the *Serratia* genus.

Received 26 September 2015 **Accepted** 5 October 2015 **Published** 19 November 2015

Citation Bonnin RA, Girlich D, Imanci D, Dortet L, Naas T. 2015. Draft genome sequence of the *Serratia rubidaea* CIP 103234^T reference strain, a human-opportunistic pathogen. Genome Announc 3(6):e01340-15. doi:10.1128/genomeA.01340-15.

Address correspondence to Thierry Naas, thierry.naas@aphp.fr.

Serratia species are Gram-negative rods responsible for human-opportunistic infections. Despite the fact that *Serratia* species are widespread in the environment, they are also encountered in human fecal flora. *Serratia marcescens*, the main representative of *Serratia*, was discovered in the early 19th century by the Italian microbiologist Bizio (1).

Now, the genus comprises 18 species recovered from environment and clinical specimens (http://www.bacterio.net/). Among pathogenic species, *S. marcescens* is the most frequently identified, along with *Serratia liquefaciens*. Infections caused by these organisms are varied, including urinary tract infections (UTIs), endocarditis, and wound and pulmonary infections (1). *Serratia rubidaea*, although rarely recovered from human specimens, is recognized as the fourth common cause of *Serratia*-related infections (1). Infections caused by *S. rubidaea* are mainly reported in patients with severe trauma or with underlying diseases, including sepsis, bacteremia, and UTIs (2–5). *Serratia* spp. may be a source of difficult-to-treat infections, since many of these strains are resistant to β-lactams mediated by the production of chromosomally encoded β-lactamases of either Ambler class C (AmpC-type of *S. marcescens*), Ambler class A (FonA and SFC-1 of *Serratia fonticola*), or Ambler class B (Sfh-I of an environmental *S. fonticola*) (6, 7).

Genomic DNA was extracted using the UltraClean microbial DNA isolation kit (Mo Bio Laboratories) from overnight cultures in LB agar (Bio-Rad, Marnes-la-Coquette, France). Genomic DNA quantification was performed using a Qubit fluorometer (Life Technologies, Carlsbad, CA) and adjusted to 0.2 ng/μl. Library preparation was performed using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA). Sequencing was performed on an Illumina MiSeq 2000 sequencer with V3 chemistry using 2 × 75-bp paired-end reads.

Illumina sequencing resulted in 4,367,802 reads of an average length of 74.31 nucleotides, giving a total 324,574,495 nucleotides. These generated reads were assembled using Velvet (8) and computed using CLC Workbench version 8.5. Two hundred forty contigs, giving a genome of 4,929,307 bp with a G+C% of 59.3%, were obtained from these raw data and then annotated using the RAST server (http://rast.nmpdr.org/). The RAST system predicted 4,522 coding sequences involved in essential functions, such as cell wall synthesis or RNA/DNA metabolism. One hundred ninety-eight coding sequences (CDSs) were predicted in cell wall and capsule synthesis, with 106 involved in virulence, disease, and defense; 38 involved in cell division and cell cycle; 153 involved in fatty acid and lipid metabolism; 134 involved in the stress response; and 216 and 231 involved in protein and RNA metabolism, respectively.

We hope that this sequence will help for genomic comparisons of the *Serratia* genus.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LJZP00000000. The version described in this paper is version LJZP01000000.

ACKNOWLEDGMENT

This work was funded by Paris-Sud University, France.

REFERENCES

1. **Mahlen SD.** 2011. *Serratia* infections: from military experiments to current practice. Clin Microbiol Rev **24:**755–791. http://dx.doi.org/10.1128/CMR.00017-11.
2. **Saito H, Elting L, Bodey GP, Berkey P.** 1989. *Serratia* bacteremia: review of 118 cases. Rev Infect Dis **11:**912–920. http://dx.doi.org/10.1093/clinids/11.6.912.
3. **Menezes EA, Cezafar FC, Andrade Mdo S, Rocha MV, Cunha FA.** 2004. Frequency of *Serratia* sp. in urine infections of intern patients in the Santa Casa de Misericórdia in Fortaleza. Rev Soc Bras Med Trop **37:**70–71.
4. **Gentille D, Pérez M, Centelles MJ.** 2014. Bacteremia by a *Serratia rubidaea* with an atypical quinolones resistance phenotype. Rev Chilena Infectol **31:**351–352. (In Spanish.)
5. **Litterio ML, Arazi S, Hernández C, Lopardo H.** 2012. Isolation of *Serratia rubidaea* from a mixed infection after a horse bite. Rev Argent Microbiol **44:**272–274.

6. **Fonseca F, Sarmento AC, Henriques I, Samyn B, van Beeumen J, Domingues P, Domingues MR, Saavedra MJ, Correia A.** 2007. Biochemical characterization of SFC-1, a class A carbapenem-hydrolyzing β-lactamase. Antimicrob Agents Chemother **51:**4512–4514. http://dx.doi.org/10.1128/AAC.00491-07.
7. **Saavedra MJ, Peixe L, Sousa JC, Henriques I, Alves A, Correia A.** 2003. Sfh-I, a subclass B2 metallo-β-lactamase from a *Serratia fonticola* environmental isolate. Antimicrob Agents Chemother **47:**2330–2333. http://dx.doi.org/10.1128/AAC.47.7.2330-2333.2003.
8. **Zerbino DR, Birney E.** 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res **18:**821–829. http://dx.doi.org/10.1101/gr.074492.107.