Draft Genome Sequences of *Acinetobacter parvus* CM11, *Acinetobacter radioresistens* CM38, and *Stenotrophomonas maltophilia* BR12, Isolated from Murine Proximal Colonic Tissue

Azadeh Saffarian, a Céline Mulet, a Tomoaki Naito, a,b Christiane Bouchier, a Magali Tichit, d Laurence Ma, d Gianfranco Grompone, a Philippe J. Sansonetti, a,b Thierry Pédroña

Unité de Pathogénie Microbiennne Moléculaire, INSERM U1202, Institut Pasteur, Paris, France; Chaire de Microbiologie et Maladies Infectieuses, Collège de France, Paris, France; Yakult Central Institute, Yakult Honsha Co., Ltd, Izumi, Kunitachi-shi, Tokyo, Japan; Plate-forme Génomique, Département Génomes et Génétique, Institut Pasteur, Paris, France; Microbiota Unit, Bioaster, Paris, France

Here, we report three genome sequences of bacteria isolated from murine proximal colonic tissue and identified as *Acinetobacter parvus* CM11, *Acinetobacter radioresistens* CM38, and *Stenotrophomonas maltophilia* BR12.

Recently, by laser capture microdissection and pyrosequencing, we identified bacteria located inside murine proximal colonic crypts (1). These bacteria were aerobic, nonfermentative, and mainly belong to the genus *Acinetobacter*, *Delftia* and *Stenotrophomonas* spp. were also identified. In order to study the impact of these bacteria on the intestinal epithelium, the first step was to cultivate them. Proximal colonic tissues from C57BL/6 mice (Ellevage Janvier) were washed with bleach and homogenized in 2 ml of sterile phosphate-buffered saline (PBS) using the Precellys system (Evage Janvier) were washed with bleach and homogenized in 2 ml of sterile phosphate-buffered saline (PBS) using the Precellys system. This mixture was then added to 30 ml of a minimum medium (30°C for 48 h, with shaking at 300 rpm/min in a Multitron incubation shaker (Infors) and isolated on agar plates (GTCS, MacCosy, Herellea, and CHROMagar). Selected colonies were reisolated on CHROMagar to obtain a pure colony. The colonies were identified using the Biolog system with a GEN III MicroPlate. Strain identification was confirmed by Sanger sequencing of 16S, rpoB, and gyrB genes after genomic DNA extraction by the Wizard genomic DNA purification kit, according to the manufacturer’s instructions (Promega). The genomes were sequenced with the Illumina HiSeq 2000 technology (paired-end libraries) at the Institut Pasteur of Paris, France.

The numbers of paired-end reads for all samples are indicated in Table 1. For *Acinetobacter parvus* CM11 and *Acinetobacter radioresistens* CM38, the average base quality for Read 1 and Read 2 is >30, and for *Stenotrophomonas maltophilia* BR12, it is >32 and 20, respectively. The 100-base reads were filtered out using Prinseq-lite 0.20.3 (3).

The parameters of filtering were fixed to remove all reads with a quality score of <30 for bases and/or an average quality score of <35 for read sequences (for *A. parvus* CM11 and *A. radioresistens* CM38) and <33 for *S. maltophilia* BR12. Exact or a reverse complementary duplicate (for both R1 and R2), reads containing ambiguous base N for >1% of their length, and reads of low complexity (entropy value, <70) were removed. The numbers of paired-end reads remaining after filtering are given in Table 1. Those reads have been used for producing the contigs using the assembly de novo option of CLC-Assembler 4.2.0 and CLC Genomics Workbench (CLC bio).

Moreover, the contigs were cleaned: all contigs <1,000 bases were trimmed, and all contigs containing more than 1% of compounds not involved in resistance to antibiotics and toxic compounds were removed. Moreover, the contigs were cleaned: all contigs <1,000 bases were trimmed, and all contigs containing more than 1% of compounds not involved in resistance to antibiotics and toxic compounds were removed.

### Table 1

| Species             | Length of genome (Mb) | G+C content (%) | No. of paired-end reads | No. of contigs obtained from assembly de novo with CLC Assembler | Avg length of contigs (bp) | Total of assembled contigs (Mb) | N90 (bp) | No. of contigs after cleaning | Total of bases after cleaning (Mb) | No. of coding sequences | No. of genes involved in resistance to antibiotics and toxic compounds | Accession no. |
|---------------------|-----------------------|-----------------|-------------------------|---------------------------------------------------------------|--------------------------|-----------------------------|---------|-------------------------------|-----------------------------------|-----------------------|---------------------------------------------------------------|------------------|
| A. parvus CM11      | 3.34                  | 38.70           | 37,132,842              | 9,039,763                                                     | 4,511,26                 | 213,844                     | 118     | 3.45                          | 3,259                             | 45                    | LACJ00000000                                                  | LACJ00000000    |
| A. radioresistens CM38 | 3.14                 | 41.50           | 29,979,045              | 7,018,315                                                     | 62,364.14                | 165,532                     | 41      | 3.17                          | 2,974                             | 39                    | LATS00000000                                                  | LATS00000000    |
| S. maltophilia BR12  | 4.85                  | 66.30           | 57,576,810              | 2,864,688                                                     | 46,920.68                | 92,072                      | 79      | 4.4                           | 3,905                             | 49                    | LATR00000000                                                  | LATR00000000    |

*The contigs are merged into a single accession number.*

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Address correspondence to Philippe J. Sansonetti, philippe.sansonetti@pasteur.fr, or Thierry Pédro, thierry.pedron@pasteur.fr.
and/or containing the ambiguous base N for >15% of their length were removed. The numbers of contigs before and after cleaning are shown in Table 1.

Functional annotation was carried out on cleaned contigs using tools from RAST (4, 5) (http://rast.nmpdr.org/) and from the MicroScope platform (6) (http://www.genoscope.cns.fr/agc/microscope/mage/). RAST annotation (Table 1) showed the genes involved in antibiotic resistance, and interestingly, the gene encoding the β-lactamase was present in the three strains. The knowledge of the complete sequence of these strains will allow us to better understand the impact of these bacteria on the intestinal epithelium.

**Nucleotide sequence accession numbers.** The draft genome sequences have been deposited at DDBJ/EMBL/GenBank under the accession numbers listed in Table 1.

**ACKNOWLEDGMENTS**

This work was supported by the European Research Council and from grants from Danone Research and Yakult Research. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Tomoaki Naito is an employee of Yakult Honsha Co., Ltd.

High-throughput sequencing was performed on the Genomics Platform, a member of the France Génomique consortium (ANR10-INBS-09-08). We thank Philippe Bouvet and Sylvain Brisse for helpful discussions.

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