# 'Beduinella massiliensis', gen. nov., sp. nov. a new genus representing a new family in the phylum Firmicutes, and proposal of Beduinellaceae fam. nov.

S. I. Traore<sup>1</sup>, E. I. Azhar<sup>2,3</sup>, M. Yasir<sup>2</sup>, F. Bibi<sup>2</sup>, J. Delerce<sup>1</sup>, P.-E. Fournier<sup>1</sup>, A. A. Jiman-Fatani<sup>4</sup>, J.-C. Lagier<sup>1</sup> and D. Raoult<sup>1,2</sup>

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France, 2) Special Infectious Agents Unit, King Fahd Medical Research Centre, King Abdulaziz University, Jeddah, Saudi Arabia, 3) Medical Laboratory Technology Department, Faculty of Applied Medical Sciences and 4) Department of Medical Microbiology and Parasitology, Faculty of Medicine, King Abdulaziz University, Jeddah, Saudi Arabia

### **Abstract**

We report here the main characteristics of a new bacterium named 'Beduinella massiliensis' strain Marseille-P2846<sup>T</sup> (CSURP2846P) that was isolated from a faecal specimen of a 50-year-old Saudi Bedouin female and propose the creation of a new family 'Beduinellaceae'.

© 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Beduinella massiliensis, culturomics, genomics, taxono-genomics, taxonomy

Original Submission: 30 June 2016; Accepted: 25 July 2016

Article published online: 29 July 2016

Corresponding author: D. Raoult, Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, 13385, Marseille cedex 05, France E-mail: didier.raoult@gmail.com

As a part of culturomics [1], we isolated in 2016, a bacterial strain that could not be identified by our systematic matrix-assisted laser desorption—ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2,3]. This strain (Marseille-P2846<sup>T</sup>) was isolated from the stool sample of a 50-year-old healthy Bedouin female living in the Jazan region of Saudi Arabia. This healthy individual gave an informed consent. This study was performed in Saudi Arabia with approval from the Ethical Committee of the King Abdulaziz University (Saudi Arabia), and the local ethics committee of the IFR48 (Marseille, France) under the numbers 014-CEGMR-2-ETH-P and 09-022, respectively.

The stool sample was pre-incubated for 3 days at 37°C in a blood culture bottle (BD Diagnostics, Le Pont-de-Claix, France) supplemented with 2 mL of rumen fluid filter-sterilized through a 0.2-µm pore filter (Thermo Fisher Scientific, Villebon sur

Yvette, France) and 2 mL of sheep blood (bioMérieux, Marcy l'Etoile, France). After 2 days of pre-incubation, the sample was inoculated on 5% sheep blood agar that was incubated at 37°C in anaerobic conditions generated using AnaeroGen TM (bio-Mérieux). The strain Marseille-P2846<sup>T</sup> was isolated after a 72-hour incubation.

Agar-grown colonies were transparent with a diameter from 0.2 to 0.5 mm. Bacterial cells were non-motile, non-sporeforming, Gram-negative and rod-shaped with pointed ends, ranging in length from 2.6 to 4 µm and in width from 0.4 to 0.6 µm. Strain Marseille-P2846<sup>T</sup> was catalase-negative and oxidase-negative. To identify this strain as Marseille-P2846<sup>T</sup>, the complete 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [4], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain Marseille-P2846<sup>T</sup> exhibited an 86.6% sequence identity with Christensenella minuta strain YIT 12065<sup>T</sup> (GenBank Accession number NR\_112900.1), the phylogenetically closest species with standing nomenclature (Fig. 1), which putatively classifies it as a member of the new family 'Beduinellaceae' within the order Clostridiales in the phylum Firmicutes. Christensenella minuta strain YIT 12065<sup>T</sup> is a strictly anaerobic, non-motile, non-sporeforming, Gram-negative rod that was first isolated from human faeces [5].

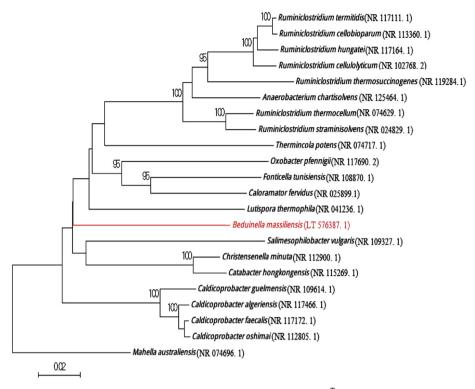


FIG. 1. Phylogenetic tree showing the position of 'Beduinella massiliensis' strain Marseille P2846<sup>T</sup> relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes are percentages of bootstrap values obtained by repeating the analysis 500 times to generate a majority consensus tree. Only the bootstraps score at least 95% were retained. The scale bar indicates a 2% nucleotide sequence divergence.

Strain Marseille P2846P exhibited a 16S rRNA sequence divergence >12% with its phylogenetically closest species with standing in nomenclature [6]; hence, we propose the creation of the new family 'Beduinellaceae' fam. nov., of the new genus 'Beduinella' fam. nov., gen. nov., and of the strain Marseille-P2846<sup>T</sup> as the type strain of 'Beduinella massiliensis' fam. nov, gen. nov, sp. nov., the first representative species of this new family. 'Beduinella massiliensis' fam. nov., gen. nov., sp. nov. (Be.dui.nel.'la. N.L fem.n. Beduinella from the Latin name of nomadic Bedouin population from Saudi Arabia where the strain was collected), (mas.si.li.en'sis, L., fem. adj., massiliensis for Massilia, the Roman name of Marseille, where strain Marseille-P2846<sup>T</sup> was isolated).

**MALDI-TOF-MS spectrum accession number.** The MALDI-TOF-MS spectrum of 'B. massiliensis' is available at: http://mediterranee-infection.com/article.php?laref=256&titre=urms-database

**Nucleotide sequence accession number.** The 16S rRNA gene sequence was deposited in GenBank under Accession number LT576387.

**Deposit in a culture collection.** Strain Marseille-P2846<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2846P.

## **Conflict of interest**

None to declare.

# **Funding sources**

This work was funded by the Mediterrannée-Infection Foundation. This project was also funded by the Deanship of Scientific Research (DSR), King Abdulaziz University, Jeddah, under Grant No. (3-140-1434-HiCi). The authors, therefore, acknowledge DSR for technical and financial support.

### References

- Lagier JC, Armougom F, Million M, Hugon P, Pagnier I, Robert C, et al. Microbial culturomics: paradigm shift in the human gut microbiome study. Clin Microbiol Infect 2012;18:1185–93.
- [2] Seng P, Abat C, Rolain JM, Colson P, Lagier JC, Gouriet F, et al. Identification of rare pathogenic bacteria in a clinical microbiology laboratory: impact of matrix-assisted laser desorption ionization-time of flight mass spectrometry. J Clin Microbiol 2013;51:2182–94.

- [3] Lagier JC, Hugon P, Khelaifia S, Fournier PE, La SB, Raoult D. The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. Clin Microbiol Rev 2015;28:237–64.
- [4] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. 16S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentifiable bacterial isolates. J Clin Microbiol 2000;38: 3623–30.
- [5] Morotomi M, Nagai F, Watanabe Y. Description of Christensenella minuta gen. nov., sp. nov., isolated from human faeces, which forms a distinct branch in the order Clostridiales, and proposal of Christensenellaceae fam. nov. Int J Syst Evol Microbiol 2012;62:144–9.
- [6] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of metagenomic data. Genome Res 2007;17:377–86.