Marseillibacter massiliensis gen. nov., sp. nov., a new bacterial genus isolated from the human gut

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Abstract

In this manuscript, we report the main characteristics of *Marseillibacter massiliensis* gen. nov., sp. nov., strain Marseille-P2840^T (CSUR P2840), a new member of the family *Oscillospiraceae* that was isolated from the stool of a healthy 29-year-old Senegalese woman.

Keywords: Culturomics, emerging bacterium, gut microbiota, *Marseillibacter massiliensis*, taxonomy
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As a part of culturomics study [1] dedicated to exploring the gut microbiota using culture techniques, a bacterial strain named Marseille-P2840 was isolated in April 2016 from the stool sample of a healthy, 29-year-old Senegalese female. The study was approved beforehand by the Institut Fédératif de Recherche 48 (Faculty of Medicine, Marseille, France), under agreement number 09-022. Systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening using a MicroFlex spectrometer (Bruker Daltonics, Bremen, Germany) [2] was unable to identify this strain. Growth of strain Marseille-P2840 was obtained after 3 days of incubation on 5% sheep blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France) at 37°C in anaerobic conditions using AnaeroGen™ (bioMérieux). The colonies on 5% sheep blood-enriched agar were circular, beige, with a diameter of 0.5–1 mm. Gram staining showed Gram-negative, non-motile rods. Bacterial cells observed using electron microscopy were rods, ranging in length from 1.7 to 3 µm and with a diameter ranging from 0.4 to 0.6 µm. The catalase and oxidase tests were negative. Molecular identification of the isolate was performed by sequencing the 16S rRNA gene, as previously described [3] using a 3130-XL sequencer (Applied Biosciences, Saint-Aubin, France). Strain Marseille-P2840 showed 94.4% sequence identity with *Oscillibacter valericigenes* Sjm18-20 (GenBank Accession number NR_074793) the phylogenetically closest species with standing in nomenclature. This similarity, which is <95%, putatively classifies strain Marseille-P2840 as a member of a new genus within the family *Oscillospiraceae*, belonging to the phylum *Firmicutes* (Fig. 1). *Oscillibacter valericigenes* is a strictly anaerobic bacterium that was isolated from the digestive microbiota of a *Corbicula* clam. It is a Gram-negative, rod-shaped, motile bacterium (0.5 × 2.5–6.0 µm) that is not sporulating and exhibits negative catalase activity [4].

The 16S rRNA sequence of strain Marseille-P2840 diverged by more than 5% from other members of the genus *Oscillibacter*, which is the phylogenetically closest species with a validly published name [5]. From these results, we propose the creation of the new genus, *Marseillibacter* gen. nov. (Mar.seil.li.bac′ter. N.L. masc. n. composed of *Marseilli* referring to Marseille where the type strain was isolated, and *bacter*, a rod).

Strain Marseille-P2840^T is the type strain of the new species *Marseillibacter massiliensis* gen. nov., sp. nov., (ma.si.li.en′sis. L. gen. masc. adj. *massiliensis*, of *Massilia,* the Latin name of Marseille).

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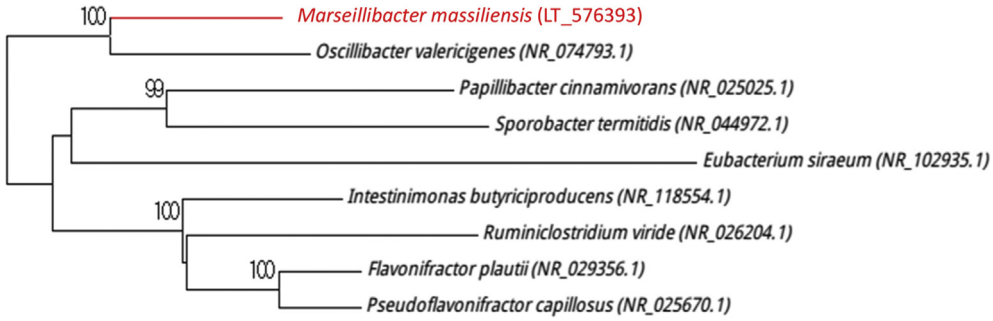

FIG. 1. Phylogenetic tree highlighting the position of *Marseillibacter massiliensis* strain Marseille-P2843^T (red) relative to other phylogenetically close members of the family *Oscillospiraceae*. Numbers at the nodes are percentages of bootstrap values obtained by repeating the analysis to generate a majority consensus tree 500 times. Only values >95% are displayed. The scale bar represents a 2% nucleotide sequence divergence.

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

Nucleotide sequence accession number. The 16S rRNA gene sequence was deposited in GenBank under accession number LT576393.

Deposit in a culture collection. Strain Marseille-P2840^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2840.

Conflict of interest

The authors certify that they do not have any conflict of interest in relation to this research.

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References

[1] Lagier J-C, Hugon P, Khelaifia S, Fournier P-E, La Scola B, 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.
[2] Seng P, Abat C, Rolain JM, Colson P, Lagier J-C, 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] 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.
[4] Iino T, Mori K, Tanaka K, Suzuki K-I, Harayama S. *Oscillibacter valericigenes* gen. nov., sp. nov., a valerate-producing anaerobic bacterium isolated from the alimentary canal of a Japanese *Corbicula* clam. Int J Syst Evol Microbiol 2007;57:1840–5.
[5] Kim M, Oh HS, Park SC, Chun J. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 2014;64:346–51.