NEW SPECIES

“Raoultibacter massiliensis” gen. nov., sp. nov., a new bacterium isolated from the human gut of a Saudi Bedouin

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Abstract

We propose the description of a new bacterial genus and new bacterial species, “Raoultibacter massiliensis,” isolated from faecal specimen from a 19-year-old healthy Saudi Bedouin. © 2016 Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturoomics, emerging bacteria, human gut microbiota, “Raoultibacter massiliensis”, taxonomy

Original Submission: 17 June 2016; Revised Submission: 23 June 2016; Accepted: 28 June 2016
Article published online: 5 July 2016

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In 2016, we isolated the Marseille-P2849 strain from the stool of a 19-year-old healthy Bedouin living in Saudi Arabia. This study was part of an effort to explore the human gut microbiota using culturomics [1]. The patient gave a signed informed consent, and the study was validated by the ethics committee of the Institut Federatif de Recherche 48 under number 09-022.

The bacterium could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening (score <0.7) using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. Consequently, we sequenced the 16S rRNA gene of the bacterium using fD1 and rP2 primers as previously described [3].

The stool sample from the Bedouin was subjected to the conditions of culture developed by culturomics [1,4]. The stool was preincubated for 7 days at 37°C in an anaerobic atmosphere in a culture bottle containing blood-enriched Columbia agar liquid medium (bioMérieux, Marcy l’Etoile, France) supplemented with 5 mL of rumen fluid filter-sterilized through a 0.2 μm pore filter (Thermo Fisher Scientific, Villebon sur Yvette, France). The initial growth of the Marseille-P2849T strain was obtained 4 days after the seeding of the liquid medium in a 5% sheep’s blood agar that was incubated at 37°C in anaerobiosis generated using AnaeroGen (bioMérieux). Raoultibacter massiliensis forms transparent microcolonies on blood agar with a mean diameter of 0.1 to 0.3 mm. Bacterial cells are motile Gram-negative, short rods/coccobacilli ranging in length from 0.8 to 1.2 μm and diameter ranging from 0.4 to 0.6 μm. The Marseille-P2849T strain was found to be a strictly anaerobic, non-sporoforming coccobacilli and was catalase positive and oxidase negative.

The sequence of the 16S rRNA gene of this strain showed a similarity of 91.4% with Gordonibacter urolithinfaciens strain Marseille-AA00211T and 91.3% with Gordonibacter pameleae strain 7-10-1-bT (GenBank accession numbers LT223667 and NR102934, respectively), the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classifies the bacterium as a member of a new genus within the family Eggertellaceae that we named “Raoultibacter.” Gordonibacter urolithinfaciens and Gordonibacter pameleae are anaerobic, non-sporoforming, Gram-positive coccobacilli isolated...
from the healthy human gut and from the colon of a patient with acute Crohn disease, respectively [5,6].

Because strain Marseille-P2849\(^T\) exhibits a 16S rRNA sequence divergence of >5% with its phylogenetically closest species with a validly published name with standing in nomenclature [7], we propose the creation of the new genus named “Raoultibacter” (ra.ou.l.ti.bac’ter, N.L. masc. gen. n. Raoultibacter, composed of Raoult, in honor of French microbiologist Didier Raoult, who created the concept of culturomics, and bacter, “bacterium”). Marseille-P2849\(^T\) is the type strain of the new species “Raoultibacter massiliensis” gen. nov., sp. nov. (mas.i-li.en’sis, L. gen. masc. n. massiliensis, “of Massilia,” the Latin name of Marseille where the strain Marseille-P2849\(^T\) was first isolated).

**Nucleotide sequence accession number**

The 16S rRNA gene sequence was deposited in GenBank under accession number LT576395.

**Deposit in a culture collection**

Marseille-P2849\(^T\) strain was deposited in the Collection de Souches de l’Unité des Rickettsies (CSUR, WDCM 875) under number P2849.

**Acknowledgements**

This project was funded by the Deanship of Scientific Research (DSR), King Abdulaziz University, Jeddah, under grant 3-140-1434-HiCi. The authors acknowledge with thanks DSR’s technical and financial support. This study was funded by the Fondation Méditerranée Infection.

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**FIG. 1.** Phylogenetic tree showing position of “Raoultibacter massiliensis” strain Marseille-P2849\(^T\) relative to other phylogenetically close species with standing in nomenclature. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values (≥95%) obtained by repeating analysis 500 times to generate majority consensus tree. Scale bar indicates 1% nucleotide sequence divergence.
Conflict of Interest

None declared.

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