



HAL
open science

'Ileibacterium massiliense' gen. nov., sp. nov., a new bacterial species isolated from human ileum of a patient with Crohn disease.

M. Mailhe, D. Ricaboni, V. Vitton, J.-C. Lagier, Pierre-Edouard Fournier,
Didier Raoult

► To cite this version:

M. Mailhe, D. Ricaboni, V. Vitton, J.-C. Lagier, Pierre-Edouard Fournier, et al.. 'Ileibacterium massiliense' gen. nov., sp. nov., a new bacterial species isolated from human ileum of a patient with Crohn disease.. *New Microbes and New Infections*, 2017, 17, pp.25–26. 10.1016/j.nmni.2016.11.022 . hal-01795942

HAL Id: hal-01795942

<https://amu.hal.science/hal-01795942v1>

Submitted on 26 Aug 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

'*Ileibacterium massiliense*' gen. nov., sp. nov., a new bacterial species isolated from human ileum of a patient with Crohn disease

M. Mailhe¹, D. Ricaboni^{1,3}, V. Vitton², J.-C. Lagier¹, P.-E. Fournier¹ and D. Raoult¹

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 2) Service de Gastroentérologie, Hôpital Nord, Assistance Publique-Hôpitaux de Marseille, Marseille, France and 3) Département des sciences cliniques et biomédicales, Luigi Sacco, Division des Maladies Infectieuses III, Université de Milan, Milan, Italy

Abstract

We propose here the main characteristics of '*Ileibacterium massiliense*' strain Marseille-P3115, which was isolated from the ileum liquid sample of a patient with Crohn disease.

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

Keywords: Culturomics, gut microbiota, *Ileibacterium massiliense*, microbiota, taxonogenomics

Original Submission: 10 November 2016; **Revised Submission:** 20 November 2016; **Accepted:** 23 November 2016

Article published online: 28 November 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

Culturomics is a complementary approach to metagenomics in studying the human microbiota [1]. We used this technique in April 2016 to study the gut microbiota from stepped samples from the digestive tract of patients who underwent upper endoscopy and colonoscopy simultaneously. Thus, we identified strain Marseille-P3115 from the ileum liquid sample of a 25-year-old patient with Crohn disease. The patient provided informed signed consent, and the ethics committee of the Institut Fédératif de Recherche IFR48 validated the study under number 2016-010.

Strain Marseille-P3115 was first isolated through a pre-incubation of 30 days in an anaerobic blood culture bottle (BD BACTEC, Plus Anaerobic/F Media, Le Pont de Claix, France) earlier enriched with 5 mL of 0.2 µm filtered rumen and 5 mL of sheep's blood. This liquid culture medium was then seeded on Columbia agar supplemented with sheep's blood (Columbia agar + 5% sheep's blood; bioMérieux, Marcy l'Etoile, France). The first growth was obtained after 1 day of incubation at 37°C in an anaerobic atmosphere (anaeroGEN Compact, Oxoid,

Thermo Scientific, Dardilly, France). After a growth of 48 hours on Columbia agar (bioMérieux), the microcolonies had a mean diameter of 0.08 mm and were white and circular. Bacterial cells were Gram-negative bacilli, with a mean diameter of 0.3 µm and a mean length of 1 µm. Strain Marseille-P3115 had no catalase activity and no oxidase activity. This strain was also nonmotile and non-endospore forming.

Given that our systematic matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) screening (Microflex LT; Bruker Daltonics, Bremen, Germany) [2] could not identify strain Marseille-P3115, the 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [3] using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain Marseille-P3115 exhibited a 90.7% sequence similarity with *Mogibacterium neglectum* ATCC 700924^T (GenBank accession no. AB037875), the phylogenetically closest species with standing in nomenclature (Fig. 1). *Mogibacterium neglectum* was first isolated from the human oral cavity in 2002 [4].

The 16S rRNA gene sequence divergence exceeded 5% [5] with its phylogenetically closest species with standing in nomenclature, so we propose the creation of the new genus '*Ileibacterium*' gen. nov. (il.ei.bac.te'ri.um, Gr. n. *ilei*, 'ileum'; Gr. n. *bakterion*, 'bacterium'; N.L. neut. n. *Ileibacterium*, 'bacterium isolated from the human ileum sample'). '*Ileibacterium massiliense*' gen. nov., sp. nov. (mas.si.li.en'se, L. neut. adj., *massiliense*

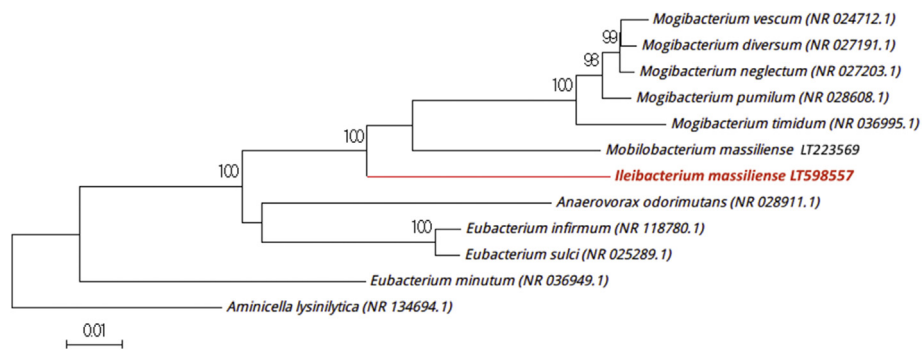


FIG. 1. Phylogenetic tree showing position of *Ileibacterium massiliense* strain Marseille-P3115^T relative to other phylogenetically close neighbours. Sequences were aligned using Musclev v3.8.31 with default parameters, and phylogenetic inferences were obtained using neighbour-joining method with 1000 bootstrap replicates within MEGA6 software. Only bootstrap values >95% are shown. Scale bar represents 1% nucleotide sequence divergence.

for Massilia, the Latin name of Marseille, where the strain was first isolated), is classified as a member of the *Eubacteriaceae* family. The type strain of the new species '*Ileibacterium massiliense*' gen. nov., sp. nov., is strain Marseille-P3115^T.

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of '*Ileibacterium massiliense*' strain Marseille-P3115^T is available online (<http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>).

Nucleotide sequence accession number

The 16S r RNA gene sequence of '*Ileibacterium massiliense*' strain Marseille-P3115^T was deposited in GenBank under accession number LT598557.

Deposit in a culture collection

'*Ileibacterium massiliense*' strain Marseille-P3115^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3115 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) under number DSM 103486.

Conflict of Interest

None declared.

Acknowledgements

This study was funded by the Fondation Méditerranée Infection. The authors thank M. Lardière for English-language review.

References

- [1] Lagier JC, Khelaifia S, Tidjani Alou M, Ndongo S, Dione N, Hugon P, et al. Culture of previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol* 2016;1:16203.
- [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] Drancourt M, Bollet C, Carlouz 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] Nakazawa F, Poco SE, Sato M, Ikeda T, Kalfas S, Sundqvist G, et al. Taxonomic characterization of *Mogibacterium diversum* sp. nov. and *Mogibacterium neglectum* sp. nov., isolated from human oral cavities. *Int J Syst Evol Microbiol* 2002;52(Pt 1):115–22.
- [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(Pt 2):346–51.