'*Mobilibacterium massiliense*' gen. nov. and '*Mobilibacterium timonense*' sp. nov., identified in a human stool specimen

M. Bilen[1], S. Ndongo[1], F. Cadoret[1], G. Dubourg[1], Z. Daoud[2], P.-E. Fournier[1] and D. Raoult[1]

1) *Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and* 2) *Clinical Microbiology Department, Faculty of Medicine and Medical Sciences, University of Balamand, Amioun, Lebanon*

Abstract

This study presents the main characteristics of '*Mobilibacterium massiliense*' strain P2510 (CSUR P2510) and '*Mobilibacterium timonense*' strain P3194 (CSUR P3194), isolated from a stool sample of a patient at the Timone hospital and from a stool sample of a healthy 50-year-old pygmy *(Baka)* woman, respectively.

Keywords: Culturomics, emerging bacteria, gut microbiota, '*Mobilibacterium massiliense*', '*Mobilibacterium timonense*'
Original Submission: 17 October 2016; **Revised Submission:** 3 November 2016; **Accepted:** 9 November 2016
Article published online: 15 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

'*Mobilibacterium massiliense*' and '*Mobilibacterium timonense*' were both isolated as part of the study of the human microbiome based on culturomics techniques [1,2]. Samples were kept at +4°C. Validation from the ethics committee of the Institut Fédératif de Recherches IFR48 was obtained under number 09022.

Samples were diluted with 1 mL of phosphate-buffered saline and incubated for 30 days under anaerobic condition at 37°C in a blood culture bottle supplemented with 5 mL sheep's blood and 5 mL filtered sheep rumen. The strain Marseille-P2510 and the strain Marseille-P3194 were isolated at days 7 and 10, respectively, on 5% sheep's blood–enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). Both colonies could not be identified by our systematic matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4]. Colonies appeared smooth with a mean diameter of 0.3 to 0.5 mm. Bacterial cells were Gram negative, catalase and oxidase negative, appearing as bacilli shaped with an average diameter of 1.4 µm. The 16S rRNA gene sequencing was performed using fD1-rP2 primers (Eurogentec, Seraing, Belgium) as previously described with a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) [5]. Strain Marseille-P2510 exhibited a 91.06% sequence identity with *Mogibacterium diversum*, which is equivalent to >5% sequence dissimilarity with the closest species with standing in nomenclature [6]. Thus, we propose the creation of a new genus '*Mobilibacterium*' (mo.bi′li.bac.te′ri.um, N.L. masc. gen. n. *Mobilibacterium*, for the fact that these bacteria are mobile). Marseille-P2510 is the type strain of the new species '*Mobilibacterium massiliense*' gen. nov., sp. nov. (mas.il.i.en′se, L. gen. masc. n. *massiliense,* pertaining to Massilia, the antic name of the city of Marseille, where this bacterium was discovered).

For strain Marseille-P3194, the 16S rRNA sequence exhibited a 96.01% sequence identity with '*M. massiliense*' which is equivalent to >1.3% sequence divergence with its phylogenetically closest species (Fig. 1) [6]. Thus, we propose the creation of a new species '*Mobilibacterium timonense*' (ti.mo.nen′se, N.L. masc. adj. *timonense* from the Latin name of Hôpital de la Timone, where strain Marseille-P3194 was isolated). Strain Marseille-P3194 is the type strain of the new species '*Mobilibacterium timonense*'.

http://dx.doi.org/10.1016/j.nmni.2016.11.008

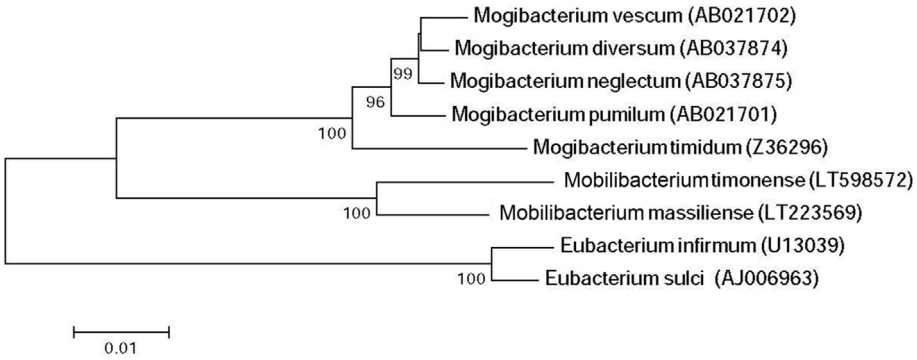

FIG. 1. Phylogenetic tree representing position of '*Mobilibacterium massiliense*' strain Marseille-P2510 and '*Mobilibacterium timonense*' strain Marseille-P3194 among other phylogenetically close neighbors. Sequences of strains involved in this tree were aligned using CLUSTALW tool, and phylogenetic inferences were obtained by MEGA software using maximum-likelihood method. Bootstrap values obtained after 500 repeats are shown on nodes. Only bootstrap score of at least 90% were kept. Scale bar indicates 2% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S rRNA gene sequence of '*M. massiliense*' and '*M. timonense*' were deposited in GenBank under accession numbers LT223569 and LT598572, respectively.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectra of '*M. massiliense*' and '*M. timonense*' are available online (http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database).

Deposit in a culture collection

Strain Marseille-P3194 and strain Marseille-P2510 were deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under numbers P3194 and P2510, respectively.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

[1] Lagier JC, Hugon P, Khelaifia S, Fournier PE, 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] 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.
[3] 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.
[4] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. Microbiol Today 2006;33:152–5.
[5] 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.
[6] 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.