# 'Gabonibacter timonensis' sp. nov., a new bacterium isolated from the human gut of a Pygmy woman 

M. Bilen ${ }^{1,2}$, F. Cadoret ${ }^{1}$, G. Dubourg ${ }^{\prime}$, Z. Daoud ${ }^{2}$, P.-E. Fournier ${ }^{\text {' }}$ and D. Raoult ${ }^{1}$<br>I) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRDI98, 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 supports the main characteristics of a new genus 'Gabonibacter timonensis' strain Marseille-P3388 (CSUR P3388); a new member of the Gabonibacter genus and Porphyromonadaceae family, that was isolated from a stool sample of a healthy 47-year-old Pygmy woman. © 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, emerging bacteria, Gabonibacter timonensis, gut microbiota, human microbiota
Original Submission: 2 December 2016; Revised Submission: 16 December 2016; Accepted: 23 December 2016
Article published online: 29 December 2016

Corresponding author: D. Raoult, Aix-Marseille Université, URMITE, UM63, CNRS7278, IRDI98, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, I3385, Marseille Cedex 05, France.
E-mail: didier.raoult@gmail.com

As part of the project aiming to describe the human microbiome by culturomics, stool samples were collected in 2015 from Congo and work was initiated after receiving an authorization from the Institut Fédératif de Recherche under the number 09-022 [1].

Phosphate buffered saline was used for stool sample dilution. Then, diluted samples were inoculated in a blood-culture bottle supplemented with 5 ml sheep blood and 5 ml filtered rumen. The culture bottle was incubated at $37^{\circ} \mathrm{C}$ and follow up was performed for 30 days. A 'Gabonibacter timonensis’ colony was isolated at day 10 on 5\% blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). The first identification trial of Strain Marseille-P3388 by matrix-assisted laser desorption/ ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany) was unsuccessful [2]. Hence, 16 S rRNA gene sequencing was carried out for strain identification. Briefly, a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France)
was used along with fDI-rP2 primers (Eurogentec, Seraing, Belgium) as previously described [3]. Strain Marseille-P3388 exhibited a $97 \%$ sequence identity with Gabonibacter massiliensis strain $\mathrm{GM7}^{\top}$ (LN88I588.I), the phylogenetically closest species (Fig. I). Hence, strain Marseille-P3388 can be classified as a new species within the genus Gabonibacter [4]. Colonies were smooth with a mean diameter of $0.8-2.5 \mathrm{~mm}$. Bacterial cells were Gram-positive bacilli, catalase and oxidase negative with a mean diameter of $1.06 \mu \mathrm{~m}$.

We propose the discovery of the new species 'Gabonibacter massiliensis' (mas.il.i.en'sis. L. gen. masc. n. massiliensis pertaining to Massilia, the ancient name of the city of Marseille where strain P3388 was discovered.). Strain Marseille-P3388 ${ }^{\top}$ is the type strain of the new species 'Gabonibacter massiliensis'.

MALDI-TOF MS spectrum accession number. The MALDI-TOF MS spectrum of 'Gabonibacter massiliensis' is available online (http://www.mediterranee-infection.com/ article.php?laref=256\&titre=urms-database).

Nucleotide sequence accession number. The 16 S rRNA gene sequence was deposited in GenBank under Accession number LT63I520.

Deposit in a culture collection. Strain Marseille-P3388 ${ }^{\top}$ was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3388.


FIG. I. Phylogenetic tree showing the position of 'Gabonibacter timonensis' strain Marseille-P3388 between the phylogenetically closest species. CLUSTALW tool was used for sequence alignment and phylogenetic inferences were generated using the MeGA software by the maximum-likelihood method. Bootstrap values obtained after 500 repeats are shown on the nodes. Bootstrap scores of at least $90 \%$ were kept. The scale bar indicates a $2 \%$ nucleotide sequence divergence.

## Transparency declaration

The authors have no conflicts of interest to declare.

## Funding

This work was funded by Mediterrannée-Infection Foundation.

## References

[I] Lagier J-C, 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] 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 ionizationtime of flight mass spectrometry. J Clin Microbiol 2013;5I: 2182-94.
[3] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. I6S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentifiable bacterial isolates. J Clin Microbiol 2000;38: 3623-30.
[4] Kim M, Oh H-S, Park S-C, Chun J. Towards a taxonomic coherence between average nucleotide identity and I6S rRNA gene sequence similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 2014;64:346-5I.

