

## “*Prevotellamassilia timonensis*,” a new bacterial species isolated from the human gut

S. Ndongo<sup>1</sup>, J.-C. Lagier<sup>1</sup>, P.-E. Fournier<sup>1</sup>, D. Raoult<sup>1,2</sup> and S. Khelaifia<sup>1</sup>

1) Aix Marseille Université, URMITE, UM63, CNRS 7278, IRD 198, INSERM 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France and 2) Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

### Abstract

We describe here the main characteristics of “*Prevotellamassilia timonensis*” gen. nov., sp. nov., strain Marseille-P2831<sup>T</sup> (CSUR P2831), a new member of the *Prevotellaceae* family that was isolated from stool samples from a 45-year-old patient.

© 2016 The Author(s). Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

**Keywords:** Culturomics, *Prevotellamassilia timonensis*, taxonomy, taxonogenomics, human gut

**Original Submission:** 20 June 2016; **Revised Submission:** 24 June 2016; **Accepted:** 28 June 2016

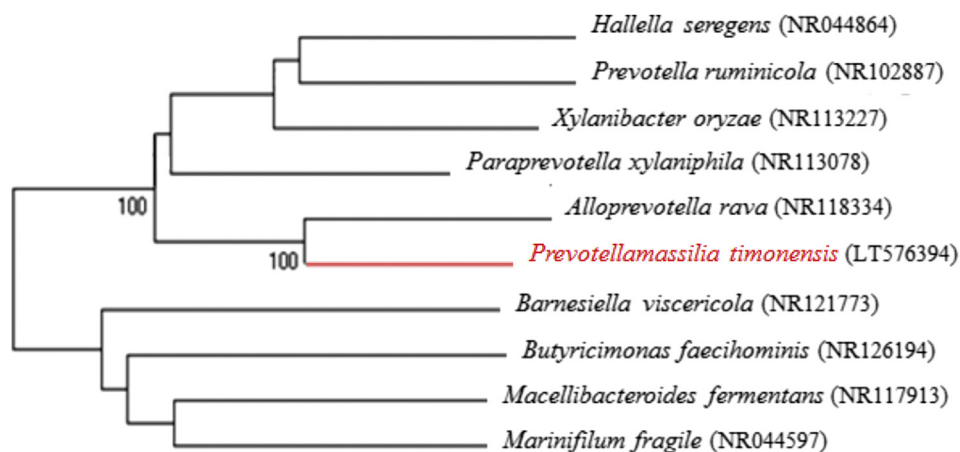
**Article published online:** 5 July 2016

**Corresponding author:** S. Khelaifia.  
**E-mail:** [khelaifia\\_saber@yahoo.fr](mailto:khelaifia_saber@yahoo.fr)

By culturomics study [1], we isolated a new bacterial strain from the stool specimen of a 45-year-old patient hospitalized in March 2016 for the treatment of a melanoma in Marseille, France. We obtained the patient’s consent, and the study was approved by the Institut Fédératif de Recherche 48 (Faculty of Medicine, Marseille, France) under agreement number 09-022. Growth of the strain Marseille-P2831 was obtained on 5% sheep’s blood–enriched Columbia agar (bioMérieux, Marcy l’Etoile, France) after 48 hours’ incubation at 37°C under an anaerobic atmosphere generated by AnaeroGen (bioMérieux). Strain Marseille-P2831 was a strictly anaerobic, Gram-negative cocci, non–spore forming, motile, with no catalase and no oxidase activities. The colonies were irregular and beige, with a diameter of 0.8 to 1.5 mm on blood-enriched Columbia agar (bioMérieux) after 72 hours’ incubation. Individual cells exhibited a diameter of 0.7 to 1.2 µm and a length of 1.5 to 2.5 µm measured by electron microscopy using a DMI1000 photonic microscope (Leica, Wetzlar, Germany). Our 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 not be able to identify this strain. The complete 16S rRNA gene was sequenced using a 3130-

XL sequencer (Applied Biosciences, Saint Aubin, France) using the universal primers FD1 and RP2 (Eurogentec, Angers, France) as previously described [3]. The sequence of strain Marseille-P2831 (GenBank accession number LT576394) showed a similarity of 90% with *Alloprevotella rava* strain F0323<sup>T</sup> (GenBank accession number GU470887), the phylogenetically closest species with standing in nomenclature (Fig. 1), which classifies it as a new genus within the *Prevotellaceae* family in the *Bacteroidetes* phylum [4]. Isolated from the human oral cavity and described in 2013, *Alloprevotella rava* is an obligatory anaerobic, Gram-negative nonmotile bacilli.

Strain Marseille-P2831 exhibited a 16S rRNA sequence divergence of >5% with the other phylogenetically closest species within the *Alloprevotella* genus with a validly published name with standing in nomenclature [5]. From these results, we propose the creation of a new genus “*Prevotellamassilia*” (pre.vo.tel’la.ma.si.lia, related to pre.vo.tel’la; N.L. fem. n. *Prevotella*, a bacterial generic name, and ma.si.lia, “of Massilia,” the Latin name of Marseille, where the strain was isolated; N.L. fem. n. “*Prevotellamassilia*,” organism different from, but related to, the genus *Prevotella* and *Massilia*, where our hospital is situated). “*Prevotellamassilia timonensis*” gen. nov., sp. nov. (ti.mo.nen’sis, L. masc. adj. *timonensis*, related to Timone, the name of the main university hospital in Marseille, France, from where the strain was isolated) is a new species within this new genus.



**FIG. 1.** Phylogenetic tree highlighting position of “*Prevotellamassilia timonensis*” strain Marseille-P2831<sup>T</sup> relative to other Bacteroidetes. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Scale bar represents 2% nucleotide sequence divergence.

### MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of “*P. timonensis*” is available online (<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 LT576394.

### Deposit in a culture collection

Strain Marseille-P2831<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number P2831.

### 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] 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, 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] Downes J, Dewhirst FE, Tanner ACR, Wade WG. Description of *Alloprevotella rava* gen. nov., sp. nov., isolated from the human oral cavity, and reclassification of *Prevotella tannerae* Moore et al. 1994 as *Alloprevotella tannerae* gen. nov., comb. nov. *Int J Syst Evol Microbiol* 2013;63:1214–8.
- [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.