

Pacaella massiliensis gen. nov., sp. nov., a new bacterial species isolated from the human gut

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Abstract

Herein, we report the main characteristics of a new species named *Pacaella massiliensis* gen. nov., sp. nov., strain Marseille-P2670^T (CSUR P2670) that was isolated from the gut microbiota of a 45-year-old French patient.

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Keywords: Culturomics, emerging bacterium, gut microbiota, *Pacaella massiliensis*, taxonomy

Original Submission: 5 August 2016; **Revised Submission:** 29 November 2016; **Accepted:** 5 December 2016

Article published online: 30 December 2016

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A 45-year-old patient with melanoma was hospitalized in March 2016 in Timone Hospital, Marseille, France. A systematic stool specimen was collected from this patient. Using the culturomics strategy [1], we isolated from this sample a bacterial strain that could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a MicroFlex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. Informed and signed consent was obtained from the patient and the study was approved by the ethics committee of the IFR48 (Marseille, France) under number 09-022. The initial growth was observed after pre-incubation of the stool sample at 37°C in an anaerobic blood-culture bottle enriched with 5 ml sterile-filtered sheep rumen for 3 days. Pure subculture of strain Marseille-P2670 was obtained on 5% sheep-blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France)

incubated at 37°C for 72 h in an anaerobic atmosphere using AnaeroGenTM (bioMérieux). Agar-grown colonies were beige and ranged from 1 to 2 mm in diameter. Cells from strain Marseille-P2670 are Gram-negative rods forming chains. Bacterial cells are 0.3–0.4 µm in diameter and 1.8–2.2 µm in length as observed using electron microscopy, and are non-motile and non-spore-forming. Strain Marseille-P2670 is strictly anaerobic and is negative for catalase and oxidase activities. The 16S rRNA gene of this strain was sequenced using fD1-rP2 primers (Eurogentec, Angers, France) as previously described [3]. The obtained amplicon showed a 91% similarity with *Pyramidobacter piscolens* strain W5455 (GenBank Accession number NZ_ADFP00000000), the phylogenetically closest species with standing in nomenclature (Fig. 1), which classifies strain Marseille-P2670 as a member of the family Synergistaceae in the phylum Synergistetes [4]. *Pyramidobacter piscolens* is an obligately anaerobic, non-motile bacillus. To date, it is the sole representative of the genus *Pyramidobacter* with a published and validated name. Its type strain W5455^T was first isolated from the human oral cavity [4].

Strain Marseille-P2670 showed a 16S rRNA sequence divergence of more than 5% with its phylogenetically closest

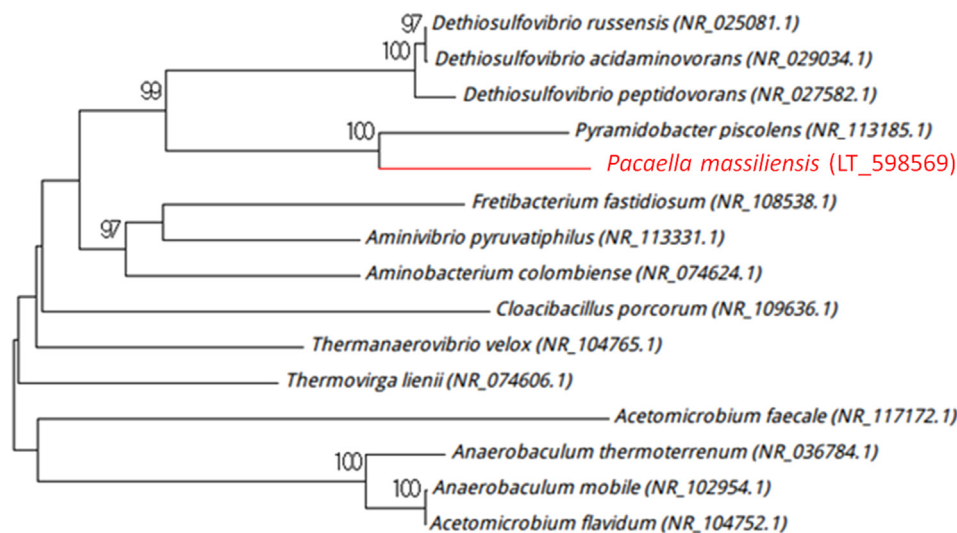


FIG. 1. Phylogenetic tree highlighting the position of *Pacaella massiliensis* strain Marseille-P2670^T (red) relative to other phylogenetically close members of the family Synergistaceae. Numbers at the nodes are percentages of bootstrap values obtained by repeating the analysis to generate a majority consensus tree 500 times. Only values >95% are displayed.

species with a validly published name standing in nomenclature [5]. Based on these results, we propose strain Marseille-P2670 as a member of the new genus *Pacaella* gen. nov. (pa.ca.el'la. L. N. Fem. n. *pacaella*, of PACA, the acronym of Provence Alpes Côte d'Azur, the region where *Pacaella massiliensis* was isolated). Strain Marseille-P2670^T is the type strain of the new species *Pacaella massiliensis* gen. nov., sp. nov. (ma.si.li.en'sis. L. fem. adj. *massiliensis*, of *Massilia*, the Latin name of Marseille where *P. massiliensis* was isolated).

MALDI-TOF MS spectrum accession number. The MALDI-TOF MS spectrum of *P. massiliensis* is available at <http://www.mediterraneeinfection.com/article.php?leref=256&titre=urms-database>.

Nucleotide sequence accession number. The 16S rRNA gene sequence was deposited in GenBank under Accession number LT598569.

Deposit in a culture collection. Strain Marseille-P2670^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2670.

Transparency declaration

The authors have no conflicts of interest to declare.

Acknowledgements

This research was funded by the Fondation Méditerranée Infection.

References

- [1] 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.
- [2] Lagier JC, Hugon P, Khelaifa 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.
- [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, Vartoukian SR, Dewhirst FE, Izard J, Chen T, Yu W-H, et al. *Pyramidobacter piscolens* gen. nov., sp. nov., a member of the phylum 'Synergistetes' isolated from the human oral cavity. *Int J Syst Evol Microbiol* 2009;59:972–80.
- [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.