'*Angelakisella massiliensis*' gen. nov., sp. nov., a new bacterial species isolated from human ileum

M. Mailhe[1], D. Ricaboni[1,2], V. Vitton[3], F. Cadoret[1], 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,* 2) *Département des sciences cliniques et biomédicales, Luigi Sacco, Division des Maladies Infectieuses III, Université de Milan, Milan, Italy and* 3) *Service de Gastroentérologie, Hôpital Nord, Assistance Publique-Hôpitaux de Marseille, Marseille, France*

Abstract

We present here a summary of the main characteristics of '*Angelakisella massiliensis*' strain Marseille-P3217^T (= CSUR P3217) that was isolated from the ileum liquid sample of a 76-year-old woman.
© 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: *Angelakisella massiliensis*, culturomics, genomics, gut microbiota, taxonomy
Original Submission: 15 December 2016; **Revised Submission:** 4 January 2017; **Accepted:** 9 January 2017
Article published online: 13 January 2017

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

In May 2016, as part of the culturomics study [1] of the human microbiome [2], a bacterial strain was isolated from the ileum liquid sample [3] of a 76-year-old woman who underwent a colonoscopy for colonic polyp control. Our systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening (Microflex, Bruker Daltonics, Wissembourg, France) [4] was not able to identify this strain. The ethics committee of the Institut Fédératif de Recherche IFR48 validated the study under number 2016-010 and the patient gave signed consent after clear information.

Pre-incubation of 7 days in a blood-culture bottle (BD BACTEC®, Plus Anaerobic / F Media, Le Pont-de-Claix, France) previously supplemented with 5 mL of sheep blood and 5 mL of 0.2-µm-filtered rumen was managed before seeding on Columbia agar supplemented with 5% sheep blood (bioMérieux, Marcy l'Etoile, France). This solid medium was then inoculated for 1 day in an anaerobic atmosphere (AnaeroGen™ Compact, OXOID Ltd, Thermo Scientific, Dardilly, France) at 37°C to obtain the initial growth of strain Marseille-P3217^T. This strain was also able to grow at 45°C in the same conditions.

Agar-grown colonies were yellow, with a mean diameter of 0.2 mm. Bacterial cells were Gram-negative bacilli with a very elongated shape. The length varied from 2300 to 5500 nm and the width varied from 300 to 500 nm. Strain Marseille-P3217^T was motile and non-spore-forming. This strain had neither oxidase activity nor catalase activity.

The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [5] and using a 3130-XL sequencer (Applied Biosciences, Saint-Aubin, France). Strain Marseille-P3217^T exhibited a 92.4% sequence identity with the *Ruminicoccus champanellensis* type strain 18P13^T (accession number AJ515913), the phylogenetically closest species with standing in nomenclature [6] (Fig. 1), which was first isolated in 2012 from the human gut microbiota [7].

The 16S rRNA sequence divergence was >5.0% [8] with its phylogenetically closest species with standing in nomenclature, so we propose the creation of the new genus '*Angelakisella*' gen. nov. (An.ge.la.ki.sel'la N.L. fem. n. *Angelakisella*, in honour of the French microbiologist Emmanouil Angelakis who is part of the culturomics team). '*Angelakisella massiliensis*' gen. nov., sp. nov.

© 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/)
http://dx.doi.org/10.1016/j.nmni.2017.01.003

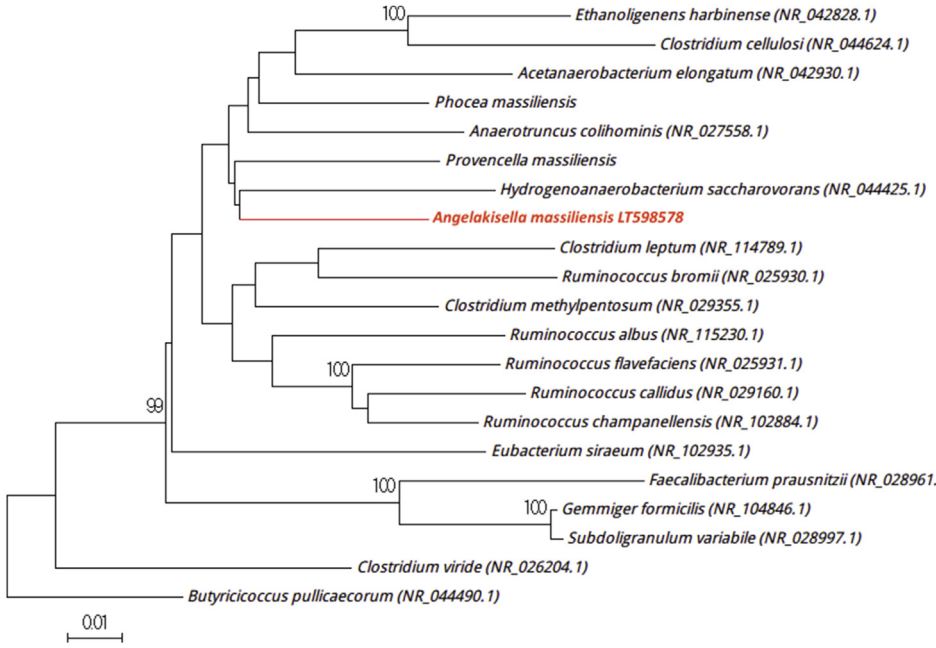

FIG. 1. Phylogenetic tree showing the position of '*Angelakisella massiliensis*' strain Marseille-P3217^T relative to other phylogenetically close neighbours. Sequences were aligned using MUSCLE v3.8.31 with default parameters and phylogenetic inferences were obtained using the neighbour-joining method with 1000 bootstrap replicates, within MEGA6 software. Only bootstrap values >95% are shown. The scale bar represents a 1% nucleotide sequence divergence.

(mas.si.li.en'sis N.L. fem. adj. *massiliensis*, belonging to Massilia, the Latin name of Marseille where the type strain was first isolated) is classified as a member of the family *Ruminococcaceae* in the phylum *Firmicutes*. Strain Marseille-P3217^T is the type strain of the new species '*Angelakisella massiliensis*' gen. nov., sp. nov.

MALDI-TOF MS spectrum accession number. The MALDI-TOF MS spectrum of '*Angelakisella massiliensis*' strain Marseille-P3217^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 was deposited in GenBank under Accession number LT598578.

Deposit in a culture collection. Strain Marseille-P3217^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under the number P3217.

Conflict of interest

The authors have no conflicts of interest to declare.

Funding

This work was funded by the Méditerranée-Infection Foundation.

Acknowledgements

The authors thank Magdalen Lardière for reviewing the English of this article.

References

[1] 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 Off Publ Eur Soc Clin Microbiol Infect Dis 2012;18:1185–93.

[2] Lagier JC, Hugon P, Khelaifia S, Fournier P-E, 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] Raoult D, Henrissat B. Are stool samples suitable for studying the link between gut microbiota and obesity? Eur J Epidemiol 2014;29:307–9.

[4] 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 ionization-time of flight mass spectrometry. J Clin Microbiol 2013;51:2182–94.

[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 H-S, Park SC, Chun J. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence

© 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases, *NMNI*, **16**, 51–53
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 2014;64:346–51.

[7] Chassard, Delmas, Robert, Lawson PA, Bernalier-Donadille A. *Ruminococcus champanellensis* sp. nov., a cellulose-degrading bacterium from human gut microbiota. Int J Syst Evol Microbiol 2012;62:138–43.

[8] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of metagenomic data. Genome Res 2007;17:377–86.

© 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases, *NMNI*, **16**, 51–53
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).