



**HAL**  
open science

# '*Ndongobacter massiliensis*' gen. nov., sp. nov., a new bacterial genus isolated from a human urine sample after de novo kidney transplantation

S Brahimi, Frederic Cadoret, Pierre-Edouard Fournier, Valérie Moal, Didier Raoult

## ► To cite this version:

S Brahimi, Frederic Cadoret, Pierre-Edouard Fournier, Valérie Moal, Didier Raoult. '*Ndongobacter massiliensis*' gen. nov., sp. nov., a new bacterial genus isolated from a human urine sample after de novo kidney transplantation. *New Microbes and New Infections*, 2016, 16, pp.34-36. 10.1016/j.nmni.2016.12.018 . hal-01474940

HAL Id: hal-01474940

<https://amu.hal.science/hal-01474940v1>

Submitted on 3 Sep 2024

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

# '*Ndongobacter massiliensis*' gen. nov., sp. nov., a new bacterial genus isolated from a human urine sample after *de novo* kidney transplantation

S. Brahimi<sup>1,2</sup>, F. Cadoret<sup>1</sup>, P.-E. Fournier<sup>1</sup>, V. Moal<sup>1,3</sup> and D. Raoult<sup>1</sup>

1) Aix-Marseille Université, Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes (URMITE), CNRS 7278, IRD 198, INSERM 1095, UM63, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Marseille, France, 2) Université Blaise Pascal, Clermont-Ferrand, UFR Sciences et Technologies, Campus Universitaire des Cézeaux, Aubière, France and 3) AP-HM, Hôpital Conception, Centre de Néphrologie et Transplantation Rénale, Centre Hospitalo-Universitaire Conception, Marseille, France

## Abstract

We report the main characteristics of '*Ndongobacter massiliensis*' strain Marseille-P3170<sup>T</sup> (= CSUR P3170), which was isolated from the urine sample of a 37-year-old man who had just received a kidney transplant for genetic focal segmental glomerulosclerosis.

© 2017 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

**Keywords:** Culturomics, kidney transplant, '*Ndongobacter massiliensis*', taxonomy, urine

**Original Submission:** 6 December 2016; **Revised Submission:** 15 December 2016; **Accepted:** 23 December 2016

**Article published online:** 29 December 2016

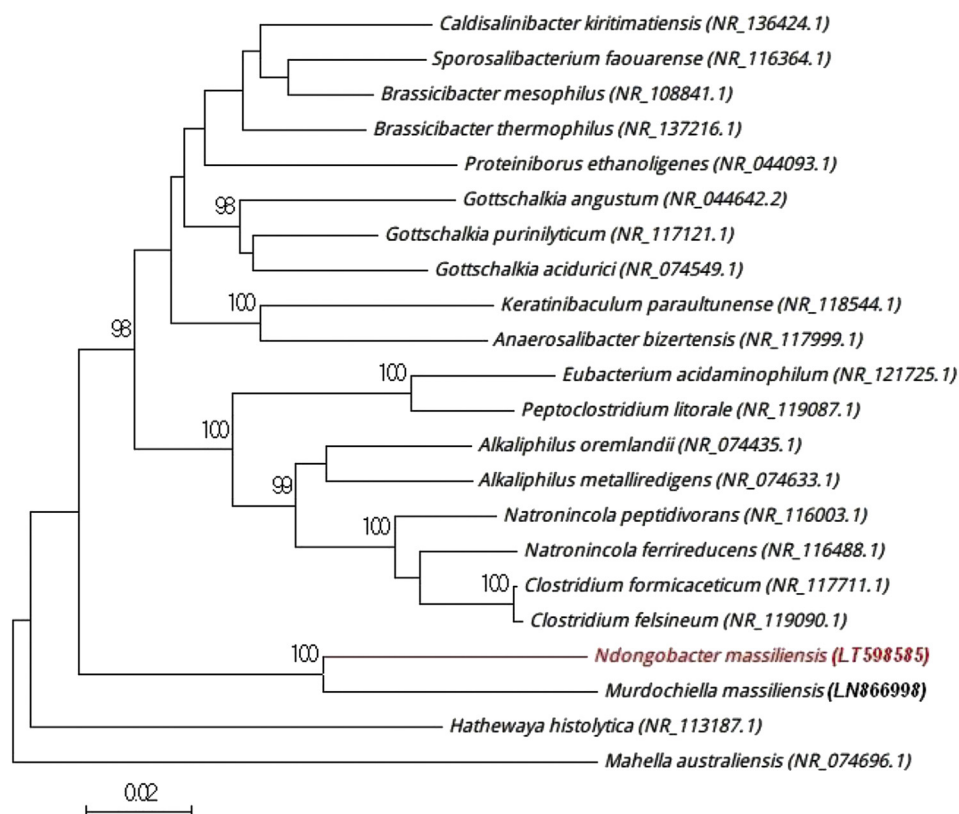
**Corresponding author:** D. Raoult, Aix-Marseille Université, Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes (URMITE), CNRS 7278, IRD 198, INSERM 1095, UM63, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, 13385, Marseille cedex 5, France  
**E-mail:** [didier.raoult@gmail.com](mailto:didier.raoult@gmail.com)

As a part of the study exploring the diversity of the urinary microbiota by culturomics [1,2], we investigated urine samples collected from adult kidney transplant recipients. The bacterial strain Marseille-P3170, which was not identified by our systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3], was isolated from a urine sample of a 37-year-old man, after kidney transplantation for genetic focal segmental glomerulosclerosis. The patient provided signed informed consent, and the agreement of the local ethics committee of the IFR48 (Marseille, France) was obtained under number 09-022. We initially pre-incubated the urine sample at 37°C for 10 days in an anaerobic blood-culture bottle (BACTEC™ Lytic/10 Anaerobic/F Culture Vials; Becton-Dickinson, Pont de Claix, France) enriched with 5% sterilized rumen by microfiltration (0.2-µm pore diameter). Then, the pre-incubated sample was seeded on 5% sheep blood Columbia agar medium (bioMérieux, Marcy

l'Étoile, France). A pure culture of the strain Marseille-P3170 was obtained after 3 days of incubation at 37°C in an anaerobic atmosphere (AnaeroGen™, Oxoid Ltd, Dardilly, France). Agar-grown microcolonies were translucent glistening with a mean diameter <0.5 mm. The strain Marseille-P3170 cells were Gram-negative cocci, non-motile, ranging in diameter from 400 to 600 nm and did not exhibit oxidase or catalase activities.

The complete 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [4] and a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). The strain Marseille-P3170 exhibited sequence similarity of 89.7% with *Murdochiella massiliensis* strain SIT12 (GenBank Accession number LN866998), which is the phylogenetically closest published species (Fig. 1). The genus *Murdochiella* was first discovered and published by Ulger-Toprak *et al.* in 2010, the strain was isolated from a sacral pilonidal cyst aspirate from an immunocompetent patient, the cells were cocci, Gram-positive staining, non-motile and obligate anaerobic [5]. *Murdochiella massiliensis* was first isolated by Vicino *et al.* in May 2015 from the stool of a healthy 2-year-old Senegalese boy, by cultivation on marine medium in anaerobic atmosphere after 21 days of incubation. *Murdochiella massiliensis* is a Gram-positive, coccus-shaped, non-motile, non-spore-forming bacterium [6].

As the strain Marseille-P3170 showed a 16S rRNA gene sequence divergence >5% from its phylogenetically closest



**FIG. 1.** Phylogenetic tree showing the position of 'Ndongobacter massiliensis' strain Marseille-P3170<sup>T</sup> relative to other phylogenetically close neighbours. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes are percentages of bootstrap values obtained by repeating the analysis 500 times to generate a majority consensus tree. Only bootstrap scores of at least 90% were retained. The scale bar indicates a 2% nucleotide sequence divergence.

species with standing in nomenclature [7], it is putatively classified as a new representative strain of the new genus 'Ndongobacter' among the Firmicutes phylum. We propose the creation of the new genus 'Ndongobacter' gen. nov. (N.don.go.bac'ter N. L. masc. n. *Ndongo* referring to the microbiologist Sokhna Ndongo N.L. masc. n. *bacter*, a rod). The strain Marseille-P3170<sup>T</sup> is the type strain of 'Ndongobacter massiliensis' gen. nov., sp. nov., the first representative species of this new genus (mas.si.li.en'sis, L., fem. adj., *massiliensis* for *Massilia*, the Latin name of Marseille, France, where the organism was first isolated).

**MALDI-TOF MS spectrum accession number.** The MALDI-TOF MS spectrum of 'Ndongobacter massiliensis' strain Marseille-P3170<sup>T</sup> is available online (<http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>).

**Nucleotide sequence accession number.** The 16S rRNA gene sequence was deposited in GenBank under Accession number LT598585.

**Deposit in a culture collection** Strain Marseille-P3170<sup>T</sup> was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3170

## Transparency declaration

The authors have no conflicts of interest to declare.

## Funding

This work was funded by the Fondation Méditerranée Infection.

## References

- [1] Hilt EE, McKinley K, Pearce MM, Rosenfeld AB, Zilliox MJ, Mueller ER, et al. Urine is not sterile: use of enhanced urine culture techniques to detect resident bacterial flora in the adult female bladder. *J Clin Microbiol* 2014;52:871–6.
- [2] Lagier J-C, 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. *J Clin Microbiol Rev* 2015;28:237–64.
- [3] 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.
- [4] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral J-P, 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.
- [5] Ulger-Toprak N, Liu C, Summanen PH, Finegold SM. *Murdochella asaccharolytica* gen. nov., sp. nov., a Gram-stain-positive, anaerobic coccus isolated from human wound specimens. *Int J Syst Evol Microbiol* 2010;60:1013–6.
- [6] Vicino E, Traore SI, Cimmino T, Dubourg G, Labas N, Andrieu C, et al. Noncontiguous finished genome sequence and description of *Murdochella massiliensis* strain SIT12 sp. nov. *New Microbes New Infect* 2016;14:31–4.
- [7] Kim M, Oh H-S, Park S-C, 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.