

“*Varibaculum massiliense*” sp. nov., a new bacterial species isolated from human urine

S. E-H. Brahimi^{1,3}, S. Khelaifia¹, D. Raoult¹ and V. Moal^{1,2}

1) Aix-Marseille Univ, 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, 2) APHM, Hôpital Conception, Centre de Néphrologie et Transplantation Rénale, 13385, Marseille and 3) Université Blaise Pascal, Clermont-Ferrand, UFR Sciences et Technologies, Campus Universitaire des Cézeaux, Aubière, France

Abstract

We report the main characteristics of “*Varibaculum massiliense*” strain Marseille-P2802^T (=CSUR P2802), which was isolated from urine sample of a 59-year-old man with end-stage renal disease.

© 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, kidney disease, taxonomy, urine, “*Varibaculum massiliense*”

Original Submission: 7 June 2016; **Revised Submission:** 13 June 2016; **Accepted:** 22 June 2016

Article published online: 28 June 2016

Corresponding author: V. Moal, Centre de Néphrologie et Transplantation Rénale, Centre Hospitalo-Universitaire Conception, 147 Boulevard Baille, 13385, Marseille cedex 5, France
E-mail: valerie.moal@ap-hm.fr

As a part of microbial culturomics project [1], we investigated the urinary microbiota [2] in adult kidney transplant recipients. The bacterial strain Marseille-P2802, which could not be 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 59-year-old man treated with chronic hemodialysis for diabetic nephropathy. 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. A pure culture of the strain Marseille-P2802 was initially obtained after 7 days of direct seeding culture of the urine sample on a 5% sheep’s blood Columbia agar medium (bioMérieux, Marcy l’Étoile, France) incubated at 37°C in anaerobic atmosphere generated using the GENbag Anaer systems (bioMérieux). Agar grown microcolonies were entire edged, translucent greyish, and glistening with a mean diameter of 0.5 mm. Strain Marseille-

P2802 cells were bacilli Gram positive, small rod shaped, and slightly curved, ranging in diameter from 500 to 600 nm. The strain Marseille-P2802 did not exhibit catalase or oxidase 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-P2802 exhibited a 98.65% sequence similarity with *Varibaculum cambriense* strain CCUG 44998^T (GenBank accession number NR042127) [5,6]. *V. cambriense* is the phylogenetically closest species with standing nomenclature (Figure 1). Consequently, it putatively classifies the strain Marseille-P2802 as a new member of the genus *Varibaculum* within the family *Actinomycetaceae* in the phylum *Actinobacteria*. *V. cambriense* was first described by Hall *et al.* in 2003 as an anaerobic, Gram-positive, diphtheroid-shaped bacterium [5,6].

For the strain Marseille-P2802, showing a 16S rRNA sequence divergence of >1.3% with its phylogenetically closest species with standing in nomenclature [7,8], we propose the creation of “*Varibaculum massiliense*” sp. nov. (L. neut. adj. *massiliense*, of or pertaining to Massilia, the Latin name of Marseille, France, where the organism was first isolated), and the strain Marseille-P2802^T is the type strain of “*Varibaculum massiliense*” sp. nov.

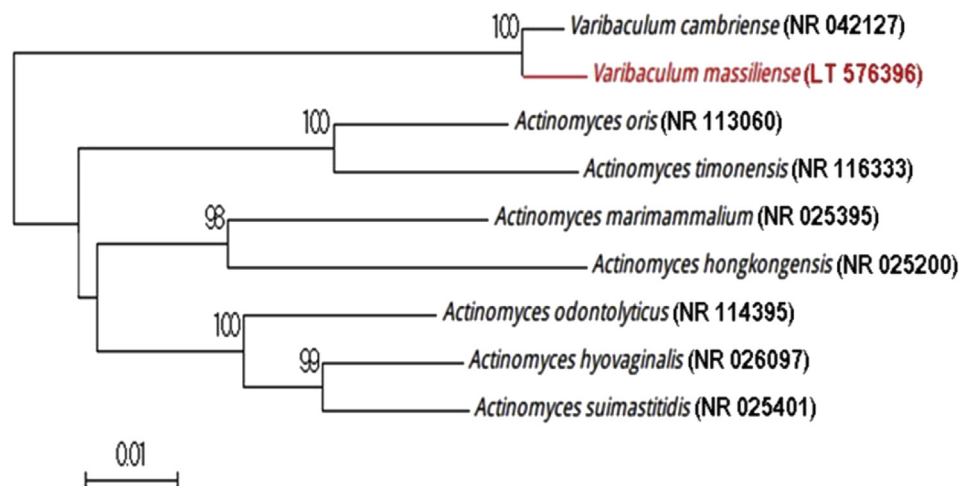


FIG. 1. Phylogenetic tree showing position of “*Varibaculum massiliense*” strain Marseille-P2802^T relative to other phylogenetically close neighbours. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstrap scores of at least 90% were retained. Scale bar indicates 1% nucleotide sequence divergence.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of “*Varibaculum massiliense*” strain Marseille-P2802^T 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 LT576396.

Deposit in a culture collection

Strain Marseille-P2802^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2802.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [1] 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.
- [2] 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.
- [3] 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.
- [4] Drancourt M, Bollet C, Carlizot 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.
- [5] Hall V, Collins MD, Lawson PA, Hutson RA, Falsen E, Inganas E, et al. Characterization of some actinomyces-like isolates from human clinical sources: description of *Varibaculum cambriense* gen. nov., sp. nov. *J Clin Microbiol* 2003;41:640–4.
- [6] Validation of publication of new names and new combinations previously effectively published outside the IJSEM. *Int J Syst Evol Microbiol* 2003;53:627–8.
- [7] Huson DH, Auch AF, Qi J, Schuster SC. MEGAN analysis of metagenomic data. *Genome Res* 2007;17:377–86.
- [8] 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.