

'*Khoudiadiopia massiliensis*' gen. nov., sp. nov., strain Marseille-P2746^T, a new bacterial genus isolated from the female genital tract

A. Diop¹, D. Raoult^{1,2}, F. Fenollar^{1,2} and P.-E. Fournier¹

1) Aix-Marseille Université, Institut hospitalo-universitaire Méditerranée-infection, URMITE, UM63, CNRS 7278, IRD 198, Inserm U1095, Marseille, France and 2) Campus International UCAD-IRD, Dakar, Senegal

Abstract

We report the main characteristics of '*Khoudiadiopia massiliensis*' gen. nov., sp. nov., strain Marseille-P2746^T (= CSUR P2746), a new member of the *Peptoniphilaceae* family isolated from a vaginal swab of a patient suffering from bacterial vaginosis.

© 2017 The Author(s). Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, human microbiome, *Khoudiadiopia massiliensis*, taxono-genomics, vaginal microbiota

Original Submission: 14 April 2017; **Revised Submission:** 23 May 2017; **Accepted:** 2 June 2017

Article published online: 8 June 2017

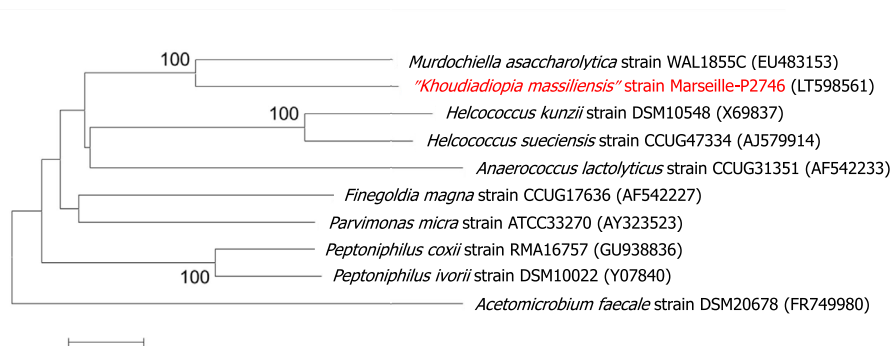
Corresponding author: P.-E. Fournier, Aix-Marseille Université, Institut hospitalo-universitaire Méditerranée-infection, URMITE, UM63, CNRS 7278, IRD 198, Inserm U1095, 19-21 Boulevard Jean Moulin, 13005 Marseille, France
E-mail: pierre-edouard.fournier@univ-amu.fr

The study of the vaginal microbiota diversity from patients with bacterial vaginosis is part of the ongoing microbial culturomics revolution in our laboratory [1]. A new member from the new family *Peptoniphilaceae* was isolated during this study that could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry screening on a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany), from a vaginal sample of a 26-year-old French woman suffering from bacterial vaginosis in the hospital Nord in Marseille (France). The patient gave her informed and signed consent and the study was authorized by the local ethics committee of the IFR48 (Marseille, France) under agreement 09-022. Strain Marseille-P2746^T was first cultivated in April 2016 after 48 h of incubation in an anaerobic atmosphere at 37°C on Schaedler agar and Trypticase soy agar (BD Diagnostics, Le Pont de Claix, France), after 4 days of pre-incubation in a blood culture bottle enriched with rumen and sheep blood. Colonies were bright grey. Bacterial cells were Gram-positive, non-motile and non-spore-forming with a mean diameter of 0.55 µm. Strain

Marseille-P2746^T is a strictly anaerobic coccus and exhibits oxidase activity but no catalase activity. Using the universal primer pair FD1 and rp2 as previously described [2], and a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France), the 16S rRNA gene was sequenced. Strain Marseille-P2746^T exhibited an 89.28% 16S rRNA gene sequence identity with *Murdochiella asaccharolytica* strain WAL 1855C^T (GenBank Accession number EU483153), the phylogenetically closest species with a validly published name (Fig. 1). This value was lower than the 95% 16S rRNA gene sequence threshold proposed by Stackebrandt and Ebers [3] to define a new genus without carrying out DNA–DNA hybridization and classifies it as a new genus within the *Peptoniphilaceae* family (phylum *Firmicutes*), first created in 2014 [4]. *Murdochiella asaccharolytica* is an obligate anaerobic species isolated from a sacro-pilonidal cyst aspirate from an immunocompetent patient. It is also Gram-stain-positive, non-motile, non-spore-forming, and also shows a negative catalase activity [5].

Strain Marseille-P2746^T has >10% 16S rRNA gene sequence divergence with its closest phylogenetic neighbour [6], so we propose the creation of a new genus named '*Khoudiadiopia*' gen. nov. (*khou.dia.dio*'*opia*, N.L. fem. n. *khoudiadiopia* from the contraction of the first and last names of the Senegalese microbiologist Khoudia Diop). Strain Marseille-P2746^T is the type strain of '*Khoudiadiopia massiliensis*' gen. nov., sp. nov., the type species of the new genus '*Khoudiadiopia*' gen. nov.

FIG. 1. Phylogenetic tree highlighting the phylogenetic position of 'Khouidiopia massiliensis' gen. nov. strain Marseille-P2746^T relative to other close species. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and the tree was constructed with the Neighbour-joining method and 500 bootstrap replicates using the MEGA6 software. Numbers at the nodes are percentages of bootstrap values > 95%. The scale bar indicates a 2% nucleotide sequence divergence.



Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in EMBL-EBI under Accession number LT598561.

Deposit in a culture collection

'*Khouidiopia massiliensis*' gen. nov., sp. nov. was deposited in the 'Collection de Souches de l'Unité des Rickettsies' (CSUR, WDCM 875) under number CSUR P2746.

Acknowledgement

This research is funded by the Méditerranée-Infection Foundation.

Transparency declaration

No conflicts of interest 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] 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.
- [3] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152–5.
- [4] Johnson CN, Whitehead TR, Cotta MA, Rhoades RE, Lawson PA. *Peptoniphilus stercorisuis* sp. nov., isolated from a swine manure storage tank and description of *Peptoniphilaceae* fam. nov. *Int J Syst Evol Microbiol* 2014;64:3538–45.
- [5] Ulger-Toprak N, Liu C, Summanen PH, Finegold SM. *Murdochiella 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] Yarza P, Richter M, Peplies J, Euzéby J, Amann R, Schleifer KH, et al. The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of all sequenced type strains. *Syst Appl Microbiol* 2008;31:241–50.