

'*Congobacterium massiliense*' gen. nov. sp. nov., a new bacterium isolated from the gut of a pygmy (*Baka*) woman

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Abstract

We report the main characteristics of a new genus, '*Congobacterium*,' and a new species, '*Congobacterium massiliense*,' strain Marseille-P3295 (CSUR P3295), a new member in the order *Coriobacteriacea*, which was isolated from a stool sample of a healthy 50-year-old pygmy (*Baka*) woman. © 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Culturomics, '*Congobacterium massiliense*', emerging bacteria, gut microbiota, human microbiota

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In 2015, stool samples were collected from Congolese persons as part of the project aiming to describe the human gut microbiome by culturomics [1]. An approval from the ethics committee under the number 09-022 was obtained from the Institut Fédératif de Recherches IFR48 (Marseille, France).

Samples were inoculated in blood culture media after being diluted with 1 mL of phosphate-buffered saline. Then 5 mL of sheep's blood was added to the culture bottle along with 5 mL of filtered rumen and incubated at 37°C under anaerobic conditions. On day 10, strain Marseille-P3295 was isolated on 5% sheep's blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). Colonies were smooth with a mean diameter of 0.4 to 0.8 mm. Strain Marseille-P3295 cells were Gram-positive bacilli, catalase and oxidase negative with an average length of 1.58 µm. Colonies could not be identified by our systematic matrix-assisted desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. Thus, 16S rRNA gene sequencing was done using fD1-rP2 primers (Eurogentec, Seraing, Belgium) on a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) as previously described [3].

'*Congobacterium massiliense*' strain Marseille-P3295 exhibited a 93.8% 16S rRNA gene sequence similarity with *Mogibacterium neglectum* type strain P9a-h (Z36274), the phylogenetically closest species with standing in nomenclature (Fig. 1). Thus, strain Marseille-P3295 can be classified as a new genus because it exhibits a 16S rRNA gene sequence divergence of more than 5% with its phylogenetically closest species with a validly published name with standing in nomenclature [4]. We propose the creation of the new genus, '*Congobacterium*' (con.go.bac.ter'ium, N.L. masc. gen. n. *Congobacterium*, for Congo, the originary country of samples out of which strain Marseille-P3295 was isolated). Marseille-P3295 is the type strain of the new species '*Congobacterium massiliense*' gen. nov., sp. nov. (mas.il.i.en'se, L. gen. masc. n. *massiliense*, pertaining to Massilia, the antic name of the city of Marseille where this bacteria was discovered).

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of '*C. massiliense*' 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 LT623899.

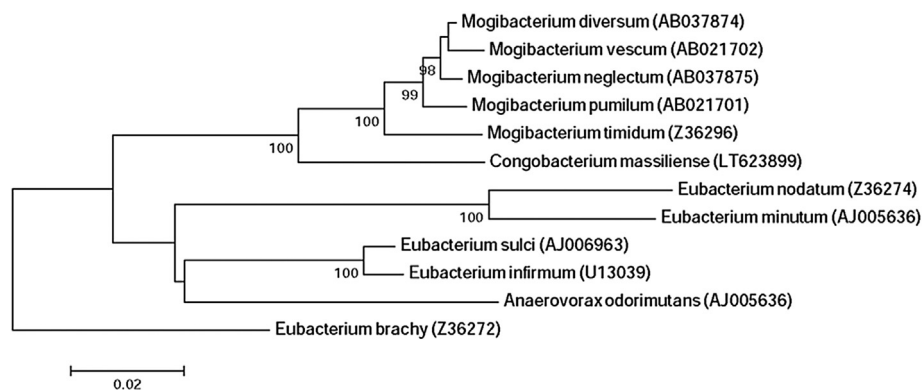


FIG. 1. Phylogenetic tree showing position '*Congobacterium massiliense*' strain Marseille-P3295 among phylogenetically closest species. Multiple sequence alignment was performed using CLUSTALW, and phylogenetic inferences were done using maximum-likelihood method by MEGA software. Bootstraps values are shown on nodes after 500 repeats, and values less than 90% were eliminated. Scale bar indicates 2% nucleotide sequence divergence.

Deposit in a culture collection

Strain Marseille-P3295 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3295.

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Conflict of Interest

None declared.

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