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'*Bacteroides ihuae*' sp. nov., a new bacterial species isolated from the human respiratory microbiome

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Abstract

We present the main features of '*Bacteroides ihuae*' sp. nov., strain Marseille-P2824^T (CSUR P2824), isolated from the sputum of healthy Frenchwoman living in Marseille.

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Keywords: '*Bacteroides ihuae*', culturomics, genomics, taxonogenomics, taxonomy

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We applied the culturomics strategy [1,2] to a sputum sample from a healthy French woman living in Marseille. We obtained the participant's oral consent as well as authorization from the ethics committee of the Institut Federatif de Recherche IFR48 under number 09-022. After day 10 of preincubation of the sample in an aerobic blood culture bottle (Becton Dickinson, Le Pont-de-Claix, France) supplemented with filter-sterilized rumen at 30°C, strain Marseille-P2824^T was subcultured on 5% sheep's blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France) at 30°C in an anaerobic atmosphere with 5% CO₂. Colonies appeared to be smooth with a diameter ranging from 1 to 3 mm. Bacterial cells were Gram-positive and rod shaped, with a diameter ranging from 0.5 to 0.64 µm and a length ranging from 1.0 to 1.6 µm. Strain Marseille-P2824^T was negative for catalase and oxidase production.

Strain Marseille-P2824^T was not identified by our systematic matrix-assisted desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) (<http://mediterranean-infection.com/article.php?laref=256&titre=urms-database>) on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4]. Consequently, 16S rRNA gene sequencing was performed using fD1-rP2 primers as previously described [5], with a 3130-XL

sequencer (Applied Biosciences, Saint-Aubin, France). Strain Marseille-P2824^T was classified as a member of the genus *Bacteroides* within family *Bacteroidaceae* in the phylum *Bacteroidetes* because it shares a 96% sequence identity with *Bacteroides graminisolvens* strain JCM 15093 (GenBank accession no. NR_113069) [6], which is the phylogenetically closest species with standing in nomenclature (Fig. 1). Because this similarity value was lower than the 98.65% threshold recommended to define a new species [7] when DNA-DNA hybridization is not performed, we propose that strain Marseille-P2824^T may be the representative strain of a new species named '*Bacteroides ihuae*' (*i.hum.i'i*, N.L. gen. n. *ihuae*, based on the acronym IHUMI, the Institut Hospitalo-Universitaire Méditerranée-Infection in Marseille, France, where the type strain was isolated). Strain Marseille-P2824^T is the type strain of the new species '*Bacteroides ihuae*'.

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of '*Bacteroides ihuae*' strain Marseille-P2824^T is available online (<http://mediterranean-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 LT576386.

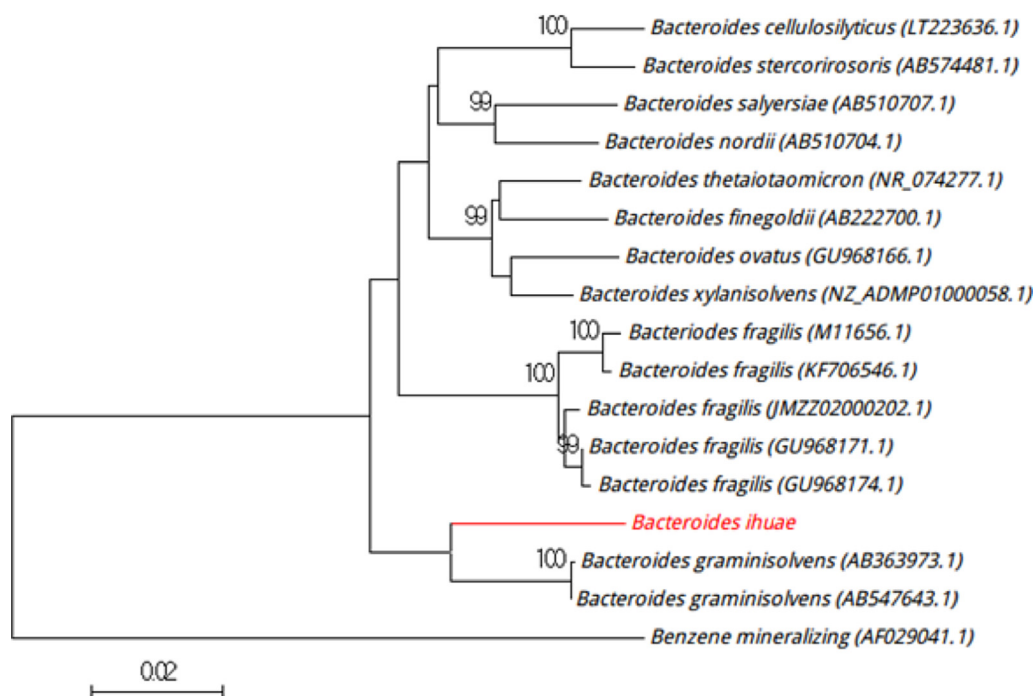


FIG. 1. Positioning of 'Bacteroides ihuae' strain Marseille-P2824^T relative to other phylogenetically close strains in phylogenetic tree. CLUSTALW was used to align sequences, and phylogenetic inferences were generated using MEGA software with maximum likelihood method. Scale bar indicates 2% nucleotide sequence divergence. Numbers at nodes are percentages of 500 bootstrap values obtained in order to generate consensus tree. Only bootstraps with minimum of 90% score were retained.

Deposit in a culture collection

Strain Marseille-P2824^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2824.

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Conflict of Interest

None declared.

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