'Merdibacter massiliensis' gen. nov., sp. nov., isolated from human ileum

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Abstract

We report here the main characteristics of *'Merdibacter massiliensis'* strain Marseille-P3254^T (= CSUR P3254 = DSM 103475), which was isolated from human ileum.

Keywords: Culturomics, human gut microbiota, *'Merdibacter massiliensis'*, new species, taxonogenomics
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In order to increase our knowledge about the human gut microbiome, we combined two highly complementary approaches, culturomics [1,2] and metagenomics, to study samples from the gastrointestinal tract (stomach, duodenum, ileum, right and left sides of the colon). The patient was informed and provided signed consent. The study was validated by the ethics committee of the Institut Hospitalo-Universitaire Méditerranée Infection under number 2016-010.

We isolated from the ileal wash sample of a 76-year-old patient, who underwent upper and lower digestive tract endoscopy as follow-up, a bacterial strain that escaped identification by our matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3].

Strain Marseille-P3254^T first growth was obtained on 5% sheep's blood–enriched Columbia agar medium (bioMérieux, Marcy l'Etoile, France) under anaerobic atmosphere (anaeroGEN, Oxoid, Dardilly, France) after 7 days' enrichment of the fresh ileal wash sample in an anaerobic blood culture bottle (Becton Dickinson, Pont de Claix, France) completed with 5 mL of sterile sheep's blood (bioMérieux) and 5 mL of 0.2 µm filter-sterilized (Thermo Fisher Scientific, Villebon-sur-Yvette, France) rumen fluid, incubated at 37°C. After 5 days of anaerobic incubation on 5% sheep's blood–enriched agar (bioMérieux) at 37°C, the colonies were circular, raised with entire edges and translucent. The mean diameter was of 0.5 to 1.5 mm. Neither haemolysis nor pigmentation was observed.

Bacterial cells were Gram-negative, nonmotile rods with a width of 0.3 to −0.5 µm and a length of 1.1 to 2.2 µm. Strain Marseille-P3254^T was catalase and oxidase negative. Different temperatures (20, 28, 37, 45 and 55°C) and atmospheres (anaerobic, aerobic and microaerophilic (CampyGEN, Oxoid) were tested on 5% sheep's blood–enriched Columbia agar (bioMérieux). Growth was achieved only under anaerobic atmosphere at 37°C and 45°C. The sporulation test (20 minutes at 80°C) was negative.

The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [4], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain Marseille-P3254^T exhibited a 90.70% sequence identity with *Eubacterium dolichum* strain JCM 10413^T (GenBank accession no. NR113409), the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classifies it as a member of a new genus within the family *Erysipelotrichaceae* in the phylum *Firmicutes*. The family *Erysipelotrichaceae* is composed of 13 genera with validly published names (*Allobaculum, Bulleidia, Catenibacterium, Catenisphaera, Coprobacillus,*

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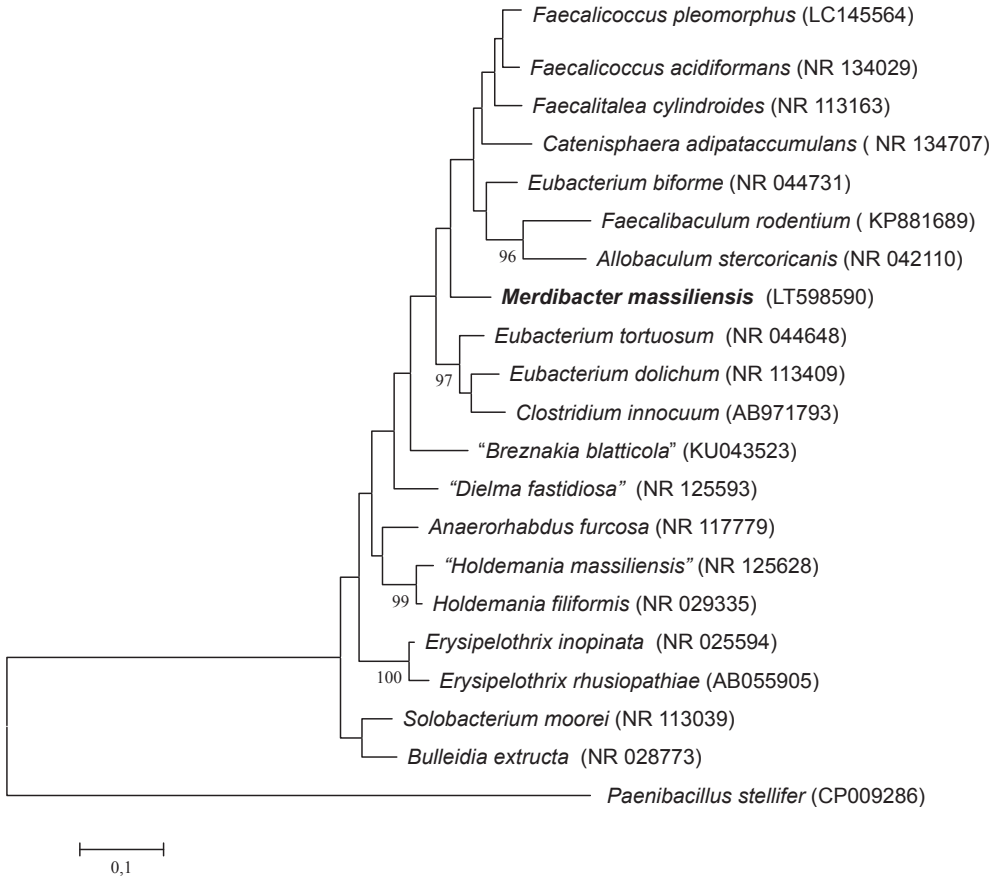

FIG. 1. Phylogenetic tree showing position of *'Merdibacter massiliensis'* strain Marseille-P3254^T relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 1000 times to generate majority consensus tree. Only bootstraps values of at least 90 were retained. Species highlighted between inverted commas have been effectively published but are still not considered validly published under International Code of Bacteria rules.

Eggerthia, Erysipelothrix, Faecalicoccus, Faecalitale, Holdemanella, Holdemania, Solobacterium and *Turicibacter*) [5]. Members within this family are generally Gram positive, but another candidate not yet validly named, the *Erysipelotrichaceae* genus *Dielma,* exhibits a Gram-negative stain [6]. The existence of Gram-negative-staining microorganisms within the *Firmicutes* phylum is accepted and at least partially understood [7].

On the basis of a 16S rRNA gene sequence divergence of strain Marseille-P3254^T with the phylogenetically closest species with standing in nomenclature [8], we propose here the creation of the new genus *'Merdibacter'* (Mer.di.bac.ter, L. fem. n. *merda,* 'faeces'; N.L. masc. n. *bacter,* 'a rod'; N.L. masc. n. *Merdibacter,* 'a rod from faeces') for which the strain Marseille-P3254^T (= CSUR P3254 = DSM 103534) is the type strain. Strain Marseille-P3254^T is the type strain of *'Merdibacter massiliensis'* gen. nov., sp. nov (mas.si.li.en′sis, L. masc. adj. *massiliensis,* for Massilia, the Roman name of Marseille).

Nucleotide sequence accession number

The 16S r RNA gene sequence was deposited in GenBank under accession number LT598590.

Deposit in a culture collection

Strain Marseille-P3254^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3254 and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen under number DSM 103534.

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Conflict of Interest

None declared.

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