

“*Anaerotruncus massiliensis*,” a new species identified from human stool from an obese patient after bariatric surgery

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Abstract

We report the main characteristics of a new bacterial species strain AT3^T (CSUR = P2007, DSM = 100567) that was isolated from the stool sample collected from a 47-year-old obese French man after he underwent bariatric surgery.

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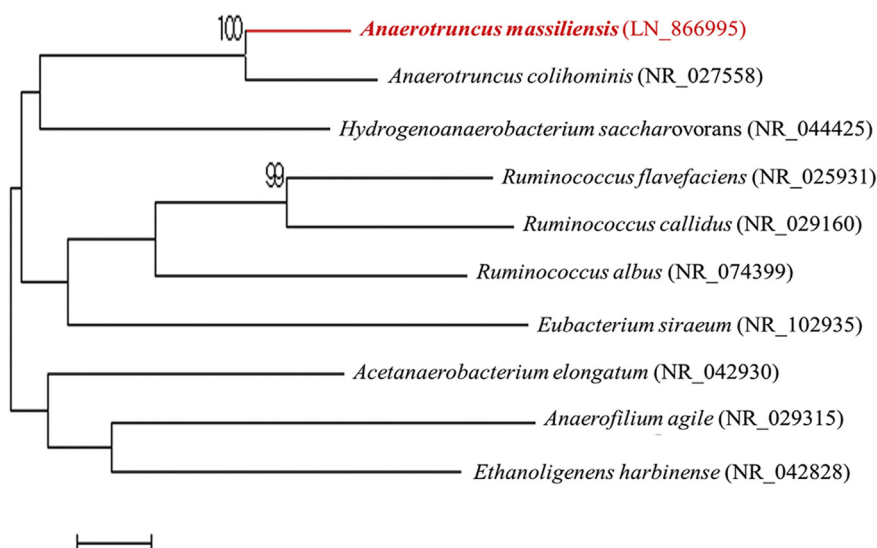
We performed an exploratory study of gut microbiota from obese patients before and after bariatric surgery by a microbial culturomics approach, as previously described [1]. The patient provided signed informed consent, and the study was validated by the ethics committee of the Institut Federatif de Recherche IFR48 under number 09-022. The first growth was obtained after 30 days of culture in a blood culture bottle (BACTEC Lytic/10 Anaerobic/F culture vials; Le Pont de Claix, Isère, France) enriched with 4 mL of sheep’s blood and 4 mL of rumen under anaerobic atmosphere at 37°C medium. Agar-grown (Columbia agar + 5% sheep’s blood; bioMérieux, Marcy l’Etoile, France) colonies were opalescent with a mean diameter of 0.5 to 1.5 mm. The strain AT3^T is a bacterial strain, whose spectrum could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Germany) [2]. The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [3] using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France).

Strain AT3^T exhibited a 96.6% sequence similarity with *Anaerotruncus colihominis* strain WAL 14565^T = CCUG 45055^T = CIP 107754^T, the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classifies it as a member of the genus *Anaerotruncus* established in 2004 by Lawson *et al.* [4] within the *Clostridiaceae* family in the *Firmicutes* phylum. Bacterial cells were negative for Gram stain and rod shaped with a size of 0.3 × 2.9 µm. The strain AT3^T was catalase positive and oxidase negative. The closest species, *Anaerotruncus colihominis*, is a Gram-positive bacillus whereas the strain AT3^T remained Gram-negative after three assays. Strain AT3^T exhibits a 16S rRNA gene sequence divergence higher than 1.35% (3.4%) with its phylogenetically closest species with standing in nomenclature [5]. We propose the creation of a new species called *Anaerotruncus massiliensis* (ma.si.li.en’sis, N.L. fem. adj. *massiliensis*, “of Massilia,” the Latin name of Marseille, where *A. massiliensis* was first isolated). The strain AT3^T is the type strain of the new species *A. massiliensis*.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of this strain is available at <http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>.

FIG. 1. Phylogenetic tree showing position of strain AT3^T relative to other phylogenetically closest species. Sequences were aligned using CLUSTALW, and phylogenetic inferences obtained using maximum-likelihood method within MEGA software. Numbers at nodes depict bootstrap values obtained by repeating analysis 500 times to yield consensus tree. Only bootstrap values of at least 90% were retained. Scale bar indicates 1% nucleotide sequence divergence.



Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank as accession number LN_866995.

Deposit in a culture collection

Strain AT3^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) and Deutsche Sammlung von Mikroorganismen (DSM) under number CSUR = P2007 and DSM = 100567.

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Conflict of Interest

None declared.

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