

“*Bariatricus massiliensis*” as a new bacterial species from human gut microbiota

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Abstract

We report here the main phenotypic characteristics of “*Bariatricus massiliensis*” strain AT12 (CSUR P2179), isolated from the stool of a 58-year-old woman who underwent bariatric surgery.

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Keywords: “*Bariatricus massiliensis*”, Culturomics, genomics, taxonogenomics, taxonomy

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In 2015, as part of our culturomics project aiming at identifying all bacterial species within the human microbiota [1,2], we analysed a stool specimen from a 58-year-old-woman who benefitted from bariatric surgery for obesity, with a body mass index of 36.65 kg/m² before surgery. 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.

We isolated the strictly anaerobic strain AT12, which could not be identified by matrix-assisted desorption ionization–time of flight mass spectrometry (MALDI-TOF MS; Microflex; Bruker Daltonics, Leipzig, Germany) [3]. The MALDI-TOF MS spectra are available in our database (<http://www.mediterraneeinfection.com/article.php?laref=256&titre=urms-database>). The initial growth was obtained in anaerobic conditions at 37°C after 10 days of culture on 5% sheep blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). Agar-grown colonies were greyish and ranged in diameter from 0.5 to 1.5 mm. Strain AT12 is a rod-shaped and polymorphic Gram-positive bacillus, ranging in length from 1.25 to 2.5 µm. Strain AT12 is catalase and oxidase negative. The complete 16S

rRNA gene was sequenced using a 3130-XL sequencer (Applied Biotechnologies, Villebon sur Yvette, France). Strain AT12 exhibited a sequence identity of 94.37% with *Clostridium nexile* strain ATCC 27757 (GenBank accession no. X73443), its closest phylogenetic neighbour with a validly published name (Fig. 1). This putatively classified strain AT12 within a new genus within the order Clostridiales.

Clostridium nexile strain ATCC 27757 is a strictly anaerobic Gram-positive bacterium initially detected in human faeces in 1974. It was later isolated again from the faecal flora of 20 healthy Japanese Hawaiians [4]. In addition, it has been shown that *Clostridium nexile* possesses a gene encoding a trypsin-dependent lantibiotic ruminococcin A (RumA) [5]. This protein may be an effective bacteriocin against *Clostridium perfringens* [5].

Another bacterium closely related to “*B. massiliensis*” strain AT12 is *Lactonifactor longoviformis*, another member of the order Clostridiales. It was isolated for the first time in 2007 from a fresh stool sample from a healthy man. The first isolate was a strictly anaerobic Gram-positive, helically coiled rod [6].

Because of a 16S rRNA difference greater than 5% with its closest phylogenetic neighbour [7], we propose that strain AT12 is the representative strain of a new genus with the order Clostridiales, for which we propose the name “*Bariatricus*” gen. nov. after bariatrics, the medical specialty that deals with the causes, prevention and treatment of obesity. Strain AT12^T is the type species of “*Bariatricus massiliensis*” sp. nov.

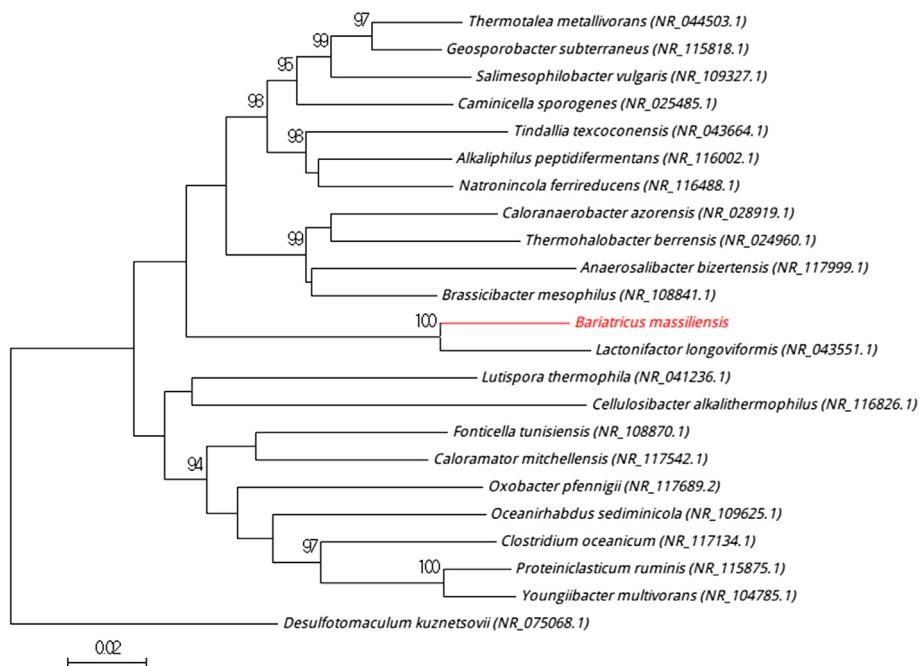


FIG. 1. Phylogenetic tree showing position of “*Bariatricus massiliensis*” strain AT12^T relative to other phylogenetically close members of order Clostridiales. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstraps scores at least 90% were retained. Scale bar = 2% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S RNA gene sequence was deposited in GenBank under accession number LN898273.

Deposit in a culture collection

Strain AT12^T was deposited in the Collection de Souches de l’Unité des Rickettsies (CSUR; WDCM 875) under number P2179.

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Conflict of Interest

None declared.

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