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'*Eisenbergiella massiliensis*', a new species isolated from human stool collected after bariatric surgery

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Abstract

We report the principal characteristics of '*Eisenbergiella massiliensis*' sp. nov. strain AT11 (CSURP = P2120, DSM = 101499) that was isolated from a stool sample collected after bariatric surgery of a 56-year-old obese French woman.

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Keywords: Culturomics, *Eisenbergiella massiliensis*, human gastrointestinal microbiome, obesity, taxonomy

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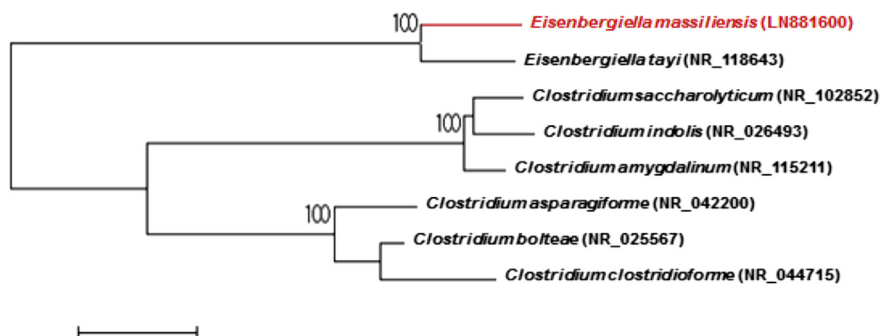
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In April 2011, as part of a culturomics study [1,2] to explore the gut microbiota from obese patients before and after bariatric surgery, we isolated a strain that did not correspond to any

previously known species. The patient provided signed informed consent and the study was approved by the ethics committee of the Institut Federatif de Recherche IFR48 under number 09-022, 2010. The first growth was obtained after 21 days of culture in a blood culture bottle enriched with sheep blood and rumen medium under an anaerobic 37°C atmosphere as described elsewhere [3]. Agar-grown (Columbia agar + 5% sheep blood; bioMérieux, Marcy l'Etoile, France) grey colonies exhibited an irregular form with a mean diameter of 0.5 mm after 48–72 h of culture. A bacterium whose

FIG. 1. Phylogenetic tree showing the position of '*Eisenbergiella massiliensis*' strain AT11 relative to other phylogenetically related species. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes depict bootstrap percentage values obtained by repeating the analysis 500 times to yield a consensus tree. The bootstrap values of at least 95% were retained. The scale bar indicates a 1% nucleotide sequence divergence.



spectrum could not be identified by our systematic matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF-MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) was identified by the 16S rRNA gene sequencing [4]. The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [5], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). It displays 97.7% sequence similarity with *Eisenbergiella tayi* strain B086562 (= LMG 27400 = DSM 26961 = ATCC BAA-2558), the phylogenetically nearest species with standing nomenclature (Fig. 1). This fact putatively classifies strain AT11 as a member of the genus *Eisenbergiella* within the *Lachnospiraceae* family in the phylum *Firmicutes*. However, this percentage remains lower than the 98.7% 16S rRNA gene sequence threshold recommended by Stackebrandt and Ebers to delineate a new species [6]. Strain AT11 exhibited a 16S rRNA sequence divergence of 2.24% with its phylogenetically closest species with standing in nomenclature [7]. The strain AT11 was catalase-positive and oxidase-negative. Cells are Gram-negative staining, non-motile, non-spore-forming with a mean diameter of 2 µm by electron microscopy. Based on phenotypic and phylogenetic characteristics we propose the creation of a new species named '*Eisenbergiella massiliensis*' (ma.si.li.en'.sis. L. fem. adj. *massiliensis*, of Massilia, the Latin name of Marseille where '*Eisenbergiella massiliensis*' was first isolated). Strain AT11 is the type strain of the new species '*Eisenbergiella massiliensis*'.

MALDITOF-MS Spectrum Accession Number

The MALDITOF-MS spectrum of this strain is available at <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 LN881600.

Deposit in a Culture Collection

Strain AT11 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number P2120.

Conflicts of Interest

No conflict of interest to declare.

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