Anaerococcus urinomassiliensis sp. nov., isolated from a urine sample of a 17-year-old boy affected by autoimmune hepatitis and membranoproliferative glomerulonephritis

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Abstract

We report the main characteristics of '*Anaerococcus urinomassiliensis*' strain FC4^T (CSURP2143) that was isolated from a urine sample of a 17-year-old boy affected by autoimmune hepatitis and membranoproliferative glomerulonephritis.

Keywords: *Anaerococcus urinomassiliensis*, culturomics, genomics, taxono-genomics, taxonomy
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In 2015, as part of a culturomics study [1,2] of the human microbiome, a bacterial strain that could not be identified by matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3] was isolated from the urine of a 17-year-old boy affected by autoimmune hepatitis and membranoproliferative glomerulonephritis. The patient's parents gave signed informed consent and the ethics committee of the Institut Federatif de Recherche IFR48 approved the study under number 09-022.

The initial growth was obtained after 10 days of incubation in an anaerobic blood culture vial (Becton Dickinson, Le Pont-de-Claix, France) supplemented with 5 mL of 0.2-µm filtered rumen fluid. A pure culture of strain FC4 was then obtained after 48 h of incubation at 37°C on 5% sheep blood–Columbia agar medium (bioMérieux, Marcy l'Etoile, France) in anaerobic atmosphere generated using the GENbag Anaer system (bioMérieux). Agar-grown colonies were small with a mean diameter of 50 µm and were translucent white. Bacterial cells were Gram-positive cocci with a diameter ranging from 400 to 600 nm. Strain FC4 did not exhibit catalase or oxidase activities. The 16S rRNA gene was sequenced using the fD1-rP2 primers as previously described [4], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain FC4 exhibited sequence similarities with *Anaerococcus octavius* strain NCTC 98 IOT (GenBank accession number NR-026360) [5], its phylogenetically 94.73% closest species with standing nomenclature in the range of 92.3% to 97.2% observed among *Anaerococcus* species (Fig. 1). This putatively classifies strain FC4 as a member of the genus *Anaerococcus* in the family *Peptostreptococcaceae* within the phylum *Firmicutes*.

Strain FC4 presents a 16S rRNA gene sequence divergence with its phylogenetically closest species with standing in nomenclature [6], so we propose the creation of the new species '*Anaerococcus urinomassiliensis*' sp. nov. strain FC4^T as the type strain of '*Anaerococcus urinomassiliensis*' (u.ri.no.mas.sil.ien'sis composed of u.ri.no L. V. intransitive. of *urino*, the Latin name for the verb to swim, closed of u.ri.na. L. N. gen. fem. *urina*, of *urina*, the Latin name of urine as this strain FC4 was first found in a paediatric urine sample and mas.si.li.en'sis. L. fem. adj. *massiliensis*, of Massilia, the ancient Greek and Roman name for Marseille, France, where the type strain was isolated).

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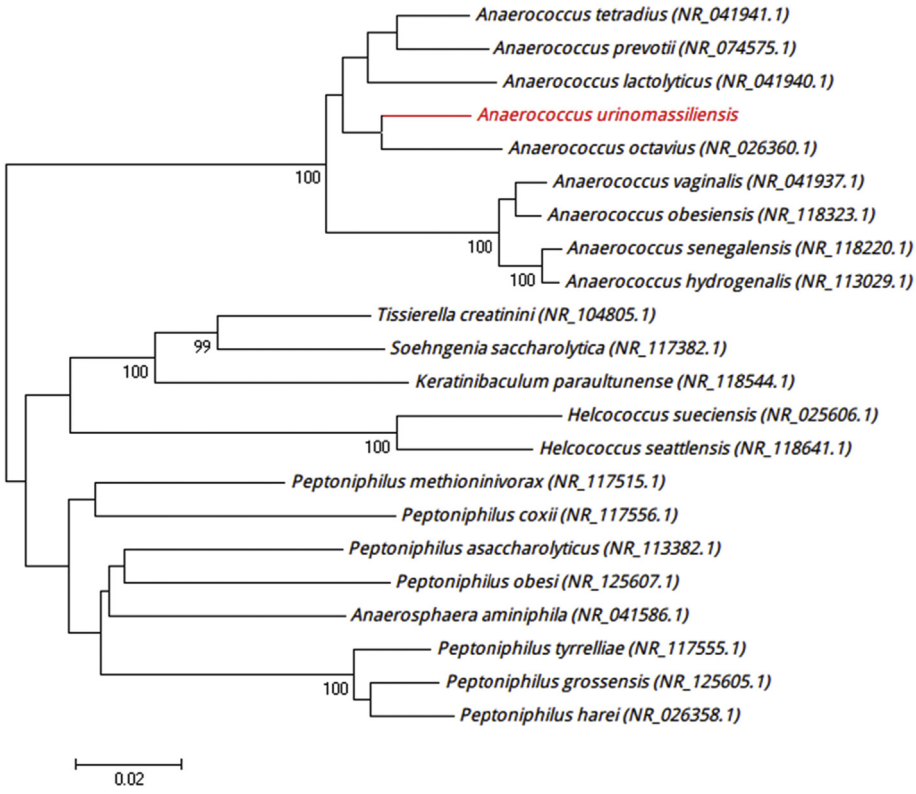

FIG. 1. Phylogenetic tree showing the position of '*Anaerococcus urinomassiliensis*' strain FC4 relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes are percentages of bootstrap values (≥ 95%) obtained by repeating the analysis 500 times to generate a majority consensus tree. GenBank accession numbers are indicated in parentheses. The scale bar indicates a 2% nucleotide sequence divergence.

MALDI-TOF Spectrum

MALDI-TOF spectrum of '*Anaerococcus urinomassiliensis*' strain FC4^T is available at http://mediterranee-infection.com/article.php?laref=256&titre=urms-database.

Nucleotide Sequence Accession Number

The 16S r RNA gene sequence was deposited in GenBank under Accession number LN898272.

Deposit in a Culture Collection

Strain FC4^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2143.

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Conflict of Interest

The authors have no conflicts of interest to declare.

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