

'*Urinacoccus massiliensis*' gen. nov. sp. nov., identified in urine sample of a 7-year-old boy hospitalized for dental care under general anaesthesia

A. Morand^{1,2}, F. Cornu³, M. Tsimaratos³, F. Cadoret^{1,2}, J.-C. Lagier^{1,2}, P. E. Fournier^{1,2} and D. Raoult^{1,2}

1) Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, CNRS (UMR 7278), IRD (198), INSERM (U1095), AMU (UM63), 2) Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, Aix-Marseille Université and 3) Pédiatrie Multidisciplinaire—Hôpital de la Timone, Marseille, France

Abstract

We report here the main characteristics of '*Urinacoccus massiliensis*' gen. nov. sp. nov., strain FC2 (CSURP1992). This strain was isolated from the urine of an asymptomatic 7-year-old boy.

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Corresponding author: D. Raoult, URMITE, CNRS (UMR 7278), IRD (198), INSERM (U1095), AMU (UM63), Faculté de Médecine, Aix-Marseille Université, 27 Boulevard Jean Moulin, 13385 Marseille Cedex 5, France
E-mail: didier.raoult@gmail.com

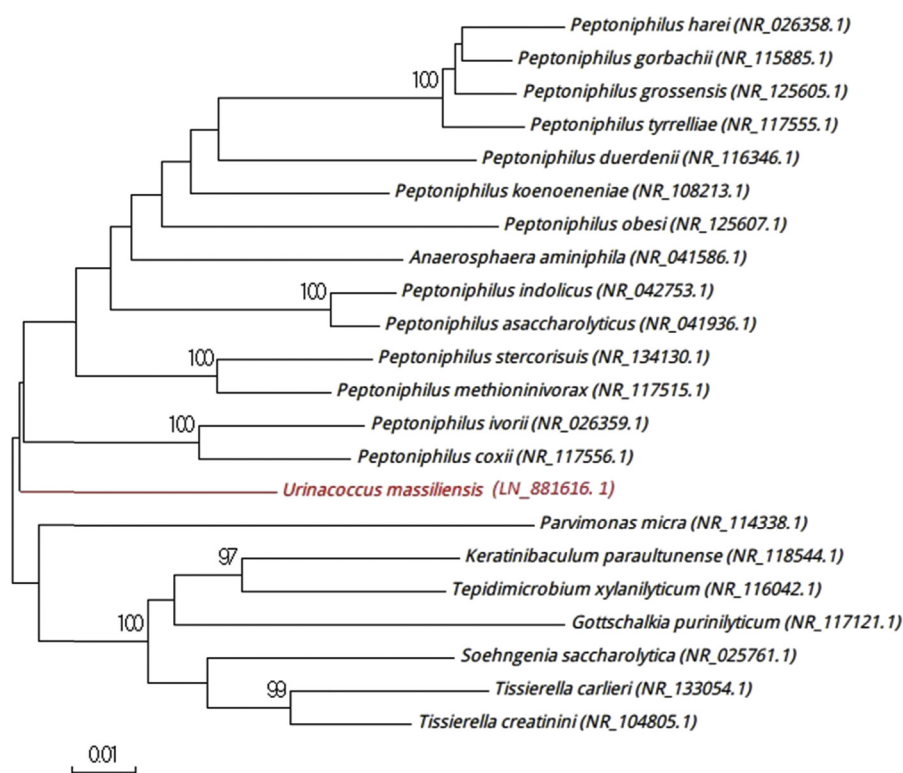
As part of a culturomics study [1,2] of the human microbiome, in 2015 we isolated from the urine of a 7-year-old boy hospitalized for dental care under general anaesthesia a bacterial strain that was not identified by matrix-assisted laser desorption–ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3]. The patient's parents provided signed informed consent and the ethics committee of the Institut Federatif de Recherche IFR48 validated 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 subculture of strain FC2 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 systems

(bioMérieux). Agar-grown colonies were microscopic and translucent with a mean diameter of 1 µm. Bacterial cells were Gram-positive cocci, ranging in length from 300 to 500 nm. Strain FC2 was catalase and oxidase negative. 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 FC2 exhibited a 91% sequence identity with *Peptoniphilus coxii* strain RMA 16757^T (GenBank Accession number GU938836) [5], the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classifies it as a new genus member of the family *Peptoniphilaceae* in the phylum *Firmicutes*.

Strain FC2 presents a 16S rRNA gene sequence divergence >5% with its phylogenetically closest species with standing in nomenclature [6], so we propose the creation of the new genus '*Urinacoccus*' gen. nov. (u.ri.na.coc'cus, N. L. masc. n. composed of u.ri.na, L. N. gen. fem. *urina*, from *urina*, the Latin name of urine and coc'cus, L. N. gen. masc. *coccus*, from *coccus*, the Latin name of bacterium having a spherical or spheroidal shape) as strain FC2 is a coccus and was first isolated from a paediatric urine sample. We propose the new species '*Urinacoccus massiliensis*' sp. nov. (mas.sil.ien'sis, L. Adj. gen. fem. *massiliensis*, of *massilia*, the Latin name of Marseille) because strain FC2 was first found in the city of Marseille.

FIG. 1. Phylogenetic tree showing the position of 'Urinacoccus massiliensis' strain FC2 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. GenBank Accession numbers are indicated in parentheses. Numbers at the nodes are percentages of bootstrap values ($\geq 95\%$) obtained by repeating the analysis 500 times to generate a majority consensus tree. The scale bar indicates a 1% nucleotide sequence divergence.



MALDI-TOF spectrum accession number. The MALDI-TOF spectrum of 'Urinacoccus massiliensis' strain FC2^T is available at: <http://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 LN881616.

Deposit in a culture collection. Strain FC2 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P1992.

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Conflict of Interest

None declared.

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