"*Lagierella massiliensis*," a new bacterium detected in human feces

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Abstract

We report here the main characteristics of *"Lagierella massiliensis"* strain SIT14 (CSUR P2012), which was isolated from a stool specimen from a healthy 28-month-old Senegalese boy.

Keywords: Culturomics, emerging bacterium, gut microbiota, *"Lagierella massiliensis"*, taxonomy
Original Submission: 12 June 2016; **Revised Submission:** 5 July 2016; **Accepted:** 25 July 2016
Article published online: 29 July 2016

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The bacterial strain SIT14 was isolated in 2015 as a part of a culturomics study of the human microbiome [1,2]. However, the strain could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3,4]. The stool had been collected in Senegal with the informed consent of the boy's parents and the validation of the ethics committee of the Institut Federatif de Recherche IFR48 under number 09-022. It was then preserved at 4°C before being shipped to Marseille, where it was frozen at −80°C before cultivation.

The stool specimen was preincubated for 30 days in an anaerobic blood culture bottle enriched with 37 g/L of Difco Marine Broth (Becton Dickinson, Le Pont de Claix, France) at 37°C. It was then subcultured on 5% sheep blood–enriched agar (bioMérieux, Marcy L'Etoile, France). Strain SIT14 grew after 7 days of incubation at 37°C. Agar-grown colonies were white and concave with a diameter ranging from 0.2 to 0.6 mm. Bacterial cells were Gram positive and coccus shaped, ranging in diameter from 0.7 to 0.9 µm. Strain SIT14 was catalase positive but oxidase negative. The 16S rRNA gene was sequenced using the fD1-rP2 primers as previously described [5], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain SIT14 exhibited a 90.5% sequence identity with *Finegoldia magna* strain ATCC 29328^T (GenBank accession no. NR_074677. 1), the phylogenetically closest species with standing in nomenclature (Fig. 1). *Finegoldia magna* is a Gram-positive anaerobic bacterium that was originally isolated from an abdominal wound and was described in 2008 [6].

Because strain SIT14 exhibited a 16S rRNA sequence divergence of >5% with the phylogenetically closest species with standing in nomenclature [7], we propose that it is the representative strain of a new genus within the family *Peptoniphilaceae* in the phylum *Firmicutes* that we name *"Lagierella"* (la.gi.e.rel'la, N.L. fem. n. *lagierella,* in honor of the French scientist Jean-Christophe Lagier). Strain SIT14^T is the type strain of the new species *"Lagierella massiliensis"* (ma.si.li.en'sis L., fem. adj., *massiliensis,* "of Massilia," the Roman name of Marseille, where strain SIT14^T was isolated).

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of *"L. massiliensis"* is available at http://www.mediterraneeinfection.com/article.php?laref=256&titre=urms-database.

http://dx.doi.org/10.1016/j.nmni.2016.07.005

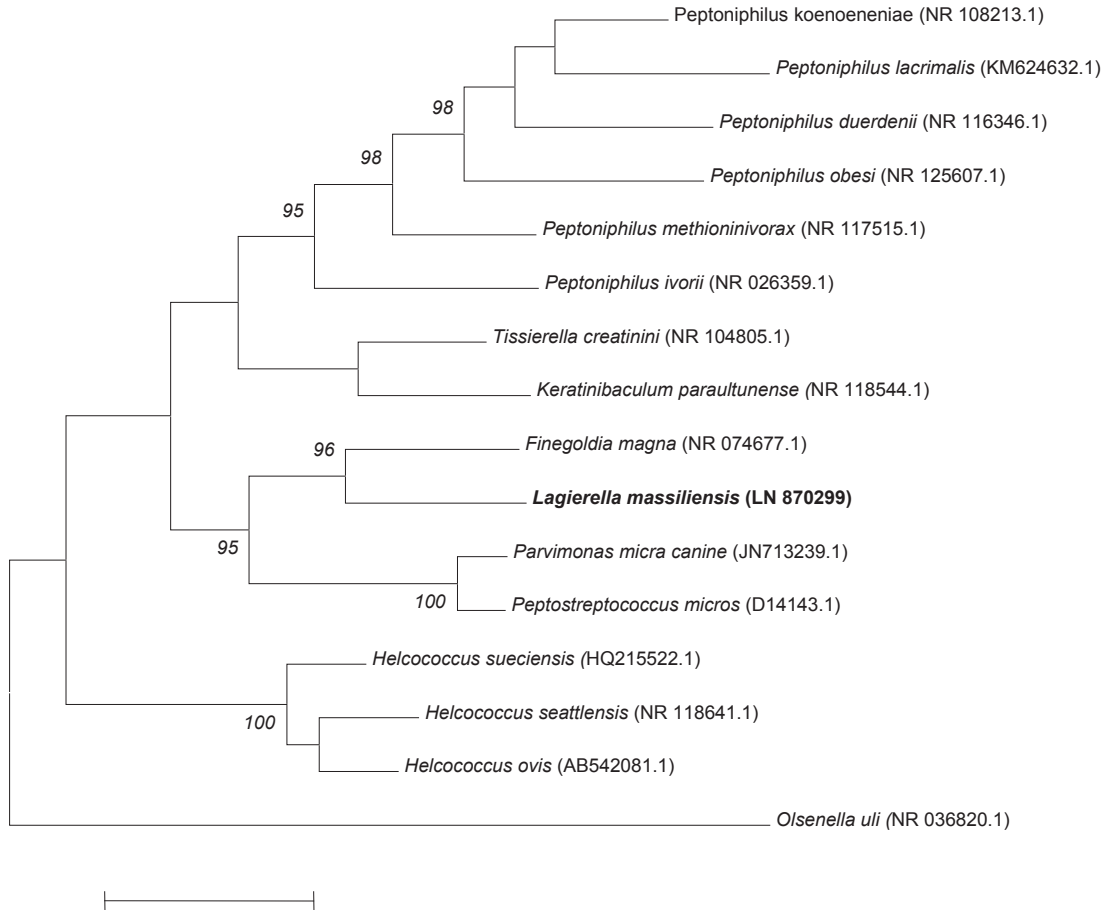

FIG. 1. Phylogenetic tree showing position of *"Lagierella massiliensis"* strain SIT14 relative to other phylogenetically close species with a validly published name. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Accession numbers are indicated in parentheses. Numbers at nodes are percentages of bootstrap values (>95%) obtained by repeating analysis 500 times to generate majority consensus tree. Scale bar indicates 5% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN870299.

Deposit in a culture collection

Strain SIT14 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2012.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

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