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“*Massiliomicrobiota timonensis*,” a new bacterial species isolated from the human gut

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Abstract

We report the main characteristics of a new bacterium, “*Massiliomicrobiota timonensis*” strain SNI16 (= CSUR P2264), which was isolated from the stool of a 87-year-old patient.

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Keywords: Culturomics, emerging bacterium, gut microbiota, *Massiliomicrobiota timonensis*, taxonomy

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After applying the culturomics strategy to study the bacterial diversity of a stool specimen collected from a 87-year-old patient [1], we isolated a bacterial strain that could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a MicroFlex spectrometer (Bruker Daltonics, Leipzig, Germany) [2]. This strain was isolated from a stool specimen collected from an 87-year-old patient hospitalized in September 2015 at the Timone Hospital in Marseilles, France, for cognitive impairment complicated by weight loss. The patient’s family provided a signed informed consent. Approval of the study by the local ethics committee of IFR48 (Marseille, France) was obtained under agreement 09-022.

The initial growth of strain SNI16 was obtained after a 5-day incubation in a 5% sheep’s blood– and filter-sterilized rumen-enriched anaerobic blood culture vial (Becton-Dickinson, Pont de Claix, France) at 37°C. Then strain SNI16 was subcultured on 5% sheep’s blood–enriched Columbia agar (bioMérieux,

Marcy l’Etoile, France) at 37°C in anaerobic atmosphere generated by AnaeroGen (bioMérieux). After 72 hours of incubation, colonies of strain SNI16 are pale grey, slightly translucent and exhibit a diameter of 1 to 2 mm. Cells from strain SNI16 are Gram-negative and rod shaped in chains. Cells are not mobile, do not form spores and exhibit a diameter of 0.3 to 0.4 µm and a length of 1.8 to 2.2 µm in electron microscopy. Strain SNI16 is strictly anaerobic and exhibits no catalase or oxidase activity. The 16S rRNA gene was sequenced using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) as previously described [3]. Strain SNI16 exhibits a 91% sequence identity with *Coprobacillus cateniformis* strain JCM10604^T (GenBank accession no. NR_024733), the phylogenetically closest species with standing in nomenclature (Fig. 1), which potentially classifies it as a member of a new genus within the family *Erysipelotrichaceae* in the *Firmicutes* phylum [4].

Strain SNI16 shares with *Coprobacillus cateniformis* strain JCM10604^T several features including an isolation from human faeces, obligate anaerobic growth, cell shape and absence of spore and motility [5].

For strain SNI16^T, exhibiting a 16S rRNA gene sequence divergence of more than 5% with the phylogenetically closest species with a validly published name [6], we formally propose the creation of the new genus, “*Massiliomicrobiota*” gen. nov.

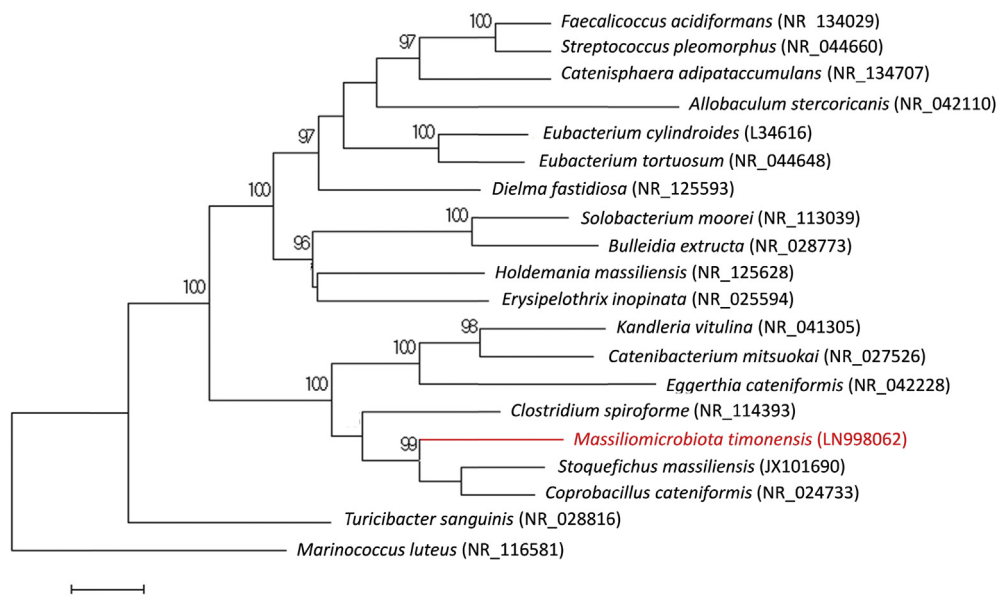


FIG. 1. Phylogenetic tree showing position of *Massiliomicrobiota timonensis* strain SNI6^T (red) relative to other phylogenetically close members of family *Erysipelotrichaceae*. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences 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 values greater than 95% are displayed. *Marinococcus luteus* was used as outgroup. Scale bar indicates 2% nucleotide sequence divergence.

(mas.si.lio.mi.cro.bio'ta N.L. fem. n., a combination of Massilio, the Latin name of Marseille, and microbiota, in reference to the human gut flora from which strain SNI6^T was isolated). Strain SNI6^T is the type strain of “*Massiliomicrobiota timonensis*” gen. nov., sp. nov. (ti.mo.nen'sis. L. masc. adj., from timonensis, pertaining to Timone, the name of the main university hospital in Marseille, France, at which the strain was isolated).

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of *M. timonensis* 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 LN998062.

Deposit in a culture collection

Strain SNI6^T was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number CSUR P2264.

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Conflict of Interest

None declared.

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