

“*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

Original Submission: 25 April 2016; **Revised Submission:** 3 May 2016; **Accepted:** 9 May 2016

Article published online: 17 May 2016

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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.

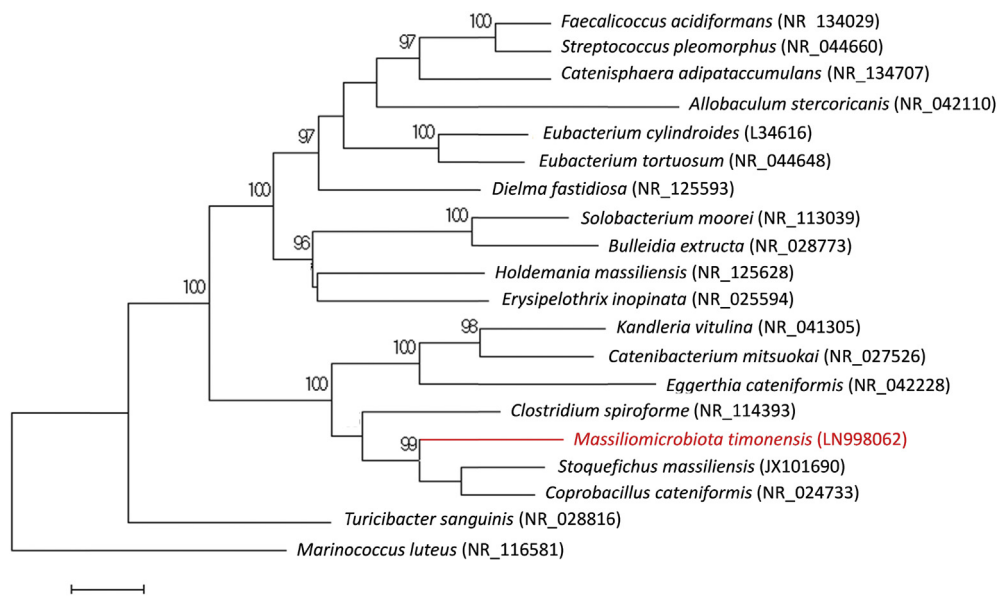


FIG. 1. Phylogenetic tree showing position of *Massiliomicrobiota timonensis* strain SNI6^T (red) relative to other phylogenetically close members of family *Erysipelotrichaceae*. GenBank accession numbers are indicated in parentheses. Sequences were aligned using CLUSTALW, and phylogenetic inferences 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.

Acknowledgement

This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [1] Lagier JC, Hugon P, Khelaifa S, Fournier PE, La Scola B, Raoult D. The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. *Clin Microbiol Rev* 2015;28:237–64.
- [2] Seng P, Abat C, Rolain JM, Colson P, Lagier JC, Gouriet F, et al. Identification of rare pathogenic bacteria in a clinical microbiology laboratory: impact of matrix-assisted laser desorption/ionization–time of flight mass spectrometry. *J Clin Microbiol* 2013;51:2182–94.
- [3] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. 16S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentified bacterial isolates. *J Clin Microbiol* 2000;38:3623–30.
- [4] Euzéby J. Validation list n° 74. *Int J Syst Evol Microbiol* 2000;50:949–50.
- [5] Kageyama A, Benno Y. *Coprobacillus cateniformis* gen. nov., sp. nov., a new genus and species isolated from human feces. *Microbiol Immunol* 2000;44:23–8.
- [6] Kim M, Oh HS, Park SC, Chun J. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. *Int J Syst Evol Microbiol* 2014;64:346–51.