# *"Senegalia massiliensis,"* a new bacterium isolated from the human gastrointestinal tract

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## Abstract

We report the main characteristics of *"Senegalia massiliensis"* strain SIT17 (= CSUR P2130) that was isolated from the stool of a healthy 13-month-old Senegalese boy.



**Keywords:** Culturomics, emerging bacterium, gut microbiota, *Senegalia massiliensis*, taxonomy
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In 2015, using culturomics, a strategy combining several culture conditions to study the human gut microbiome [1,2], we isolated from the stool of a healthy 13-month-old Senegalese boy 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) [3]. The child's parents provided a signed informed consent, and the study was approved by ethics committee of the Institut Fédératif de Recherche IFR48 under number 09-022.

The sample was frozen at −80°C in Senegal and then transported in dry ice to Marseille, France, where it was used for bacterial culture. The stool was incubated at 37°C in an anaerobic blood culture bottle (Becton-Dickinson, Pont de Claix, France) enriched with 37 g/L of Difco Marine Broth (Becton Dickinson). Colonies subcultured on 5% sheep's blood–enriched Columbia agar (bioMérieux, Marcy l'Etoile, France), and were grey and translucent with a mean diameter of 0.5 to 1 mm. Bacterial cells were Gram positive, rod shaped and motile but formed no spores. Cells ranged in length and width from 2 to 4.5 µm and 0.3 to 0.5 µm, respectively. Strain SIT17 exhibited catalase but no oxidase activity. The 16S rRNA gene was sequenced using the fD1-rP2 primers as previously described, using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain SIT17 exhibited a 92.72% sequence identity with *Sporosalibacterium faouarense* strain SOL3f37 (GenBank accession no. NR_116364), the phylogenetically closest species with standing nomenclature (Fig. 1). *S. faouarense* was isolated from a hydrocarbon-polluted soil surrounding a deep petroleum environment located in south Tunisia [4]. Cells of strain SOL3f37 are Gram-positive, rod shaped and motile.

For strain SIT17, exhibiting a 16S rRNA gene sequence divergence >5% with its phylogenetically closest species with standing in nomenclature [5], we propose the creation of the new genus *"Senegalia"* gen. nov. (se.ne.ga'lia N.L. fem. n., of Senegal, where the patient from whom strain SIT17$^T$ was isolated lived). Strain SIT17$^T$ is the type strain of *"Senegalia massiliensis"* gen. nov., sp. nov. (mas.il.i.en'sis. L. gen. fem. n., massiliensis, of Massilia, the Latin name of Marseille, where strain SIT17$^T$ was characterized.



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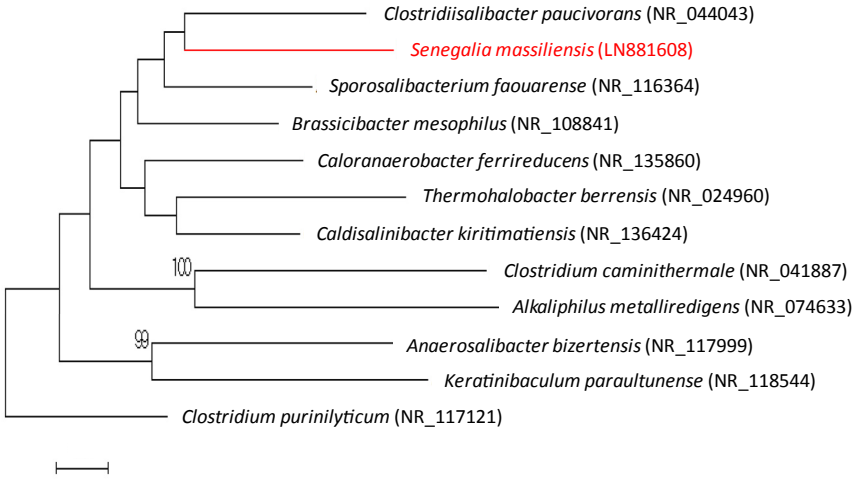


**FIG. 1.** Phylogenetic tree showing position of *"Senegalia massiliensis"* strain SIT17 relative to other phylogenetically close species with validly published names. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values (≥95%) obtained by repeating analysis 500 times to generate majority consensus tree. GenBank accession numbers are indicated in parentheses. Scale bar indicates 1% nucleotide sequence divergence.

## MALDI-TOF MS spectrum accession number

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

## Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN881608.

## Deposit in a culture collection

Strain SIT17 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P2130.

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## Conflict of Interest

None declared.

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