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# “*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.

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**Keywords:** Culturomics, emerging bacterium, gut microbiota, *Senegalia massiliensis*, taxonomy

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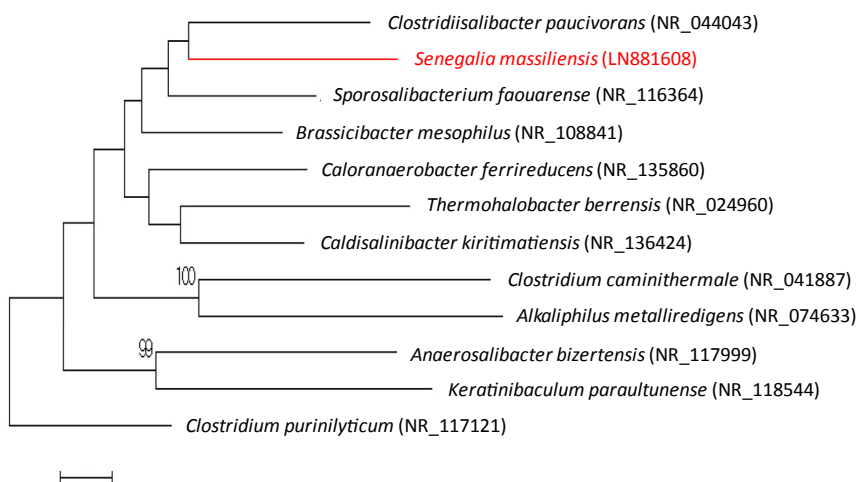
In 2015, using culturomics, a strategy combining several culture conditions to study the human gut microbiome [1,2], we isolated from the stool of a healthy 13-month-old Senegalese boy a bacterial strain that could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (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  $-80^{\circ}\text{C}$  in Senegal and then transported in dry ice to Marseille, France, where it was used for bacterial culture. The stool was incubated at  $37^{\circ}\text{C}$  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  $\mu\text{m}$  and 0.3 to 0.5  $\mu\text{m}$ , 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 faouarens* strain SOL3f37 (GenBank accession no. NR\_116364), the phylogenetically closest species with standing nomenclature (Fig. 1). *S. faouarens* 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<sup>T</sup> was isolated lived). Strain SIT17<sup>T</sup> is the type strain of “*Senegalia massiliensis*” gen. nov., sp. nov. (mas.i.li.en'sis. L. gen. fem. n., massiliensis, of Massilia, the Latin name of Marseille, where strain SIT17<sup>T</sup> was characterized.

**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 ( $\geq 95\%$ ) 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?leref=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.

### Acknowledgement

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### Conflict of Interest

None declared.

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