

## NEW SPECIES

# Isolation of new species “*Peptoniphilus phoceensis*” from human gut

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## Abstract

Taxonogenomics coupled with culturomics leads to descriptions of new bacteria. Thanks to this strategy, we report the main characteristics of “*Peptoniphilus phoceensis*” strain SIT15, a new bacterium isolated from a stool sample of a 1-year-old healthy Senegalese boy.

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**Keywords:** Culturomics, gut microbiota, human, “*Peptoniphilus phoceensis*” sp. nov., taxonogenomics

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Culturomics, a recently developed alternative to traditional culture methods, improves the likelihood of detecting bacteria [1,2]. When we applied this strategy to a stool sample from a healthy 1-year-old boy from Senegal, bacterium strain SIT15 was isolated by matrix-assisted desorption ionization–time of flight mass spectrometry but failed to provide systematic identification (<http://www.mediterranee-infection.com/article.php?leref=256&titre=urms-database>) on a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany). The stool was collected in 2014 after the protocol was accepted by the national ethics committee of Senegal and IFR48 (Marseille, France) under numbers 11-017 and 09-12-022, respectively.

Parents' written informed consent was obtained. Strain SIT15 was isolated after 15 days of culture in a sterile bottle containing a marine medium (bioMérieux, Marcy l'Étoile, France), followed by subculture in 5% sheep's blood–enriched Columbia agar (bioMérieux) under anaerobic conditions at 37°C [4–6]. Gram-positive coccus, strain SIT15, exhibited catalase activity without oxidase and grew after 24 hours. Individual colonies are opaque and have a diameter of 1 mm on agar plates; individual cells exhibit a diameter of 1.5 μm. Motile and

non–spore forming, it grows between 28°C and 40°C (with 37°C optimal) and supports a salinity of approximately 0 (range, 0–5%) and pH ranging from 6 and 8.5.

Identification was completed by sequencing the 16S rRNA using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) and an adequate set of primer rP2-fD1 [4–6]. The 16S rRNA sequence obtained was corrected and assembled by ChromasPro 1.34 (Technelysium, Tewantin, Australia). A BLASTn analysis was performed against the online GenBank database (<http://blast.ncbi.nlm.nih.gov/gate1.inist.fr/Blast.cgi>). The results demonstrated that the 16S rRNA sequence of strain SIT15 (GenBank accession no. LN881605) exhibited 96.95% identity with the closest species, *Peptoniphilus grossensis* strain ph5 (Fig. 1) [7]. This value is lower than the threshold recommended to delineate a new species [8]. Therefore, strain SIT15 was putatively classified as a new species, “*Peptoniphilus phoceensis*” sp. nov. strain SIT15, belonging to the genus *Peptoniphilus* within the family Peptoniphilaceae created in 2014 by Johnson *et al.* [9].

The closest species of *P. phoceensis* (*P. grossensis* strain ph5, *Peptoniphilus obesi* strain ph1, *Peptoniphilus timonensis* strain JC401, *Peptoniphilus gorbachii* strain WAL10418) are anaerobic Gram-positive microorganisms without oxidase and nitrate reductase activities [7]. *P. grossensis* strain ph5, *P. obesi* strain ph1 and *P. timonensis* strain JC401 are nonmotile [7]. In contrast to strain SIT15, *P. grossensis* strain ph5 and *P. timonensis* strain JC401 can produce endospores [7].

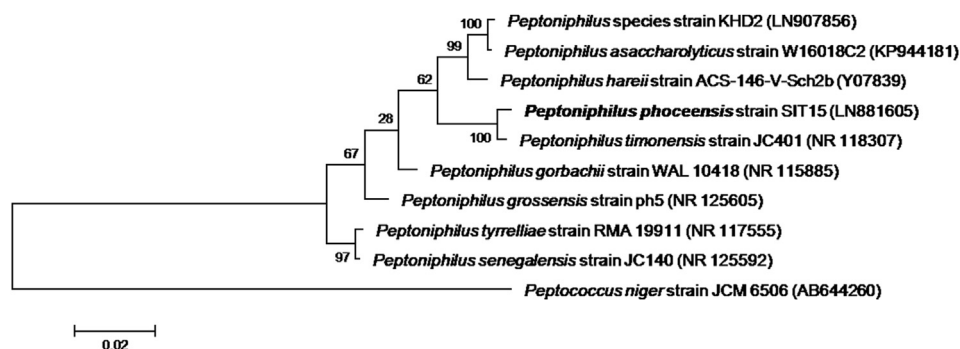


FIG. 1. Phylogenetic tree highlighting position of "Peptoniphilus phoceensis" strain SIT15. Scale bar = 0.02% nucleotide sequence divergence.

The divergence of 16S rRNA sequences between *P. phoceensis* strain SIT15 and the phylogenetically closest species was more than 2%, exceeding the recommended threshold value of 1.3% [8]. Thus, we propose the creation of the new species "Peptoniphilus phoceensis" sp. nov., named for Phocaea, the Hellenic city of sailors who settled in Marseille, France, where this bacterium was isolated, 2600 years ago. Strain SIT15<sup>T</sup> is the type strain of the new species "Peptoniphilus phoceensis" sp. nov.

Description of gut anaerobes, previously shown to be depleted in malnutrition [10], is of critical importance in deciphering the links between gut microbiota and human health.

### Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN881605.

### Deposit in a culture collection

Strain SIT15 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under accession number P2336.

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### Conflict of Interest

None declared.

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