'*Phoenicibacter massiliensis*' gen. nov., sp. nov., a new bacterium isolated from the human gut of a pygmy woman

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Abstract

This study supports the main characteristics of the new genus and new species '*Phoenicibacter massiliensis*' strain Marseille-P3241^T (CSUR P3241), a new bacterium isolated from a stool sample of a healthy 47-year-old pygmy woman.

Keywords: Culturomics, emerging bacteria, gut microbiota, human microbiota, *'Phoenicibacter massiliensis'*
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In 2015, stool samples were collected in Congo for analysis as part of a project of the human microbiome description via culturomics [1]. Before the study began, approval was obtained by the ethics committee of the Institut Federatif de Recherche IFR48 (Marseille, France) under number 09-022.

One millilitre of phosphate-buffered saline was used to dilute stool samples before inoculation in blood culture media supplemented with 5 mL filtered rumen and 5 mL sheep's blood. The culture bottle was incubated at 37°C under anaerobic conditions. After 10 days of growth, strain Marseille-P3241 was isolated on 5% blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France). Colonies were smooth with a diameter ranging between 0.1 and 0.5 mm. Strain Marseille-P3241 cells are coccobacillus, Gram positive, and catalase and oxidase negative, with an average diameter of 2.9 µm. This strain could not be identified using our systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2]. Therefore, sequencing of the 16S rRNA gene was performed by the mean of the fD1-rP2 primers as previously described (Eurogentec, Seraing, Belgium) using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) [3].

Strain Marseille-P3241 exhibited an 87.7% sequence identity with *Gordonibacter pamelaeae,* the phylogenetically closest published species with standing in nomenclature (Fig. 1). Having a 16S rRNA gene sequence similarity <5% with the phylogenetically closest species with standing in nomenclature, we propose the creation of the new genus [4], *Phoenicibacter* (Phoe.ni.ci.bac′ter, N.L. masc. gen. n., for 'Phoenician,' the cultural ancestry of the person who cultivated strain Marseille-P3241). Marseille-P3241^T is the type strain of the new species '*Phoenicibacter massiliensis*' gen. nov., sp. nov. (mas.il.i.en′sis, L. gen. masc. n., *massiliensis,* pertaining to Massilia, the antic name of the city of Marseille, where this bacteria was discovered).

MALDI-TOF MS spectrum

The MALDI-TOF MS spectrum of *P. massiliensis* is available online (http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database).

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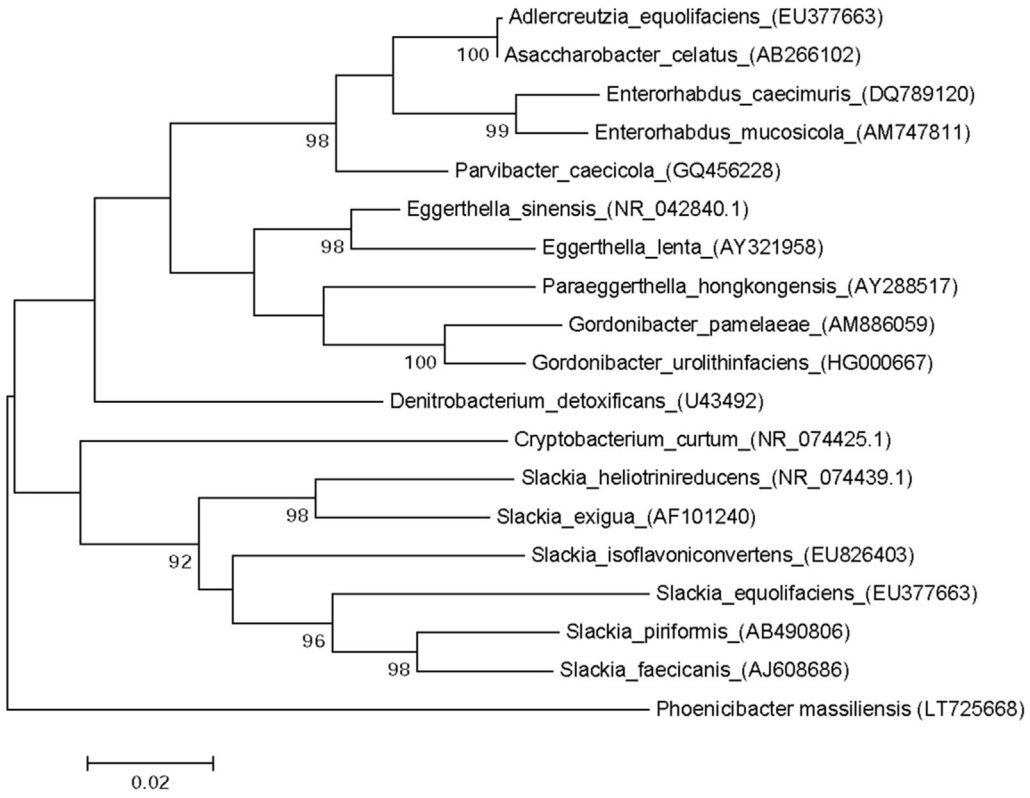

FIG. 1. Phylogenetic tree showing positioning of '*Phoenicibacter massiliensis*' strain Marseille-P3241 among its phylogenetically closest species. Sequence alignment was performed by CLUSTALW, and phylogenetic inferences were generated by MEGA software with maximum-likelihood approach. Five hundred repeats were used for bootstrap value generation and are shown on nodes. Minimum 90% bootstrap value was only considered for tree. Scale bar indicates 2% nucleotide sequence divergence.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LT725668.

Deposit in a culture collection

Strain Marseille-P3241^{T} was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P3241.

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Conflict of Interest

None declared.

References

[1] Lagier JC, Hugon P, Khelaifia 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 unidentifiable bacterial isolates. J Clin Microbiol 2000;38:3623–30.

[4] 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.