

'*Helcococcus massiliensis*' sp. nov., a new bacterial species isolated from the vaginal sample of a woman with bacterial vaginosis living in Dielmo, Senegal

N. S. Fall¹, D. Raoult², C. Sokhna¹ and J. C. Lagier²

1) Aix Marseille Univ, IRD (Dakar, Marseille, Papeete), AP-HM, IHU-Méditerranée Infection, UMR Vecteurs—Infections Tropicales et Méditerranéennes (VITROME) and 2) Aix Marseille Univ, IRD, APHM, UMR MEPHI, Institut Hospitalo-Universitaire Méditerranée-Infection, Marseille, France

Abstract

We report here the isolation of a new bacterial species '*Helcococcus massiliensis*' strain Marseille P4590 (CSURP4590), isolated from the vaginal sample of a woman with bacterial vaginosis.

© 2018 Published by Elsevier Ltd.

Keywords: Culturomics, Genomics, *Helcococcus massiliensis*, Taxonogenomics, Taxonomy

Original Submission: 23 March 2018; **Revised Submission:** 1 June 2018; **Accepted:** 5 June 2018

Article published online: 12 June 2018

Corresponding author: J.-C. Lagier, Aix Marseille Univ, IRD, AP-HM, IHU-Méditerranée Infection, UMR Microbes Evolution Phylogénie (MEPHI), 19-21 Boulevard Jean Moulin, 13005 Marseille, France.
E-mail: jclagier@yahoo.fr

In 2017, as a part of the human microbiota exploration using culturomics [1,2], a vaginal swab was collected from a 36-year-old woman with bacterial vaginosis living in Dielmo, rural Senegal, West Africa. The study and consent procedures were approved by the Senegalese Comité National d'Ethique pour la Recherche en Santé ethics committee in accordance with the SEN protocol 16/04 under number 00039 as well as by the ethics committee of the Institut Hospitalo-Universitaire Méditerranée Infection under number 2016-011.

The initial growth of the bacterium was obtained after 15 days of preincubation in anaerobic liquid medium enriched with sheep's blood and rumen. The solution was then seeded on 5% sheep's blood agar under anaerobic conditions at 37°C. Agar-grown colonies were beige, circular and opaque with a mean diameter of 1 mm. The bacterium was a Gram-negative, non-spore forming and nonmotile anaerobic coccus. Strain P4590 was catalase negative and oxidase negative. The colonies

could not be identified by our systematic matrix-assisted laser desorption-ionization time-of-flight screening (<http://mediterranean-infection.com/article.php?laref=256&titre=urms-database>) on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [3] (Fig. 1). The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described, using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain P4590 exhibited a 95.5% sequence identity with *Helcococcus seattlensis*, the phylogenetically closest species with standing in nomenclature (Fig. 2), which putatively classified it as a member of the genus *Helcococcus* within the family incertae sedis in the phylum *Firmicutes*. This value is under the threshold of 98.7% that defines a new species, as established by Stackebrandt and Ebers [4]. We therefore propose the creation of the new species '*Helcococcus massiliensis*' (ma.si.li.en.sis, L. fem. adj., *massiliensis*, 'of Massilia,' the Latin name of Marseille where *H. massiliensis* was first isolated). Strain 4590 is the type strain of the new species P4590.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LT934442.

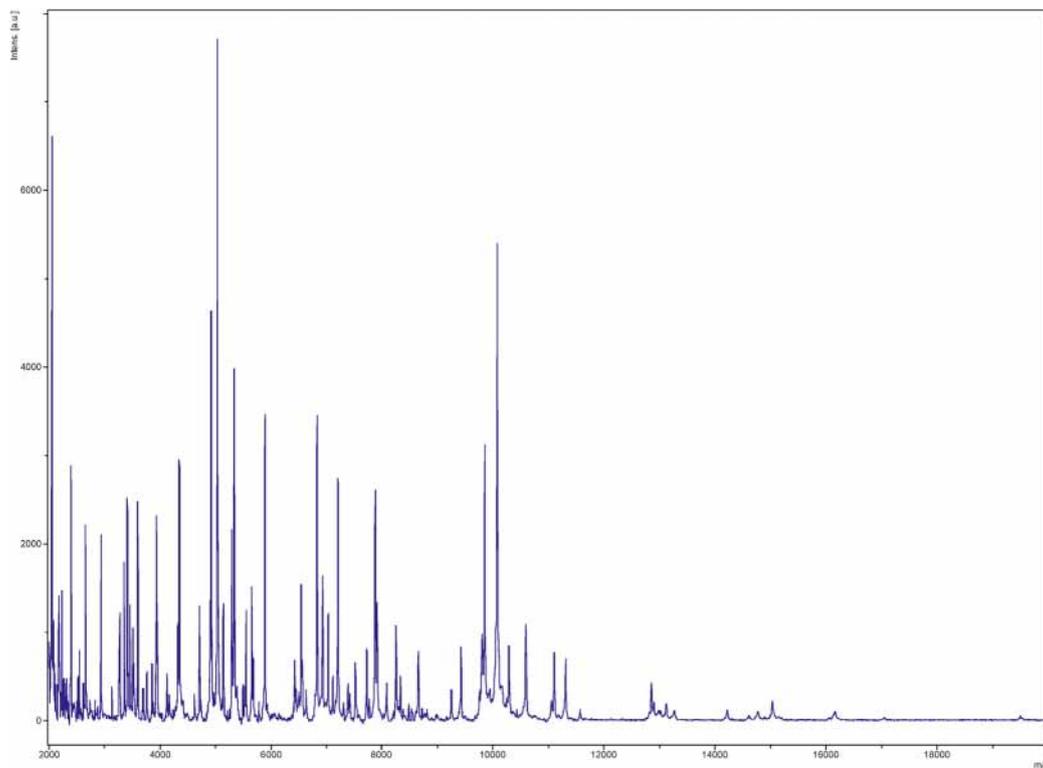


FIG. 1. Reference matrix-assisted desorption ionization–time of flight mass spectrometry analysis of *Helcococcus massiliensis* strain Marseille P4590 (CSUR P4590).

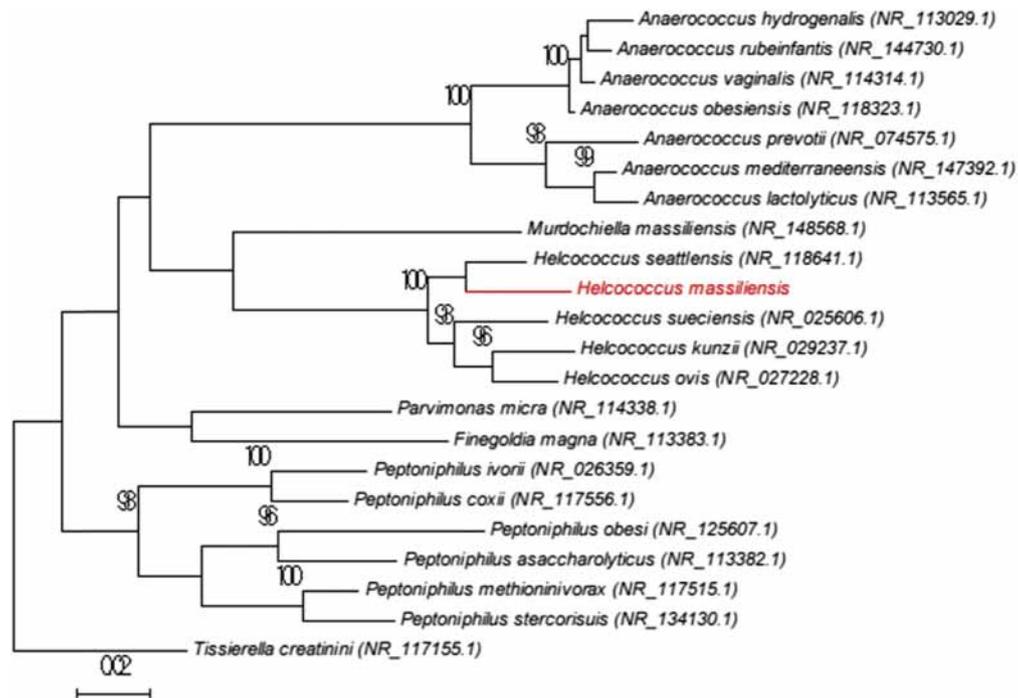


FIG. 2. Phylogenetic tree showing position of '*Helcococcus massiliensis*' strain P4590 relative to its phylogenetically closest neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstraps scores of at least 90% were retained. Scale bar indicates 2% nucleotide sequence divergence.

Deposit in a culture collection

Strain P4590 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR, WDCM 875) under number P4590.

Acknowledgements

This work has benefited from the support of the French state, managed by the 'Agence Nationale pour la Recherche' including the 'Programme d'Investissement d'avenir' under reference Méditerranée Infection 10-IAHU-03. This work was supported by Région Provence Alpes Côte d'Azur and European funding FEDER PRIMI.

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] Lagier JC, Khelaifia S, Alou MT, Ndongo S, Dione N, Hugon P, et al. Culture of previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol* 2016;1:16203.
- [3] Seng P, Drancourt M, Gouriet F, La Scola B, Fournier PE, Rolain JM, et al. Ongoing revolution in bacteriology: routine identification of bacteria by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. *Clin Infect Dis* 2009;49:543–51.
- [4] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152–5.