'*Corynebacterium fournierii*,' a new bacterial species isolated from the vaginal sample of a patient with bacterial vaginosis

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Abstract

Here we describe briefly *'Corynebacterium fournierii'* strain Marseille P2948 (= CSUR P2948 = DSM103271), a new bacterium that was isolated from the vaginal sample of a 21-year-old woman with bacterial vaginosis.

Keywords: Bacterial vaginosis, *'Corynebacterium fournierii'*, culturomics, taxonomy, vaginal microbiota
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As part of the study of the vaginal microbiota by the microbial culturomics [1], we isolated from the vaginal swab of a 21-year-old Frenchwoman with bacterial vaginosis [2] a bacterial strain that could not be identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; Microflex spectrometer, Bruker Daltonics, Leipzig, Germany) [3]. The study was authorized by the local ethics committee of the IFR48 (Marseille, France; agreement 09-022). The patient gave also her written consent.

The initial growth of strain Marseille P2948 was obtained after 30 days of preincubation of the vaginal sample in a blood culture bottle (Becton Dickinson, Le Pont-de-Claix, France) enriched with 4 mL of rumen that was filter-sterilized through a 0.2 µm pore filter (Thermo Fisher Scientific, Villebon-sur-Yvette, France) and 3 mL of sheep's blood (bioMérieux, Marcy l'Etoile, France), then subcultured on Chocolat Poly-ViteX agar (Becton Dickinson) and incubated for 2 days in an aerobic atmosphere. Bacterial cells were facultative anaerobic Gram positive and rod shaped, with good growth under aerobic conditions and very weak growth under anaerobic conditions. They were nonmotile and non–spore forming, and had a mean breadth of 0.7 µm and a mean length of 1.4 µm. After 2 days of incubation at 37°C under aerobic conditions on Columbia blood agar supplemented with 5% sheep's blood, colonies were very small, slightly greyish and circular with an approximate diameter of 1 mm. Catalase reaction was positive but oxidase activity was negative.

The 16S rRNA gene sequence was obtained after amplification using the universal primer pair fD1 and rp2 and a 3130-XL sequencer (Applied Biosciences, Saint-Aubin, France), as previously reported [4]. 16S rRNA gene sequence–based identification of strain Marseille P2948 showed 98.7% of identity with *Corynebacterium ureicelerivorans* strain IMMIB RIV-2301 (GenBank accession no. NR_042558.1), the phylogenetically closest bacterium with a validly published name (Fig. 1). Strain Marseille P2948 exhibited also 93.4% *rpoB* gene sequence similarity with *Corynebacterium ureicelerivorans*. Because the 16S rRNA gene sequence was in the range of 98.7% to define a new species [5], strain Marseille P2948 was considered as a new species within the *Corynebacterium* genus in the *Coriobacteriaceae* family.

Strain Marseille P2948 presents a 16S rRNA gene sequence divergence of around 1.3% with its phylogenetically closest species [6], and we propose that strain Marseille P2948 may be

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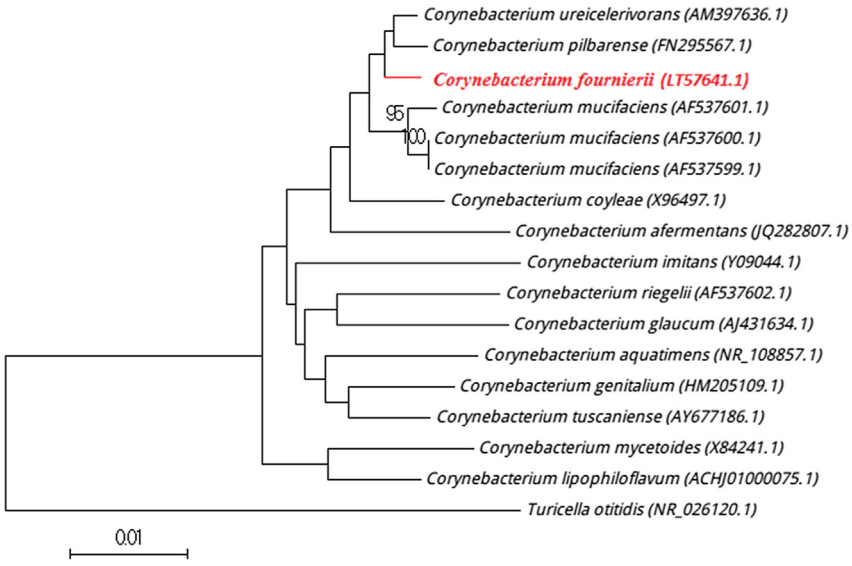

FIG. 1. Phylogenetic tree highlighting position of *'Corynebacterium fournierii'* strain Marseille P2948^T relative to other closest species. GenBank accession numbers are indicated after name. Sequences were aligned by Muscle v3.8.31 with default parameters, and phylogenetic inferences were obtained by neighbour-joining method with 500 bootstrap replicates, within MEGA6 software. Only bootstrap values ≥95% are shown. Scale bar indicates 1% nucleotide sequence divergence.

the putative representative of a novel species named *'Corynebacterium fournierii'* sp. nov. (four.nier'ii, L. gen. n. *fournierii,* in honor of French scientist P.-E. Fournier for his outstanding contributions to medical microbiology and taxonogenomics). Strain Marseille P2948^T is the type strain of the new species *'Corynebacterium fournierii'* sp. nov.

MALDI-TOF MS spectrum

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

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in EMBL-EBI under accession number LT576414.1.

Deposit in a culture collection

Strain Marseille P2948 was deposited in both the 'Collection de Souches de l'Unité des Rickettsies' (CSUR, WDCM 875) and the collection 'Deutsche Sammlung von Mikroorganismen' (DSM) under numbers P2948 and 103271 respectively.

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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] Menard JP, Fenollar F, Henry M, Bretelle F, Raoult D. Molecular quantification of *Gardnerella vaginalis* and *Atopobium vaginae* loads to predict bacterial vaginosis. Clin Infect Dis 2008;20:33–43.
[3] 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.
[4] 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.
[5] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. Microbiol Today 2006;33:152–5.
[6] Yarza P, Richter M, Peplies J, Euzeby J, Amann R, Schleifer KH, et al. The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of all sequenced type strains. Syst Appl Microbiol 2008;31:241–50.