NEW SPECIES

‘Peptoniphilus vaginalis’ sp. nov., a new species isolated from human female genital tract

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Abstract

We relate here the main characteristics of ‘Peptoniphilus vaginalis’, strain KHD2 (= CSUR P0125 = DSM 101742), a new member of the Peptoniphilus genus, cultivated from a vaginal sample of a woman with bacterial vaginosis.

Keywords: bacterial vaginosis, culturomics, ‘Peptoniphilus vaginalis’, taxonomy, vaginal flora

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As part of the study of the human vaginal microbiota by culturomics in our laboratory (Marseille, France) [1], we isolated from the genital tract of a 33-year-old woman with bacterial vaginosis [2], a new bacterial strain of the Peptoniphilaceae family for which identification using matrix-assisted laser desorption–ionization time-of-flight mass spectrometry (MALDI-TOF MS) with a MicroFlex spectrometer (Bruker Daltonics, Leipzig, Germany) failed [3].

The agreement number of the National Ethics Committee of the IFR48 (Marseille, France) for this study is 09-022. The patient has also given her written consent.

The vaginal sample was first pre-incubated for 24 hours in a blood culture (BD Diagnostics, Le Pont-de-Claix, France) supplemented 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 blood (bioMérieux, Marcy l’Étoile, France) at 37°C. Then, the pre-incubated sample was inoculated on Colistin nalidixic acid (CNA) agar (BD Diagnostics) and Trypticase Soy Agar plates. Strain KHD2 was isolated in anaerobic condition at 37°C after a 4-day incubation on both Colistin nalidixic acid (CNA) and Trypticase Soy Agar plates. Colonies were translucent and grey with a diameter of 1–1.5 mm on Columbia agar with 5% sheep blood (bioMérieux). Bacterial cells are Gram-positive cocci with a diameter ranging from 0.5 to 0.7 μm, catalase-negative and oxidase-negative.

The amplification of the 16S rRNA gene was performed using the universal pair of primers fD1 and rp2 as previously reported [4]. Amplicon was sequenced with 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain KHD2 exhibited a 98.2% sequence similarity with Peptoniphilus harei (GenBank NR_026358.1), the phylogenetically closest validated species (Fig. 1). This value is lower than the 98.7% 16S rRNA sequence threshold recommended to delineate a new species in the phylum Firmicutes without carrying out DNA–DNA hybridization [5]. Hence, the strain KHD2 may be classified as the representative strain of a novel species within the genus Peptoniphilus in the Peptoniphilaceae family. Created in 2001 by Ezaki et al., after the subdivision of the genus Peptostreptococcus into three genera (Anaerococcus, Peptoniphilus and Gallicola), the genus Peptoniphilus contains only strictly anaerobic bacteria [6]. Besides, this genus currently includes 13 species that have been identified in diverse human clinical specimens like sacral

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ulcer, vaginal discharge, and ovarian, peritoneal and lachrymal gland abscesses [7].

As strain KHD2 is >1.8% divergent in the 16S rRNA gene sequence from its closest phylogenetic neighbour [8], we propose that it may be the representative strain of a novel species named ‘Peptoniphilus vaginalis’ sp. nov (va.gi.na’lis. L. n. vagina sheath, vagina; L. masc. suff. -alis suffix denoting pertaining to; N.L. masc. adj. vaginalis pertaining to vagina, of the vagina). Strain KHD2 is the type strain of the new species of ‘Peptoniphilus vaginalis’ sp. nov.

MALDI-TOF-MS spectrum accession number

The MALDI-TOF-MS spectrum of ‘Peptoniphilus vaginalis’ is available at http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database.

Nucleotide sequence accession number

The 16S rRNA gene sequence of strain KHD2 was deposited in EMBL-EBI under this accession number: LN907856.

Deposit in culture collection

The isolate of ‘Peptoniphilus vaginalis’ was deposited in the ‘Collection de Souches de l’Unité des Rickettsies’ (CSUR, WDCM 875, number P0125) and in the collection ‘Deutsche Sammlung von Mikroorganismen’ (DSM, number 101742).

Conflicts of interest

The authors have no conflict of interest.

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