‘Olegusella massiliensis’ strain KHD7, a new bacterial genus isolated from the female genital tract

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Abstract

We report the main characteristics of ‘Olegusella massiliensis’ gen. nov., sp. nov., strain KHD7 (= CSUR P2268 = DSM 101849), a new member of the Coriobacteriaceae family isolated from the vaginal flora of a patient with bacterial vaginosis.

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As part of the ongoing microbial culturomics study of the human microbiota in our laboratory [1], we studied the diversity of the vaginal microorganisms of patients with bacterial vaginosis. In Hospital Nord, Marseille, France, we isolated from a vaginal sample of a 33-year-old French woman a new member of the Coriobacteriaceae family that could not be identified by matrix-assisted laser desorption–ionization time-of-flight mass spectrometry (MALDI-TOF MS) using a Microflex spectrometer (Bruker Daltonics, Leipzig, Germany). The study was authorized by the local ethics committee of the IFR48 (Marseille, France) under agreement 09-022, and the patient provided written informed consent.

Strain KHD7 was first isolated in November 2015 after 48-hour incubation under anaerobic conditions at 37°C on 5% sheep’s blood–enriched CNA agar (BD Diagnostics, Le pont de Claix, France) after 10-day preincubation in a blood culture bottle enriched with rumen that was filter sterilized through a 0.2 μm pore filter (Thermo Fisher Scientific, Villebon sur Yvette, France) and sheep’s blood. Colonies were pale white and translucent and had a diameter of 1 to 1.2 mm. Bacterial cells were Gram-positive, nonmotile and non-spore-forming coccobacilli with a mean diameter of 0.35 μm and a mean length of 0.42 μm. Strain KHD7 is strictly anaerobic and has no catalase and oxidase activities.

The 16S rRNA gene amplification was done using the primer pair fD1–rp2 as previously described [2], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). Strain KHD7 exhibited the highest 16S rRNA sequence identity of 93.5% with Olsenella uli strain DSM 7084T (GenBank accession no. NR_074414), the phylogenetically closest species with a validly published name (Fig. 1). This value was lower than the 95% 16S rRNA gene sequence threshold proposed by Stackebrandt and Ebers [3] to define a new genus without carrying out DNA-DNA hybridization, and it classifies strain KHD7 as the representative strain of a new genus within the Coriobacteriaceae family in the phylum Actinobacteria [4]. Olsenella uli [5] was isolated from human gingival crevices [5]. It is a Gram-positive, strictly anaerobic, nonmotile and non-endospore-forming bacillus, with no catalase or oxidase activity. Olegusella umbonata, another closely related anaerobic...
species isolated from sheep rumen, exhibits similar phenotypic properties [6].

Because strain KHD7 is more than 6% divergent in the 16S rRNA gene sequence with its closest phylogenetic neighbour [7], we propose that it may be the representative strain of a novel genus named Olegusella. The gen. nov. Olegusella (O.le.gu.sel’a. M.L. dim. suffix usel’la; M.L. fem. n.) was chosen to honor Dr Oleg Mediannikov for his contribution to medical microbiology. Strain KHD7 is the type strain of the new species ‘Olegusella massiliensis’ gen. nov., sp. nov.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of O. massiliensis is available at http://www.mediterraneeinfection.com/article.php?laref=256&titre=urms-database.

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in European Molecular Biology Laboratory—European Bioinformatics Institute (EMBL-EBI) under accession number LN998058.

Deposit in culture collection

Strain KHD7 was deposited in the Collection de Souches de l’Unité des Ricketties (CSUR, WDCM 875) under number P2268

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Conflict of Interest

None declared.

References

[1] Lagier J.C., Hugon P., Khelifa S., Fournier P.E., La Scola B., Raoult D. The rebirth of culture in 49 microbiology through the example of culturotics to study human gut microbiota. Clin Microbiol Rev 2015;28: 237–64.
[2] Drancourt M., Bollen C., Carlizou A., Martelin R., Gayral J.P., 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.
[3] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. Microbiol Today 2006;33:152–5.

[4] Stackebrandt E, Rainey FA, Ward-Rainey NL. Proposal for a new hierarchical classification system, Actinobacteria classis nov. Int J Syst Bacteriol 1997;47:479–91.

[5] Dewhirst FE, Paster BJ, Tzellas N, Coleman B, Downes J, spratt da, et al. Characterization of novel human oral isolates and cloned 16S rDNA sequences that fall in the family Coriobacteriaceae: description of Olsenella gen. nov., reclassification of Lactobacillus uli as Olsenella uli comb. nov. and description of Olsenella profusa sp. nov. Int J Syst Evol Microbiol 2001;51:1797–804.

[6] Kraatz M, Wallace R, Svensson L. Olsenella umbonata sp. nov., a microaerotolerant anaerobic lactic acid bacterium from the sheep rumen and pig jejunum, and emended descriptions of Olsenella, Olsenella uli and Olsenella profusa. Int J Syst Evol Microbiol 2011;61:795–803.

[7] Yarza P, Richter M, Peplies J, Ezpeleta 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.