

'*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 7084^T (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

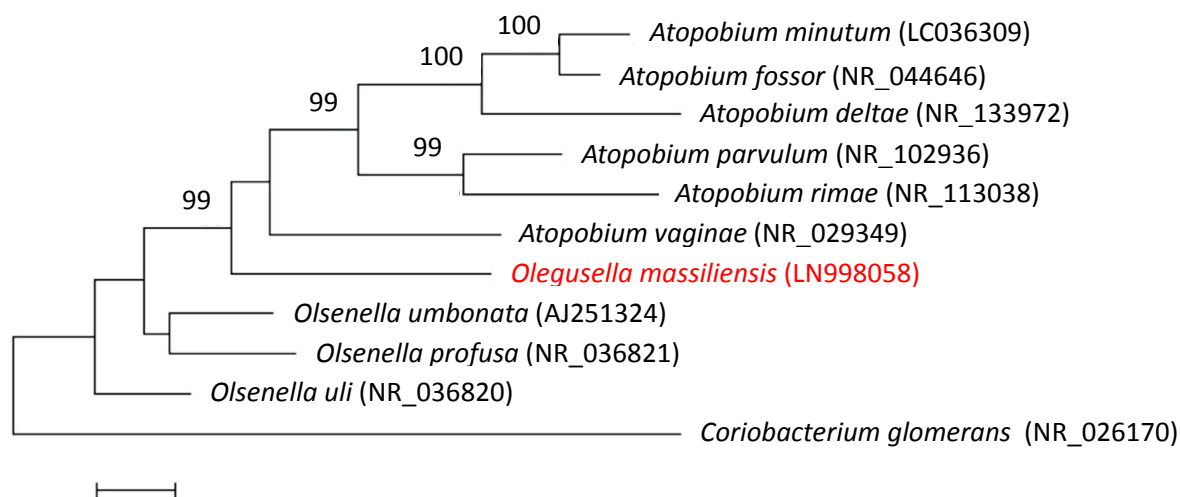


FIG. 1. Phylogenetic tree highlighting position of 'Olegusella massiliensis' strain KHD7 (red) relative to other phylogenetically close members of family Coriobacteriaceae. GenBank accession numbers are indicated in brackets. Sequences were aligned using Muscle, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA6 software. Numbers at nodes are percentages of bootstrap values ($\geq 95\%$) obtained by repeating analysis 500 times to generate majority consensus tree. Scale bar = 1% nucleotide sequence divergence.

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.

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