

ABSTRACT BOOK



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PT384 *Lactobacillus femina* sp. nov., a new species of *Lactobacillus delbrueckii* group

Joana Rocha¹, João Francisco Tomaz Santos Botelho¹, Magdalena Ksiezarek¹, Teresa Goncalves Ribeiro¹, Miguel Paulo Machado², Joao Andre Carrico², Lígia Pimentel³, Sofia Salsinha³, Luís M. Rodríguez-Alcalá³, Manuela Pintado³, Svetlana Ugarcina Perovic¹, Luisa Maria Vieira Peixe¹

¹UCIBIO/REQUIMTE. Faculdade de Farmácia, Universidade do Porto

²Universidade de Lisboa, Faculdade de Medicina, Instituto de Microbiologia and Instituto de Medicina Molecular

³Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia

The *Lactobacillus* genus is a paraphyletic group of lactic acid bacteria. In the human body, lactobacilli colonize different niches playing important roles in preventing infection and maintaining health. Two strains, c10Ua161M^T and c10Ua232AE, were preliminary identified by MALDI-TOF-MS as *Lactobacillus jensenii*, but *pheS* gene phylogenetic analysis did not confirm this species attribution.

To define the taxonomic position of two strains isolated from urine sample of a reproductive-age healthy woman, using a polyphasic taxonomic approach.

Individual phylogenetic analysis of 16S rRNA and *pheS* genes, average nucleotide identity (ANI), genome-to-genome distance calculation (GGDC), cellular fatty acids and biochemical tests were performed for taxonomic classification.

Phylogenetic analysis based on 16S rRNA gene assigned both strains to the genus *Lactobacillus*. Additionally, *pheS*-based phylogenetic analysis revealed that c10Ua161M^T and c10Ua232AE shared >99% of similarity and formed a well discriminated cluster in the *Lactobacillus delbrueckii* group, with *L.jensenii* and *L.psittaci* type strains (92.6 and 84.6%, respectively) as the closely related species. However, ANI and GGDC values of these strains were clearly below the proposed criterion for bacterial species delineation (87.9<95% and 34.3<70%, respectively) when compared with the genome sequence of *Lactobacillus* type strains. The type strain c10Ua161M^T G+C content was 34.2 mol%. The main cellular fatty acid was oleic acid (C_{18:1 ω9}). The ability to metabolize melibiose and starch further discriminated the two strains from other closely related *Lactobacillus* species. These results support the description of a novel species of the genus *Lactobacillus*, for which the name *Lactobacillus femina* sp. nov. is proposed (c10Ua161M^T).