

Alicyclobacillus consociatus sp. nov., isolated from a human clinical specimen.

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Abstract

A Gram-stain-positive, aerobic organism, isolated from a blood sample from a 51-year-old woman, was studied for its taxonomic position. Based on 16S rRNA gene sequence similarity comparisons, strain CCUG 53762(T) was grouped into the genus *Alicyclobacillus*, most closely related to the type strain of *Alicyclobacillus pohliae* (94.7 %). The 16S rRNA gene sequence similarity to other species of the genus *Alicyclobacillus* was ≤ 91 % and similarity to species of the genus *Tumebacillus* was 91.3-93 %. The occurrence of menaquinone MK-7 as the major respiratory quinone, meso-diaminopimelic acid as the diagnostic diamino acid of the cell wall and the fatty acid profile supported the allocation of the strain to the genus *Alicyclobacillus*. Major fatty acids were iso- and anteiso-branched fatty acids. The polar lipid profile consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine and three unknown phospholipids. The absence of the iso-branched fatty acids iso-C16 : 0 and iso-C17 : 0 allowed differentiation of strain CCUG 53762(T) from *A. pohliae* CIP 109385(T). In addition, the results of physiological and biochemical tests also allowed phenotypic differentiation of strain CCUG 53762(T) from this most closely related species. The G+C content of the DNA was 47 mol%.

Strain CCUG 53762(T) therefore represents a novel species of the genus *Alicyclobacillus*, for which we propose the name *Alicyclobacillus consociatus* sp. nov., with CCUG 53762(T) (= CCM 8439(T)) as the type strain.

Beteiligte Forschungseinheiten

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