

Revision of the genus *Massilia* La Scola et al. 2000, with an emended description of the genus and inclusion of all species of the genus *Naxibacter* as new combinations, and proposal of *Massilia consociata* sp. nov.

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Abstract

A Gram-stain-negative, rod-shaped, non-spore-forming bacterium originating from a human clinical specimen was studied for its taxonomic position. 16S rRNA gene sequence similarity studies clearly allocated this strain (CCUG 58010(T)) to the class Betaproteobacteria, closely related to members of the genera *Massilia* and *Naxibacter*. *Naxibacter varians* was shown to be the most closely related species on the basis of 16S rRNA gene sequence similarity (97.5 %), followed by *Massilia niastensis* (96.8 %) and *Massilia aerilata* (96.4 %). Similarities to all other species of the genera *Naxibacter* and *Massilia* were in the range 93.9-96.2 %. Chemotaxonomic data (major ubiquinone: Q-8; major polar lipids: phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol; and major fatty acids: summed feature 3 (C(16 : 1) ω 7c and/or iso-

C(15 : 0) 2-OH), C(16 : 0), C(18 : 1) ω 7c and C(12 : 0), with C(10 : 0) 3-OH as hydroxylated fatty acid) supported the affiliation of the isolate to these genera, which share these chemotaxonomic traits. DNA-DNA hybridization of strain CCUG 58010(T) with the type strain of *N. varians* CCUG 35299(T) resulted in a relatedness value of 39.2 % (reciprocal, 50 %) and physiological and biochemical tests also allowed phenotypic differentiation of the isolate from the most closely related species. There is currently no justification for a division of the genera *Massilia* and *Naxibacter* and for this reason a proposal is made to transfer all species of the genus *Naxibacter* to the genus *Massilia*, as *Massilia alkalitolerans* comb. nov., *Massilia varians* comb. nov., *Massilia haematophila* comb. nov. and *Massilia suwonensis* comb. nov. Strain CCUG 58010(T) represents a novel species, for which the name *Massilia consociata* sp. nov. is proposed, with the type strain CCUG 58010(T) (= CCM 7792(T)).

Beteiligte Forschungseinheiten

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