

***Isoptericola cucumis* sp. nov., isolated from the root tissue of cucumber (*Cucumis sativus*).**

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Abstract

A Gram-positive, aerobic organism, showing an irregular cell morphology was isolated from the root tissue of cucumber (*Cucumis sativus*) and investigated in detail for its taxonomic position. On the basis of the 16S rRNA gene sequence analysis strain AP-38T was shown to be most closely related to *Isoptericola variabilis* (99.1%), and *Isoptericola nanjingensis* (98.9%). The 16S rRNA gene sequence similarity to all other *Isoptericola* species was $\leq 98.5\%$. DNA-DNA similarities to *Isoptericola variabilis* DSM 10177T and *Isoptericola nanjingensis* DSM 24300T were 31%/41% (reciprocal) and 34%/34% (reciprocal), respectively. The diagnostic diaminoacid of the peptidoglycan was L-lysine. The quinone system contained predominantly menaquinones MK-9(H4) and MK-9(H2). In the polar lipid profile major compounds were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and two phosphatidylinositol-mannosides. The polyamine pattern contained the major components spermidine and spermine and significant amounts of tyramine. In the fatty acid profile, anteiso-C15:0, and iso C15:0 were present in major amounts. These data support the allocation of the strain to the genus *Isoptericola*. The results of

physiological and biochemical characterization additionally provides a phenotypic differentiation of strain AP-38T from *N. variabilis* and *N. nanjingensis*. AP-38T represents a new species of the genus *Isoptericola*, for which we propose the name *Isoptericola cucumis* sp. nov., with AP-38T (= LMG 29223T = CCM = 8653T) as the type strain.

Beteiligte Forschungseinheiten

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