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Sanguibacter soli sp. nov, isolated from of a ginseng field

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Strain DCY22^T, a Gram-positive, non-spore-forming, rod-shaped, motile bacterium was isolated from soil of a ginseng field in South Korea and characterized in order to determine its taxonomic position. 16S rRNA gene sequence analysis revealed that strain DCY22^T belongs to the family *Sanguibacteraceae,* and the highest degree of sequence similarity was found with *Sanguibacter marinus* 1-19^T (96.8%), *Sanguibacter suarezii* ST-26^T (96.0%), *Sanguibacter inulinus* ST-50^T (95.9%), *Sanguibacter keddieii* ST-74^T (95.5%), *Terrabacter terrae* PPLB^T (94.0%) and *Terrabacter tumescens* DSM20308^T (93.8%). Chemotaxonomic data revealed that strain DCY22^T possesses menaquinone MK-9 common in the genus *Sanguibacter* and predominant fatty acids, unknown ECL13.961 (45.81%), 17:0 anteiso (23.46%), 18:0 iso (15.42%) and unknown ECL14.966 (8.70%). The results of physiological and biochemical tests clearly demonstrated that strain DCY22^{T}represents a distinct species. Based on these data, DCY22^T (= KCTC 13155^T = JCM 14841^T) should be classified as the type strain for a novel species, for which the name *Sanguibacter soli* sp. nov. has been proposed. This work was supported by a grant from the Plant Diversity Research Center of the 21st Century Frontier Research Program (code # PF06222-00) funded by Ministry of Science and Technology of the Korean government.
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Molecular Identification of the Medicinal Plant *Anemarrhena asphodeloides* "Ji-Mo" by PCR

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Expensive herbs like oriental medicinal plants are always a possible target for fraudulent labeling in many countries including China, Japan, Korea, Russia, Canada, and the USA. Phylogenetic analyses, using the neighbor joining method and the parsimony method, based on sequences in nuclear ribosomal DNA and tRNA coding sequences (*trn*LF) in chloroplast DNA were presented in this study. For the first time, tRNA coding sequences (*trn*LF) of *A. asphodeloides* were PCR-amplified using universal primers and sequenced. In the phylogenetic tree, the ITS and *trn*LF sequences of *A. asphodeloides* were clustered with those of the genera *Hesperocalis, Agave* and *Hosta*. Most material that were marketed commercially in the name of "Ji-Mo" were found to have the same ITS and *trn*LF sequences with original *A. asphodeloides* plants and turned out to be genuine products. Specific PCR primers were designed from this polymorphic site within the sequence data, and were used to detect true plants via multiplex PCR. The described method has important implications in both the production and sale of the medicinal products, allowing for the prevention of fraud, and also revealing the possible presence of other, cheaper plant material.

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