A021

Dyella koreensis sp. nov., a β-glucosidase Producing Bacterium

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A bacterial strain (BB4^T), which has β-glucosidase activity, was isolated from soil around the bamboo roots. It was a Gram-negative, aerobic, non-motile, and straight rod-shaped bacterium Phylogenetic analysis of 16S rRNA sequences revealed a clear affiliation with members of the family "Xanthomonadaceae" The G+C content of the genomic DNA was 63.8 mol% The major fatty acids were branched fatty acid, especially large amounts of iso $C_{15\,0,}$ iso $C_{17\,0}$ and iso $C_{17\,1}$ ω9c were detected, which were similar to those of genus Dyella. The results of DNA-DNA hybridization with Dyella japonica XD53^T and Frateuria aurantia LMG 1558^T, in combination with phenotypic characteristics and 16S rRNA sequence analysis, demonstrated that strain BB4^T should be classified as a novel Dyella species. The name Dyella koreensis sp. nov. is proposed, with strain BB4^T(= KCTC 12359^T = NBRC 100831^T) as the type strain.

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A022

Description of *Shinilla granuli* gen. nov., sp. nov., and Proposal of the Reclassification of *Zoogloea ramigera* IAM 12669 as *Shinilla zoogloeoides* com. nov.

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The strain studied was aerobic or facultative anaerobic, heterotrophic, motile, Gram-negative and oxidase-, catalase-positive. 16S rRNA gene sequence phylogenetic analysis indicated that the strain occupied a distinct lineage within '*Rhizobiaceae* group' of α-*Proteobactia.* The major respiratory quinine was Q-10 and the predominant fatty acids were $C_{16\,0}$ and $C_{18\,1}$. On the basis of phenotypic, chemotaxonomic and phylogenetic characteristics, the novel bacteria is proposed that the strain Ch06 should be placed in a new genus for which the names *Shinilla* gen nov , sp. nov. is proposed with the type strain Ch06^T (= KCTC 12237^T = NBRC XXXX ^{T}).

From the results of the 16S rRNA gene sequence analysis, phenotypic features, and genomic distinctiveness, the species *Zoogloea ramigera* IAM 12669 is proposed to be reclassified in the new genus *Shinilla* as *Shinilla zoogloeoides* com. nov , with type strain IAM 12669^T(= ATCC 19623^T = K T CrabtreeI-16-M^T)

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A023

Cultivation and Characterization of the Novel Bacterial Strains in the Rare-Isolated Phylum Lineage from the Soil of the Ginseng Field

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The culturability of bacteria in the soil of the ginseng field (Pocheon, Korea) was investigated by using 1/2R2A and 1/10 R2A agar as the growth medium. 180 isolates obtained from plate counting experiments performed were identified by comparative analysis of partial 16S rRNA gene sequences. A large proportion of these isolates can be genomic novel species or genus of globally distributed group of soil bacteria within the divisions *Actinobacteria*, *Proteobacteria*, and *Bacteroidetes*. Among these 180 strains, designated GSW5-05 was closely related with lineage of *Acidobacterium* which were actively cultured in the soil by Janssen *et al* (AEM 2005, 826-834) and designated GSW4-04 and GSW4-15 were distant from any cultured isolate or uncultured clone in the lineage of *Verrucomicrobia.* About these three strains, we performed polyphasic taxonomic studies for placing these strains as taxonomic marker strains.

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A024

Flavobacterium xylanilyticum sp. nov. and *Flavobacterium cheongjuense* sp. nov., Novel Xylan-degrading Bacteria Isolated from Sewage

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Phenotypic and phylogenetic studies were performed on 6 strains isolated from sewage of Cheongju industrial complex The isolates were xylanolytic, Gram-negative and yellow-pigmented and grew on R2A agar Chemotaxonomic investigations revealed that all the isolates belonged to the genus *Flavobacterium.* Phylogenetic analysis of the 16S rDNA sequences of six isolates showed that two strains of them represented new sublines in the genus *Flavobacterium,* with *Flavobacterium saccharophilum* and *Flavobacterium johnsoniae* as their nearest phylogenetic neighbours. Pheno-typic properties, DNA G+C contents and whole-cell fatty acid profiles of these strains were consistent with those of the genus *Flavobacterium* Level of DNA-DNA relatedness to the closest phylogenetic neighbours of both strains were between 11 and 38%. Based on the phylogenetic and phynotypic distinctiveness of the isolates, the name *Flavobacterium xylanilyticum* sp nov is proposed for the strain CC8^T and *Flavobacterium cheongjuense* is proposed for strain CC9^T.

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