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***Dyella koreensis* sp. nov., a β -glucosidase Producing Bacterium**Hee-Chan Yang^{1*}, Wan-Taek Im¹, Dong-Shan An¹, Jun-Woen Lee², Doek-Chun Yang², and Sung-Taik Lee¹¹Korea Advanced Institute of Science and Technology, ²Kyung Hee University

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} ω 9c were detected, which were similar to those of genus *Dyella*. The results of DNA-DNA hybridization with *Dyella japonica* XD53^T and *Fraterura 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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Description of *Shinilla granuli* gen. nov., sp. nov., and Proposal of the Reclassification of *Zoogloea ramigera* IAM 12669 as *Shinilla zoogloeoides* com. nov.Dong-Shan An^{*}, Wan-Taek Im, Hee-Chan Yang, and Sung-Taik Lee

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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 quinone 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 Crabtree16-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 FieldWan-Taek Im^{1*}, Xiu-li Zhang Zhang¹, Qing-mei Liu¹, Leonid N Ten^{1,2}, and Sung-Taik Lee¹¹Department of Biological Sciences, Korea Advanced Institute of Science and Technology, ²Department of Chemistry, National University of Uzbekistan, Uzbekistan

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**Hye Yoon Park^{*}, Kwang Kyu Kim, and Sung-Taik Lee

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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. Phenotypic 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 phenotypic 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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