

A013

***Clostridium ganghwense* sp. nov., Isolated from Tidal Flat Sediment**Seil Kim¹, Hyunyoung Jeong, and Jongsik Chuk
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A Gram-negative, strictly anaerobic, halophilic, motile, sporulating and rod-shaped bacterium, designated strain HY-42-06^T, was isolated from tidal flat sediment from Ganghwa Island in South Korea. The isolate produced glycerol, ethanol and CO₂ as fermentation end products from glucose. Strain HY-42-06^T grew optimally at 35°C, pH 7.5 and 3 (w/v)% artificial sea salts. No growth was observed in the absence of sea salts. In phylogenetic analyses based on 16S rDNA sequence, strain HY-42-06^T showed a distinct phyletic line within the members of cluster I of the order *Clostridiales*. The closest phylogenetic neighbor to strain HY-42-06^T was *Clostridium novyi* ATCC 17861^T (94.91% 16S rDNA sequence similarity). Several phenotypic characters readily differentiate the tidal flat isolate from phylogenetically related clostridia. On the basis of polyphasic evidence, strain HY-42-06^T should be classified as a novel species, for which the name *Clostridium ganghwense* sp. nov. is proposed, the type strain is HY-42-06^T (=IMSNU 40027^T = KCTC 5146^T = JCM 13193^T).

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A014

***Hymenobacter woopoensis* sp. nov., Isolated from Freshwater**Keun Sik Baik^{1*}, Eun Mi Kim^{1,2}, Hoa Kieuquynh¹, Seong Chan Park¹, Mi Sun Kim¹, Se Il Moon¹, and Chi Nam Seong¹¹*Department of Biology, College of Natural Sciences, Suncheon National University,* ²*Department of Dental Hygiene, Kwangyang Health College*

A Gram-negative, designated WPCB131^T, was isolated from freshwater of Woopo wetland, Republic of Korea. Phylogenetic analysis based on 16S rDNA sequences indicated that this strain belongs to the *Cytophaga-Flavobacterium-Bacteroides* group and is related to the genus *Hymenobacter*, with 95.5% sequence similarity to *Hymenobacter actinoscleris* and 94.5% to *Hymenobacter aerophilus*, nearest phylogenetic neighbours. The major fatty acids were C_{15:0} iso (34.8%), C_{16:1} ω5c (15.0%), C_{17:1} anteiso B/i (14.4%) and C_{16:1} ω7c/15 iso-2OH (13.8%). The DNA G+C content was 47%. The polyphasic data showed that our freshwater isolate is affiliated to the genus *Hymenobacter* with a novel species status. The name *Hymenobacter woopoensis* sp. nov. is therefore proposed for the strain WPCB131^T.

A015

Two Novel Species of the Genus *Sporosarcina* Isolated from Activated SludgeByung-Yong Kim^{1*}, Hang-Yeon Weon², Seung-Beom Hong¹, Soon-Wo Kwon¹, and Seung-Joo Go¹¹*Korean Agricultural Culture Collection, Genetic Resources Division, National Institute of Agricultural Biotechnology, Rural Development Administration,* ²*Applied Microbiology Division, National Institute of Agricultural Science and Technology, Rural Development Administration*

Two bacterial strains designated as F73^T and I80^T were isolated from activated sludge of industrial sewage. A polyphasic taxonomic study was performed. Both isolates are Gram-positive, aerobic and spore-forming rods. The phylogenetic analysis of 16S rDNA sequences placed both isolates within the genus *Sporosarcina*, which was grouped into *Bacillus* rRNA group 2. The closest cultured bacterial relatives with validly published names were *Sporosarcina psychrophila* (96.5% for strain F73^T) and *Sporosarcina aquamarina* (96.6% for strain I80^T). The 16S rDNA sequence similarity between strains F73 and I80 was 98.0%. The major cellular fatty acids of both strains were anteiso-C_{15:0} and iso-C_{15:0}. The major menaquinone of both strains was MK-7. The diaminopimelic acid was absent in both strains. However, the mean level of DNA-DNA relatedness between two isolates F73^T and I80^T was 28.0%.

On the basis of the polyphasic data, it is proposed that strains F73^T (=KACC 11299^T =DSM 16921^T) and I80^T (=KACC 11300^T =DSM 16920^T) should be placed in the genus *Sporosarcina* as the type strains of two novel species.

A016

Diversity and Dominant Members of the Bacterial Soil Community in a Different Layers of Forest Soil as Determined by ARDRAYun-Ji Kim^{*}, So-Young Choi, and Kyung-Sook Whang
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Microbial community diversity in *Coniferous* forest soil were analyzed using a 16S rDNA-based cloning approach. Total DNA was directly extracted from fermented litter layer (F layer), rhizosphere soil (A layer) and 16S rDNA were amplified using PCR primers based on the universally conserved sequences. Bacterial clone libraries were constructed, 106 clones from F layer and 111 clones from A layer were examined by ARDRA using *Hae*III. Clones were clustered based on restriction patterns using GelCompar II. Eighteen different RFLP types were detected from 106 clones (F layer) and 30 different RFLP types were detected from 111 clones (A layer). In the case of F layer 18 selected clones sequenced fell into two bacterial phyla, alpha-, beta-, gamma-, delta-Proteobacteria, and *Actinobacteria*. Thirty select clones from A layer fell into four bacterial phyla, alpha-, gamma-, delta-Proteobacteria, *Planctomycetes*, *Acidobacteria*, and *Actinobacteria*.

A large proportion of soil bacterial populations belonging to beta-Proteobacteria in F layer and alpha-Proteobacteria in A layer. Eighty percentage of the clones belonged to yet-unnamed family-level groups belonging to novel lineages.