

A005

***Photobacterium aplysiae* sp. nov., a Lipolytic Marine Bacterium Isolated from Eggs of a Sea Hare (*Aplysia kurodai*)**

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A bacterial strain, GMD509^T, showing lipolytic activity was isolated from the eggs of sea hare, *Aplysia kurodai* collected at Mogiyeo of the South Sea (depth, 12 m), Korea. The strain is Gram-negative, motile, facultative anaerobic, mesophilic and weakly halophilic. Optimal growth condition of the strain GMD509^T is 3.0 % (w/v) NaCl, pH 8 and 25 °C. The whole cell fatty acid profiles of the isolate include C16:1, C16:0 and C18:1 as major fatty acids and a DNA G+C content is 45 mol%. Phylogenetic analyses of 16S rDNA sequences place this bacterium in the γ -Proteobacteria, within the genus *Photobacterium*. 16S rDNA gene sequence of GMD509^T is most similar to that of *P. frigidiphilum* (97.8%), *P. profundum* (97.5%) and *P. indicum* (97.4%). The DNA-DNA relatedness levels between the isolate and its closest known phylogenetic relatives, *P. frigidiphilum* and *P. indicum*, are 25.3 and 13.7%, respectively. The strain GMD509^T therefore represents a new species for which we propose the name *Photobacterium aplysiae* sp. nov., and provide the type strain is GMD509^T (=KCTC12383 =JCM12948)

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A007

Two Novel *Paenibacillus* Species, *Paenibacillus hakamense* sp. nov. and *Paenibacillus taeanense* sp. nov. Isolated from Root of Sand Dune Plants

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Two Gram-positive, endospore forming bacteria (PHA2-4^T and PBA10-1^T) were isolated from two sand dune plant species, *Lathyrus japonicus* and *Glehnia littoralis* growing along the coastal areas in Tae-an, Korea, and their taxonomic status was investigated. Complete 16S rRNA gene sequence analysis indicated that both of the organisms should be placed in the genus *Paenibacillus*. Levels of 16S rRNA gene sequence similarity between existing *Paenibacillus* species and the two novel strains PHA2-4^T and PBA10-1^T were 92.1-97.0% and 93.6-97.5%, respectively. The major fatty acids for both strains were anteiso-C15:0, n-C16:0, and iso-C16:0. The DNA G+C contents of strains PHA2-4^T and PBA10-1^T were 43.3 and 42.9 mol%, respectively. On the basis of phenotypic and phylogenetic data, it is evident that these strains should be assigned to new species of the genus *Paenibacillus*, for which the names *Paenibacillus hakamense* sp. nov. (type strain = PHA2-4^T) and *Paenibacillus taeanense* sp. nov. (type strain = PBA10-1^T) are proposed.

A006

Comparison of *Anabaena* and *Trichormus* (Cyanobacteria), Inferred from 16S rRNA Gene and *cpcBA*-Intergenic Spacer Sequence Analyses

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The genera *Anabaena* and *Trichormus* have been classified into the filamentous heterocystous cyanobacteria (subsection IV, family I). Traditionally, the classification of cyanobacteria has been based on morphological characters, which can vary in different environmental or growth conditions and even be lost during cultivation. Moreover, new strains were isolated to avoid identification problems caused by morphological changes during cultivation. Sequencing analysis of the 16S rRNA gene and a part of the phycocyanin operon (*cpc*), specifically the intergenic spacer (IGS) between *cpcB* and *cpcA*, was performed on 6 *Anabaena* and 8 *Trichormus* strains isolated from several rivers and reservoirs in Korea and preserved in Biological Resource Center, KRIBB. The 16S rRNA gene sequence similarities of *Anabaena variabilis* and *Trichormus variabilis* were 95.9 - 100% and 97.8 - 99.7%, respectively. Phylogenetic trees based on the 16S rRNA gene showed that *Anabaena* strains were distinguishable from *Trichormus* strains and were divided into two groups. However, phylogenetic trees based on *cpcBA*-IGS regions of 6 *Anabaena* and 8 *Trichormus* strains showed that the genera are intermixed.

A008

***Psychroserpens mesophilus* sp. nov. and *Rhodobacter incheonensis* sp. nov., Isolated from Young Marine Biofilm**

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Two bacterial strains (KOPRI 13537 and KOPRI 13650) among the marine bacteria isolated from young biofilm were investigated to determine taxonomic status. Based on the 16S rRNA sequence, KOPRI 13537 and KOPRI 13650 should be placed in the genus *Rhodobacter* and genus *Psychroserpens*, respectively. Major fatty acids of KOPRI 13537 were C18:1w9t, C16:0 and C16:1w9 and could assimilate arabinose, mannitol, maltose and citrate. Unlikely to the other members of genus *Rhodobacter* the isolate has no photosynthetic pigments. Major fatty acids of KOPRI 13650 were C18:1w9, C16:1w9 and a-C17:0. The isolate was non-motile rod form. Optimal growth was observed at 30 °C and 4-5% of NaCl concentration. Based on the phenotypic and phylogenetic data, it is proposed that KOPRI 13537 should be proposed as *Rhodobacter incheonensis* sp. nov., and KOPRI 13650 as *Psychroserpens mesophilus* sp. nov.

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