A053

Lysobacter granulense sp. nov., Isolated from Anaerobic Granules in an Upflow Anaerobic Sludge Blanket (UASB) Reactor

Wan-Taek Im[1*], Hee-Sung Bae[2], and Sung-Taik Lee[1]

[1]Department of Biological Sciences, Korea Advanced Institute of Science and Technology, [2]Department of Biological Science, Louisiana State University, USA

To clarify the taxonomic position of the *Lysobacter* species and a novel organism, strain Ko07^T, isolated from an up-flow anaerobic sludge blanket (UASB) reactor treating a brewery wastewater, a polyphasic taxonomy investigation was conducted. Phylogenetic inference based on 16S rDNA sequences showed that strain Ko07^T was related with the *Lysobacter* species in the range of 95.9-96.5%. Ubiquinone Q-8 and branched fatty acids, $C_{15:0}$ iso, $C_{16:0}$ iso, iso $C_{17:1}$ ω9c, and $C_{11:0}$ iso 3OH, predominantly appeared in strain Ko07^T as well as in all the *Lysobacter* species. The DNA relatedness value of strain Ko07^T to those of the *Lysobater* species was estimated to be 2.1-20.4%. Strain Ko07^T was distinguished from the *Lysobacter* species with validly published names by the comparatively low DNA G+C mol% value (63.8%), substrate utilization, and some physiochemical characteristics. On the basis of the results obtained in this study, we propose the *Lysobacter* species as the novel *Lysobacter granulensis* sp. nov.

[This work was supported by the 21C Frontier Microbial Genomics and Applications Center Program, Ministry of Science & Technology (Grant MG02-0101-001-2-2-0), Republic of Korea.]

A054

Arctic Bacteria Isolated from Marine Environments

Hyun Hee Cho*, Ki Cheol Sung, Kyeung Hee Cho, Yoo Kyung Lee, and Hong Kum Lee

Korea Polar Research Institute, Korea Ocean Research and Development Institute

Various marine bacterial strains were isolated from sediment, macroalgae and biofilm samples around the Korean Arctic Research Station Dasan located at Ny-Alsund, Svalbard, Norway (79°N, 12°E). The collected samples were diluted in distilled seawater, and spread on marine agar plates. They cultured at 10℃, and total 500 bacterial isolates were preserved in glycerol media (15%, v/v) at –80℃. Phylogenetic analysis of 16S rDNA sequences indicated that the marine bacteria belong to alpha-, beta-, and gamma-Proteobacteria, the CFB group, and High GC Gram-positive bacteria. Among them, eight bacterial isolates from sediment, three isolates from macroalgae, and four isolates from Arctic biofilm were candidates for new species; the closest cultured bacteria with validly published names were *Aequorivita antarctica*, *Colwellia piezophila*, *Formosa algae*, *Loktanella vestfoldensis*, *Marinobacter lipolyticus*, *Marinosulfonomonas methylotropha*, *Pibocella ponta*, *Pseudomonas denitrificans*, *Pseudomonas fluorescens*, *Psychromonas antarcticus*, *Psychroserpens burtonensis*, and *Roseobacter gallaeciensis*. These Arctic bacteria may offer good sources of useful enzymes with activity at low temperature.

A055

Analysis of the β-tubulin Gene in a Tooth Fungus *Hericium erinaceum*

Han-Gyu Ko[1*], Hyuk-Gu Park[1], Seong Hwan Kim[2], and Won-Mok Park[1]

[1]School of Life Sciences and Biotechnology, Korea University, [2]Department of Microbiology and Institute of Basic Science, Dankook University

Hericium erinaceum is a medicinal mushroom belonging to Hericeaceae of Basidiomycota. In order to study its genetic relationship to other *Hericium* species, the β-tubulin gene was analyzed. Degenerate primers (BTP1-BTP4) designed based on known sequences of basidiomycete β-tubulin gene were tested for their ability of amplification against 23 isolates of seven *Hericium* species originated from different countries. We could successfully amplify PCR amplicons ranged from 1,646bp to 1,676bp in size from the *Hericium* isolates tested, and their nucleotide sequences were determined. Database searches through GenBank showed that the determined sequences are basidiomycete β-tubulin genes. The amplified sequences contain coding and non-coding regions. Non-coding regions show more sequence variation than coding sequences. Nucleotide sequence identity among *Hericium* species ranged 80 to 95%. Intraspecies variation of the β-tubulin gene was clearly found in *H. erinaceum* and allowed to dissect *H. erinaceum* isolates into a few groups.

[This study was Supported by Specific Research-Promoting Joint Projects, RDA]

A056

Phylogenetic Implications of Internal Transcribed Spacer Sequences of Nuclear Ribosomal DNA in *Cordyceps*

Hyuk-Gu Park[1*], Han-gyu Ko[1], Seong Hwan Kim[2], Jae-Mo Sung[3], and Won-Mok Park[1]

[1]School of Life Sciences and Biotechnology, Korea University, [2]Department of Microbiology and Institute of Basic Science, Dankook University, [3]Department of Applied Biology, Kangwon National University

The present study was carried out to determine the phylogenetic relationships of 8 *Cordyceps* species using rDNA sequences data of ITS and 5.8S. For this work, the target rDNA regions were amplified by PCR using ITS1F-ITS4 primers form genomic DNA of 22 isolates of *Cordyceps* and their nucleotide sequences determined. Analysis of sequence data showed that the size of ITS regions of all isolates of *Cordyceps militaris* is 567 bp, while that of *C. pentatomi*, *C. longissima* and *C. yongmoonensis* is 660bp, 630bp and 670bp, respectively, indicating there is size variation in ITS rDNA among *Cordyces* spp. Phylogram based on the rDNA sequence analysis revealed that the 22 isolates could be divided into four groups. The first group was *C. pentatomi*, *C. yongmoonensis*, and *Shimizuomyces poradox*. The second group included *C. longissima*, *Paecilomyces tenuipes*, and *C. pruinosa*. The third group was *C. scarabaeicola* and the forth was *C. militaris*. With the comparison of ten isolates of *C. militaris*, we found that intraspecific variation exists in the ITS2 regions of *C. militaris*.

[This study was supported by Specific Research-Promoting Joint Projects, RDA]