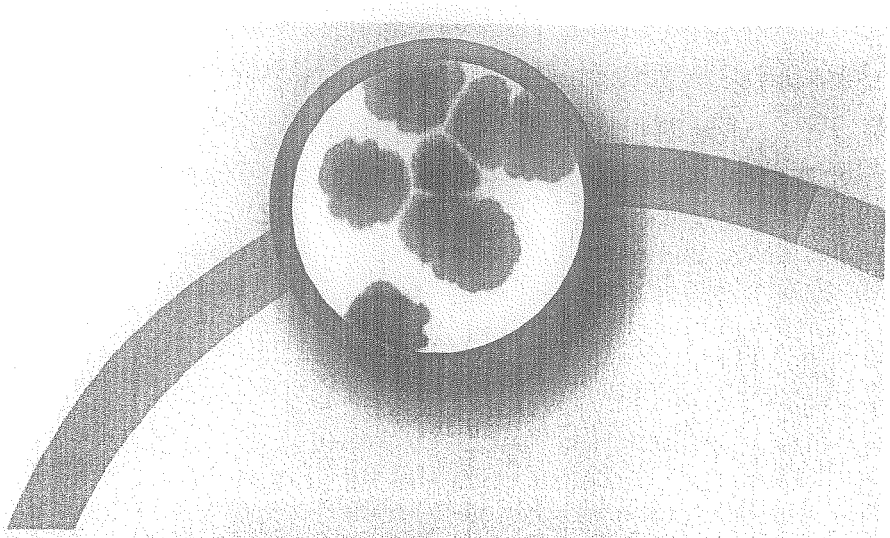

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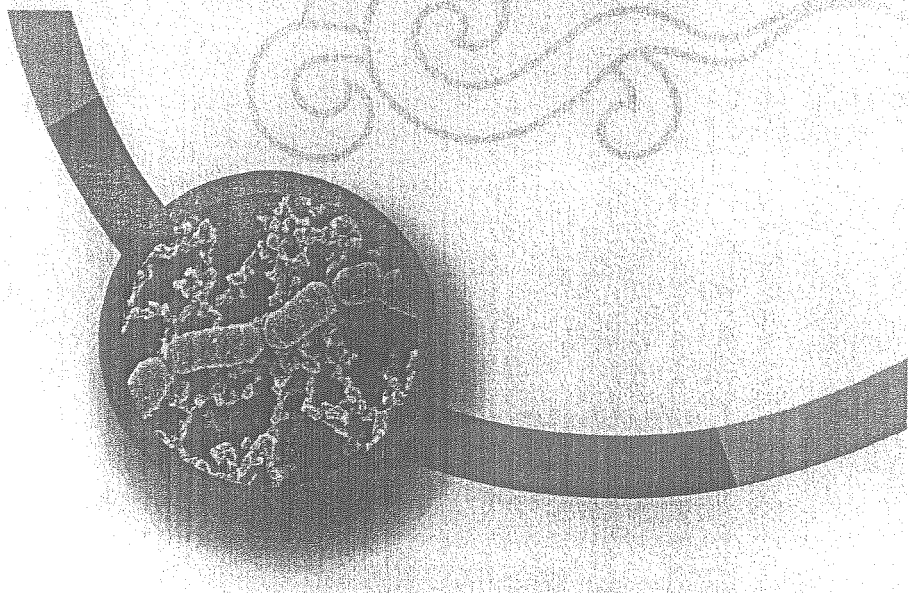

▌일 자 : 2007년 5월 10일(목) ~ 11일(금)

▌장 소 : 보광 휘닉스파크 (강원도 평창 소재)

후원: 한국과학기술단체총연합회, 한국학술진흥재단

사단법인 한국미생물학회 한국생명공학연구원

Final Circular

B040 **Influence of Pulsed Electric Field Generated Around Hot Pepper Plant on Growth and Wilt Diseases**

Byung Kwan Na* and Doo Hyun Park
Department of Biological Engineering, Seokyeong University

B041 **Methodology Study for Classifying Soil Ecological Quality using Microbial Diversity Information**

Dongwon Ki*, Jaejin Lee, and Joonhong Park
School of Civil and Environmental Engineering, Yonsei University

B042 **A New Cultivation Method Development for Antibiotic Resistant Bacteria under Wide Range of Nutrient Levels from Water Samples**

Hyangkyun Oh*, Jaejin Lee, Il Han, and Joonhong Park
Department of Civil and Environmental Engineering, Yonsei University

B043 **Biosorption of Chromium (VI) from Aqueous Solution onto Dead Biomass from Activated Sludge**

Kaliannan Thamaraiselvi[1,2*], Kangsuk Kim[1], Shankar Congeevaram[1], and Joonhong Park[1]
[1]Department of Civil Environmental Engineering, Yonsei University, [2]Department of Environmental Biotechnology, Bharathidasan University, India

B044 **A Possible Natural Alternative to Antibiotics**

Young Ho Kim[1*], Min Hee Kim[1], Yong Nam Kim[1], and Ji Young Kim[2]
[1]Department of Life Science, The University of Suwon, [2]Department of Life Science, The University of Suwon

B045 **Phylogenetic Characteristics of Bacterial Populations in Pine Mushroom (*Tricholoma matsutake*) Habitat Soil and Purification of *Acidobacteria* Phylum**

Yun-Ji Kim[1*] and Kyung-Sook Whang[1,2]
[1]Institute of Microbial Ecology and Resources, Mokwon University, [2]Department of Microbiology, Mokwon University

B046 **Assessment of Fungal Diversity in Western Islands Soil by Amplified Ribosomal DNA Restriction Analysis and Pyrosequencing**

Young Woon Lim[1*], Changmu Kim[2,3], Byung Kwon Kim[2], Jae-Hak Lee[4], Hyo Jin Kim[2], Jongsik Chun[2], and Hack Sung Jung[2]
[1]Institute of Molecular Biology and Genetics, Seoul National University, [2]School of Biological Sciences, Seoul National University, [3]Division of High-risk Pathogen Research Center, Korea Center for Disease Control and Prevention, [4]Interdisciplinary Program in Bioinformatics, Seoul National University

B047 **Biosorption of Chromium and Nickel by Isolated Heavy Metal Resistant *A. niger* [CSR-mbl1], *M. halobius* [CSR- mbl2], *M. varians* [CSR – mbl3] Isolates**

Shankar Congeevaram[1,2*], Sridevi Dhanarani[1], Joonhong Park[2], Michael Dexilin[1], and Kaliannan Thamaraiselvi[1,2]
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B045

Phylogenetic Characteristics of Bacterial Populations in Pine Mushroom (*Tricholoma matsutake*) Habitat Soil and Purification of *Acidobacteria* Phylum

Yun-Ji Kim[1*] and Kyung-Sook Whang[1,2]

[1]*Institute of Microbial Ecology and Resources, Mokwon University,* [2]*Department of Microbiology, Mokwon University*

Phylogenetic characteristic of the bacterial populations in the pine mushroom (*Tricholoma matsutake*) habitat soil were analyzed by direct extracting of DNA and 16S rDNA-ARDRA. The 115 clones from pine mushroom habitat soil were clustered into 31 different RFLP phylotypes by ARDRA. Based on the 16S rDNA sequences, 31 ARDRA groups were classified into 6 phylogenetic groups: *α-*, *β-*, *γ-Proteobacteria*, *Acidobacteria*, *Actinobacteria* and *Firmicutes*. Eighty-five percent of the total clones were *Acidobacteria* phylum, it was shown to dominant members of bacterial populations in the pine mushroom habitat soil. The *Acidobacteium* group is a newly recognized bacterial division with only three cultivated representatives: *Acidobacterium capsulatum*, *Holophaga foetida*, and *Geothrix fermentans*. Three isolates of *Acidobacteria* were successfully isolated using by improved media. These isolates had a 16S rRNA sequence of 90~92% identical to *Acidobacterium capsulatum*^{T}(D26171). On the bases of phylogeny and genomic distinctiveness, we propose to these isolates are represent a new species of the genus *Acidobacterium*.

B046

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As the fungal community is influenced by environmental factor changes, it has been used as an indicator. In order to generate extensive fungal diversity from the soils of three western islands in Korea which were located between Korea and China, we have assessed two molecular approaches, amplified ribosomal DNA restriction analysis (ARDRA) and pyrosequencing, a rapid and relatively inexpensive sequencing technology. Similar fungal structures were obtained from both approaches; the major group of fungal community was Ascomycota and Basidiomycota, while Zygomycota, Chitridiomycota and Glomeromycota were recovered at much lower frequencies. Many sequences closely matched sequences from mycorrhizal, plant pathogenic and saprophytic fungi. Comparing two approaches using the same DNA samples, we showed that a much higher fungal diversity was observed when pyrosequencing was used. We will use this new approach to monitor the change of fungal community from soils in three islands due to global warming and air pollution from the rapid development of China.

B047

Biosorption of Chromium and Nickel by Isolated Heavy Metal Resistant *A. niger* [CSR- mbl1], *M. halobius* [CSR- mbl2], *M. varians* [CSR - mbl3] Isolates

Shankar Congeevaram[1,2*], Sridevi Dhanarani[1], Joonhong Park[2], Michael Dexilin[1], and Kaliannan Thamaraiselvi[1,2]

[1]*Department of Environmental Biotechnology, Bharathidhasan University, India,* [2]*School of Civil and Environmental Engineering, Yonsei University*

Microbes play a significant role in bioremediation of heavy metal contaminated soil and wastewater. Heavy metal resistant fungi (*Aspergillus niger* [CSR - mbl1]) and bacteria (*Micrococcus halobius* [CSR -*Micrococcus varians* [CSR - mbl3]) were isolated from a world third ranking contaminated site *Ranipet*, India (Black smith institute, USA). The bioaccumulation of Cr(VI) and Ni(II) by these isolates were studied to evaluate their applicability for heavy metal removal from industrial wastewaters. Optimum pH and temperature conditions were standardized for the removal efficiency of the metals. The isolated strains were characterized for genus and species level using universal 18S and 16S primer. Results show that expanded SRTs can be recommended while using the Cr-resistant fungal and bacterial isolates for removing Cr(VI). In the case of Ni-resistant bacterial isolate, a non-expanded SRT was recommended for designing CFCS bioreactor. The Cr-resistant isolates (*Aspergillus niger* [CSR- mbl1]), was able to grow upto 10,000mgL^{-1}Cr(VI). Results indicate the applicability of the three isolated strains for the removal of Cr(VI) and Ni(II).

B048

Pathogenicity of *Pseudomonas anguilliseptica* Against Striped Beakperch, *Oplegnathus fasciatus*

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In recent years, 2-30% mortality of striped beakperch suffered by a bacterial infection had broken out in several southern coastal farms of Korea at spring season. A bacterium isolated from diseased striped beakperch was identified as *Pseudomonas anguilliseptica* by biochemical test and 16S rDNA gene sequence analysis. To evaluate the susceptibility of striped beakperch against *P. anguilliseptica*, 4.39×10^7 and 4.39×10^5 CFU/fish of bacteria was intraperitoneally injected into 5.5 g fish at 18±1°C. Cumulative mortality reached 100% and 45% in the 4.39×10^7 and 4.39×10^5 CFU/fish infected group, respectively. Experimentally infected fish showed cell associated inflammation and bacteria in the kidney and spleen. These results suggest that *P. anguilliseptica* has pathogenicity to striped beakperch and is the first report of striped beakperch mortality caused by *P. anguilliseptica*.

[This research was partially supported by the MIC (Ministry of Information and Communication), Korea, under the ITRC (Information Technology Research Center) support program supervised by the IITA (Institute of Information Technology Advancement) (IITA-2006-C1090-0602-0001)]