

Enrichment of Uncultured Ammonium Oxidizing and Denitrifying Bacteria from Antarctic Soil

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Bacteria are contribution a large role in the nitrogen cycle of ecosystems, especially in limited habitat, such as Antarctica. For the cultivation of bacteria involved in the nitrogen cycle of the Antarctica, three soils of King George Island were enriched for nitrogen fixation (NF), ammonium oxidation (AO) and denitrification (DN). Changes in N₂O gas, ammonium, nitrite and nitrate concentrations were measured every 14 days. Ammonium oxidation and denitrification were confirmed by measuring changes in nitrogen concentration, and 16S rRNA gene was amplified and analyzed for bacterial communities. Functional gene *amoA*, which is an ammonium oxidizing gene, and *nirK*, *nirS* and *nosZ*, denitrifying genes, were confirmed. As a result of the bacterial community analysis, it was found that the culture of ammonium oxidizing bacterium were cultivated with *Micavibrio*, *Oxalobacteraceae* and *Pseudomonadaceae*. *Oxalobacteraceae*, *Pseudomonadaceae* and *Propionibacteriaceae* were cultivated in denitrifying bacteria enriched culture. The denitrification pathway and the dissimilatory nitrite reductase pathway were found in the DN_1B and DN_3A denitrifying bacterium cultured in the SEED profile. The ammonia assimilation pathway was more abundant in AO_2C cultured with ammonium oxidizing bacteria. And environmental genetic analysis of the cultures obtained by enrichment will help to understand the ecological function and role of bacteria in the ecosystem.

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B015

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B016

A Novel Bacterial Strain from the Tomato Rhizosphere Resistant to Bacterial Wilt Has an Antagonistic Activity against *Ralstonia solanacearum*

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B017

Microbial Mercury Transformations in Methane Hydrate Sediments of Arctic Sea

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B018

Evaluation of the Nematicidal Activity of Endophytic Bacterial Populations from *Pinus* spp. and Isolation of Bioactive Metabolites from *Streptomyces* sp. AE170020 against *Bursaphelenchus xylophilus*

Min-Jiao Liu^{1,2}, Chun-Zhi Jin^{1,2}, Dong-Jin Park¹, Min-Kyoung Kang^{1,3}, Jun-Heon Kim⁴, Sang-Hyun Koh⁴, and Chang-Jin Kim^{1,2*}

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B019

Rapid Determination of *Salmonella enterica* Serotypes Using Pan-genome Based on Real-Time PCR Method

So-Young Lee, Yun-Kyung Ki, Hoon-Jae Jeong, Joon-Gi Kwon, You-Tae Kim, and Ju-Hoon Lee*

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B020

Nematocide Active Substances for *Bursaphelenchus xylophilus* Isolated from Actinomycetes

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B021

Comparison of Enkephalin and Gramicidin-S as Internal Standard in Measuring Microcystins from Cyanobacterial Biomass

Ji-Min Hwang, Bo-Ri Kim, Ji-Soo Shin, Jae-Hun Lee, Hye-Ryoung Kim, Kyoung-Hee Oh, and Young-Cheol Cho*

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B022

Distribution of Antibiotic Resistance Genes within Viral Metagenomes of Urban Wastewater Treatment Plants

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B023

Development and Optimization of Methods to Quantify Microcystins in Fish Tissues and Cyanobacterial Biomass

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B024

Transcriptomic Response of *Bacillus mesoane* H20-5 to Salt Induced Osmotic Stress

Shailesh Sawant, Songhwa Kim, Ju Hee An, Mee Kyung Sang, Hang-Yeon Weon, and Jaekyeong Song*

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B025

Relationship between Cyanobacterial Numbers and Cyanobacterial Biomass Determined by Phycocyanin Concentration

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