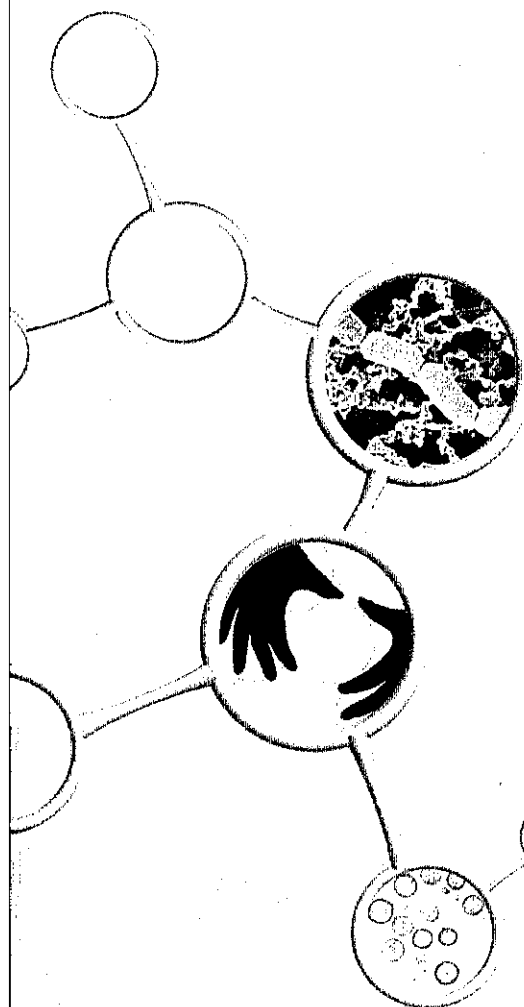


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## [B049]

### Uncultured Bacterial Diversity from Arctic Coastal Seawaters Revealed by 16S rRNA Gene Cloning

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Using the 16S rDNA-based approach the uncultured bacterial community was analyzed for 5 coastal seawater samples around Dasan Arctic Station in Svalbard, Norway. Sequences of 524 total clones belonged to *α-Proteobacteria* (32%), *β-Proteobacteria* (5%), *γ-Proteobacteria* (12%), *Actinobacteria* (12%), *Bacteroidetes* (29%), *Cyanobacteria* (5%), and *Verrucomicrobia* (4%). Clones of the SAR11 clade were less abundant in coastal (PSW1) and intermediate (PSW2) zones compared to those from near open ocean (PSW3), and glacia-melting zones (PSW4 and PSW5). The SAR11 subclades 2 & 3 were found in PSW3 & 4 while the SAR11 subclade 1 could be found abundantly in every samples analyzed. The OM42 and RCA clades dominated any region except for PSW3. Clones of the *γ-proteobacterial* SAR86 clade could be demarcated except for PSW2 whilst methylotrophic *β-proteobacterial* OM43 clones were pertinent to PSW3, PSW4, and PSW5. SSU clones from other phylogenetic groups were not clearly differed among the samples, but several intriguing phylogenetic lineages represented habitat-specific abundance [Supported by KOPRI and 21C Frontier program from MOST]

## [B050]

### Archaeal, Bacterial, and Eukaryal Diversity of Human Guts

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Bacterial, archaeal and eukaryal diversities were analyzed and compared from 10 unrelated different individuals using denaturing gradient gel electrophoresis (DGGE), a PCR-fingerprinting method. In this study, bacterial diversity was distributed only in *Firmicutes* and *Bacteroidetes* phylums, which were already known as dominant in human intestine. Most archaeal sequences were belonged to methane-producing archaea but, unexpectedly, some halophilic archaea related sequences were revealed. Fungi (*Candida* sp. and *Saccharomyces* sp.) and Stramenopiles (*Blastocystis hominis*) related sequences were revealed from eukaryotic diversity. While some distinct bands are observed, some prominent bands are found through the all samples in archaeal and bacterial DGGE analysis. However there are no totally distributed eukaryotic sequences through the samples. In UPGMA clustering analysis, archaeal and bacterial communities have relatively higher relatedness (68.9% for archaea and 59.2% for bacteria average dice coefficient values) but eukaryotic community show very low relatedness (31.26%) between samples.

## [B051]

### Halophilic Bacterial and Archaeal Diversity in Seven Kinds of Jeotgal, the Korean Salt-Fermented Seafood

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The halophilic bacterial and archaeal diversity in seven kinds of jeotgal, the Korean traditional, salt-fermented seafood was examined through culture-independent and culture-dependent approaches. Culture-independent method using DGGE revealed that different archaea coexisted and affiliated within the genus *Natronococcus*, *Halalkalicoccus*, *Haloarcula* and identified bacteria affiliated within the genus *Lactobacillus*, *Psychrobacter*, *Weissella*, *Halomonas*, *Salinivibrio*, *Vibrio*, *Streptomyces* depending on the different fish sources. By using complex halophilic media as a culture-dependent approach, we isolated diverse archaea for example, *Halorubrum saccharovorum*, *Halobacterium salinarum*, *Halobacterium noricense*, and 15 new species of halophilic archaea which closely related to the genus *Natrialba*, *Halobacterium* and *Halorubrum* were isolated. Through the research of cultivation procedure along with molecular DGGE technique represented most of dominant microbes identified with molecular method in jeotgals can be cultivable in genus level by cultivation-dependent method and halophilic archaea in extreme environment is more diverse than we expected.

## [B052]

### Preliminary Assessment of Microbial Degradation Capabilities in Petroleum-Spilled Taean Tidal Flat Sediments

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Tidal flat sediments, as active buffer zones between land and sea, have environmentally important roles including providing valuable natural resources and detoxifying anthropogenic pollutants. However, improper influx of BTEX and chlorinated solvents and oil spill incidents cause imbalances between natural capacity and contaminant loads. Although tidal flats harbor a vast diversity of microbes, the potential of bacteria capable of biodegradation have not been sufficiently monitored. In this work, biodegradation capability was preliminarily examined from the from Taean tidal flat sediments, where a severe oil spill accident was occurred. For examining aerobic degradability, biphenyl oxidizing microbes were enriched using Stable Isotope Probing (SIP) technique. Even at deep locations, significant amounts of biphenyl oxidizing bacteria were detected. While exploring anaerobic degradability, dechlorinating bacteria including *Geobacter* were stimulated in microcosms amended with tetrachloroethene (PCE). These results suggest that the microbial communities of Taean tidal flats have a variety of degradation capabilities. [Supported by Korea Ministry of Environment.]