

# Detection of Potential Pathogenic Bacteria in Bioremediation Microbial Consortia Using Metagenomics Techniques

**Jihoon Yang** (holyrood\_@hotmail.com) (Yonsei University, Seoul, Republic of Korea)

**Joonhong Park** (parkj@yonsei.ac.kr) (Yonsei University, Seoul, Republic of Korea)

**Background/Objectives.** Soil and groundwater had been contaminated with harmful substances such as petroleum and chlorinated compounds due to storage tank leakage, an illegal discharge. In order to effectively restoring the polluted environment, a bioremediation method that is more economical than chemical treatment and does not generate harmful secondary products was being applied. In most cases of bioremediation, microbial consortia were used rather than single bacteria because of site adaptability and interaction with indigenous microorganisms. In America and Canada, it was stipulated that the microbial consortia applied to the environment should not contain pathogenic microorganisms. In Korea, however, the relevant regulations were applied only to medicines, agriculture and aquatic products, so that the pathogenic of microbial consortia used for bioremediation was not managed. Therefore, this study detected potential pathogenic bacteria in chlorinated compound degrading microbial consortia in Korea and abroad using metagenomics technique.

**Approach/Activities.** This study was performed with JL-1 which Korean chlorinated compound degrading microbial consortia and KB-1, ANAS, Donnas II which were commercialized in America. The whole genome of JL-1 was analyzed using the Illumina Hiseq technique, and metagenomic data of KB-1, ANAS, and Donnas II were get from the MG-RAST (Metagenomics RAST Server). Functional analysis was performed with KEGG (Kyoto Encyclopedia of Genes and Genomes) database, and NMPDR (National Microbial Pathogen Data Resource) database was used for potential pathogenic micro-organisms detection.

**Results/Lessons Learned.** The MSDS of the KB-1 reported that *Salmonella sp.*, *Listeria monocytogenes*, *Vibrio sp.*, *Campylobacter sp.*, *Clostridia sp.*, *Bacillus anthracis*, *Pseudomonas aeruginosa*, *Yersinia sp.*, *Yeast and Mold*, *Fecal coliforms*, *Enterococci* were not detected. However, as a result of the analysis with "Human diseases" category in the KEGG database, all the microbial consortia showed disease inducing functions. The rates were 0.74% for ANAS, 0.64% for Donna II, 0.61% for JL-1, And 0.62% respectively. The "Epithelial cell signaling in Helicobacter pylori infection [PATH: ko05120]" and "Viral carcinogenesis [PATH: ko05203]" were the highest pathogenically function in every microbial consortium. From the analysis using the KEEG database, it was confirmed that all microbial consortia have potential pathogenicity. The results of pathogenic bacteria detection using NMPDR database is shown that potential pathogenic microbes accounted for less than 1% of the entire sequence, but it was confirmed that *Treponema pallidum* causing syphilis and *Listeria monocytogenes* causing listeriosis were included in the microbial community. According to the MSDS reports based on culturing, no pathogenic microorganisms were present in commercial microbial consortia. However, the function and phylogenetic analysis of the microbial community using the metagenomics technique revealed that it contains disease-inducing functions and pathogenic microorganisms. It was confirmed that metagenomics technique is effective in detecting the potential pathogenicity of microorganisms that are difficult to cultivate, or in detecting unknown pathogenic microorganisms. Therefore, companies producing microbial consortia used for bioremediation should not only submit results based on culturing, but also require pathogenicity verification using metagenomics technique.