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Improved application of microbial genomics and ecology tools in soil-groundwater bioremediation

Joonhong Park
School of Civil and Environmental Engineering, Yonsei University

1. Introduction

Predicting and assessing pollution risk and bioremediation capability requires understanding microbial functional and ecological behaviors in nature as well as in engineered system. Microbial genome sequencing and modern biotechnology development have led to the development of high-throughput detection technologies such as DNA microarrays. The purpose of this study is to illustrate the applicability of DNA microarray and other molecular tools in providing useful information regarding soil bioremediation. The first part of this presentation shows the examples of use of genome-wide microarray gene expression analysis in providing useful information for PCB (polychlorinated biphenyl) bioremediation. In a PCB-degrading bacterial strain, *Burkholderia xenovorans* LB400, the genome-wide gene expressions were analyzed under more environmentally relevant conditions such as carbon limitation, biofilm-forming conditions, and PCB-mediated stresses. The second part of this study is to expand the applicability of DNA microarray in detecting microbial biodegradative functions in soil microbial communities. DNA microarray has a limited sensitivity to detect biodegradative genes in soil microbial communities (ref. 1). To improve detection resolution, PCB-degrading populations were selectively labelled with heavy 13C by cultring soil communities with 13C-labeled biphenyl, and this heavy DNA fraction was separated by density-gradient ultracentrifugation.

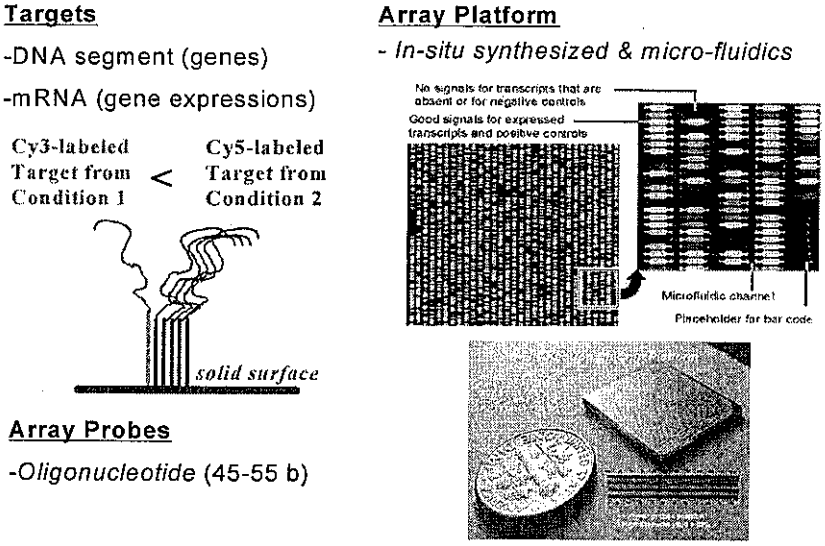

Figure 1. Principle of DNA microarray hybridization and the scheme of Xeotron chip used in this study.