

## Exploration of Soil Microbial Resources from Soil Metagenome

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Culture-independent studies on microbial diversity revealed that tiny fraction of total microorganisms in soil (less than 1% of total microbes) were identified and characterized by pure culture technique. This is because the majority of them are not culturable. Therefore, ecological function of the majority of microbial population in soil environments are not characterized and their potential in industrial application was not exploited. A genetic strategy, metagenome, came from the idea that much more microbial resources could be tapped from the viable but non-culturable (VBNC) bacteria compared to the small portion of culturable microbes. Soil metagenome is a total microbial genome obtained from soils directly, thus contain the most of VBNC DNA. Our aim in this study is to construct metagenomic library from various soil environments and to search microbial products, which can serve for chemical biotechnology application. We have constructed soil metagenomic libraries in a fosmid from four different soils. Heavy-metal specific responses of the selected copper tolerant clones to several heavy metals suggested that our libraries cover the genome of diverse microorganisms. Sequencing of insert DNA ends from randomly selected clones also exhibited the diverse microbial genes cloned in our libraries. We have also selected several number of lipolytic active clones and novel antimicrobial activities from the libraries. The characterization of the lipolytic active clones and an antimicrobial active clone will be presented. Many useful genes could be exploited from our metagenomic libraries for chemistry applications.

### References

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