

## **Detection and isolation of genes involved in heterocyclic compounds degradation from Antarctic psychrophilic bacteria**

Azham Zulkharnain<sup>1</sup>, Seiryu Take<sup>1</sup>, Tatsuya Niwano<sup>1</sup>, Siti Aqlima Ahmad<sup>2</sup>

<sup>1</sup>*Department of Bioscience, Faculty of Systems Engineering and Science, Shibaura Institute of Technology*

<sup>2</sup>*Department of Biochemistry, Faculty of Biotechnology & Biomolecular Sciences, Universiti Putra Malaysia*

The extensive usage of petroleum derived chemicals has introduced various recalcitrant compounds into the environment. Among of these compounds, we are focused on heterocyclic compounds such as carbazole (CAR), dibenzothiophene (DBT) and dibenzofuran (DBF) as they are more complicated to be degraded by microorganisms as they contain not only hydrogen and carbon atoms. Ignoring the fate of these compounds could lead to more disastrous effects not just to the environment, but also to humans due to the accumulative effects of bioconcentration. Previous reports regarding heterocyclic compounds have revealed that these compounds are ubiquitous in every environment studied and bacteria with heterocyclic compounds degrading ability have been isolated accordingly. We believe Antarctica is equally contaminated with heterocyclic compounds as we had successfully isolated bacteria with the ability to utilize CAR as sole carbon source. In relation to this, we aim to study the genetic structure of these bacteria, to understand their mechanisms for effectiveness in extreme low temperatures. Initial detection of genes was conducted using set of primers designed based on conserved regions for terminal dioxygenase *carA* genes collected from previous studies. Degenerative primer designed for detecting Rieske iron-sulfur cluster domain which is usually available in dioxygenases involved in aromatic hydrocarbon was also used. Findings from this study will be a first step before extensive studies using next generation sequencing technologies. Comparative analyses will be conducted using reported homolog genes and gene clusters to understand the origin and evolution of heterocyclic compounds degradation history in the Antarctic region.