

## **Metagenomic data of soil microbial community in relation to basal stem rot disease**

### **ABSTRACT**

The oil palm industry, especially in Indonesia and Malaysia is being threatened by Basal Stem Rot (BSR) disease caused by *Ganoderma boninense*. There is no conclusive remedy in handling this disease effectively. In this study, metagenomics analysis of soil were analyzed for a better understanding of the microbial diversity in relation to BSR disease. Study was conducted in three plantation sites of Sabah, Malaysia which incorporated different disease management and agronomic practices. The estates are located at Sandakan (Kam Cheong Plantation), Lahad Datu (FGV Ladang Sahabat) and Tawau (Warisan Gagah). Soil samples were collected from disease free, high and low BSR incidence plots. Illumina MiSeq metagenomic analysis using V3–V4 region of 16S rRNA gene was employed to study the microbial diversity. Bacteria (97.4%) and Archaea (0.2%) were found majority in kingdom taxonomy level. The most abundant phyla were *Proteobacteria*, *Acidobacteria*, *Actinobacteria*, and *Verrucomicrobia*. Higher alpha diversity of all species was observed among all tested soil from each estates. Beta analysis was analyzed using non phylogenetic UnifRac matrix and visualized using Principal Coordinates Analysis (PCoA). The tested soil samples in Kam Cheong Plantation were found to have similar bacterial communities. The data provided is useful as an indicator in developing biology controls against *Ganoderma boninense*.