

Analysis of tropical soil bacterial communities in Sabah using high-throughput sequencing

ABSTRACT

Aims: Soils contain a diverse bacterial population that is essential in various ecological processes such as biogeochemical cycling, soil quality improvement, plant growth and the maintenance of a balanced ecosystem. Hence, there is a need to understand the bacterial diversity and sustainability of various geographical regions. Nonetheless, despite growing knowledge of soil microbial diversity in many parts of the world, there is little data on the bacterial diversity of tropical soils such as Malaysia. Hence, this research was conducted to determine the bacterial communities of soils from selected areas in East Malaysia using the 16S rRNA gene-based metagenomic high-throughput sequencing and analysis approach.

Methodology and results: Soil samples (n=3) were collected from three sites within the same vicinity in Kota Kinabalu, Sabah. DNA was extracted from bacteria in the soil samples and the mix of bacterial 16S rRNA genes was amplified, sequenced and aligned to those in the Genbank. A total of 39 different bacteria phyla were found in the soil samples. The most abundant phyla in the analysed soils were Proteobacteria (19.90%), followed by Acidobacteriota (15.73%), Actinobacteriota (12.79%), Firmicutes (9.40%), Chloroflexi (9.23%), Planctomycetota (7.19%), Verrucomicrobiota (5.53%), Myxococcota (5.43%), Latescibacterota (2.72%) and Desulfobacterota (2.38%).

Conclusion, significance and impact of study: Research findings provided an overview of the most prevalent bacterial phyla in the selected Sabah soils, allowing the effects of environmental change on bacterial population shift to be tracked in the future.