

# マレーシア熱帯泥炭地における微生物群集構造とそれらの生物地球化学的循環への寄与

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**Resume of Doctoral Dissertation**

Microbial Community Structure and Their Contribution to  
Biogeochemical Cycles in Malaysian Tropical Peatland

Agriculture  
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**1 Research goal**

This study aims to understand better how tropical peatlands respond to disturbance by investigating GHG emissions, physicochemical variables, peat characteristics, peat microbial communities, and the link between these components.

**2 Summary of the chapters**

**Chapter 1**

Tropical peatland forests are a one-of-a-kind dual ecosystem that combines rainforest and peatland. Its topography is heavily influenced by hydrological conditions, which in turn determine the vegetation structure and peat types. It is considered as extreme ecosystems because of their low pH (generally below pH 4), anaerobic and oligotrophic conditions. Tropical peatland plays a vital role in nutrient cycling, serving as a source of groundwater, reducing excess nutrient flows from surface waters, and sequestering and storing atmospheric carbon. Southeast Asian peatland forests have been rapidly deforested in recent years, owing to agricultural expansion fuelled by rising global population, which has resulted in increased demand for food and renewable energy sources. The major drivers for deforestation in peatlands are expansion of industrial plantations, timber extraction and agriculture. The oil palm plantation experience aerobic condition with a long-term draining and drying peat. Drainage canal networks associated with oil palm plantation are a major contributor to peatland degradation. These canals are used to control water table level and make the soil suitable for planting, yet their presence has the negative impact of drying out peat soils near the ground surface. Peat soil considered to be poor soil due to acidic conditions and limited nutrient availability. The addition of fertilizer to promote palm productivity is likely to generate peat mineralization; The oil palm plantations associated drainage in peatlands expose surface peat to aerobic decomposition, presumably resulting in higher CO<sub>2</sub> emissions. This reverses the role of peatlands as a carbon sink to carbon source. The composition of organic matter is a crucial factor, by which above ground diversity influences the below ground

diversity. The soil biota depends on soil organic matter for their nutrients and C supply.

## Chapter 2:

The first field study was conducted to investigate the temporal GHG emissions corresponding to the environmental variables and peat characteristic of three land-use in Malaysian peatland systems, (i) natural peat swamp forest (NF), (ii) recovery peat swamp forest (RF), and (iii) oil palm plantation (OP). Biweekly temporal measurements of CO<sub>2</sub>, CH<sub>4</sub>, and N<sub>2</sub>O fluxes were conducted using a closed-chamber method from July 2017 to December 2018, along with the continuous measurement of environmental variables and a one-time measurement of the soil physicochemical properties. The results indicated that the changes in environmental conditions resulting from draining (OP) or rewetting historically drained peatland (RF) affected CH<sub>4</sub> and N<sub>2</sub>O emissions more than CO<sub>2</sub> emissions. The cumulative CH<sub>4</sub> emission was significantly higher in the forested sites (RF and NF), which was linked to these sites having a significantly higher water table (WT) level ( $p < 0.05$ ). Similarly, the high cumulative CO<sub>2</sub> emission trends at the RF and OP sites indicated that the RF rewetting-restored peatland system continued to have high decomposition rates despite having a significantly higher water table level (WT) than the OP site ( $p < 0.05$ ). The highest cumulative N<sub>2</sub>O emission at the drained-fertilized OP and rewetting-restored RF sites was linked to the available substrates for high decomposition (low C/N ratio) together with soil organic matter mineralization that provided inorganic nitrogen (N), enabling ideal conditions for microbial mediated N<sub>2</sub>O emissions. Overall, the measured peat properties did not vary significantly between the three land uses. However, the lower C/N ratio at the OP and the RF sites indicated higher decomposition rates in the drained and historically drained peat than in the undrained natural peat (NF), which was associated with high cumulative CO<sub>2</sub> and N<sub>2</sub>O emissions.

## Chapter 3:

The second field study was conducted to explore the variation of tropical peat microbial communities between undisturbed-peat natural peat swamp forest (NF) and disturbed-peat oil palm plantation (OP) at different peat depths and how it related to biogeochemical cycling using the high-throughput sequencing (NGS). Peat samples at three different depths, 0–5cm (surface layer), 20–25cm (sub-soil layer), and 40–50cm (bottom layer), were collected in September 2019 (dry season) from both sites. DNA was extracted from three replicate soil samples at each depth using the ISOIL beat beating soil extraction kit, and were sent to GENEWIZ for Next Generation Sequencing (NGS). This study shows that the peat microbial community structure in tropical peatlands was dominated by bacteria and responded to depth and land-use change. The dominant microbial taxa observed at the forest in this study are selectively similar to those in other studies on tropical peatland forest, yet their proportion of abundances are different that might suggest that there is a distinct degrading process of plant residues and formation of peat under different environmental conditions. The dominant phyla that accounted for more than 3% of the mean relative abundance of the overall microbial communities of both sites were *Acidobacteria*, followed by *Proteobacteria*, *Thermoplasmata*, and *Actinobacteria*. Alpha-diversity shows no significant difference between forest and oil palm peatland, yet Beta-diversity reveals significant differences between soil depths and sites. The ordination plots of PCoA (Beta-diversity) demonstrated that microbial communities in the

forest surface soil (0-5cm) were closely related to the surface and subsurface soils of the oil palm site (0-5cm and 20cm depths). However, approximately 60.5% of the sequences were not classified to any known genera, suggesting that there could be new, unknown microbial biota present in the extremely acid ecosystem.

#### **Chapter 4:**

Based on the findings, The findings of this study can assert that the rewetting-restored efforts of tropical peatland may not immediately reduce GHGs, because it depends on the length of time since the peatland started recovering. The higher total GHG emissions at the RF site in this study (rewetting restoration started 6-7 years previously), mainly due to increased CH<sub>4</sub> emissions, suggest that emissions may not be fall during the initial stage of peatland recovery. Therefore, further research is needed to clarify the timeline for changes in emissions after the start of peatland restoration. In addition, research on restored peatlands should be widened to include different types of restored sites and different histories of previous land-used before the implementation of rewetting-restoration efforts. Also, this study has demonstrated the differences in structure of microbial communities between a natural peat swamp forest (NF) and a drained and cultivated peatland oil palm plantation (OP). The peat microbial community structure in both tropical peatlands was dominated by bacteria, but varied with depth and land-use. The microbial communities in the oil palm plantation were closely related to the soil surface communities of the natural forest system. The dominant microbial taxa observed in the forest system in this study are similar to those in other studies on tropical peatland forest in Malaysia, yet the proportions of their abundances were different, which might reflect the distinct degrading process of plant residues and formation of peat under different environmental conditions. In this study, approximately 60.5% of the sequences were not classified to any known genera, suggesting that there could be new, unknown microbial biota present in this extremely acid ecosystem. To connect taxonomic composition and function is a challenge, and to connect microbial community structure and ecosystem functioning is even more of a dilemma. Therefore, future studies should focus on specific taxa that have demonstrated a significant response to land-use change in order to gain a more detailed understanding of the implications of microbial turnover for peatland ecosystem functioning.