



Title	Study on the diversity and vertical distribution of soil microorganisms in tropical peatlands of Sarawak, Malaysia, and characterization of nitrous oxide (N ₂ O)-emitters and quenchers from the tropical peat soils [an abstract of dissertation and a summary of dissertation review]
Author(s)	LAU, Sharon Yu Ling
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学位論文内容の要旨

博士の専攻分野名称：博士（農学）

氏名：Sharon Yu Ling Lau

学位論文題名

Study on the diversity and vertical distribution of soil microorganisms in tropical peatlands of Sarawak, Malaysia, and characterization of nitrous oxide (N₂O)-emitters and quenchers from the tropical peat soils

(サラワク・マレーシア熱帯泥炭地における土壌微生物の多様性と垂直分布、および熱帯泥炭土壌から分離した亜酸化窒素 (N₂O) の産生および消去に関わる微生物の特徴に関する研究)

1. Improved DNA Extraction Method to Access Microbial Diversity of Tropical Peatlands

Woody tropical peat soil is a histosol with an intermediate-to-strong acidic nature, consisting of >75% organic matter mainly with degraded wood materials extraordinarily rich in humic substances. Due to its chemical and physical properties, tropical peat soil is one of the most difficult sources for obtaining pure soil DNA. Several methods for effective and reproducible DNA extraction from woody peat soil were tested to obtain high-quality DNA suitable for use as template DNA for 16S rRNA gene-targeted denaturing gradient gel electrophoresis (DGGE), along with an appropriate choice of a humus-tolerant *Taq* polymerase. Results show that DNA extraction using a modified conventional method, followed by removal of humic substances using 1.5% agarose gel electrophoresis in Tris/Borate/EDTA (TBE) buffer as an important step, yielded the most comprehensive DNA fingerprinting profile for soil eubacteria and archaea. The DGGE profiles of the DNA samples from both top (0–50 cm) and deep (350–400 cm) layers of tropical peat soils exhibited microbial compositions including unculturable eubacteria of class Deltaproteobacteria, phyla Actinobacteria, Bacteroidetes, and Acidobacteria, and archaea of phyla Thaumarchaeota and Crenarchaeota.

2. Vertical Distribution of N₂O Emission Potentials in Tropical Peatland

Tropical peat swamp forests that have been reclaimed for agricultural use are generally active sources of nitrous oxide (N₂O) efflux; but the cause and mode for the emergence of N₂O emitters from the soil microbial communities of reclaimed tropical peat soil are unclear. Using a culture-based N₂O emission assay, the N₂O emission potentials of soil at various depths (0–450 cm) were investigated in two oil palm

plantations with a period of 2 years (E2Y) and 10 years (E10Y) after deforestation in Sarawak, Malaysia. The peat soil at E2Y showed a trend of high N₂O emission potential in deeper layers (200–400 cm), whereas the older plantation E10Y showed considerably more active N₂O emission potential in shallow soil (10–50 cm). N₂O emission potentials among the soil microbial communities at different soil depths of E10Y site showed positive correlations with NO₃⁻ and NH₄⁺ contents, whereas soils of the E2Y site had N₂O emission potentials inversely proportional to the contents of NO₃⁻. This contrasting vertical correlation between N₂O-emitting potentials and mineralized nitrogen contents suggests that active N₂O emission in deep soil of E2Y has maintained the original C/N ratio of the peat soil, whereas at E10Y, such a regulatory system has been lost due to advanced soil degradation.

3. Isolation and Characterization of N₂O Quenchers from Tropical Peatlands

Potent N₂O-quenchers were isolated and identified as *Burkholderia* sp. and *Chitinophaga* sp. from soils collected at various depths from an oil palm plantation on peat. *Chitinophaga* sp. showed an extraordinary N₂O-quenchable activity and was able to eliminate as much as 3000 ppmv (atmospheric level at 300 ppbv) of the supplemented N₂O in the headspace (22.57 mL) within 3 days. No inhibition of N₂O quenching was observed by addition of 10% acetylene, suggesting that the N₂O quenching may not be due to reduction of N₂O by N₂OR. The whole-genome sequencing for the *Chitinophaga* sp. using a pyrosequencer revealed that N₂O quenching activity of *Chitinophaga* sp. is without the *nosZ* gene, suggesting the possibility of other redox mechanisms.