



Biogeographical distribution of microbial communities along the Rajang River–South China Sea continuum

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Abstract. The Rajang River is the main drainage system for central Sarawak in Malaysian Borneo and passes through peat domes through which peat-rich material is being fed into the system and eventually into the southern South China Sea. Microbial communities found within peat-rich systems are important biogeochemical cyclers in terms of methane and carbon dioxide sequestration. To address the critical lack of knowledge about microbial communities in tropical (peat-draining) rivers, this study represents the first seasonal assessment targeted at establishing a foundational understanding of the microbial communities of the Rajang River–South China Sea continuum. This was carried out utilising 16S rRNA gene amplicon sequencing via Illumina MiSeq in size-fractionated samples (0.2 and 3.0 μm GF/C filter membranes) covering different biogeographical features and sources from headwaters to coastal waters. The microbial communities found along the Rajang River exhibited taxa common to rivers (i.e. predominance of β -*Proteobacteria*) while estuarine and marine regions exhibited taxa that were common to the aforementioned regions as well (i.e. predominance of α - and γ -*Proteobacteria*). This is in agreement with studies from other rivers which observed similar changes along salinity gradients. In terms of particulate versus free-living bacteria, nonmetric multi-dimensional scaling (NMDS) results showed similarly distributed microbial communities

with varying separation between seasons. Distinct patterns were observed based on linear models as a result of the changes in salinity along with variation of other biogeochemical parameters. Alpha diversity indices indicated that microbial communities were higher in diversity upstream compared to the marine and estuarine regions, whereas anthropogenic perturbations led to increased richness but less diversity. Despite the observed changes in bacterial community composition and diversity that occur along the continuum of the Rajang River to the sea, the PICRUSt predictions showed minor variations. The results provide essential context for future studies such as further analyses on the ecosystem response to anthropogenic land-use practices and probable development of biomarkers to improve the monitoring of water quality in this region.

1 Introduction

Biogeochemical transformations are primarily governed by microbial communities (Konopka, 2009), and it is crucial to understand their dynamics in order to predict biosphere modulations in response to a changing climate. Despite the importance of freshwater to society and despite hosting the highest microbial diversity (Besemer et al., 2013), microbial