



## **Diversity and composition of sediment bacteria in subtropical coastal wetlands of North Stradbroke Island, Queensland, Australia**

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Coastal wetlands provide a wide variety of important ecosystem services but continue to suffer disturbance, degradation and deforestation. Sediment bacteria are responsible for major nutrient transformation and recycling in these ecosystems. Insight into microbial community composition and the factors that determine them may improve our understanding of biogeochemical processes, food web dynamics, biodegradation processes and, thus, help to develop the management strategies for preserving the ecosystem health and services. Characterizing shifts in community taxa along environmental gradients has been shown to provide a useful tool for determining the major drivers affecting community structure and function.

North Stradbroke Island (NSI) in Southern Queensland presents considerable habitat diversity including variety of groundwater dependent ecosystems such as lakes, swamps, sedge-like salt marshes and mangroves. Ecological responses of continuous groundwater extraction for municipal purposes and sand mining operations on NSI are still need to be assessed in order to protect its unique environment. Changes in coastal hydrology due to either climate change or human activity may directly affect microbial populations and, thus, biogeochemical cycles of nutrients. These may result in altering/losing some ecosystem services provided by coastal wetlands.

In this study we examine microbial diversity and determine environmental controls on bacterial community structure along a natural transition from freshwater forested wetland (melaleuca woodland), sedge-like salt marsh and into mangroves located at NSI. The study area is characterized by significant groundwater flow, nutrient limitation and sharp transition from one ecosystem type to another. Sediment cores (0-5 cm and 20-25 cm depth) were collected from three representative sites of each zone (mangroves - salt marsh - freshwater wetland) along the salinity gradient in August 2012. Subsamples were set aside for use in chemical analyses, microbiological analysis and for porewater extraction.

Microbial community structure and diversity are assessed using denaturing gradient gel electrophoresis (DGGE) of 16S rRNA gene fragments and barcoded pyrosequencing. To evaluate the relationships between microbial communities and environmental variables we use bioinformatical and statistical tools. Physico-chemical parameters included measurements of sediment pH, temperature, salinity and nutrients composition. Background information regarding hydrology and vegetation is incorporated in the study.

Sediment bacteria play a vital role in wetland ecological function, and they are very sensitive to environmental changes. Considering coastal wetlands of NSI as a model area, our study may contribute to the knowledge of factors shaping microbial diversity in tropical wetlands, help to gain insight into the microbe-nutrient-plant relationships, and also serve as background for conservation plans to safeguard these ecosystems.