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Different plant species drive the microbial methane and nitrogen cycles and CH₄ and N₂O emissions on coasts affected by brackish water

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Coastal ecosystems are suffering increasing degradation in many parts of the world and the ecological integrity and biodiversity of those ecosystems have been greatly threatened due to the high load of pollutants produced largely through anthropogenic processes. Agricultural, industrial and domestic applications pollution mainly affect coastal zones via riverine inputs from contaminated urban and rural areas near shore, atmospheric deposition and direct dumping. Beside the different other pollutants, excessive nutrients have become major concerns which can completely change the functioning and appearance of coastal ecosystems. A variety of plants complete the ecological system of coasts and coastal vegetation may even govern the microbial processes and greenhouse gas emissions. With the need to better protect and manage the coastal areas, it is important to understand the decisive microbial processes of nutrients cycling in coastal ecosystem, especially in the face of the changing climate.

The aim of this study was to assess the abundances of soil bacteria and archaea and their potential to perform different carbon and nitrogen cycling processes in coastal zones and relate these nutrient transformation processes to greenhouse gas emissions. The study was carried out in Estonian and Chinese coasts which were affected by brackish water (mixed saline and fresh water) because of riverine inputs. Twice a month during the most intensive vegetation period, the gas samples (CO₂, CH₄, and N₂O) were taken and different parameters of plant (*Schoenoplectus tabernaemontanii* and *Phragmites australis* in Estonia; *Spartina alterniflora* and *Scirpus mariqueter* in China) and water were measured in situ. Soil (from the 0–10 cm top layer) and plant samples were collected in the end of study. Besides different chemical parameters measured of soil samples, the archaeal and bacterial community abundance was evaluated by quantitative PCR. To characterise methane cycle, the abundances of methanogenic marker gene *mcrA* and methanotrophic marker gene *pmoA* were assessed. Genetic potential of nitrogen transformation processes was evaluated by targeting the following functional genes: bacterial, archaeal and COMAMMOX (complete oxidation of ammonium)-specific *amoA* (nitrification); *nirS*, *nirK*, *nosZ* clade I and *nosZ* clade II (denitrification); *nifH* (N₂ fixation); *nrfA* (DNRA, dissimilatory nitrate reduction to ammonium); ANAMMOX- (anaerobic ammonium oxidation), and *n-damo*-specific 16S rRNA genes (nitrite dependent anaerobic methane oxidation).

The results concluded that different plant species played a critical role in mediating gas emissions, where their age composition and biomass was important. Relevance of n-damo process and its high genetic potential for CH₄ reduction was detected in coastal areas. Still, four times higher CH₄ emissions were observed on the Chinese coast compared to Estonia. DNRA process showed the greatest genetic potential in the Chinese research area, but this process was less likely to occur in the soil of Estonian *Phragmites australis*. As a result of nitrification and denitrification, N₂O was emitted from the coasts to the atmosphere.