



## Emergent macrophytes select for nitrifying and denitrifying microorganisms in constructed wetlands

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The use of constructed wetlands for wastewater treatment is a reliable low-cost alternative that has been widely developed during the last years. Several processes involving plants, sediments, and microbial communities contribute to nitrogen removal in wetlands. Vegetation plays an important role in this process, not only by nutrient assimilation but also by the stimulation of the plant associated microbiota. Plants supply oxygen at the close proximity of the root surface that may favour ammonia oxidizers. At the same time, exudation of organic compounds potentially speeds-up denitrification in the anoxic environment. The aim of this work was to understand the plant-microbe interactions at the root level in the Empuriabrava free water surface constructed wetland (Spain). The roots of the macrophytes *Typha latifolia*, *Typha angustifolia*, *Phragmites australis* and *Bolboschoenus maritimus* were sampled at four dates from January to September 2012, covering all the stages of plant growth. Additionally, sediment surrounding vegetation and non-vegetated sediments were sampled. Microbial community structure was analysed by pyrosequencing of bacterial and archaeal 16S rDNA and functional genes (*nirK*, *nirS*, *nosZ* and *amoA*).

Bacterial communities were significantly different in sediments of the vegetated areas compared to the root surface. Plant roots exhibited a higher proportion of proteobacteria whereas Actinobacteria were dominant in sediments. The nitrifiers *Nitrosomonas* sp. and *Nitrosococcus* sp. accounted for less than 1% of all sequences. Archaeal communities were dominated by the Miscellaneous Crenarchaeotic Groups C2 and C3 and Methanomicrobia. Higher relative abundances of MCG were found in roots of *P. australis*, *B. maritimus* and *T. angustifolia*. Ammonia oxidizing archaea accounted for less than 0.1% of all sequences but were consistently more abundant in sediment samples compared to roots. *NirK* and *NirS*-type bacterial communities showed clearly distinct distribution patterns among plant species, thus indicating different plant-microbe relationships for the two bacterial groups.

Our results show that plant roots have implications in multiple steps of the nitrogen cycle and can significantly alter nitrogen removal in wetlands.