Title:

Bacterial community dynamics in constructed wetlands with different plants for the polishing of high salinity industrial wastewater

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Abstract:

Industrial wastewaters that are able to be treated by biological means are good candidates to be addressed by constructed wetlands (CWs). CWs are man-made systems that have been conceived to enhance specific characteristics of natural wetlands ecosystems for improved treatment capacity (Kadlec and Wallace, 2009), arising as an interesting and potential option to be comprised in an integrated wastewater management. Microorganisms have the main role in transformation and mineralisation of nutrients and organic pollutants in CWs (Stottmeister et al., 2003). Research into the dynamics of wetland microbiology is needed in order to contribute to elucidating their functioning (Calheiros et al., 2009).

This study focused on the diversity of bacterial communities from two series of horizontal subsurface CWs, planted with different species, polishing high salinity tannery wastewater, under a range of hydraulic conditions. Each series was planted with *Arundo donax* (series: SA) and *Sarcocornia* sp. (series: SS) in a substrate composed by expanded clay and sand. High numbers of cultivable bacteria were obtained from rhizosphere samples plated onto marine and nutrient agar. Several bacterial isolates were retrieved from the CWs for which phylogenetic affiliations were obtained on the basis of 16S rRNA gene sequence. Changes in the bacterial community related to the roots and substrate of each series and along CW operation were examined using denaturating gradient gel electrophoresis (DGGE). For each series the diversity and equitability indexes calculated based on DGGE profiles were, in general, similar for all wetland units, suggesting that despite the high diversity, the distribution of species is even. No clear relation was established between the sample collection time, hydraulic loading applied and the bacterial diversity. The influence of the type of plant in the bacterial communities in the rhizosphere was assessed.

Keywords: constructed wetlands, bacterial communities, DGGE, industrial wastewater

References

Calheiros, C.S.C., Duque A.F., Moura, A., Henriques, I.S., Correia, A., Rangel, A.O.S.S., Castro, P.M.L. 2009. Substrate effect on bacterial communities from constructed wetlands planted with *Typha latifolia* treating industrial wastewater. Ecological Engineering. 35(5):744-753

Kadlec, R.H. and Wallace, S. 2009. Treatment Wetlands. 2nd Edition. CRC Press. Taylor & Francis Group. Boca Raton. Florida

Stottmeister, U., Wießner, A., Kuschk, P., Kappelmeyer, U., Kästner, M., Bederski, O., Müller, R.A. and Moormann, H. 2003. Effects of plants and microorganisms in constructed wetlands for wastewater treatment. Biotechnology Advances. 22:93-117