

Sulfate-reducing prokaryotes in river floodplains

Summary

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This thesis constitutes a pioneer attempt at elucidating the ecology of sulfate-reducing prokaryotes in river floodplains. These are non-typical sulfate-reducing environmental settings, given the generally low sulfate concentration that characterize freshwater habitats, and river flow regulation that makes flooding events infrequent. However many current riverine areas are polluted by sulfate, essential ion for sulfate reducers metabolism. In addition, where biodiverse wetlands restoration attempts allow rivers greater access to the floodplains, more frequent and prolonged waterlogging may create the necessary anoxic conditions for the growth of these anaerobic microorganisms.

Given the diversified and polyphyletic nature of sulfate-reducing prokaryotes and their expected low abundance in floodplains, at first it was necessary to develop a molecular high-throughput screening tool potentially able to detect, discriminate and identify at a high degree of resolution all microbes with the ability to reduce sulfate. The polymerase chain reaction-denaturing gradient gel electrophoresis strategy presented in **Chapter II** was subsequently applied in combination with other molecular, microbiological and analytical techniques to study sulfate-reducing prokaryotes in a variety of floodplain soils, in field and laboratory-scale experimental formats (**Chapter III, IV, and V**).

During the initial large-scale field survey (**Chapter III**), sulfate reducers biogeography in river floodplains was studied with a polyphasic approach consisting of polymerase chain reaction-denaturing gradient gel electrophoresis screening, microarray monitoring, and polar lipid-derived fatty acids analyses. Surprisingly, sulfate reducers were detected in diversified communities in all non- or temporarily flooded soils analyzed, suggesting a widespread ability among this microbial guild to survive periods of exposure to oxygen. Furthermore, the biogeographic pattern observed indicates differences in dominant community members; in particular *Desulfosarcina*-, *Desulfomonile*- and *Desulfobacter*-related sulfate-reducing prokaryotes showed a salinity-dependent distribution. Therefore, the response of sulfate-reducing communities in various floodplain soils may not necessarily be the same upon changing environmental conditions. This aspect was investigated in **Chapter IV**.

Summary

The locations of the Haringvliet lagoon used for the mesocosm set-up presented in **Chapter IV** had different history, *i.e.* river regulation and management practices. These factors have changed the physico-chemical characteristics of the soils, but they have altered also the sulfate-reducing microbial community, and its potential response upon flooding.

The most striking product of dissimilatory sulfate reduction is sulfide, a highly reactive chemical with a strong environmental impact. The effect of active sulfate-reducing communities on floodplain plants and *vice-versa* was investigated in a microcosm experiment with *Glyceria maxima* (reed sweetgrass) as model wetland plant (**Chapter V**). The presence of active sulfate-reducing prokaryotes promoted plant growth by enhancing sulfide-mediated phosphate release and by reducing the accumulation of toxic fermentation products in the soil in the first weeks after flooding with sulfate-rich water. The importance of iron deposits in reducing the negative phytotoxic effects of sulfide was also highlighted. Finally, molecular analyses revealed that only sulfate-reducing microorganisms belonging to the families *Desulfobulbaceae*, *Desulfovibrionaceae* and *Desulfobacteraceae* were active in the rhizosphere of *G. maxima*.