

Home

Online Library HESS

- Recent Final Revised Papers
- Volumes and Issues**
- Special Issues
- Library Search
- Title and Author Search

Online Library HESSD

Alerts & RSS Feeds

General Information

Submission

Review

Production

Subscription

Comment on a Paper

Impact
Factor
2.270

ISI
indexed

ARCHIVED IN

PORTICO

▣ Volumes and Issues ▣ Contents of Issue 1 ▣ Special Issue

Hydrol. Earth Syst. Sci., 12, 277-291, 2008
www.hydrol-earth-syst-sci.net/12/277/2008/

© Author(s) 2008. This work is distributed
under the Creative Commons Attribution 3.0 License.

Vegetation composition and soil microbial community structural changes along a wetland hydrological gradient

W. K. Balasooriya¹, K. Deneff², J. Peters¹, N. E. C. Verhoest¹, and P. Boeckx²

¹Department of Forest and Water Management, Ghent University, Coupure links 653, 9000 Gent, Belgium

²Department of Applied Analytical and Physical Chemistry, Ghent University, Coupure links 653, 9000 Gent, Belgium

Abstract. Fluctuations in wetland hydrology create an interplay between aerobic and anaerobic conditions, controlling vegetation composition and microbial community structure and activity in wetland soils. In this study, we investigated the vegetation composition and microbial community structural and functional changes along a wetland hydrological gradient. Two different vegetation communities were distinguished along the hydrological gradient; *Caricetum gracilis* at the wet depression and *Arrhenatheretum elatioris* at the drier upper site. Microbial community structural changes were studied by a combined in situ ¹³CO₂ pulse labeling and phospholipid fatty acid (PLFA) based stable isotope probing approach, which identifies the microbial groups actively involved in assimilation of newly photosynthesized, root-derived C in the rhizosphere soils. Gram negative bacterial communities were relatively more abundant in the surface soils of the drier upper site than in the surface soils of the wetter lower site, while the lower site and the deeper soil layers were relatively more inhabited by gram positive bacterial communities. Despite their large abundance, the metabolically active proportion of gram positive bacterial and actinomycetes communities was much smaller at both sites, compared to that of the gram negative bacterial and fungal communities. This suggests much slower assimilation of root-derived C by gram positive and actinomycetes communities than by gram negative bacteria and fungi at both sites. Ground water depth showed a significant effect on the relative abundance of several microbial communities. Relative abundance of gram negative bacteria significantly decreased with increasing ground water depth while the relative abundance of gram positive bacteria and actinomycetes at the surface layer increased with increasing ground water depth.

▣ [Final Revised Paper](#) (PDF, 2708 KB) ▣ [Discussion Paper](#) (HESSD)

Citation: Balasooriya, W. K., Deneff, K., Peters, J., Verhoest, N. E. C., and Boeckx, P.: Vegetation composition and soil microbial community structural changes along a wetland hydrological gradient, Hydrol. Earth Syst. Sci., 12, 277-291, 2008. ▣ [Bibtex](#) ▣ [EndNote](#) ▣ [Reference Manager](#)

 Copernicus Publications
The Innovative Open Access Publisher

Search HESS

Library Search

Author Search

News

- ▣ New Service Charges
- ▣ Financial Support for Authors
- ▣ ISI Impact Factor: 2.270

Recent Papers

01 | HESSD, 28 Apr 2009:
Integrating field and
numerical modeling methods
for applied urban karst
hydrogeology

02 | HESSD, 28 Apr 2009:
Analyzing the relationship
between peak runoff
discharge and land-use
pattern – a spatial
optimization approach

03 | HESSD, 27 Apr 2009:
Dynamically vs. empirically
downscaled medium-range
precipitation forecasts

