RCN: Enzymes in the Environment

Big questions and challenges: Linking aquatic and terrestrial environments

JÜRGEN MARXSEN

Aquatic Microbial Ecology Group,
Department of Animal Ecology,
Gießen, Germany

JUSTUS-LIEBIG-UNIVERSITÄT GIESSEN

Limnological River Station, Max Planck Institute for Limnology, Schlitz, Germany

mpil max-planck-institut für limnologie

Soil and water habitats

Macrohabitats

- characterized by varying proportions of 2 phases: solid surfaces and water
- continuum (?) of habitats: from arid deserts (no or little pore water) to offshore sea water (only traces of particulate matter, lacking nearly completely any solid surfaces)

Fundamental differences between soil and water

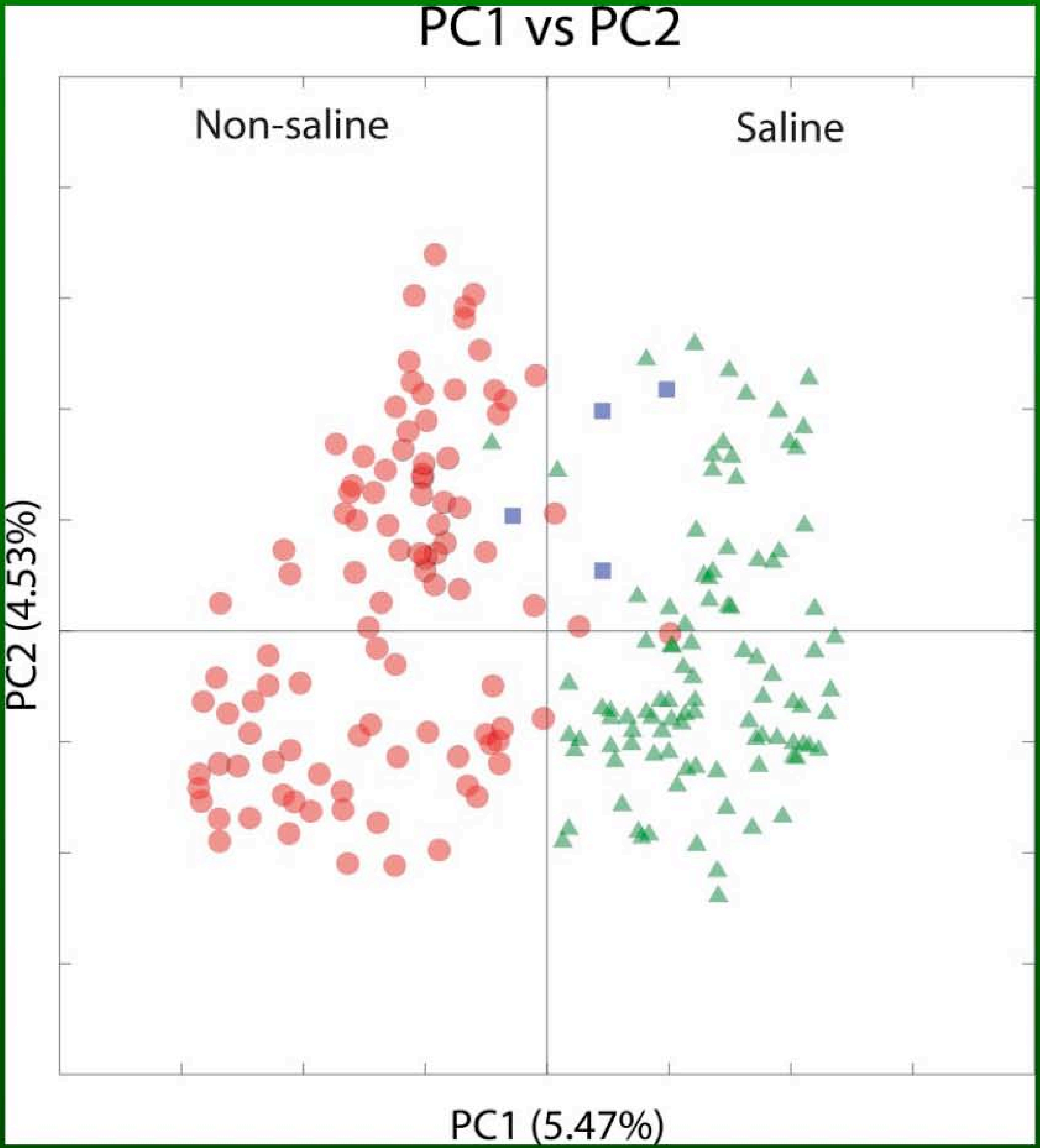
- water availability
- substrates for microbial growth
  soil: plant residues
  water: more direct coupling to primary producers
- constancy: more pronounced constancy in aquatic environm.

Microhabitats

are the effective habitats for microorganisms

- aquatic microhabitats occur also in soil

Global patterns in bacterial community composition: salinity

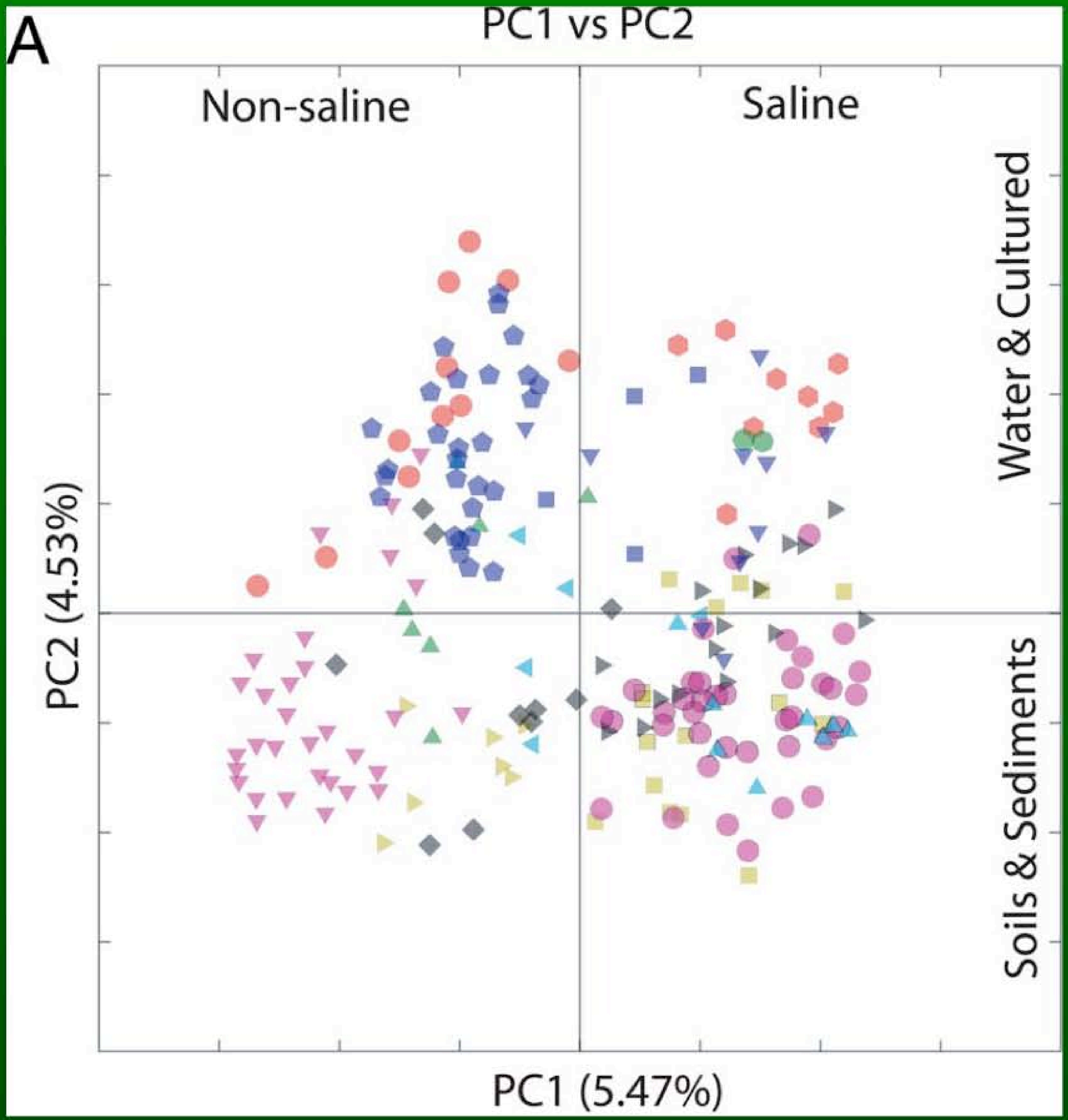


Major environmental determinant: salinity (rather than temperature, pH, or other physical and chemical factors)

red circles – non-saline environments
green triangles – saline environments
blue squares –mixed environments

From LOZUPONE, C.A., & R. KNIGHT, 2007. Global patterns in bacterial diversity. PNAS 104: 11436-11440.

Global patterns in bacterial community composition: water vs. sediment/soil



2nd most important determinant: substratum type (water vs. soil/ sediment)

blue pentagons – nonsaline water
red circles – nonsaline cultured
purple triangles – surface soils
yellow sidewise triangles – sediments
gray diamonds – submerged soils and aquifers
blue sidewise triangles – nonsaline springs
green triangles - nonsaline endolithic

From LOZUPONE, C.A., & R. KNIGHT, 2007. Global patterns in bacterial diversity. PNAS 104: 11436-11440.

Diversity in soil and aquatic sediments

- **Aquatic sediments**

  - highest phylogenetic diversity from all environments considered (highly stratified nature, chemical gradients)

- **Soil**

  - low phylogenetic diversity, but
  - very high species level diversity (more closely related species in one sample)
  - fungi not considered

Levels of analyzing structure and function of extracellular enzymes

- Genomics (DNA)
- Transcriptomics (mRNA)
- Proteomics (proteins)
- Metabolomics (metabolites)

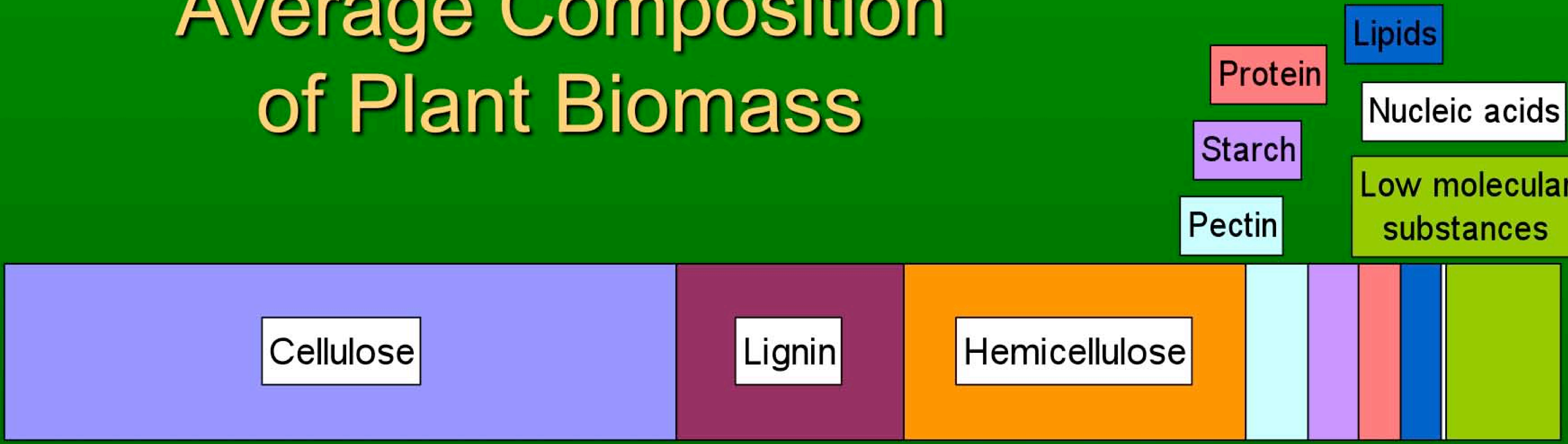
E.g.: RAES, J., & P. BORK, 2008. Molecular eco-systems biology: towards an understanding of community function. Nature Rev. Microbiol. 6: 693-699.

Broad and narrow functions *sensu* Schimel

- Broad processes
  - carried out by many organisms
  - little apparent influence of microbial community structure
- Narrow processes
  - carried out by restricted groups of organisms
  - potential for substantial ecosystem-level effects from differences in microbial diversity and community structure
  - example: litter degradation

SCHIMEL, J., 1995. Ecosystem consequences of microbial diversity and community structure. In: F.S. CHAPIN & C. KÖRNER (eds.), Arctic and Alpine Biodiversity: Patterns, Causes and Ecosystem Consequences. Ecosystem Studies 113, Springer, Berlin, p. 239-254.

Average Composition of Plant Biomass



endoglucanase,
cellobiohydrolase,
β-glucosidase,
....

phenol-oxidase,
peroxidase,
....

β-xylosidase,
....

Extracellular enzymes involved in degradation

Narrow functions among extracellular enzymes?

- Are among extracellular enzymes (esp. those involved in the degradation of refractory macromolecules) really narrow functions?
- Are the communities and functions in soil and aquatic environments sensitive to environmental changes?
- Does reduction of community diversity and/or do changes in community composition have large-scale effects on these processes?
- Is there any influence on the overall CO_2 release by soil and aquatic environments?

Water availability

- <u>Soil</u>
  - narrow processes more sensitive to be affected in soil

- <u>Aquatic environments</u>
  - exposed to drought in temporary waters
  - headwaters become more affected by more frequent and longer lasting droughts because of climate change in some regions
  - extracellular enzymes have an important role for recovery of microbial communities and re-establishing its functions after rewetting

MARXSEN, J., A. ZOPPINI & S. WILCZEK, 2010. Microbial communities in streambed sediments recovering from desiccation. FEMS Microbiol. Ecol. 71: 374-386

Possible approach

- Initial metagenome and metaproteome analysis (+ metatranscriptome analysis?)
  - select functional genes expressed at high enough levels
  - taxonomic analysis can be included

- Detailed analysis of functional genes
  - PCR-based assays (DNA, cDNA)
  - after having selected or developed suitable primers

- Data on the diversity of enzymes
  - genome, transcriptome and protein level
  - compare with activity measurements

Important questions

- How are community composition and extracellular enzyme activity linked?
- Which are the differences between typical aquatic and terrestrial environments regarding enzyme diversity and activity?
- Are there regional differences?
- What about seasonal fluctuations?
- Which is the influence of natural and anthropogenic stressors (e.g. water availability, pH, temperature, nutrient enrichment, contamination)?
- …………………?