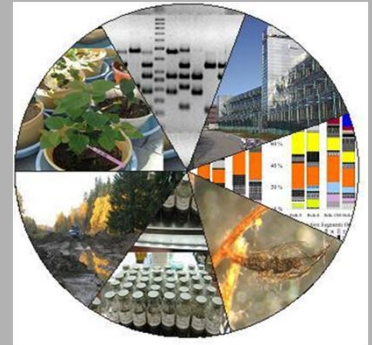


Research areas of interest

- Systems: Polluted soils and Groundwater, Plant-microbe interactions, Peatlands and Agricultural soils
- Processes: Phytoremediation, degradation of organics (*alkB*, *bphC*), heavy metal microbial transformation (Chromium), C-cycle (Methane, CO₂); soil suppressivity, agric. management
- Microbes: Archaea, Bacteria, Fungi



Members of research group



Kim Yrjälä
(Adjunct professor)



Pauli Siivonen
Master student



Shinjini Mukherjee
(PhD student)



Heli Juottonen
(Postdoc)



Sajan Raju (PhD student)



Timo Sipilä
(former Postdoc)

Methods

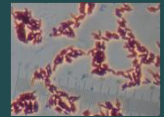
Molecular methods: DNA fingerprinting (T-RFLP, RFLP, DGGE), qPCR, 454-sequencing



Polluted field sites:
Luumäki, Läyliäinen
(Finnish Forest Research Institute, METLA)

Enzyme assays

Endophyte isolation and inoculation



Resources



Lakkasuo, and Siikaneva mires near Hyttiälä Biological station



Agricultural fields (Dept. Of Agricultural Sciences)



Greenhouses provided by METLA

Five key publications

- I. Mukherjee S., M. Heinonen, M. Dequivre, T. Sipilä, P. Pulkkinen, K. Yrjälä. 2013. Secondary succession of bacterial communities and co-occurrence of phylotypes in oil-polluted *Populus* rhizosphere. *Soil Biology and Biochemistry* 58: 188-197.
- II. Sipilä, T., Yrjälä, K., Alakukku, L., Palojärvi, A. 2012. Cross-site soil microbial communities under tillage regimes: fungistasis and microbial biomarkers. *Applied and Environmental Microbiology*. 78: 8191–8201.
- III. Yrjälä, K., Tuomivirta, T., Juottonen, H., Putkinen, A., Lappi, K., Tuittila, E-S, Penttilä, T., Minkkinen, K, Laine, J., Peltoniemi, K., & Fritze, H. 2011. CH₄ production and oxidation processes in a boreal fen ecosystem after long-term water table drawdown. *Global Change Biology*, 17: 1311-1320.
- IV. Juottonen, H., Juutinen, S., Tuittila, E-S. & Yrjälä, K. 2008. Seasonality of methane production and communities of methanogenic Archaea in a boreal fen. *The ISME Journal*, 2: 1157–1168.
- V. Sipilä, T., Riisio, H. & Yrjälä, K. 2006. Novel upper pathway extradiol dioxygenase gene diversity in polluted soil. *FEMS Microbiology Ecology* 58: 134-44.

