Fan Yang

Personal Data

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Research Experience

Current – Jan 2013

Post-doctoral researcher at Iowa State University,
Investigate the impacts of global climate change on carbon and nitrogen cycles in SPRUCE peatland, at Marcell experimental forest, MN

- Microbial metatranscriptomics in complex soil microbial communities
- Guided gene assembly with short-read metagenomic sequences
- Gene targeted sequencing of bacterial 16S rRNA genes and fungal ITS genes (Illumina paired end)
- Microbial community sequence analysis by using Quantitative Insights Into Microbial Ecology (QIIME)
- Measurements of microbial biomass and extracellular enzyme activities
- Field sampling in peat bogs

Jan 2008-Dec 2013

Doctoral research assistant at Michigan State University,
Investigate the role of bacterial populations and communities in heavy metal remediation and dairy manure co-digesters

- Anaerobic isolation and cultivation of soil and sediment bacteria
- Gene targeted 454 sequencing of bacterial 16S rRNA genes
- Construct clone libraries for microbial marker and functional genes
- Functional gene microarray of environmentally-relevant genes
- Terminal-Restriction Fragment Length Polymorphism (T-RFLP) analysis on bacterial 16S rRNA genes
- Microbial community sequence analysis by using Ribosomal Database Project (RDP, both web-based and command-line) and MOTHUR
- Construct phylogenetic trees by using Arb and Molecular Evolutionary Genetics Analysis (MEGA)
- Annotate gene sequences by using command-line Basic Local Alignment Search Tool (BLAST)
- Comparative genome analysis by using MAUVE multiple genome alignment tool
- HPLC analysis of bacterial products from growth media
- Total RNA extraction and reverse-transcription PCR

Sep 2005-Dec 2007

Master research assistant at Michigan State University,
Cooperative binding of copper by Ralstonia pickettii strains 12D and 12J

- Bioadsorption and bioaccumulation of copper by *R. picketii*
- Cell physiological responses to the presence of copper