

Microbial Interactions with Natural Organic Matter Extracted from the Oak Ridge FRC

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Project Goals: Natural organic matter (NOM) is central to microbial food webs and microbially mediated NOM transformations determine much of the carbon (C) flux in subsurface environments. However, little is known about the molecular signature of this pool of C and the microbial activities that regulate NOM turnover are still poorly resolved. The goal of this project was to study the interactions between NOM (extracted from the field site) and native microbial communities present in groundwater at a background site (FW305) at Oak Ridge Field Research Center, TN.

Water-soluble NOM was extracted from sediment samples collected from the background uncontaminated site, and the extraction efficiencies were 3.2% for organic carbon and 1.6% for inorganic carbon. Extracted NOM was used as the sole source of carbon in controlled lab incubations, and groundwater from FW305 well served as the microbial inoculum. Subsamples were harvested at several time points during a 50 day incubation for both chemical and microbial analyses. Results indicated a rapid decrease of total organic carbon within the first 1.5 days, concomitant to a rapid burst in CO₂, and increased in cell numbers. 16S rRNA gene amplicon sequencing suggested that *Massilia* spp dominated in the original inoculum, and gradually decreased to below 5% after 50 days, while *Azospirillum* spp and *Cupriavidus* spp gradually increased from < 5% to 20-30%. Advanced chemical techniques including FTICR-MS and sXAS were used to characterize the C pool that included NOM metabolites and microbial byproducts produced during the incubation period. The molecular mass of C pool generally ranged from 200-600. Relative abundance of compounds with mass around 400-600 increased with incubation time and were considered to be produced from microbial activities. Also, the C pool shifted during incubation, the proportion of lignin in cultures increased, while proteins decreased. Further, GeoChip was used to identify the changes of microbial communities and expression of functional genes during transformation of the NOM.

In conclusion, the data clearly showed that microbial community present at Oak Ridge FRC responded to NOM from the site, and that the community shifted to reveal dominant members in sequence over time in response to transformation of the different functional groups in NOM.

Funding statement: ENIGMA (<http://enigma.lbl.gov>) at LBNL supported by Office of Biological and Environmental Research US Dept of Energy Contract No: DE-AC02-05CH11231