Approaches to understanding the DOM molecular landscape

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The microbial loop model is fundamental to our understanding of biogeochemical cycling of nutrients and minerals in aquatic eco-systems. Metabolic processes are distinctly coupled in microbial communities: photosynthetic primary producers (bacteria and/or unicellular algae) release C- and N-based dissolved organic matter (DOM) comprising various biopolymers, amino acids and unknown molecules that are readily assimilated and re-mineralized by heterotrophic bacteria/archaea and protozoa. These biopolymers are produced by several mechanisms including direct release, mortality by viral lysis, regulated exocytosis of metabolites and polymers, grazing and apoptosis. These processes contribute to shape the DOM molecular landscape. Systems-wide approaches (omics) allow an integrated, and untargeted method to systematically evaluate and understand the responses of organisms to environmental forcing; on the hand, DOM targeted studies allow understanding the spatial and temporal distribution of molecules in the DOM. In this talk I will couple these approaches to understanding the DOM molecular landscape in time and space.