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Meander-Associated Riparian Zone and Hillslope Floodplain Sites Share Similar Microbial Community Structure and Metabolic Potential

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Watershed functioning relies on complex interactions among vegetation, hydrology, topography, and geology. These interactions differ in distinct subsystems of the watershed, such as river floodplains, alpine meadows, and grassland hillslopes. Microbial-mediated biogeochemical processes that occur at the micron-scale in these subsystems impact the large-scale aggregated export from the watershed, including nutrients, carbon compounds and other elements. The current study focuses on two subsystems of the East River headwaters catchment (Colorado, USA), as part of the Watershed Function SFA led by Lawrence Berkeley National Laboratory. One of the subsystems is a meander-associated floodplain (Meander L; ERML), from where 32 riparian soil samples at the 10-25 cm depth were collected (spanning an area of ~ 10,000 m²). The second subsystem is a hillslope site (Pump House Lower Montane, PLM4) ~ 360 m southeast of ERML, from which samples were collected at 5-15, 30-40, 60-70, and 90-100 cm (9 samples total). Samples were sequenced at the Joint Genome Institute. Our goal is to use these metagenomic datasets to study the soil microbial communities from each site. The research involves reconstruction of near-complete genomes that are used to determine the extent to which the functions of microbial communities of the two subsystems overlap.

Preliminary results based on profiling of community composition using scaffolds encoding ribosomal protein S3 (rpS3) show overlap between the most abundant members of the microbial communities across sites. Likewise, Bacteria are one to two orders of magnitude higher in abundance than Archaea. Thaumarchaeota, archaea that perform ammonia oxidation, are more abundant than Euryarchaeota. Notably, Candidate Phyla Radiation (CPR) taxa are more abundant in samples taken at the floodplain close to the water table (above and below). These novel bacteria are predicted to be heterotrophs and symbionts of other bacteria. Overall, we have obtained at least 250 near-complete genomes from the two subsystems. In topsoil from the two floodplain sites (hillslope and Meander L) Betaproteobacteria are the most abundant group, and based on near-complete genomes, we predicted that they are involved in sulfur oxidation. Deltaproteobacteria are the second most abundant proteobacteria, and they are predicted to carry out sulfate-reduction. Near complete genomes of Acidobacteria, Bacteroidetes, Chloroflexi, Nitrospirae, Planctomycetes, Venucomicrobia, among others; in addition to candidate phyla (CP) Rokubacteria and Latescibacteria (WS3X), and members of the candidate phyla radiation (CPR) such as Parcubacteria and Microgenomates were obtained from both sites. In-depth analysis of the metabolic potential at each site is underway.