

INTEGRATING SOIL ECOLOGY AND MICROBIAL GENOMICS: DECOMPOSITION OF CANOPY AND FOREST FLOOR SOILS IN A TEMPERATE RAINFOREST

Cody Dangerfield, Nalini Nadkarni, William Brazelton



Temperate rainforests support a high biomass of epiphytes that accumulate to form organic canopy soils within the Pacific Northwest and reach the highest accumulation in bigleaf maples (*Acer macrophyllum*). These canopy communities act as large nutrient sinks; i.e. their suspension in the canopy sequesters nutrient inputs to the forest floor. However, these nutrients are liberated via epiphyte decomposition when trees or branches fall to the forest floor. We conducted an experimental study to investigate the dynamics of epiphyte decomposition and nutrient cycling by displacing epiphytic mats within bigleaf maple canopies and driplines. Namely, we used high-depth environmental sequencing of 16S rRNA genes to identify shifts in the microbial community composition as a result of the environment relocation. This study is the first to characterize the microbial communities in canopy soils and provides initial insight into their role of facilitating the decomposition of the epiphytic material.

Our results suggested that bacterial diversity and composition shifted significantly after relocation. Canopy samples had lower richness and evenness than the treatments that were transplanted to the forest floor. We also found that there were shifts in the microbial community composition as the epiphytic mats were transplanted from the canopy to other locations in the canopy and forest floor. Using differential abundance analysis, we identified the specific taxa that cause the microbial community shifts. In doing so, we were able to track microbial succession within the treatments. We found that most of the microbial succession occurring within the treatments that were relocated to the forest floor was due to the colonization of bacteria typically found in the forest floor soil. The alternative would be that relocating the epiphytic material from the canopy may have stimulated some microbial species that were present in low abundance in the canopy to become active in the altered environmental conditions. This was observed within a few taxa, but had a lesser impact on the microbial community turnover. Additionally, we found groups of bacteria taxa that were unique to each treatment, i.e. groups of bacteria that were more abundant in the relocated treatments than the original canopy and ground soil. We also found an additional group that is present throughout the environment except within the epiphytic material in the undisturbed canopy soil. This suggests that some microbial species are present but inhibited when the epiphytic mat is connected to the canopy and gives further evidence that the forest canopy is an extreme environment for microbes.

