44. Effects of Competitors or Cheaters and Temperature on Physiological Performance and Gene Transcription of Model Fungi

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Project Goals: During the decomposition of plant materials, microorganisms take up monomers for use in respiration and biosynthesis. Plant cell wall polymers, such as cellulose, pectin and lignin, are degraded into monomers by microorganisms capable of producing extracellular enzymes. However, production of extracellular enzymes is an energy-intensive process, and some organisms may be adapted to take advantage of the activity of enzymes produced by other microbes (i.e., "cheating"). Our overall project goal is to describe in detail how substrate type and growth in a mixed community (with potential for cheating) affects gene transcription, microbial physiology, and plant litter decomposition. Here, we specifically test the hypothesis that temperature may shift the relationships among microbial species. Increased temperature is expected to increase activity of extracellular enzymes as well as aqueous diffusion of both extracellular enzymes and degradation products. Hence, we hypothesize that cheating by microbes will increase at higher temperatures due to higher availability of polymer degradation products.

Pure cultures of *Trichoderma reesei* QM6a, *Phanerochaete chrysosporium* RP-78, and *Rhodotorula sp.* were grown as monocultures and co-cultures in sand microcosms containing minimal nutrients and ground beech leaves or cellulose as the sole carbon source. The microcosms were incubated at 20°C or 30°C. Shifts in gene expression were determined by sequencing transcriptomes in replicate microcosms by Illumina HiSeq2500, resulting in ~10 million sequences per sample. Physiological measurements of microbial performance included biomass, respiration, polymer and monomer concentrations, and extracellular enzyme activity including beta-glucosidase, alpha-glucosidase, beta-xylosidase, cellobiohydrolase, nagase, and phosphatase. During growth on cellulose, *T. reesei* accumulated the most biomass, but biomass was further increased by growth in co-culture with either *P. chrysosporium* or *Rhodotorula sp.* ($P<0.05$). Respiration from cellulose microcosms reflected respiration of the organism with the highest biomass in monoculture; in particular, *T. reesei* respiration did not appear to be affected by growth in co-culture even though biomass was increased ($P>0.05$). In contrast, in beech microcosms, biomass accumulation and respiration were highest for *P. chrysosporium.* Biomass in beech co-cultures reflected the biomass of the organism with the highest biomass in monoculture ($P>0.05$), but respiration in *P. chrysosporium* microcosms was increased due to growth in co-culture ($P<0.05$). Thus, carbon use efficiency of *T. reesei* growing on cellulose appeared to increase due to co-culture, whereas carbon use efficiency of *P. chrysosporium* growing on beech leaves appeared to decrease due to co-culture. Analysis of transcript abundance and relative biomass of each organism will provide information needed to determine rates of carbon consumption relative to investment in extracellular enzymes.

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