Links between Plant and Fungal Diversity in Habitat Fragments of Coastal Sage Scrub

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Project Objectives

Habitat fragmentation is decreasing biodiversity worldwide (Virtuosic et al. 1997). Little is known about how these decreases in plant diversity will affect fungal diversity in soil and the ecosystem functions that fungi perform such as decomposition and nutrient cycling (De Deny and Van der Patten 2005). The objectives of the proposed research are to address the following questions: (1) Does habitat fragmentation result in a loss of fungal taxonomic richness and function? and (2) Is the species richness and function of fungi in habitat fragments influenced by plant species richness? To answer these questions, we are studying a native coastal sage scrub habitat at Newport Back Bay in southern California. Coastal sage scrub is the second most extensive native ecosystem type in California, but is under extraordinary threat from human development and only about 10% of the original extent of the ecosystem remains (McCall 1994).

Approach and Procedures

To investigate the effects of habitat fragmentation on the diversity and function of soil fungi, we established a series of six plots in sage scrub fragments. The fragments range in size from 23 m² to 5415 m² and the species richness of plants is directly correlated with fragment size. To assess how fungal diversity and function correspond to fragment size, we collected ten soil cores and ten surface litter samples (Oil-e horizons) from each fragment. Soil and litter samples were separately pooled for each plot and total DNA was extracted from each component. Additionally, the activity of eight enzymes involved in plant litter degradation was assayed in each soil and litter sample. We used regression analysis to determine the relationship between fragment size and enzyme activity.

To disentangle the effect of plant diversity from the effect of fragment size on fungal diversity and function, we established a plant litter diversity manipulation in the intact sage scrub habitat in November, 2007. We placed two grams of air-dried leaf litter from 1, 3, 5, or 7 species of plants into nylon mesh bags (20cm X 20cm) in a randomized block design with seven replicates per treatment (total of 28 litter bags). After one year, the bags were harvested and weighed for total mass loss. The relationship of mass loss to fragment size was evaluated with an ANOVA. Additionally, the remaining litter bag material was subsample to assay for extracellular enzyme activity and fungal species richness. Enzyme activity of the litter bags was assayed in the same way as the soil samples from each fragment. Total DNA was extracted from each litter bag for fungal-specific amplification and sequencing. To process the large number of DNA sequences required to sufficiently
describe fungal diversity, we developed (in collaboration with N. Fierer and R. Knight, University of Colorado Boulder) a high-throughput pyrosequencing protocol and bioinformatics pipeline. To our knowledge, this is the first established protocol for small-subunit rDNA of fungal communities. Taxa were defined as DNA sequences sharing ≥97% sequence identity.

Results

We found that enzyme activity in organic soil (Oe horizons) was significantly positively correlated with fragment size for five of the eight enzymes: N-acetyl-glucosaminidase (F = 35.8, df = 1, P = 0.004), β-glucosidase (F = 9.9, df = 1, P = 0.035), Glycine aminopeptidase (F = 13.15, df = 1, P = 0.022), Leucine aminopeptidase (F = 14.5, df = 1, P = 0.019), and cellobiohydrolase (F = 13.12, df = 1, P = 0.022, Fig. 1). After one year, litter decomposition was significantly faster in litter bags containing more species of plant litter (F = 6.97, df = 3, P = 0.002, Fig. 2). Moreover, fungal diversity increased strongly and significantly in relation to plant litter diversity in litterbags (Fig. 3), and marginally significantly in habitat fragments with higher plant diversity (Fig. 4). Litterbags with greater numbers of fungal taxa also decomposed significantly faster (Fig. 5).

Discussion

Critical ecosystem functions such as decomposition and nutrient cycling were significantly reduced with fragmentation of the coastal sage scrub ecosystem (Fig. 1). Fungal diversity tended to decrease as well (Fig. 4). Since direct manipulations of plant litter diversity (in litterbags) produced similar—and even stronger—effects on fungal diversity (Fig. 3), it appears that reductions in plant diversity following fragmentation are the proximate cause of changes in the fungal community. A potential underlying mechanism for the relationship between fungal and plant diversity is specialization by fungal taxa on particular organic substrates, which we have documented in situ in a companion study (McGuire et al. 2010). Since plant species vary in the chemical composition of litter, then communities with higher plant diversity should likewise produce litter that can support greater numbers of fungal taxa.

We also determined that decomposition rates were higher in litterbags that contained more plant litter species (Fig. 2). The acceleration of decomposition rates may have occurred as a consequence of increases in fungal diversity (Fig. 5). Previous microcosm studies have documented positive relationships between fungal diversity and litter decomposition, potentially owing to niche differentiation among taxa (LeBauer 2010). Alternately, the presence of multiple litter types may provide better nutrient supplies for decomposers, leading to faster decomposer activity (Gartner and Cardon 2004).

Our understanding of how plant diversity influences ecosystem functions is limited, and our results provide new mechanisms by which the number of plant species in an ecosystem is an important contributor. These data have important implications for management of coastal sage scrub ecosystems and are directly relevant to the overall Kearney mission to understand soil-ecosystem functions across spatial scales. We found that the size of the ecosystem directly influences the rate of key soil processes via changes in plant and fungal diversity.
References


Figure 1. Extracellular enzyme activity in organic soil horizons (O<sub>i</sub>-e horizons) was significantly correlated with fragment size for five of the eight enzymes. The best-fit lines are shown with corresponding $R^2$ values.
Figure 2. Percent mass remaining of litter bags with different plant species treatments after one year. Litter bags with seven species of plant leaf litter decomposed significantly faster than litter bags with fewer plant species (F = 6.97, df = 3, P = 0.002). The mean percent mass remaining ±1 SE are shown for each litter diversity manipulation.
Figure 3. Fungal diversity was significantly positively related to the number of plant species represented within litterbags. These bags decomposed for one year within the largest coastal sage scrub fragment, which also harbored the highest plant species diversity.
Figure 4. Coastal sage scrub fragments with higher plant diversity (i.e., larger fragments) supported marginally higher levels of fungal diversity. Fungal diversity was assessed in soil cores collected directly from each fragment.
Figure 5. Decomposition rates were significantly faster in litterbags with greater numbers of fungal taxa. Litterbags contained 1–7 species of plant litter, and they were incubated for one year in the largest habitat fragment of coastal sage scrub. Fungal diversity was positively related to plant litter diversity (Fig. 3). Symbols represent means (±1 SE) of plant litter diversity treatments.

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