

Linking small scale soil chemical variability to fungal niche preference

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Ectomycorrhizal fungi are root symbionts of woody plants. Their host plants, for which this symbiosis is obligate, cover the majority of forested land on earth. Estimates of diversity vary greatly, but generally 30 or more (in some cases hundreds) ectomycorrhizal fungal species can be found in a 1ha area of forest even when those forests may have just one or two ectomycorrhizal hosts. Soil heterogeneity is often proposed to be a factor driving this diversity. Significant evidence exists to suggest that, at least on the scale of horizon to horizon variation, consistent shifts in fungal (including just ectomycorrhizal) community can be found to correlate with soil chemical variables. However, significant diversity is still found in a given soil horizon, suggesting that if soil chemical factors and niche heterogeneity are driving fungal diversity then a smaller scale of sampling is necessary. We looked at a large number (150) of small (<5g) soil samples taken from a bishop pine forest at Point Reyes National Seashore in northern California. A 70 cm vertical transect was drawn across a soil profile and 10 samples were taken per vertical transect. Each pit had three vertical transects X 3 pits X 2 sites (one on granitic, one on sandstone parent material). Climate, stand age, stand history were all constant between pits. For each sample %C, %N, pH, and BaCl₂ exchangeable Na, Ca, K, and Mg were measured. Also for each sample, the fungal community was characterized using terminal restriction fragment length polymorphism in conjunction with cloning and sequencing. Spatial correlation (within and between pits) was tested for. The most significant factor shaping fungal communities was parent material, followed by pH, exchangeable Ca and exchangeable Mg. While there was a significant amount of co-correlation between these factors, soil chemistry is still significantly correlated with fungal community when the effect of parent material is removed. The overall variability of soil chemical variables is discussed, as are individual fungal species habitat preferences. To our knowledge this is the first study which links soil chemical variability in the field to fungal species presence on a scale relevant to individual hyphae.

Gene regulation of iron acquisition in *Serpula lacrymans*

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The dry rot fungus, *Serpula lacrymans*, is a major decomposer of constructional wood. In houses, its extensive mycelia connect sources of minerals (gypsum or concrete), carbon (wood) and water (leaking pipes). Long distance translocation of resources within the mycelia makes *S. lacrymans* well adapted to growth in buildings. In nature, where *S. lacrymans* is rare, it colonizes stumps and dead wood in contact with soil.

Calcium oxalate crystals are commonly observed in association with hyphae of *S. lacrymans*. Based on these observations it has been suggested that calcium is dissolved from mineral sources and translocated to the wood during decomposition. However, a pilot study demonstrated no correlation between calcium content and wood decay. Instead, increased decay was correlated with increased iron content in the decomposed wood. Supporting the idea that the Fenton reaction, involving Fe²⁺ and H₂O₂, may drive cellulose decomposition. Thus making dissolution, uptake and translocation of iron central in the wood decomposition process of *S. lacrymans*.

We here examine growth, exudation and gene expression of *S. lacrymans* in pure liquid cultures with iron supplied as iron chloride or as Goethite. Carbon was supplied as glucose or cellulose and samples were taken at 10, 20 and 30 days after inoculation. Over the experimental time, pH of the growth media decreased and the capacity to complex iron increased, as determined by the CAS assay. In a parallel experiment, *S. lacrymans* was grown in microcosms with wood and soil. In this wood decomposition, fungal biomass and gene expression was analysed over the same experimental time.

The genome of *S. lacrymans* is currently being sequenced at JGI. We used the sequenced isolate in our experiments. When the genome sequence becomes available, obtained results on expressed genes can be analysed in a whole genome context. Results obtained from systems of different complexity, ranging from liquid media with glucose, to cellulose, to wood chips on soil, will be combined to determine how genes involved in iron acquisition of *S. lacrymans* are regulated in response to form of iron as well as the form of carbon.