

Multi-dimensional mycelia interactions

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Project description: Dead wood is a massive carbon pool, globally, 7.7-9.5 Pg being released each year as a result of the activities of wood decay fungi, the only organisms that significantly break down lignin. Fungal community composition is a major determinant of wood decay rate, and interspecific mycelia interactions are the major determinant of fungal community structure and dynamics. Hence, understanding these interactions is crucial to understanding wood decay rate and carbon cycling. The overall outcome of interspecific interactions between wood decay fungi can be deadlock (where neither fungus obtains territory held by the other), replacement (where one fungus ousts another completely from its territory) and partial replacement. Such interactions have been studied intensively in pairings in artificial media, wood and soil, but since outcomes are often intransitive (i.e. sp. A beats sp. B, sp. B beats sp. C, but sp. C beats sp. A) it is not possible to predict the outcomes of interactions between 3 or more simultaneous confrontations from pairing experiments. Hardly any studies have been performed under controlled conditions with multispecies interactions, yet this is crucial to understanding wood decay in the natural environment.

This project will use our novel 'Rubix cube' experimental systems, in which cubes of wood (typically 1x1x1 cm) pre-colonised by individual wood decay fungi, are arranged in a 3D tessellated lattice in various combinations. This allows analysis of effects of, for example, different combinations of species, different initial starting volumes of wood occupied by different species, different numbers of species, and different starting states of decay. CO₂ evolution and volatile organic compounds (VOCs) can be measured throughout an experiment to estimate ongoing decay rate and semiochemicals. At the end of an experiment the Rubix cube can be deconstructed to determine current status of each individual cube component in terms of, for example, CO₂ evolution, VOCs, weight loss, species present, enzyme activity and other aspects of gene expression.

The project will also build on gene expression studies already conducted in two dimensional models and assess the activity of key genes in a more dynamic and complex 3D model system where the fungi must balance nutrition, growth and defence on multiple fronts. Quantitative PCR will be used to measure gene expression during the complex interactions and green fluorescent protein (GFP) labelling to target genes will enable functional analysis and visualisation of interacting species.

Training opportunities: Training will include use of modern molecular microbiological approaches, ecological experimental design, fungal culture, quantification and activity assessment, chemical analyses including enzyme assays and GC-MS, empirical data collection and analysis, including bioinformatics, literature reviewing and meta-analysis. Transferable skills include, scientific writing, poster and oral presentations, and project management.