Forest Health News

scion

No. 289, June 2019 ISSN 1175-9755

Microbiomes and tree health

The processes that shape the health of trees are traditionally conceptualised as a disease triangle (model), characterised by the interaction between the abiotic environment, host and pathogen factors. Rapid advances in multi-omic tools are increasing our ability to access the plant microbiome (e.g. endophytes) and its links to disease development and resistance. It is now clear that these biologically active microbes need to be integrated into disease models.

The term plant microbiome describes an ecological community of plant-associated pathogenic, mutualistic, and commensal microorganisms. Certain microbes promote plant growth and increase stress resistance, whereas others can have a negative impact for the host. The composition of plant microbiomes is determined by the plant genotype, environmental factors and interactions within the microbial community. Understanding the factors influencing plant microbial community assemblies will be crucial for any effort to manage plant microbiomes. The integration of genetic, metagenomic and bioinformatic methods will be required to unravel the diversity of microbial life, their ecological functions, as well as their impact on the health of forest trees.

The potential of the plant microbiome to support forest health could be realised by using specific taxa as biocontrol agents, as well as through microbiome engineering. The development and application of microbiome-based biological control products may be more effective than using single organisms, which have proved inconsistent in the past. Targeted engineering of forest tree microbial communities could be achieved by transplanting microbes to the environment or directly to targeted trees, or by modifying environmental conditions (e.g. through nutrient treatments). Another approach could be host-mediated artificial selection, in which the microbial community is engineered based on the host genotype. It is important to maintain diversity and ecosystem health with any strategy, given the risks associated with newly introduced microorganisms and the possibility of microbial lifestyle shifts under changing conditions.

Mandy Messal working in the lab.

Although the task to clarify the question of what specifically constitutes a healthy microbiome remains, microbial diversity can be used as a biomarker for healthy plant microbiomes, e.g. in breeding and biocontrol strategies. Tree breeders have traditionally ignored the possible influence of the microbiome on tree health and function (since the microbiome was difficult to analyse), instead focusing on selection of phenotypic traits in resistance breeding against pests and pathogens. Microbial composition seems to be strongly influenced by the host genotype and can therefore be affected by/through tree breeding. On the other hand, the microbiome can affect the expression of resistance traits in trees.

In order to integrate microbiomes into tree breeding, researchers need to start treating trees as the complex ecosystems they are and determine how microbiome composition and tree phenotypes relate. The next step would be to link the acquired knowledge on microbiomes to forest management for the benefit and improvement of forest health. In the long term, this will facilitate policy and decision making in forest health management, especially considering global climate change, shifts in land use patterns and the accidental introduction of invasive organisms.

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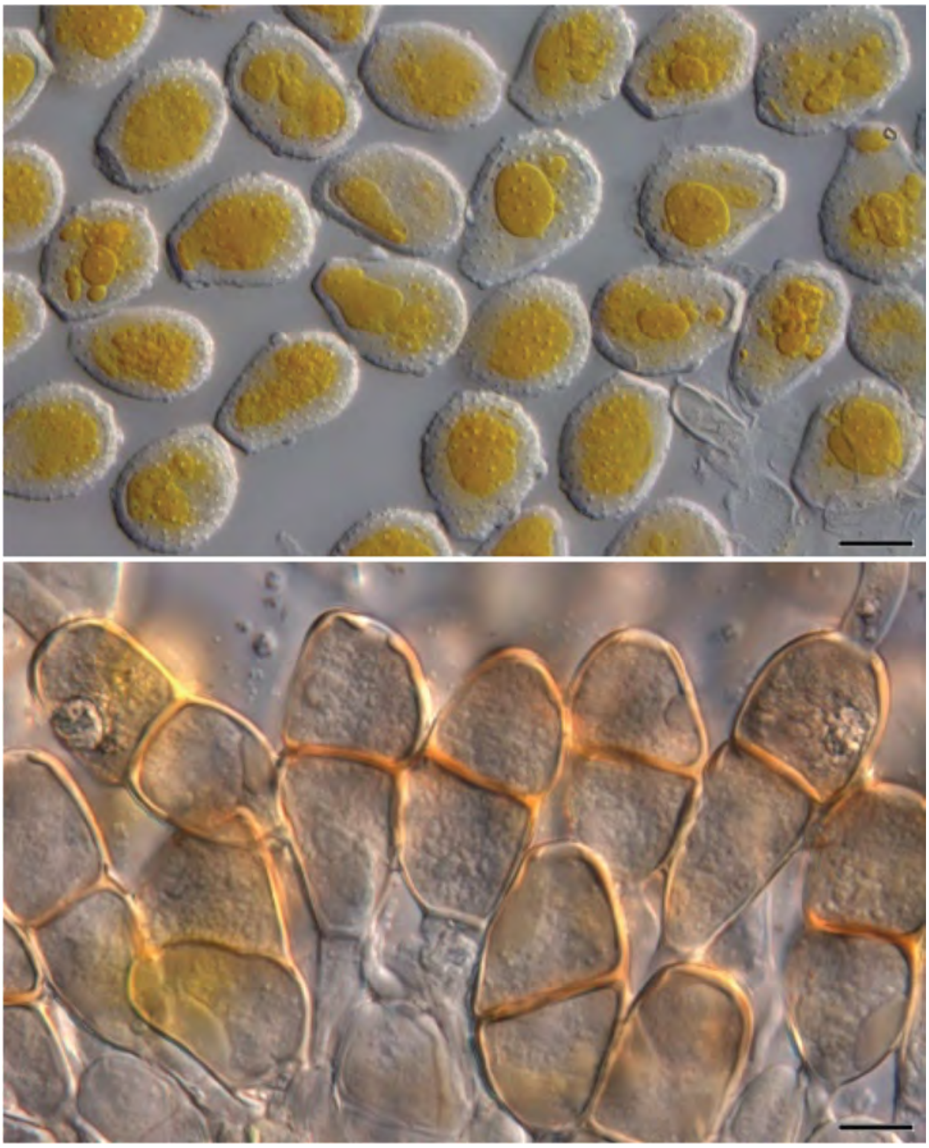
Introducing Michael Bartlett

I recently joined the Forest Protection team at Scion as a Postdoc to conduct research on myrtle rust. This research will improve our understanding of the myrtle rust pathogen (*Austropuccinia psidii*), particularly its life cycle and mode of reproduction, and forms part of the MBIE funded Beyond Myrtle Rust Programme.

Before joining Scion, I completed a PhD in Evolutionary Biology at the University of Canterbury. My PhD research examined the adaptation of male Chinook salmon (*Oncorhynchus tshawytscha*) to competition during reproduction, both before spawning opportunities for access to females and immediately after spawning when sperm from multiple males compete to fertilise eggs (sperm competition). I utilised a multidisciplinary approach that involved experiments to monitor male behaviour, microscopy to study sperm traits, separating and recombining sperm and seminal fluid from different males, *in-vitro* fertilisation trials and proteomics.

New postdoc Michael Bartlett.



Spores of Austropuccinia psidii *(myrtle rust). Top, asexual urediniospores; bottom, sexual teliospores.*

Image: Alistair McTaggart

Using this series of experiments, I determined that male Chinook salmon make rapid adjustments to their investment in sperm quality, by altering sperm swimming speed, when their social status changes from a low to a high risk of sperm competition[1]. I also found compelling evidence that these changes in speed are not due to intrinsic differences in sperm cells themselves but mediated by seminal fluid, and that this differential investment in seminal fluid directly influences paternity share and therefore reproductive success[1].

At Scion, I will apply the broad skillset I developed in my PhD and previous projects to conduct similarly multidisciplinary research on myrtle rust. This research aims to determine the extent to which *A. psidii* is reproducing sexually across a range of locations in New Zealand, by identifying sexual spore stages and using genetic markers to measure sexual recombination. We will also investigate the drivers behind change from production of urediniospores (asexual spores) to teliospores (sexual spores) using an experimental approach to collect transcriptomic (gene expression) data. The research project will provide information about the adaptive potential of the pathogen and inform management strategies for controlling the disease.

Michael Bartlett, Scion

[1] Bartlett, M.J., Steeves, T.E., Gemmell, N.J. & Rosengrave P.C. (2017) Sperm competition risk drives rapid ejaculate adjustments mediated by seminal fluid. *eLife*. 6:e28811.

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