Ross Beever Memorial Mycological Award Report

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Project Summary

Despite the overwhelming evidence that mycorrhizas are critical in determining plant community structure and ecosystem function, little is known about mycorrhizal responses to climatic change[1]. The mediating role of mycorrhizal fungi in ecosystem level responses to climate change are also understudied[2]. In addition, invasive plant species have the potential to substantially alter existing mycorrhizal interaction networks[3]. Positive feedback loops between invasive plant species and mycorrhizal communities can occur, leading to communities which are resistant to native plant recruitment for prolonged periods of time[4].

Tongariro National Park (TNP) provides habitat for a diverse native alpine ecosystem[5]. TNP is currently 1.5°C warmer and drier (-5mm of rain/year) than it was 50 years ago[6]. Alongside climate warming, a major driver of ecological change in TNP is the invasion of *Calluna vulgaris* (Ericaceae)[5]. *C. vulgaris* is facultatively mycorrhizal. This project makes use of an existing manipulative experiment employing a factorial (warming x *C. vulgaris* removal) experimental design, established in 2015 in the Rangipo desert. We use small Open Top Chamber (OTC) greenhouses to manipulate the temperature and humidity of the air and soil to simulate the climatic warming predicted for TNP. We take five soil cores from each, and using genetic barcoding techniques, build co-occurrence matrices between plants and fungi. The objectives of this project are to:

1. Reveal interaction network structure between plant and arbuscular mycorrhizal and ericoid mycorrhizal fungal species in TNP under current climatic and invasion conditions,
2. Demonstrate the degree to which experimental warming affects mycorrhizal network topology,
3. Identify the impacts of *C. vulgaris* invasion on mycorrhizal network topology and to determine whether experimental removal of the invader results in a reversal to previous network topology, indicating the strength of legacy effects, and
4. Determine whether manipulative warming decreases the legacy time of removal treatments.

Work Completed

Autumn/Winter 2016- Leaf tissue samples were collected from all vascular plants found in experimental plots. DNA was extracted and DNA amplified at the *rbc*L and the *trn*L loci to build a library of local plant barcodes.

Autumn 2017- Soil cores were collected in the manipulative experiment. Soil cores were put on ice immediately and frozen. Roots were washed and cleaned with an ultrasonic cleaner. Individual segments were frozen, ready for DNA extraction.

Work to Come

Genetic barcoding will be used to identify plant roots and ericoid and arbuscular mycorrhizal fungi. The DNA of 3 individual root samples will be extracted from each core. The plant will be identified through the amplification of plant barcoding loci and comparison to the plant barcode library. The ITS2 region will be amplified on all root fragments[2]. The amplified DNA will be investigated using either Terminal Restriction Fragment Length Polymorphisms (TRFLP) or sequencing techniques.

Costs of Completed Work

Expense	Cost
Fieldwork in Tongariro National Park: 2 trips	
• Accommodation	$80
• Transport	$400
• Field supplies	$80
Lab supplies	$500
TOTAL	**$1060**

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References

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