Population structure of an aerial *Phytophthora* species in forest systems

S. Brar[A], R.L. McDougal[B], N.M. Williams[B] and R.E. Bradshaw[A]
[A] Massey University, Private Bag 11-222, Palmerston North, 4410, NZ.
[B] Scion New Zealand Forest Research Institute Ltd, 49 Sala St, Private Bag 3020, Rotorua, 3046, NZ.

Introduction

Phytophthora pluvialis is a foliar pathogen that was recently identified as the causal agent of red needle cast on *Pinus radiata* in New Zealand. *P. pluvialis* was first isolated in Oregon (USA) in 2002 where it was recovered from Tanoak and Douglas fir trees, and was discovered on radiata pine in New Zealand in 2008. The aim of this study is to determine the genetic diversity and population structure of *P. pluvialis* in New Zealand and to compare it with the USA population.

Materials and Methods

For a preliminary analysis of genetic diversity, the *cox I* and *cox II* spacer region of the New Zealand isolates was sequenced following amplification with *Phytophthora* specific primers. All the New Zealand isolates had the same *cox* spacer region sequence as one of the seven Oregon haplotypes (haplotype 3) identified previously.

To better understand the population structure of *P. pluvialis* single nucleotide polymorphism (SNP) markers were developed. SNP markers were identified based on heterozygosity from two *P. pluvialis* genomes; one sourced from New Zealand and the second from USA (Oregon). Primers were designed around the target SNPs and tested on a panel of 8 DNA samples (6 from NZ and 2 for Oregon). The PCR products were sequenced and visually analysed for the presence of the SNP. The Ross Beever award was used to sequence some of the PCR products. The aim was to validate 30 SNP markers that can be used to genotype the *P. pluvialis* isolates.

Results and Future Work

Thirty SNP markers have been validated and will be used to genotype the *P. pluvialis* isolates. Currently there are 135 isolates from New Zealand and 94 isolates from Oregon. The genotyping work is in progress and is being carried out at the Liggins Institute in Auckland.

Part of this project is in collaboration with Oregon State University. The aim is to include more samples from Oregon and California to this study and also spend time learning population genetic software that can be used to analyze the genotypic data. The results from this study will provide information on the genetic diversity of *P. pluvialis* in NZ compared to Oregon, and will help to determine the origin of the pathogen and potential pathway of gene flow. The information from this research will be useful in building resources for monitoring the population of *P. pluvialis* in New Zealand. The SNP markers can be used as a tool to identify new polymorphisms that may be associated with virulence.