GENETIC DIVERSITY OF *DOTHISTROMA PINI* IN NEW ZEALAND

This thesis is presented in fulfilment of
the requirements for the degree of
Master of Science in Molecular Genetics
at Massey University, Palmerston North
New Zealand.

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1997

ABSTRACT

Dothistroma pini is an important pathogen of *Pinus radiata*, New Zealand's major exotic forest species. This study was undertaken to elucidate the genetic background of New Zealand's *D. pini* population as part of a research program which aims to reduce its overall effect.

Two major sampling strategies were devised and undertaken. The first involved collection from within an NZFRI field trial in which five year old host clones were available that had been scored for resistance to *D. pini* over a period of three years. This collection was designed to test the hypothesis that genetic differences would be seen between "resistant" and "susceptible" hosts.

The second collection tested the hypothesis that polymorphisms would be observed between samples from geographically isolated regions, and that more variability would be seen between these regions than within any of them. For this study, samples were collected in a "hierarchy of populations" approach from three New Zealand forests: Kinleith, Kaiangaroa and Golden Downs. Additional samples for analysis included four *D. pini* samples which were isolated during the 1960's, and DNA obtained from a Guatemalan isolate of the teleomorphic form, *Mycosphaerella pini*.

PCR amplification using 32 RAPD and 5 RAMS primers revealed no polymorphisms within two sets of five *D. pini* samples designed to be representative of the New Zealand population. Amplification was repeated with a larger number of *D. pini* samples using five RAPD and two RAMS primers, again showing no differences between any of the isolates and proving that the two sets of five samples were indeed representative of the population. However, differences were seen between *D. pini* and the isolate of *M. pini* with all primers used.

RFLP analysis of the ribosomal DNA showed no differences among five *D. pini* isolates, but revealed polymorphism between *M. pini* and *D. pini*. RFLP analysis of tthe miochondrial DNA produced a universal hybridisation pattern in all isolates.

Growth studies supported the molecular data, showing no differences between the isolates of *D. pini*. Morphological differences between *D. pini* laboratory cultures were observed, but these do not appear to correlate with any permanent genetic rearrangement.

As a result of these studies, it was concluded that the genetic diversity of *D. pini* in New Zealand is very low and that all isolates examined appear to be of a single strain.

ACKNOWLEDGEMENTS

I would like to express deep gratitude to my supervisor, Rosie Bradshaw, for her never ending support, supervision and advice, and for being a cheery and lovely person.

I am indeed grateful to the Department of Microbiology and Genetics for three years employment as a Graduate Assistant and use of resources.

Thanks to everyone in The Department for help, advice, distractions and friendship given over the years. Anita, Austen, Brendon, Carmel, Carolyn, Chris, Dianne, Karen, Kirsty, Laura, Linda, Mike, Neville, Pete, Peng, Rich, Shalome, Sheralee, Tania, Trish... too many, I'm bound to miss someone out - you should know who you are.

Scientifically speaking, thanks to: Barry Scott for primers, plasmids and freezers; Tash and Seth for their help with single sporing and growth rate experiments; Shalome for CsCl gradient mtDNA isolation and theological discussions.

Thanks to the NZFRI in Rotorua, without whose facilities it would've taken so much longer. Non-Massey scientific folks whose assistance has been invaluable, and is much appreciated, include (but are not limited to) Sue Carsons, Tom Richardson, John Lee, Luis Gea, Margaret Dick, Alan Goldstein, Raoul Thomas, Paul Bradbury.

Cheers to all my friends and flatmates for providing much needed release of tension in various ways throughout the mission. Promise I'll put less on my plate from now on. Special thanks to Carolyn, Elise, Amanda, Tania and Bannoy.

Full credit to my family who have been supportive on every level imaginable.

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