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**GENETIC DIVERSITY OF *DOTHISTROMA PINI*  
IN NEW ZEALAND**

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## 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 the mitochondrial 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.

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