Origins and Evolution of the New Zealand Forest Flora

a Molecular Phylogenetic Approach

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ABSTRACT

The origins and evolution of the New Zealand flora have puzzled the imagination of botanists world-wide. Competing hypotheses have sought to explain the floristic relationships between New Zealand and other Southern Hemisphere landmasses. Scientific approaches have involved geology, plant morphology, palynology and palaeobotany in investigations of the distribution patterns of these floras. Analyses presented in the current thesis use molecular data to investigate phylogenetic relationships of plant lineages native to the New Zealand forest flora.

In the present thesis, molecular work included amplification and sequencing of standard DNA markers such as nuclear ribosomal DNA, *ndh*F and *rbc*L gene sequence. These data were obtained for New Zealand and overseas species of Myrsinaceae, Nothofagaceae and genus *Agathis* (Araucariaceae). Analyses of these data have been presented alongside results and re-analyses of genetic data for Podocarpaceae, Proteaceae, Winteraceae and genus *Metrosideros* (Myrtaceae). These analyses aimed to synthesise recent work and provide a framework for further molecular investigations into the origins of the New Zealand woody forest flora.

Amplified fragment length polymorphism (AFLP) was used to locate polymorphic genome regions that were converted into sequence specific DNA markers. Information from AFLP and AFLP derived markers was used to elucidate evolutionary processes as well as interspecific and intraspecific relationships between closely related taxa of *Myrsine* and *Nothofagus*.

DNA analyses showed that the New Zealand forest hosts plants with very different origins and evolutionary histories. Results presented in the current thesis support hypotheses of vicariance and long-distance dispersal across Southern Hemisphere lands.

Molecular data are consistent with a continuous presence of *Agathis* (Araucariaceae), *Dacrydium* (Podocarpaceae) and *Pseudowintera* (Winteraceae) on the New Zealand archipelago since the break-up of the Gondwanan supercontinent. It is proposed that extant species of these lineages have evolved from ancestors that arrived on the New Zealand landmass during the Cretaceous. In contrast, divergence time estimates on *Nothofagus* suggest that relationships between extant *Fuscaspora* and *Lophozonia* beeches date back to the Mid Tertiary and are not explained by vicariance and continental drift.

Phylogenetic analyses substantiate fossil evidence of a Tertiary arrival of *Metrosideros* (Myrtaceae), *Myrsine* (Myrsinaceae), *Knightia* and *Toronia* (both Proteaceae). Similarly, dispersal from New Zealand to other southern lands has been inferred for *Metrosideros* and *Myrsine*. These findings and those reported earlier for

alpine plant groups suggest that trans-oceanic dispersal is likely to be an important explanation of floristic relationships between New Zealand and other distant landmasses.

Molecular studies on New Zealand *Myrsine* suggest recent speciation events, geographic differentiation and ongoing hybridisation between some morphologically and ecologically distinct species. Intraspecific analyses on *Myrsine divaricata* and *Nothofagus menziesii* show that extant distribution patterns within New Zealand are relatively recent and may have developed during the Quaternary. Although both lineages have an ancient history on the New Zealand archipelago, it is concluded that species and their distributions – including that of the monotypic genera *Elingamita* - are of recent origin.

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ABBREVIATIONS

A	Adenine
AFLP	Amplified Fragment Length Polymorphism
bp	base pairs
C	Cytosine
DNA	Deoxyribonucleic acid
G	Guanine
Indel	Insertion or deletion
ITS	Internal Transcribed Spacer
ISSR	Inter Simple Sequence Repeats
ML	maximum likelihood
MP	maximum parsimony
m.y.	million years
m.y.a.	million years ago
PAA	polyacrylamide
PCR	Polymerase Chain Reaction
QP	quartet puzzling
rDNA	ribosomal DNA
T	Thymine
RAPD	Random Amplified Polymorphic DNA markers
RFLP	Restriction Fragment Length Polymorphism
SSR	Simple Sequence Repeats

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