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**Ancient DNA studies of the New Zealand kiwi
and wattlebirds: evolution, conservation and
culture.**

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Abstract

Ancient DNA was used to provide a temporal perspective for examining a number of evolutionary, conservation and cultural questions involving members of the New Zealand avifauna. Ancient mitochondrial DNA (mtDNA) sequences were used to examine the past levels and patterns of genetic diversity in the five species of New Zealand kiwi (Apterygidae). Brown kiwi, particularly in the South Island, exhibited high levels of genetic structuring with nearly every population exhibiting private mitochondrial haplotypes. The extinction of a large number of brown kiwi populations has, therefore, led to the loss of a large amount of genetic variation in these species. The past ranges of great spotted kiwi and the three brown kiwi species, whose bones are morphologically indistinguishable, were determined. This information can aid conservation programmes aiming to re-introduce kiwi to regions where they are now extinct.

In contrast to the high level of genetic structuring in South Island brown kiwi, the majority of little spotted kiwi samples from the South Island shared a common haplotype. The difference in phylogeography between brown kiwi and little spotted kiwi is hypothesised to relate to differences in their dispersal behaviour and/or their population histories. The addition of ancient samples of little spotted kiwi from the North Island indicated a complex relationship with great spotted kiwi.

Nuclear microsatellite DNA markers were isolated from North Island brown kiwi and tested for cross amplification in the other kiwi species. Five loci were polymorphic in all kiwi species. Preliminary analyses of genotyping results indicated that the kiwi species were distinguished by assignment tests and that subdivision may occur within several of the species.

An extensive reference database of modern and ancient mtDNA sequences was used to determine species and provenance of a number of unlabelled museum subfossil bones and skins. This method was also used to examine provenance of brown kiwi feathers from Maori artefacts (cloaks and baskets).

Ancient DNA methodology was also used in a molecular examination of the relationships of a second endemic avian family, the New Zealand wattlebirds (Callaeatidae). Analyses of nuclear gene sequences, *c-mos* and RAG-1, revealed kokako, saddleback and huia comprised a strongly supported monophyletic group. A divergence time estimate for the New Zealand wattlebirds indicated that they are more likely to have arrived by transoceanic dispersal than have a Gondwanan origin. Sequences from three mtDNA genes, 12S, ND2 and cytochrome b, were also analysed but could not resolve the relationships between the three genera.

Microsatellite DNA from the extinct New Zealand huia exhibited considerable genetic variation, exceeding that found in extant North Island saddleback, from which the loci were isolated. Assignment tests indicated no genetic structuring within huia, although interpretation was complicated by a lack of provenance details for many of the skins.

The results presented here suggest that ancient DNA can not only provide information about the relationships of extinct taxa but also demonstrates the importance of placing the present day genetic diversity found in endangered taxa within the context of past patterns and levels of genetic variation.

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