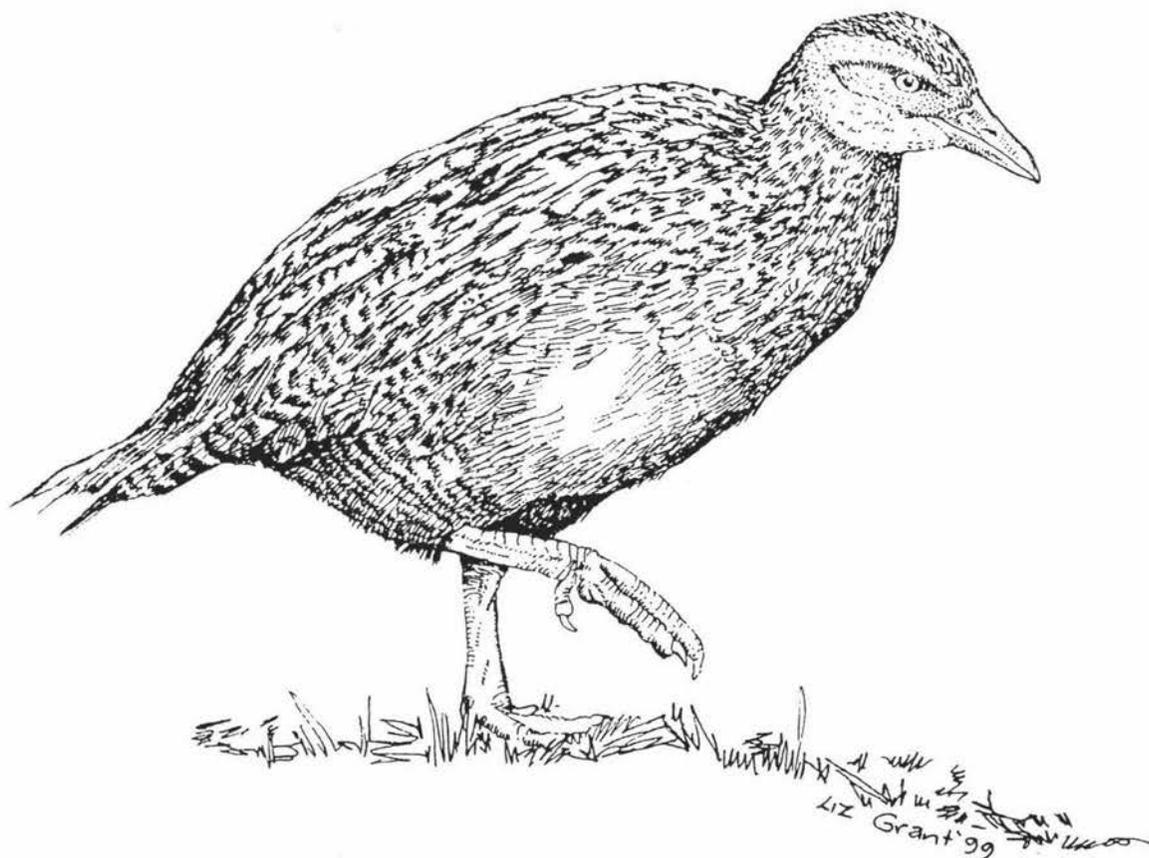


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# Conservation Genetics of the Weka, *Gallirallus australis*

By  
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A thesis presented in partial fulfilment of the requirements for the degree of  
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# Abstract

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The weka (*Gallirallus australis*) is an endangered, flightless rail endemic to New Zealand. This ground-dwelling bird has four morphologically recognised subspecies and although was once distributed throughout New Zealand, its survival is now threatened.

Genetic methods were employed to investigate aspects of weka biology relating to their conservation in order to determine if the current taxonomy reflects the genetic diversity of weka and if the provenance of weka could be determined. These results are important as they will impact on the conservation management of weka in the future.

Weka genetic diversity was investigated by sequencing four mitochondrial DNA genes: cytochrome *b*, ATPase 6, 12S and the control region. The only region that was found to exhibit variation was the control region. Through phylogenetic analysis of a 216 base pair region, the subspecific status of some weka populations was determined. The provenance of weka of unknown origin was also able to be ascertained. Nuclear variation was investigated through a preliminary study of microsatellite variation.

Molecular sexing methods were trailed to sex this monomorphic species. These results are discussed and compared with the traditional methods of sexing weka through morphometrical techniques. It was found that molecular and morphological sexing techniques produced concordant results when sexing adult weka. Molecular sexing has an advantage over morphometric sexing as it better able to accurately sex individuals of all ages.

The relationship that the terminology of "subspecies" has on conservation management is also discussed with particular reference to the weka.

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**North Island Weka**  
*Gallirallus australis greyi*  
Photo by Geoff Moon