

Population genetics of North Island Weka (*Gallirallus australis greyi*) on Rakitū Island

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Weka (*Gallirallus australis*) on Rakitū Island in the Hauraki gulf originated from the locally extinct Gisborne population. Weka may pose a threat to other species, so estimating the conservation significance of this population for North Island weka as a whole is important. We surveyed a sample of 65 Rakitū weka by making use of feathers collecting during a temporary translocation from the island in 2018 (for rat eradication), along with 31 representatives from other North Island populations (Figure 1). We used weka-specific markers including mitochondrial Control Region (Trewick et al. 2017) and novel nuclear microsatellite loci designed on our recently published weka genome (Gaspar et al. 2024).

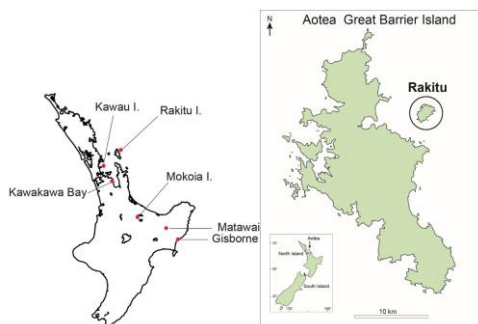


Figure 1

The Rakitū Island population contained three mtDNA haplotypes spanning diversity documented previously in Gisborne (extinct), Mokoia Island, Kawau Island as well as Opitiki (Trewick et al. 2024). Similarly, variation screened with novel microsatellite markers was highest (in the present sample) among the Rakitū weka, in terms of number of alleles, presence of private alleles and heterozygosity. Pairwise F_{ST} values among the population samples Rakitū weka were the most differentiated. Together these data suggest that the Rakitū weka contain(ed) as of 2018 a reservoir of genetic diversity that may be significant to North Island weka conservation. However, available sampling of mainland weka spans 1993 to 2017 and Rakitū in 2018. Population changes have certainly occurred in that time with the former primary native population near Gisborne going extinct. Small island populations including Rakitū, Mokoia and Kawau are likely to be subject to genetic drift, and so gradually lose diversity. Targeted sampling of North Island weka populations will allow important update of the status of this lineage and the diversity held within remaining populations. The newly developed markers promise to make further genetic screening efficient and effective and could form the basis of a revised management strategy to best protect *Gallirallus australis greyi* which has a much more restricted range than its southern cousin.

The fate of the Rakitū weka may be subject to conflicting demands but we note that although the current population of weka on Rakitū is not indigenous it is likely that the island formerly native weka population prior to human involvement. Volcanic activity in the Miocene generated landforms near the margins of mainland coastline of this region of North Island. Global sea level changes during the Pleistocene meant that for most of its subaerial existence Aotea and Rakitū were part of the mainland North Island, and would thus have shared fauna and flora.

Gasper J, Trewick SA, Gibb GC. 2024. De-novo assembly of four rail (Aves: Rallidae) genomes: A resource for comparative genomics. *Ecology and Evolution*. 14(7): e11694.

Trewick SA, Pilkington S, Shepherd LD, Gibb GC, Morgan-Richards M. 2017. Closing the gap: Avian lineage splits at a young, narrow seaway imply a protracted history of mixed population response. *Molecular Ecology*. 26(20): 5752-5772



Image by J. L. Kendrick