January 2015



RESEARCH AND CONSERVATION

ACCEPTED PAPERS, MEDIA & OUTREACH

No new papers this month

PRESENTATIONS, VISITS & NEWS conference presentations, visits to and from group members etc

- It is with sad hearts that we acknowledge the passing of Prof. Ian Jamieson. Ian was a friend and colleague of many of
 us and his work on conservation genetics and small population management has been immense. One of his most
 recent articles was published with Patricia and had a component on hihi. Abstract copied below. His help to Patricia
 and our research group in setting up on going work with toll-like receptor genes was done with genuine enthusiasm
 and wanting to help establish a new line of research questioning in hihi. I hope our continuing work on TLR genes will
 help showcase the importance of his contributions in conservation biology.
- Victoria has arrived in New Zealand to start her first field season on Tiritiri Matangi.
- Lydia is busy writing up her monitoring work from the Maungatautari hihi population.
- Anna, Patricia and John interviewed short listed candidates for a PHD studentship at Auckland University on hihi genomics.
- Donal and Rachel continue a fantastic job in the field tweaking RFID tags and monitoring hihi on Tiritiri Matangi.
- Kate, Leila, Kevin and John have been busy finishing off a final complete draft of a hihi management guide

<u>FEATURE STORY</u>: Toll-like receptor diversity in 10 threatened bird species: relationship with microsatellite heterozygosity. Conservation Genetics (2015) 10.1007/s10592-014-0685-x

Measuring individual-level heterozygosity in threatened species is one approach to understanding and mitigating losses of genetic diversity and the role of inbreeding depression in those populations. In many conservation contexts, this goal is approached by assaying levels of microsatellite diversity, and inference is often extended to functional genomic regions. Our study quantifies diversity of innate immunity toll-like receptor (TLR) genes in 10 threatened New Zealand birds across four avian orders, with an average of 20.1 individuals and 6.2 TLR loci (sequences averaging 850 bp in length) per species. We provide detailed TLR diversity statistics for these 10 species, which showed more evidence for genetic drift than balancing selection at TLR loci, with two possible exceptions (*TLR1LA* for hihi and TLR5 for kokako). Our observations also support a possible gene-duplication of *TLR7* in rock wren, indicating that a *TLR7* duplication previously observed in other passerines may have occurred early in the divergence of this order. In addition to these analyses of population-level TLR sequence diversity, we used an average of 14.6 polymorphic microsatellite loci per species to study, for the first time, the relationship between microsatellite internal relatedness (a measure of individual homozygosity) and TLR heterozygosity. There was no relationship between microsatellite and TLR heterozygosity of individuals within species, suggesting that the predictive power of microsatellites to evaluate functional diversity is poor, and highlighting the value of adding data from putatively functional genomic regions, such as TLRs, in the study of genetic diversity of threatened species. Overall this study provides valuable data for comparison with more widespread species, and facilitates research into the importance of TLR diversity in natural populations of conservation concern.

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FUNDING our major funders and new funding news

CURRENT AND PAST FUNDING – thank you!

+ British Research Council + Royal Society + Leverhulme Trust + Department of Conservation + AXA-fund + NERC + SoTM + ASAB + Massey University + NZ Safety Ltd + Royal Society of New Zealand Marsden Fund.

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