

Are hihi affected by inbreeding?

Modern genetic tools reveal inbreeding status for the threatened hihi of Aotearoa New Zealand



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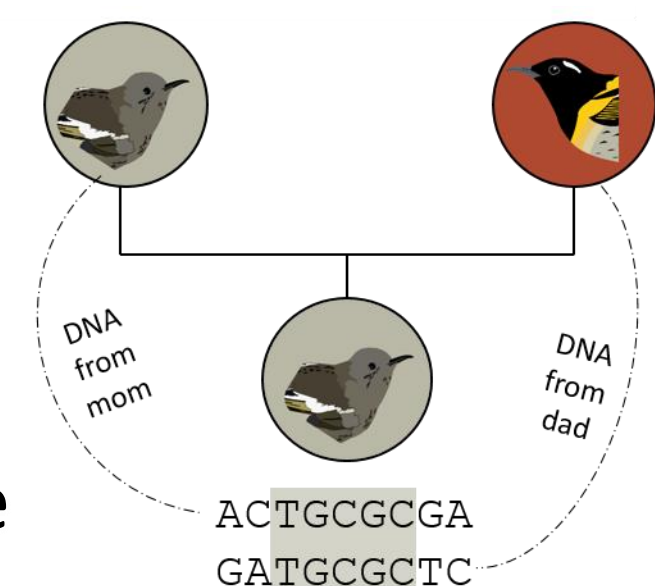
INTRODUCTION

Once abundant across the North Island, hihi now can only be found in a single remnant population and seven additional pest-free sanctuaries. Hihi are important **plant pollinators** but extremely **vulnerable** to all predators and competitors.



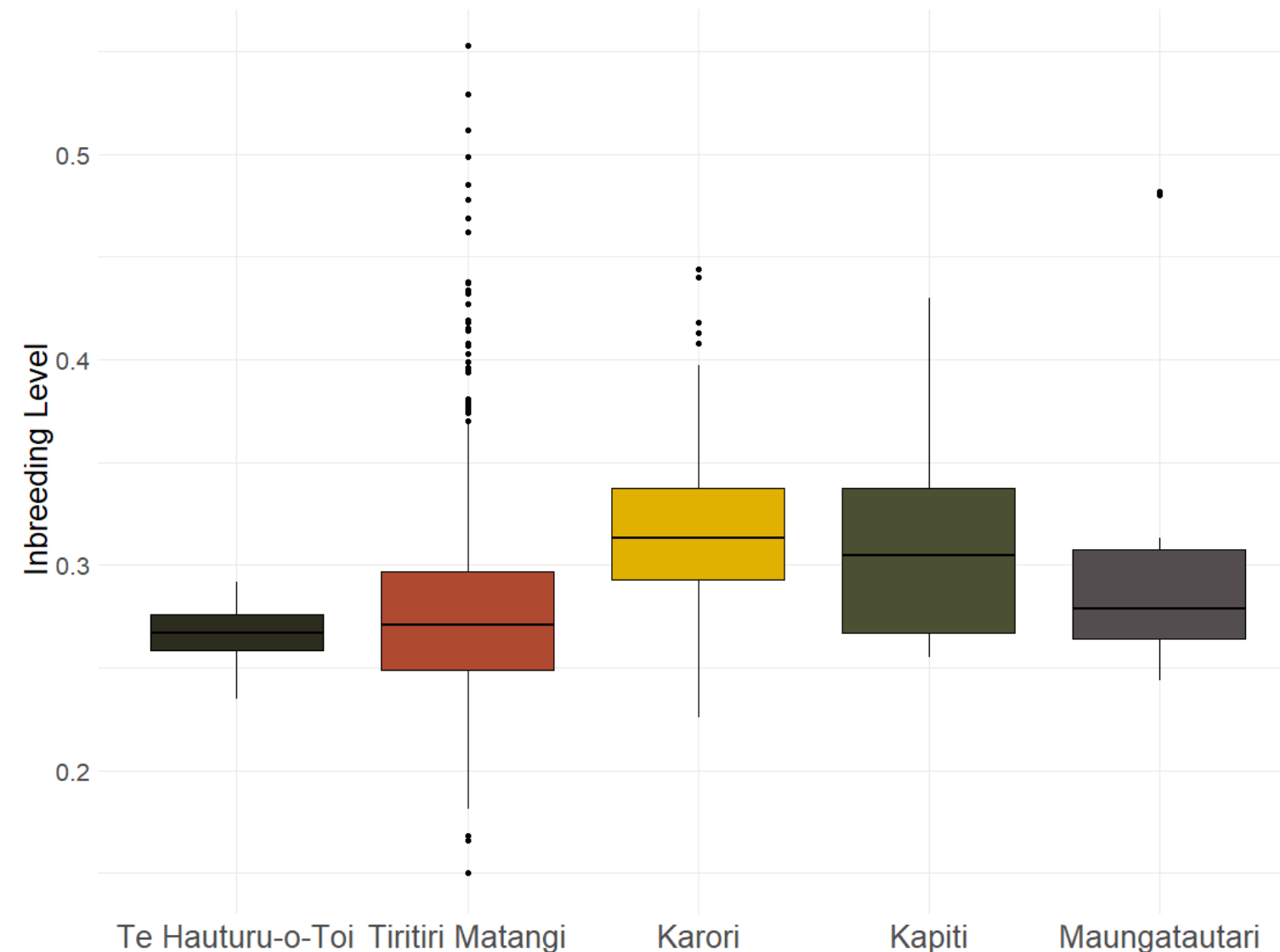
METHODS

We used hihi genomic data to infer **individual levels of inbreeding** for hihi from five populations. Inbreeding is caused by mating between close relatives, and revealed by **low variation** in the genome of an individual.



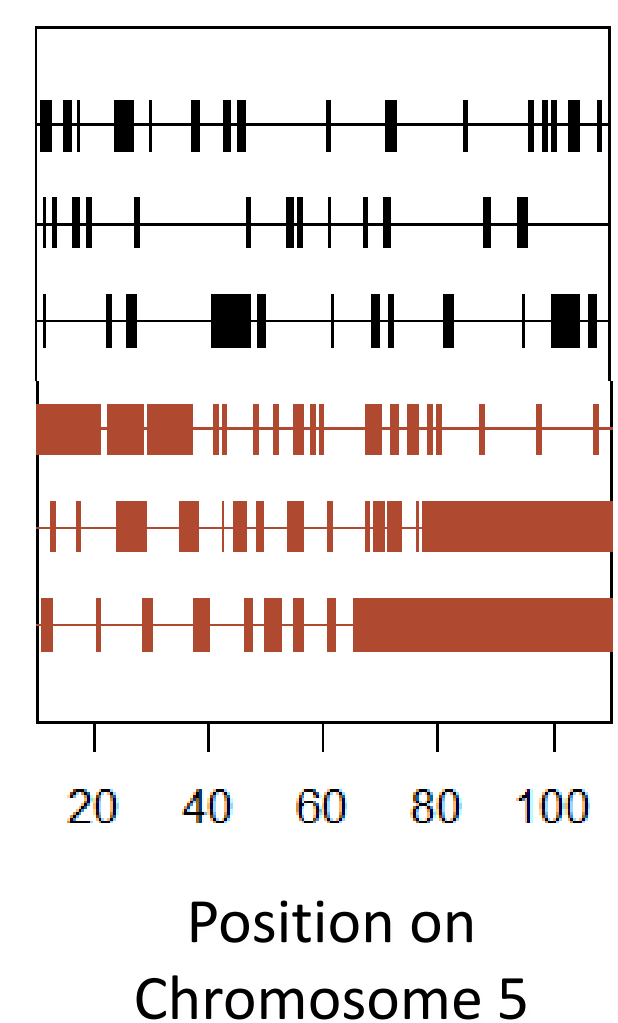
RESULT 1

Birds in the **remnant population** and in the **largest translocated population** are overall less inbred than **smaller, older** translocated populations. However, **Tiritiri Matangi** has a wide range of inbreeding levels.



RESULT 2

A closer look reveals: individuals with high total inbreeding have less variation across their chromosomes (**bottom 3 birds**) compared to those that are less inbred (**top 3 birds**).



CONCLUSION

We find that small, older translocated hihi populations such as **Karori** (Zealandia) and **Kapiti** Island have **higher inbreeding** levels than the much larger population on **Tiritiri Matangi** and the more recently established population in the **Maungatautari** sanctuary. Hihi inbreeding levels are **comparable to other bird species** of conservation concern, such as the Hawaiian Crow (‘Alalā).

