

The uses of genetic approaches in island eradications

Andrew Veale

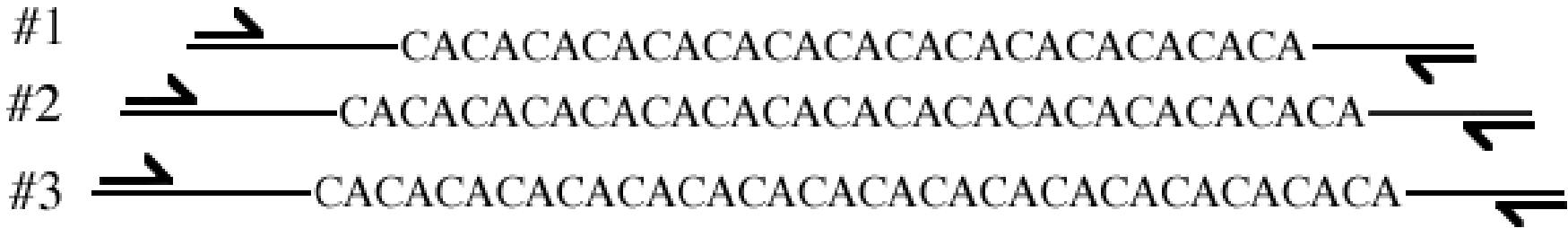
Population Connectivity and Assignment



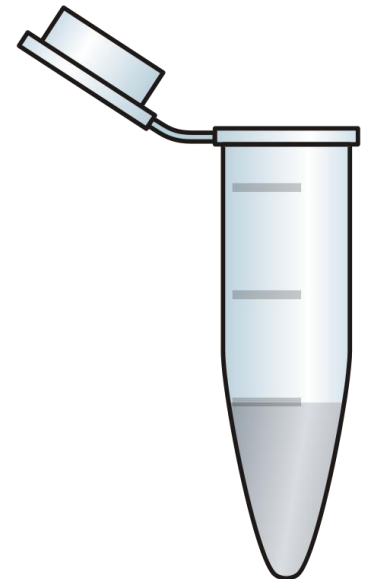
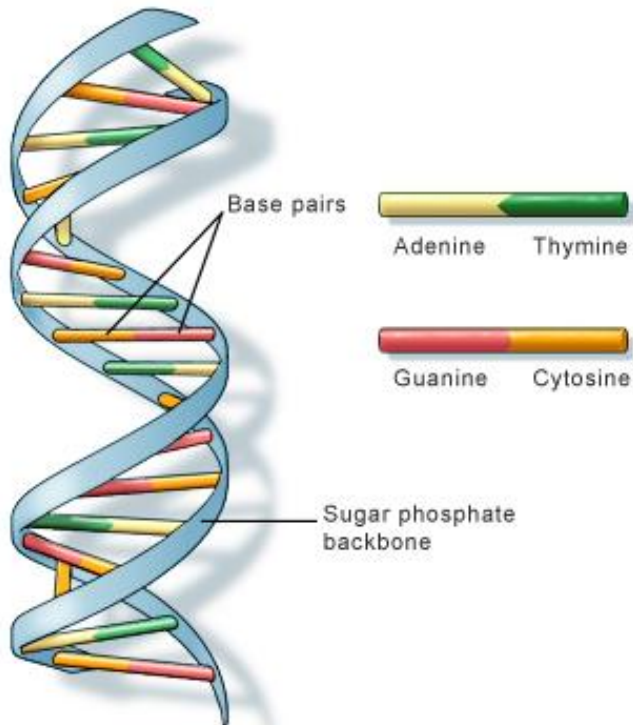
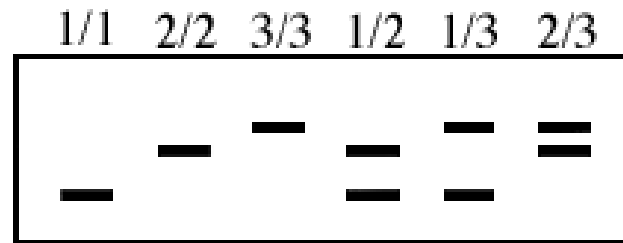
- Ideally we want to know how connected each population is.
 - To better plan control operations
 - To assess reinvasion risk
- We also want to be able to identify the source population of a given individual.
 - To evaluate invasion pathways
 - To see if reinvasion is occurring
 - To evaluate the success of control measures

DNA Microsatellites

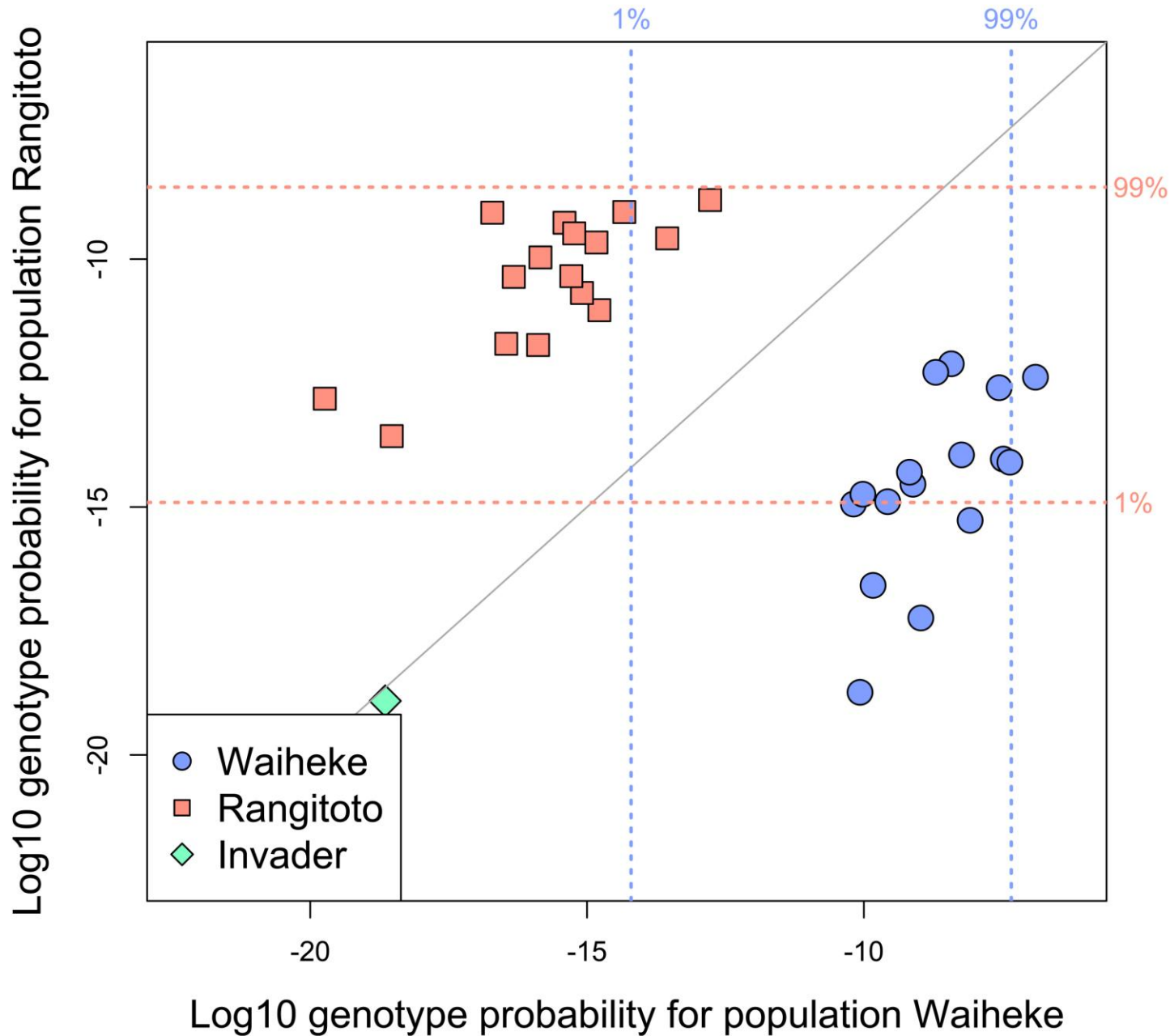
ALLELES



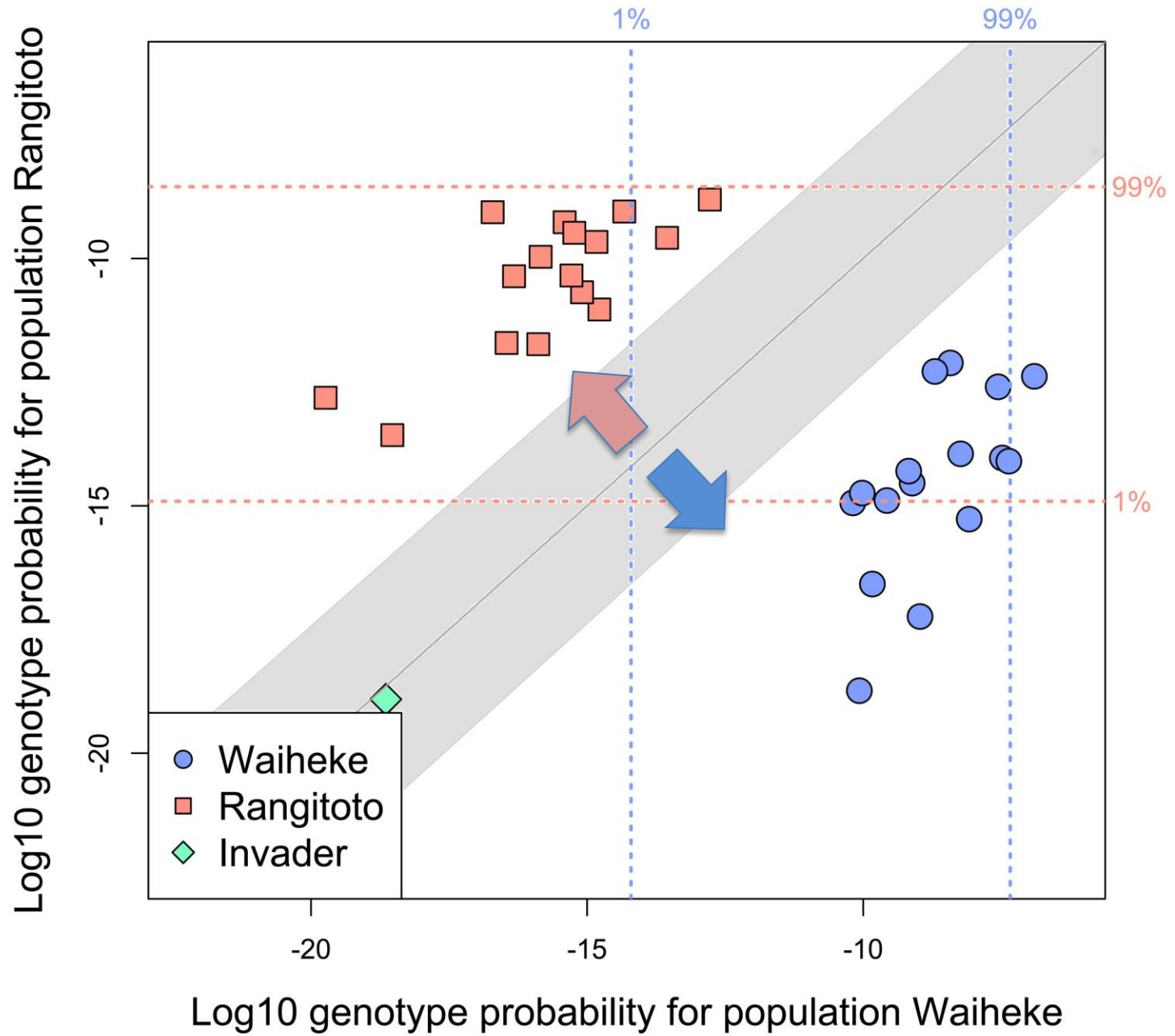
GENOTYPES

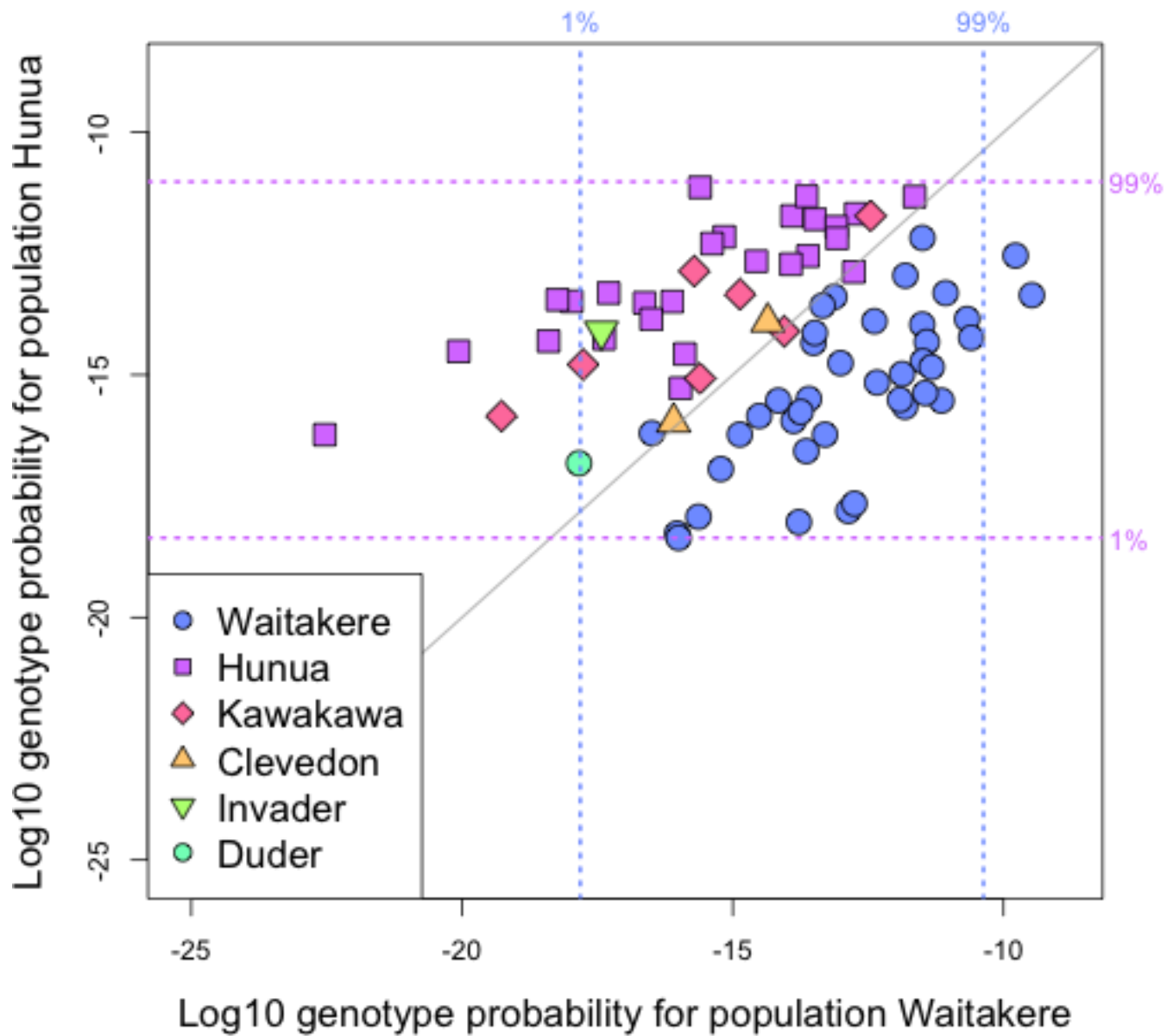


Waiheke-Rangitoto showing 'other' source for invader

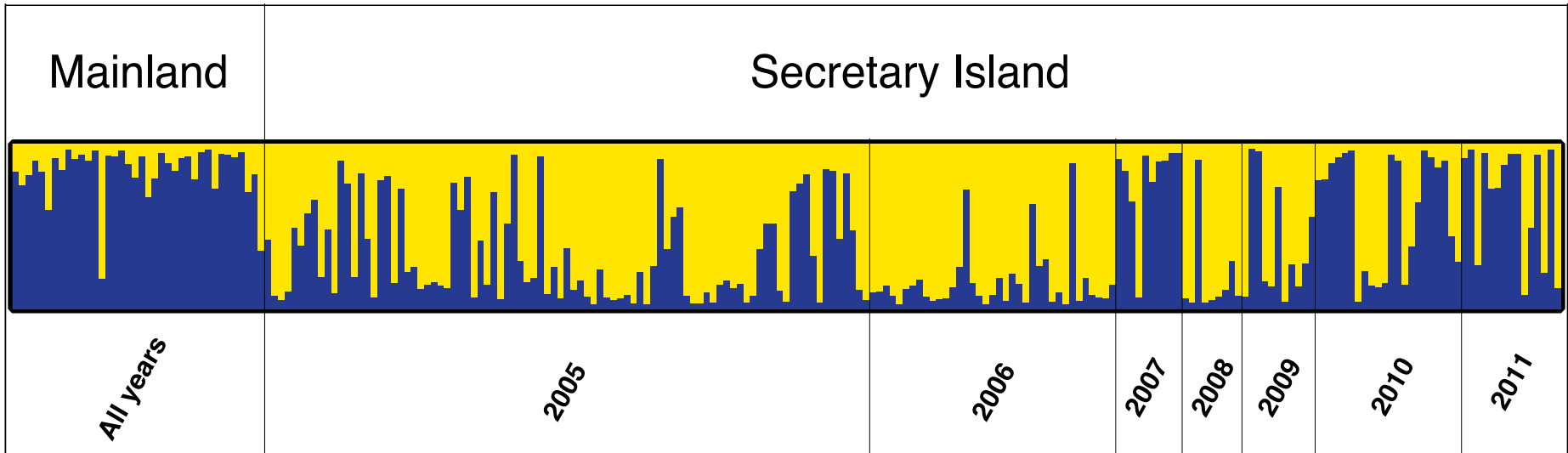
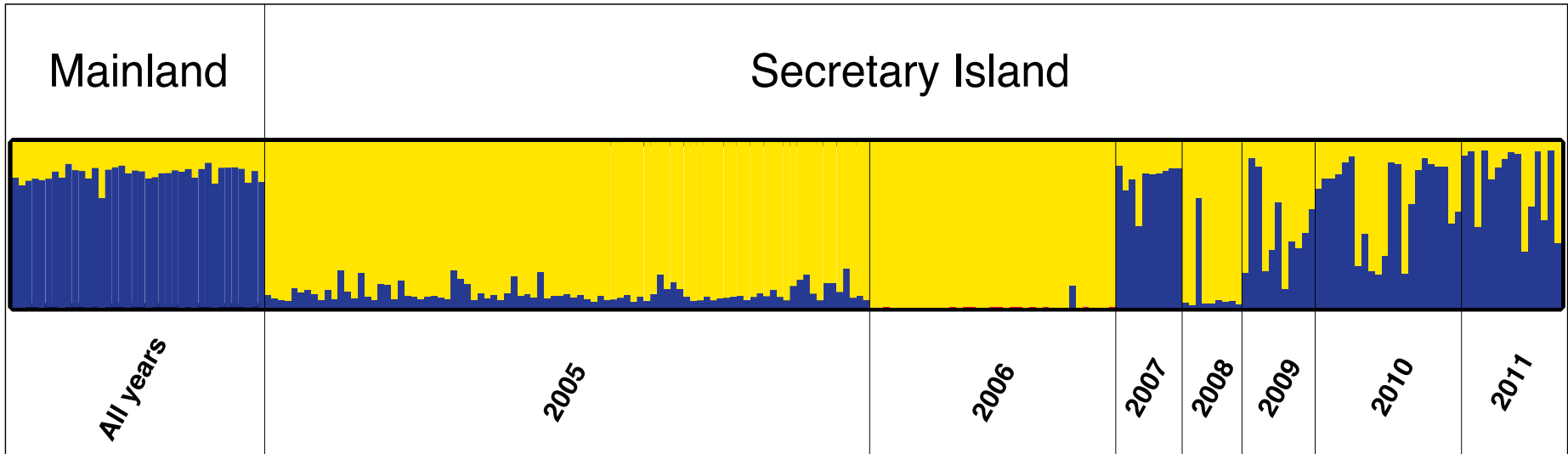


Waiheke-Rangitoto showing 'other' source for invader

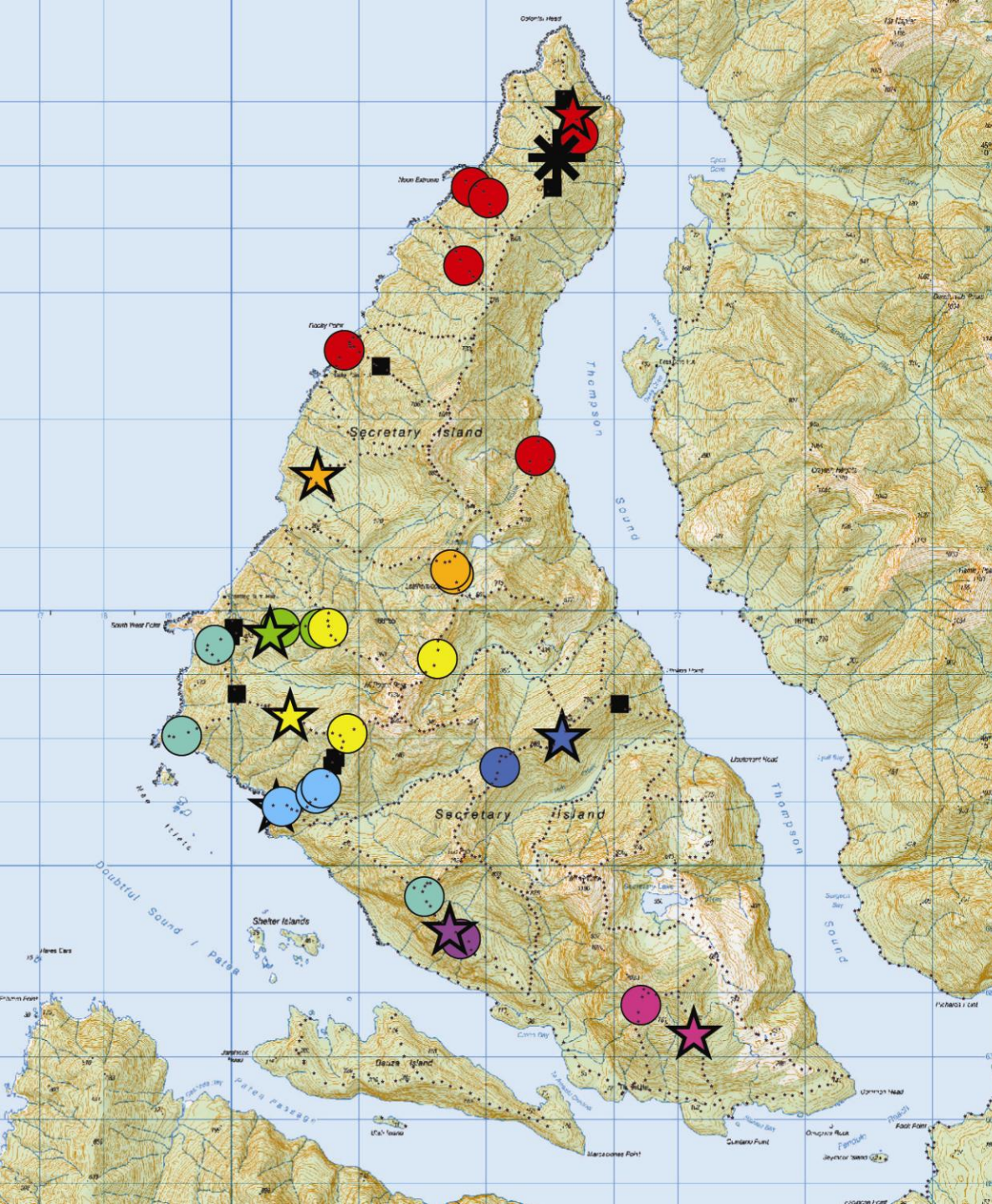




Secretary Island – Structure Admixture



Secretary Is. (2006)



Colour = Family
Circle = Juvenile
Star = Mother

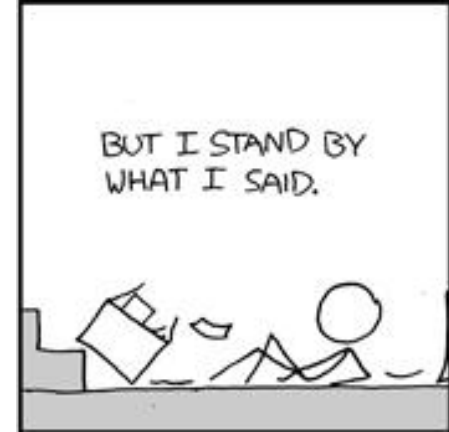
* = immigrant

Estimating migration rates



- BayesAss, Migrate & BIMR do not work!
- F_{ST} and Private Allele methods for assessing migration rates are probably correlated to migration rates: therefore useful.
- Density blocking by residents means that genetic measures of migration \lll potential migration if a population is eradicated.

Research Conclusions



- Fine-scale individual movement and levels of population connectivity are quantifiable using genetic analyses.
- Genetic Assignment (GeneCharts) is generally superior to clustering (though STRUCTURE can provide complimentary information).
- Kinship Analysis can help describe the sources of recruitment for a given population.

Recommendations

- Collect samples from 20+ geographically representative individuals for each invasive species present before attempting eradication.
- Perform genetic studies before the eradication – to define the eradication unit.
- Collect samples from across mainland sites in case they become useful later

Research Questions



- What is the spatial resolution of genetic data for different pest species in different habitats?
- What do genetic measures of population differentiation actually mean in terms of connectivity? (species specific).

Future Developments



- Individual-based genetic simulations to evaluate population connectivity for our primary predators.
- Larger numbers of markers cheaply multiplexed (possibly SNPs) to allow true kinship assessments.

Acknowledgements



- Mick Clout & Dianne Gleeson
- Elaine Murphy, Andrea Byrom, Kim King, Rachel Fewster, Oliver Hannaford
- Diana Prada & Robyn Howitt
- DoC (Pete McMurtrie, Kerri-Anne Edge, Richard Griffiths)
- University of Auckland (Joerg Kistler)
- Auckland Council (Jack Craw, Mark Mitchell, Nick Waipara)



Department of Conservation
Te Papa Atawhai



THE UNIVERSITY OF AUCKLAND
NEW ZEALAND



Landcare Research
Manaaki Whenua