Development and Validation of a Standardised Genomic Tool for Conservation Management of the Koala (*Phascolarctos cinereus*)

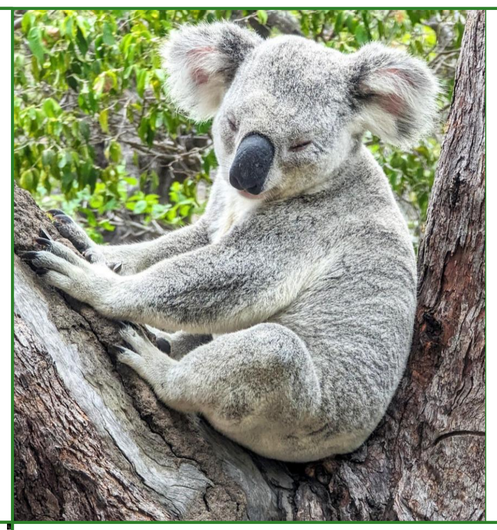
Authors: Donnelly, L.[1], Kjeldsen, S.[1,2], Lott, M.[3], Leigh, K.[4] , Field, M.[1], Cooke, I.[1] , Wright, B. [5], Zenger K.[1]

1. College of Science and Engineering, James Cook University
2. Marine Climate Change Unit, Okinawa Institute of Science and Technology
3. Australian Centre for Wildlife Genomics, Australian Museum
4. Science for Wildlife
5. Sydney School of Veterinary Science, University of Sydney

*correspondence lily.donnelly@my.jcu.edu.au

The Conservation Challenge

The Koala (*Phascolarctos cinereus*) was listed as Endangered in 2022 across most of the distribution predominantly due to habitat loss. Today, populations are highly fragmented over five jurisdictions across eastern and southeast Australia. A National Koala Management Plan developed, however understanding genomic population structure is complex for managers due to a variety of heterogenous study designs and a lack of standardised genomic tool for conservation management.



Aim & Objectives

- Develop and validate standardised monitoring tool
- Applicable for all biological koala sample types:
- (tissue, blood, archive DNA, swab, hair, scat)
- Informative for all koala populations
- Includes:
- Neutral & adaptive markers
- Host + multiple pathogen markers

Assay Development & Validation Workflow

1. Map published SNP datasets and genes to reference genome
2. Develop probe-based assay from SNP positions
3. Genotype samples on novel assay
4. Optimise and validation genotype data (Fixed, Discovery and Pathogen datasets)

Assay Composition

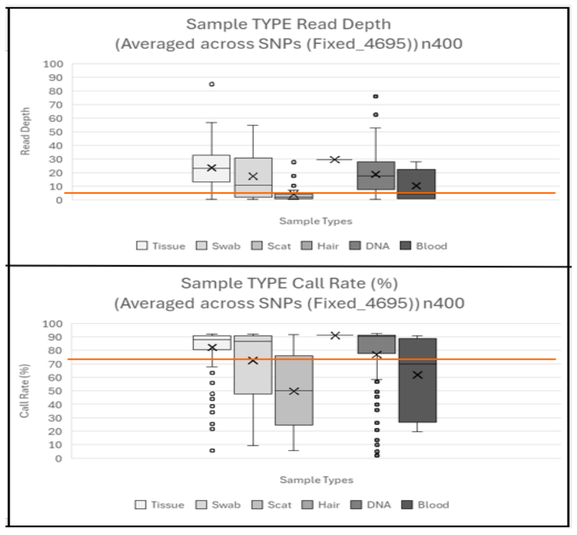
- Fixed: genomic SNP datasets (RD>10, CR>90%)
- Discovery: candidate fitness genes (RD>10, CR>90%, MAF>0.01)
- Pathogen: koala pathogen genes (presence/ absence)
- (Chlamydia, Retrovirus, Papillomavirus, Herpesvirus)

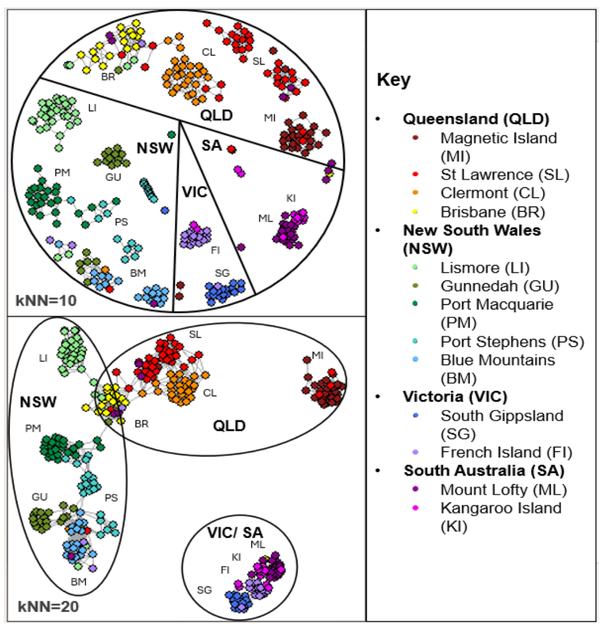
= Total 4,999 SNPs

Validation Results

Sample Type Performance (Boxplots)

- Each type passed QC (RD >5, CR>75%)
- Total n=311 passed QC
- Performance:
-Highest = Tissue, Hair, DNA
-Lowest = Scat, Blood, Swab
- No difference between replicates



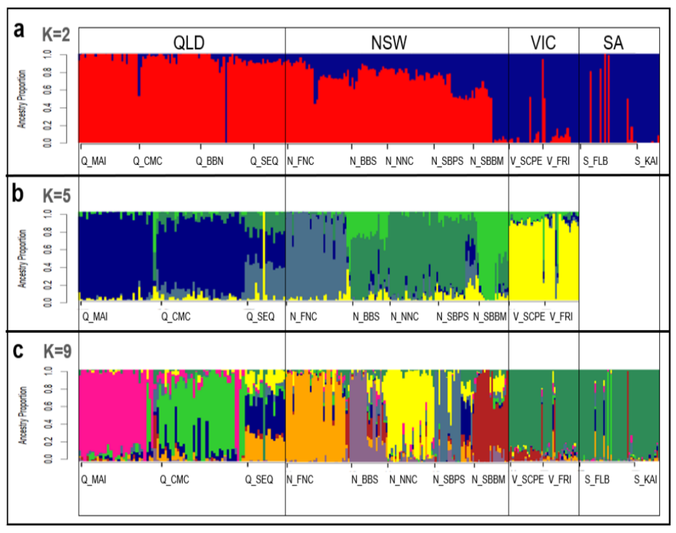


Individual clustering (NetView)

- Clear population clustering (kNN=10)
- Northern region (QLD, NSW) reflects geographic spread (kNN=20)
- Southern region (VIC, SA) has tight clustering due to bottleneck history
- Provenance dataset (n=399) able to assign sample to correct populations

Population Admixture (K=2, =4, =9)

- Northern and Southern regional divide (K=2)
- Admixture across K:
- High in NSW (complex population connectivity)
- Moderate in QLD (many isolated populations)
- Low in VIC and SA (historical bottleneck)
- Patterns consistent with literature

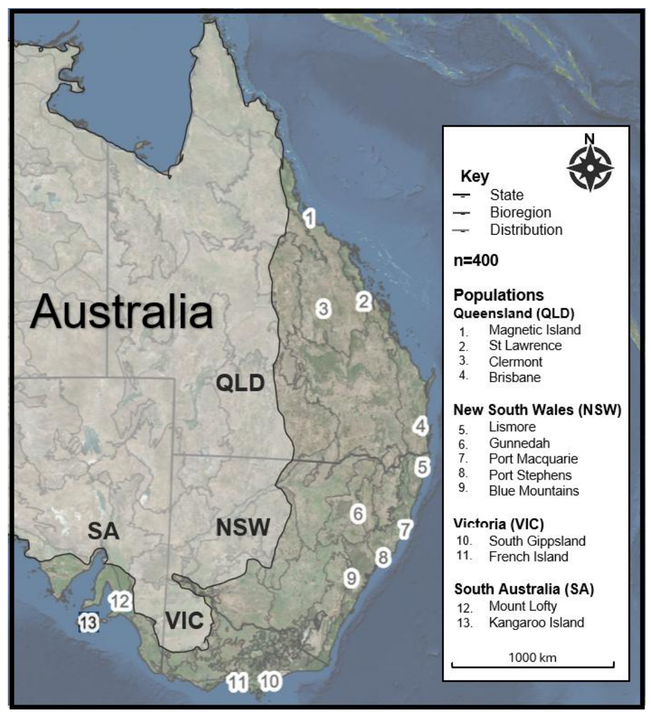


Significance

- First host (koala) & multiple pathogen markers in one assay.
- Low density <5,000 SNPs (cost effective).
- Targeted neutral & adaptive markers (highly informative)
- Applicable for all sample types (invasive & non-invasive).
- Informative for all populations across distribution.
- Standardised for conservation management

Management Applications

- Genomic monitoring
- Pedigree, kinship
- Parentage & Provenance
- Sex determination
- Pathogen screening
- Diversity & Divergence
- Population structure & connectivity



Future Directions

-Fine scale application in conservation priority region

- Broad scale application across all koala-inhabited bioregions

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A scalable genomic platform, integrating host and pathogen markers for conservation monitoring

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