



University of
Southern
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Genetic health and status of K'gari wongari (Fraser Island dingoes)

Project summary document for policy-makers and managers



Contents

About this document	2
Background information	3
Stakeholder priorities	3
Key results	6
Recommendations	7
Further information	7
Table 1. Summary of stakeholder priorities, expert recommended approaches, and the research status of these priorities.	8
References	12

About this document

This document was prepared by Dr Benjamin Allen (University of Southern Queensland), and briefly summarises the process, key results, and outcomes of the research project titled ‘*Genetic health and status of K’gari wongari (Fraser Island dingoes)*’, completed in late 2022.

This document is intended for policy-makers and managers, but might also be circulated more broadly to media outlets or the general public.



“Dingoes are observed to live in separate packs, but analysis of the number of genetically distinguishable packs revealed that there is only ‘one large pack’ on the island, from a genetic point of view.”

Background information

Subsequent to the release of the 'Ecosure review' into the conservation and management of dingoes (known locally as wongari) on K'gari (Fraser Island) in 2012 (Allen et al. 2012), there has been an increased effort to systematically address community concerns about the dingoes' status through independent scientific evaluation and open-access publication of key datasets collected and maintained by the Queensland Parks and Wildlife Service (QPWS), who are largely responsible for managing dingoes on the island.

Data on dingo numbers (Appleby and Jones 2011; Game et al. 2013; Allen et al. 2015), movements (Baxter and Davies 2018; White 2021), diet and health (Behrendorff et al. 2016), food availability (Déaux et al. 2017; Behrendorff et al. 2018), feeding behaviour (Behrendorff 2018b, 2018a), longevity (Behrendorff and Allen 2016), the frequency of serious incidents (Allen et al. 2012; Appleby 2015; Appleby et al. 2018), and the effects of humane destructions on dingo populations (Allen et al. 2015) are now all freely available and have largely quelled public concerns about most of these issues. But concern had increasingly shifted towards the genetic health and status of dingoes on the island.

Some such work to address these genetics concerns had already been undertaken (e.g. Baker 2004; Stephens 2011; Conroy et al. 2017; Cairns et al. 2018; Conroy et al. 2021), but production of these studies had not resolved community or scientific uncertainty or provided managers with actionable information. Much contention and trepidation also existed around an appropriate delivery model for this research. A novel approach was needed complete the research and make the results available, as had been done for other public concerns.

In 2018, researchers from the University of Southern Queensland proposed a stakeholder-led, expertinformed, participatory and independent co-innovation approach or process that included (1) stakeholder workshops to identify research priorities, (2) expert workshops to identify appropriate research methods, and (3) the commissioning of independent scientific research to address stakeholder priorities in accordance with experts' suggested methods (undertaken by conservation genetics experts at the University of Cape Town, South Africa). The project was eventually approved and commenced in 2020, and the overall aim of the project was to provide managers with robust and policy-ready information on the genetic health and status of dingoes K'gari – information that also met stakeholder expectations and was widely supported by the scientific community.

Stakeholder priorities

The following priorities were determined by community stakeholders at a workshop held in Hervey Bay on 19 October 2020. Priorities are ordered from the highest priority (a score of 10) to the lowest priority (a score of 0). The genetic expert group determined the most robust analytical methods to address each of these priorities at a separate workshop held a few days later. After DNA quality checks and an assessment of which priorities were answerable given the available samples (Table 1, below), the independent researchers sought to answer as many of these questions as possible.

1. Please produce a pedigree chart (or similar) from the available samples (Score = 10.0).
2. People talk about there being somewhere between 15 to 26 packs on the island: (Score = 9.5)
 - 2.1. How many 'packs' can be identified from the genetic data?

- 2.2. Do the 'humane destruction / high risk' animals come from a single bloodline (or are they closely related)?
 - 2.3. What is the estimated total population size of dingoes on the island?
3. What is the status of the population's 'genetic health'? (Score = 9.0)
 - 3.1. How common are 'bad genes' and is their frequency changing over time?
 - 3.2. Are there any obvious genetic weaknesses or vulnerabilities in the population (e.g. undescended testes, blindness, hip dysplasia)?
 - 3.3. What is the minimum breeding population size that can hold enough genetic diversity to maintain the health / viability of the population? (minimum 100 rule, 250 rule, 500 rule)
4. Do 'humane destruction / high risk' animals have similar genetic traits? (Score = 8.9)
 - 4.1. Are there common genetic traits between 'humane destruction / high risk' animals? If so, what are they?
 - 4.2. Are the traits common to 'humane destruction / high risk' animals those that are good for fitness?
 - 4.3. Some people believe animal have become more curious over time, is there any genetic evidence for this?
5. Is there any evidence of inbreeding (i.e. breeding between siblings and close relatives) and has it changed over time? (Score = 8.8)
 - 5.1. How closely related are the breeding mates?
 - 5.2. Are the levels of inbreeding on the island different from (A) nearby Butchulla country on the mainland and (B) elsewhere on the mainland?
 - 5.3. Is the observed level of inbreeding a problem for the population into the future? What does it mean for future population viability (estimate in years)?
 - 5.4. Can we detect changes in long-term rates of inbreeding, and if so, do they correlate with significant events such as natural disasters, management, anthropogenic interference, vehicle strikes etc.?
 - 5.5. What happens genetically if most of a 'pack' is removed vs just one or two? Is there a threshold where loss of individuals becomes significantly more problematic for a group? Are there particular individuals that matter more, genetically, than others?
6. How many breeders are there, what is their sex ratio, what is the effective population size, and has this changed over time? (Score = 8.3)
 - 6.1. Who are the breeders?
 - 6.2. Are they closely related?
 - 6.3. What is their age / social status (is breeding between young animals a sign of problems in the local population)?
 - 6.4. Do some litters have multiple fathers,
 - 6.5. Do some females mate with more than one male over time? How promiscuous are they?
7. What is the relationship between island animals, mainland animals, and SE Asian animals? (Score = 8.0)

- 7.1. How closely related are island animals to others from (A) nearby Butchulla country on the mainland and (B) elsewhere on the mainland?
 - 7.2. What are the origins of K'gari wongari? Where do they come from?
 - 7.3. What is the proportion of 'phenotypic genes' in the population, and has that changed over time (e.g. coat colour, tail tips etc)?
 - 7.4. What is their genetic diversity, has it changed over time (e.g. more or less domestic / endemic genes), and is it a problem for longer-term viability of the population?
 - 7.5. If mainland dingoes have contributed to the island population, how recently has this occurred?
8. Can we identify social status (rank) of animals from their genetics? (Score = 7.6)
- 8.1. Are there common genetic traits between sires?
9. Are there any spatial relationships for the genetic parameters of interest on the island, such as geographic differences in inbreeding levels, prevalence of genetic disorders, prevalence of 'cheeky dog' genes, relatedness, and/or diversity between groups? (Score = 7.4)
10. Can we determine stress levels in the dingo population and is there any relationship to external effects? (Score = 5.8)
- 10.1. Is there geographic variation in stress levels and have they changed over time (long-term and short-term, e.g. month-to-month or year-to-year)?
11. Is there evidence of domestic dog genes in the population? NOTE: domestic dogs were resident between 1860 and 1991, but since then sources may include occasional visitors' dogs (Score = 5.2)
- 11.1. Do 'humane destruction / high risk' samples differ genetically from other samples? If so, do they have more domestic dog DNA?
 - 11.2. Can we detect the arrival of domestic dogs in the 1860s and their removal at around 1990? If so, has the population 'genetically recovered' since then?
 - 11.3. Are domestic dog genes more prevalent in some areas of the island than others?
 - 11.4. How recently have domestic dog genes entered the population?
 - 11.5. If dog DNA is recent, what is the likely breed source?
12. Were there any genetic bottlenecks in the data? When did they occur? (Score = 4.4)
13. Is there still the potential for white, black and other coat colours to occur in the population? (Score = 2.8)

Key results

The following are simple summary statements expressing the key results and interpretations from the work. Complete results and analyses are available in document titled '*Report on the genetic status of K'gari wongari (Fraser Island dingoes)*', provided by independent researchers at the University of Cape Town, South Africa.

1. Tissue samples (small pieces of ear tip) from 243 dingoes were collected between 1996 and 2020, but conservative sampling requirements and DNA quality checks meant that only 144 samples needed to be analysed. Sample quality was good, and the results are considered scientifically robust by the expert group.
2. Comparisons with mainland dingoes from Rainbow Beach and other areas across Australia showed that K'gari dingoes are easily distinguishable from mainland dingoes. It is very easy to determine if a dingo found on the mainland is from K'gari, or if a dingo found on the island is from the mainland.
3. There is no evidence of recent connectivity between dingoes on the mainland and the island, or no evidence that dingoes are moving on or off the island and assimilating into local populations.
4. Dingoes are observed to live in separate packs, but analysis of the number of genetically distinguishable packs revealed that there is only 'one large pack' on the island, from a genetic point of view. In other words, dingoes from different packs mate or mix with each other frequently enough that the observed packs cannot be genetically distinguished from each other.
5. The inbreeding levels of dingoes are high on the island, and will increase over time in the absence of migrants from the mainland. But no morphological signs or physical abnormalities associated with inbreeding have been observed and their abundance does not appear to be declining, so it is likely that the population has not yet exceeded its tolerance for inbreeding. Similarly high levels of inbreeding are found in some other mainland populations of dingoes.
6. Dingoes on the island are highly related to each other, and on average, the relatedness between any two individuals is equivalent to a parent-offspring or full-sibling relationship. This means that animals destroyed for high-risk behaviour can be highly related, breeding pairs or partners can be highly related, and the dingoes successful at breeding (i.e. all the dominant males and females) can also be highly related, but these groups are no more highly related than any others.
7. The genetic ancestry or composition of the island's dingoes has changed over time, with some genes becoming more prevalent than others over the last 25 years. This shift may be the result of one (or a few) long-lived individuals becoming highly successful at raising litters and spreading their genes throughout the island over many years.
8. Something happened around the turn of the century that had a clear impact on the genetic composition of the island's dingoes. The removal of 32 dingoes in 2001 in response to the death of Clinton Gage is likely to have contributed to this, but these changes cannot be solely attributed to this widespread cull given the additional management actions occurring around the same time (e.g. fencing townships, closing rubbish dumps, reduced feeding opportunities etc.). These changes have since stabilised.
9. The dominant (and natural) process characterizing the current genetic status of the island's dingoes is enhanced genetic drift and subsequent increases in average relatedness via various levels of inbreeding, and not the occasional removal of small numbers of animals.

Recommendations

1. Continue to investigate the remaining stakeholder priorities that could not be investigated in this project, particularly the genomic priorities.
2. Routinely collect and store a tissue sample from all dingoes that are handled for any reason (i.e. those that are found deceased, or are captured for any purpose).
3. Develop a genetic management plan for the island's dingoes, inclusive of desired targets and thresholds for management action to address any issues that might arise. Immediate on-ground actions that would best provide the necessary foundation for this plan include:
 - a. Conduct a population-wide census of the dingoes on the island, or to the best extent possible, collect a genetic sample from all living dingoes within a 12 month period.
 - b. Commence formal monitoring of morphological and biological parameters that can be indicative of declines in the genetic health of the population (e.g. record the presence of floppy ears, curled tails, reduced sperm motility, pregnancy rates etc.).



“Something happened around the turn of the century that had a clear impact on the genetic composition of the island’s dingoes... These changes have since stabilised”.

Further information

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Table 1. Summary of stakeholder priorities, expert recommended approaches, and the research status of these priorities.

	ID	Stakeholder question	Expert recommended approaches	Preliminary expert assessment	Post-processing expected outcomes	Final outcome
Pedigree analyses	1.1	Produce a pedigree chart from the samples.	PEDIGREE	Possible	Insufficient data for a genetic pedigree; too many gaps.	Could not be addressed; insufficient sampling.
	2.1	How many packs / family groups can be identified?	PEDIGREE / RELATIONSHIPS	Possible	Social network analysis should be possible.	Addressed
	2.2	Are the humane destruction / high risk animals closely related?	PEDIGREE / RELATIONSHIPS	Possible	We can look at genetic relatedness between individuals that were marked as "humane destruction" compared to relatedness of other individuals, however, this may not be very useful due to confounding factors. Will be explored once we have the data.	Addressed
	5.1	How closely related are breeding mates?	PEDIGREE / GENOMICS / RELATIONSHIPS	Possible	Insufficient data (no known pairs with viable samples).	Addressed
	6.1	Who are the breeders?	PEDIGREE / POPULATION GENETICS		Insufficient data.	Could not be addressed; insufficient sampling.
	6.2	Are successful breeders closely related?	POPULATION GENETICS / RELATIONSHIPS		Insufficient data.	Addressed
	6.4	Do some litters have multiple fathers?	PEDIGREE	Low ROI. Depends on associated data	Difficult given very few known mothers sampled. More suited to microsatellite data.	Addressed
	6.5	Do females mate with more than one male, over time?	PEDIGREE	Low ROI. Depends on associated data	More suited to non-genetics methods, which might be verifiable by the available genetic data in some cases.	Addressed
Introgre ssion and	3.1	How common are alleles likely to negatively affect the health of animals?	GENOMICS	Possible	Requires genomic approach; data could be shared with appropriate experts.	Could not be addressed; requires genomics approach.

	7.3	What is the proportion of alleles responsible for phenotypes of interest, e.g. white markings, and has that changed over time?	GENOMICS		Requires genomic approach; data could be shared with appropriate experts.	Could not be addressed; requires genomics approach.
	13.1	Is there still potential for white, black and other coat colours to occur in the population?	GENOMICS	Possible - See 7.3	Requires genomic approach; data could be shared with appropriate experts.	Could not be addressed; requires genomics approach.
	11.1	Do samples from 'humane destruction / high risk' animals have more domestic dog DNA (than other samples)?	GENOMICS / POPULATION GENETICS / LANDSCAPE GENETICS	Possible - See 4.1 and 2.2	Requires genomic approach; data could be shared with appropriate experts.	Could not be addressed; requires genomics approach.
	11.3	Are domestic dog genes more prevalent in some areas of the island?	GENOMICS / POPULATION GENETICS / LANDSCAPE GENETICS	Possible - See 9	Requires genomic approach; data could be shared with appropriate experts.	Could not be addressed; requires genomics approach.
K'gari population genetics	2.3	What is the estimated total population size of dingoes on the island?	N_e	Possible	Possible by combining genetic N_e over time with any census data: N_e/N ratios.	Could not be addressed; insufficient sampling and metadata.
	3.3	What is the minimum breeding population size that can hold enough genetic diversity to maintain the health / viability of the population?	POPULATION GENETICS	Possible	Possible by modelling drift at different N_e 's to see how sensitive the population is to genetic drift.	Could not be addressed; first requires management targets, followed by simulations.
	7.4	What is their genetic diversity and has it changed over time? Is it problematic for longterm survival?	POPULATION GENETICS	Possible - See 3.3	Possible by quantifying genetic diversity over time with a variety of metrics, but given many of the older samples have not worked well we may have additional challenges with this analysis. Downward trends in all stats (if found) may be indicative of problems for longterm survival.	Addressed

	5.3	Is the observed level of inbreeding a problem for the population into the future? What does it mean for future population viability?	POPULATION GENETICS	Possible	Possible by assessing F_{is} values etc.; distribution of relatedness; or any signs of negative effects of inbreeding present. Could benefit from genomics approach to look at runs of heterozygosity (RoH); data could be shared with appropriate experts.	Addressed
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	5.4	Can we detect changes in long-term rates of inbreeding and do they correlate with significant events, e.g. 2001 cull?	POPULATION GENETICS	Possible	See 7.4	Addressed
	12.1	Are there any genetic bottlenecks evident in the data?	POPULATION GENETICS / GENOMICS (LD)	Possible, but pre- and post-'event' samples are required	Insufficient data (time scale not long enough).	Addressed
	5.2	Are observed levels of inbreeding different from nearby populations and elsewhere on the mainland?	POPULATION GENETICS	Possible	Requires good mainland data, should be possible through comparison with Cairns et al. (2018).	Addressed
	7.1	How closely related are K'gari animals to those from nearby populations and elsewhere on the mainland, and what was the 'pathway' to K'gari?	POPULATION GENETICS	Possible - See 5.2	Requires good mainland data, should be possible through comparison with Cairns et al. (2018). 'Pathway to K'gari' more difficult to answer, but will be explored once we have the data.	Addressed
Spatial	9.1	Are there spatial relationships for genetic parameters of interest: inbreeding, genetic disorder prevalence, relatedness, diversity?	POPULATION GENETICS / LANDSCAPE GENETICS	Possible, but there is no known 'cheeky dog' gene	Some of this may be possible; will be explored once we have the data.	Addressed
	3.2	Are there any obvious genetic weaknesses in the population?	N/A	Not answerable with these data	Not assessable.	Was not addressed.
	4.1	Are there common genetic traits between 'humane destruction / high risk' animals? And what are they?	GENOMICS / RELATIONSHIPS	Difficult to do well	Not assessable.	Was not addressed.

Not assessable / requires future study	4.2	Are the traits common to 'humane destruction / high risk' animals those that are good for fitness?	GENOMICS / RELATIONSHIPS		Not assessable.	Was not addressed.
	4.3	Is there any genetic evidence that animals have become more curious over time?	GENOMICS / RELATIONSHIPS	Low probability of success	Not assessable.	Was not addressed.
	5.5	What happens if most of a pack is removed vs 1 or 2?	N/A	This should be investigated at a later date	Requires future study.	Was not addressed.
	6.3	What is the age / social status of breeders?	N/A		Not assessable.	Was not addressed.
	7.2	What are the global origins of K'gari wongari	POPULATION GENETICS	This should be investigated at a later date	Requires future study.	Was not addressed.
	7.5	If mainland dingoes have contributed to the island population, how recently has this occurred?	N/A	This should be investigated at a later date	Requires future study.	Was not addressed.
	8.1	Are there common genetic traits between sires?	N/A	This should be investigated at a later date	Requires future study.	Was not addressed.
	10.1	Can we determine stress levels in the wongari population and is there any relationship to external effects?	N/A	PHENOTYPING PROBLEM	Not assessable.	Was not addressed.
	11.2	Can we detect the arrival of domestic dogs in the 1860's and removal around 1990?	N/A		Not assessable.	Was not addressed.
	11.4	How recently have domestic dog genes entered the population?	N/A	Low probability of success	Not assessable.	Was not addressed.
	11.5	If domestic dog DNA is recent what is the likely breed source?	N/A	Low probability of success	Not assessable.	Was not addressed.

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