The hybridisation capture of population-level mitochondrial genomes from environmental DNA

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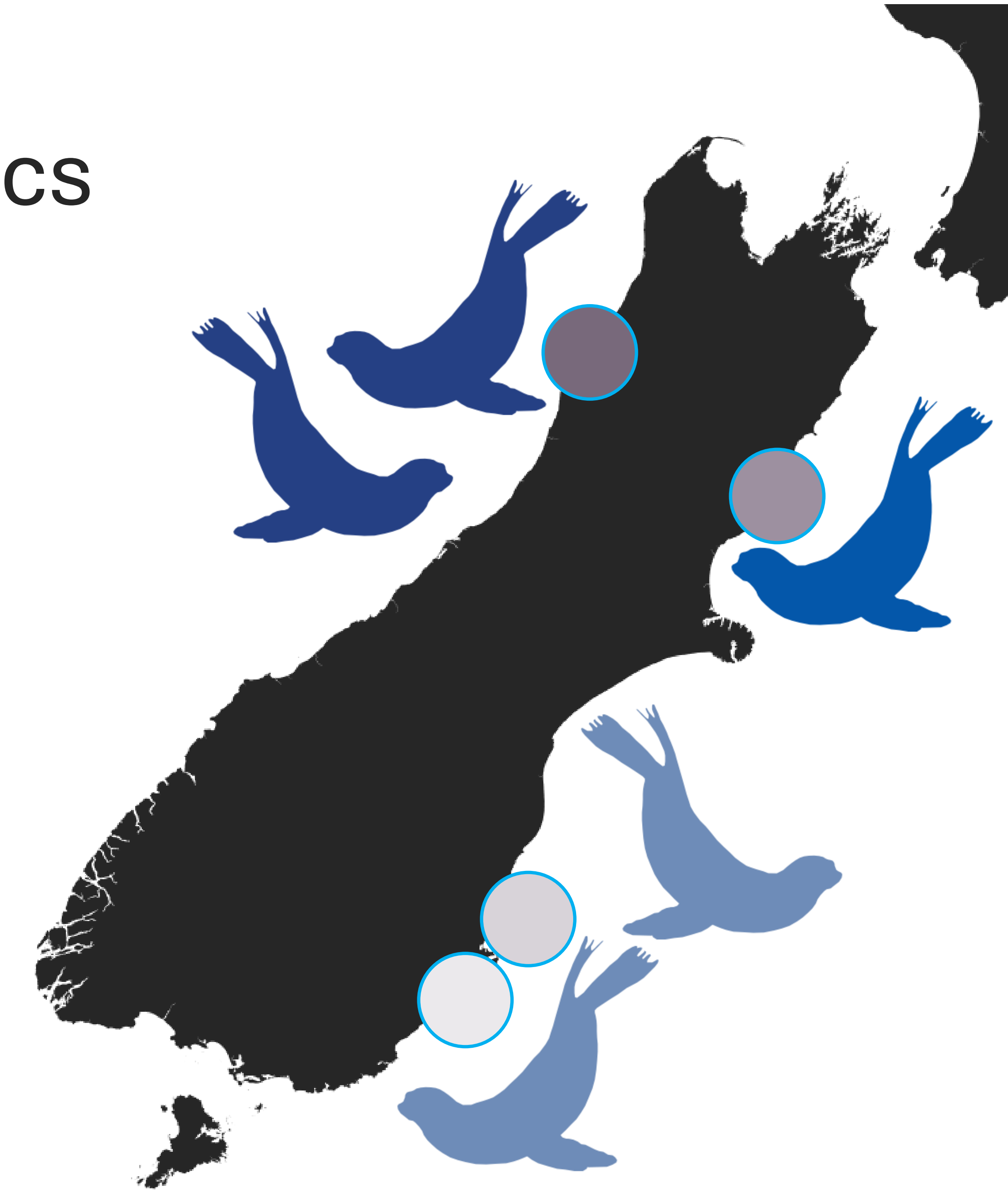
eDNA Population Genetics

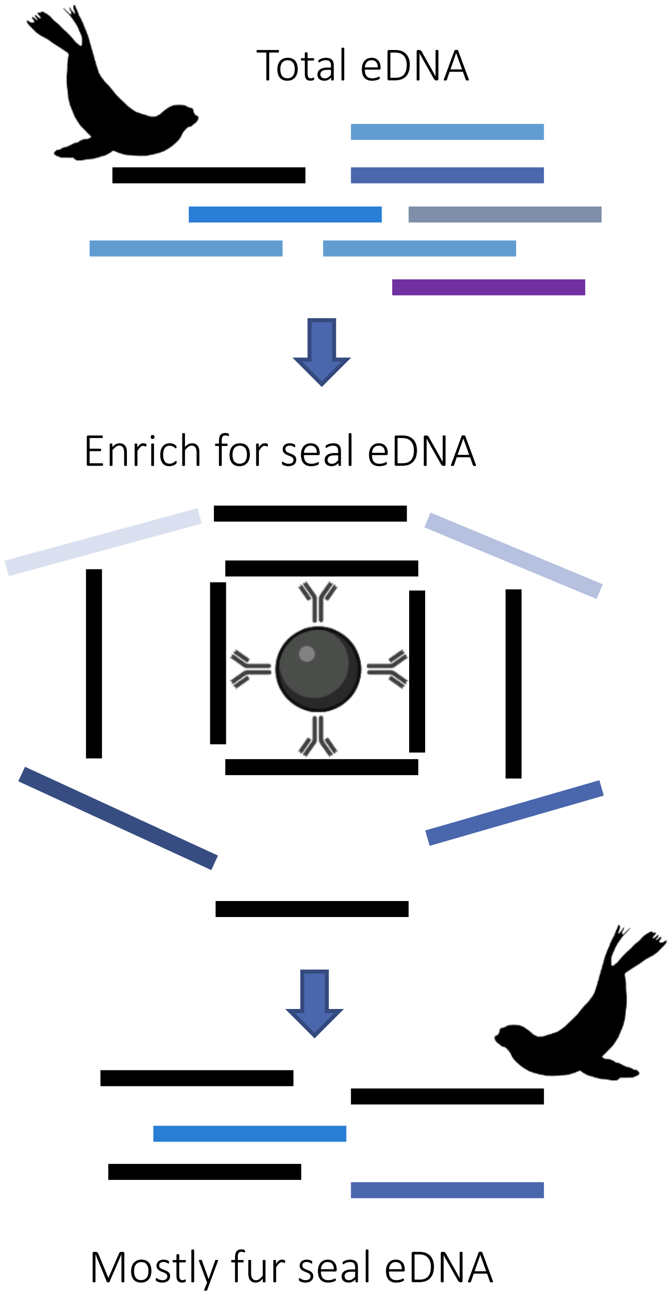
- Monitor population diversity
- Snapshot gene flow over time
- Potentially genetic identify drift, selection, other changes
- Haplotypic diversity possible

Can we get full mitogenomes?



Baited capture of eDNA data

- Capture of entire seal mtDNA genome from environmental DNA
  - Baited capture with biotinylated oligonucleotide probes complementary to target DNA sequences
  - “Fishes out” seal eDNA
  - Can be more expensive than amplicons, ($120 NZD/sample)

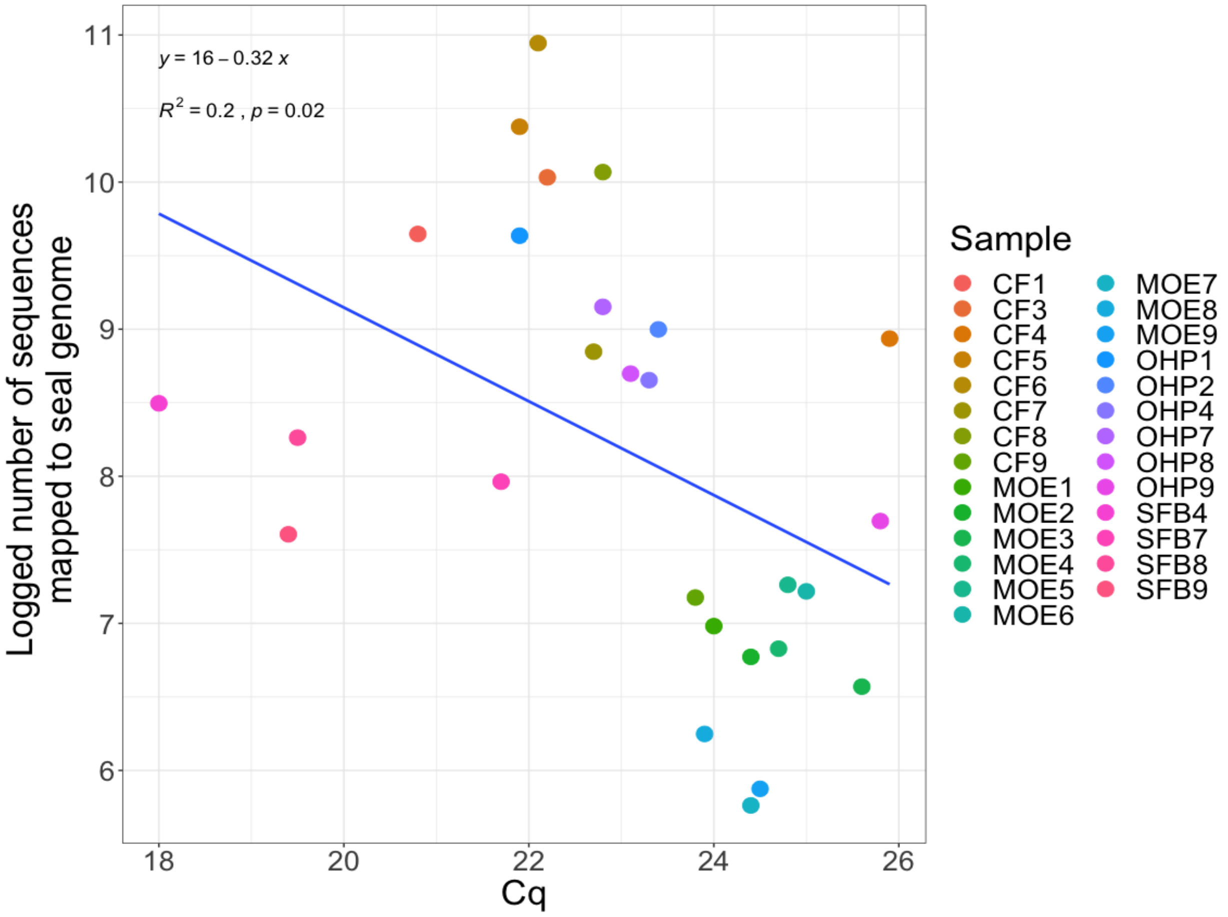


Whole Mitogenome Results

(Cytochrome B results in preprint)

Seal Mitogenome Capture

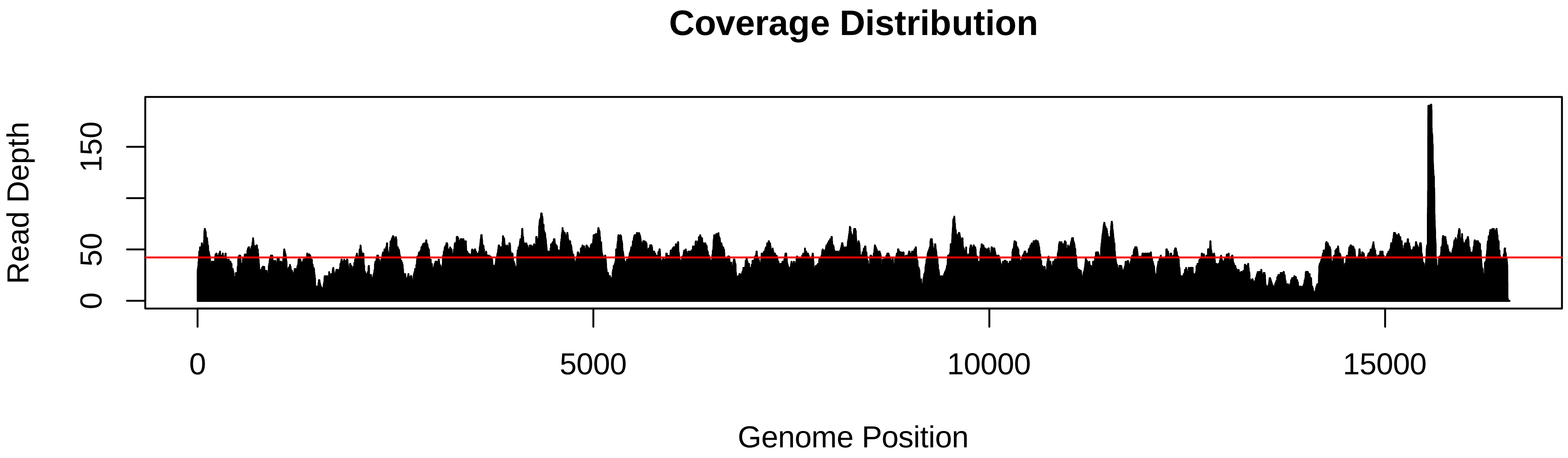
- Successful for some samples (n=27/40)
- Some sites worked better than others
- Minimum of 1x10^3 copies/µL of the target eDNA needed to reliable mitogenome recovery



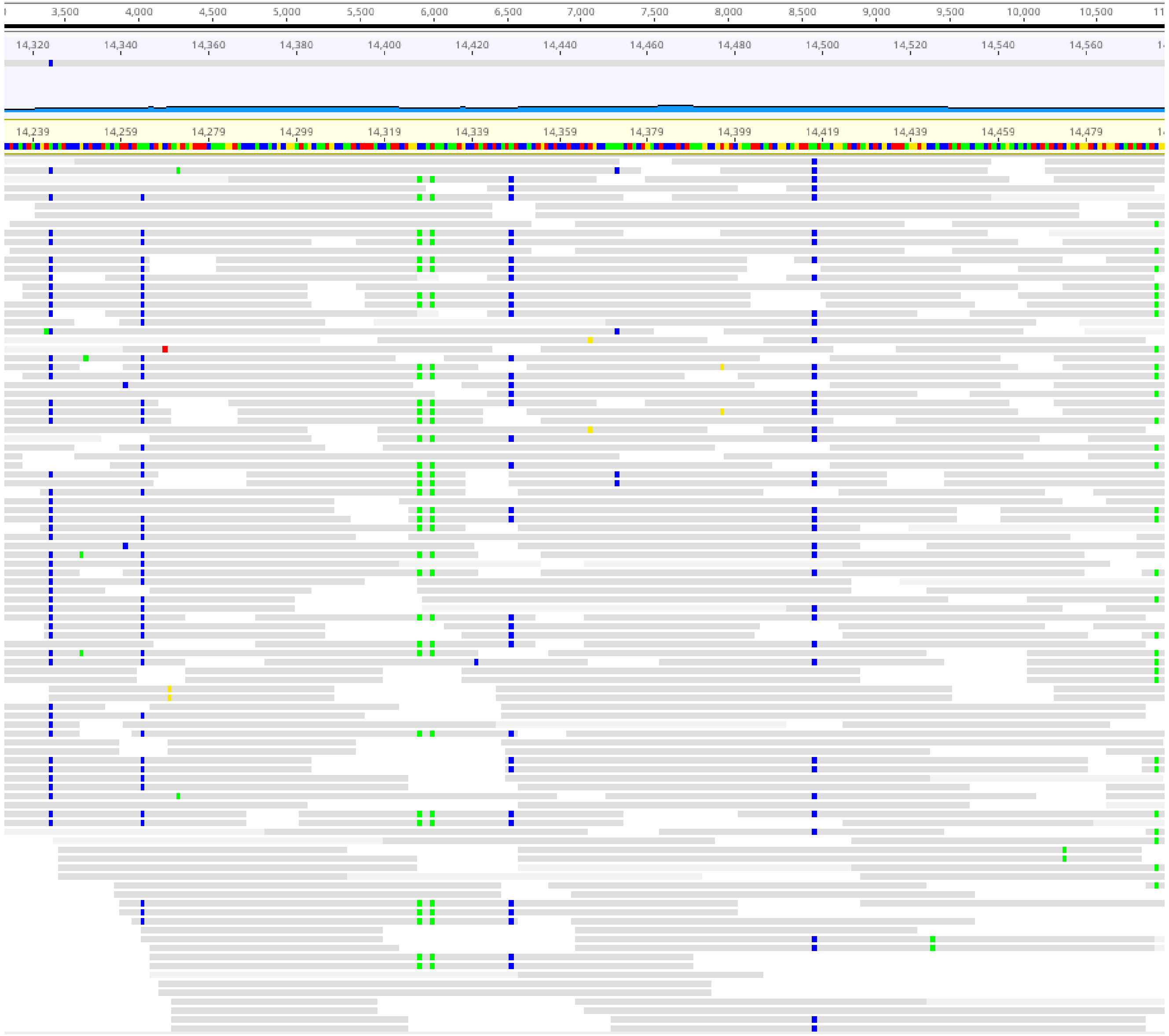
More DNA

Less DNA

Seal Mitogenome Capture



Sample 3. Cape Foulwind.
Coverage plot: 99.9% coverage, average depth 114.6 read depth, but most areas had a 40x depth.



Visualization of mapped reads to mitogenome

- Sample 21
- Moeraki Esplanade
- 15,299 reads mapped
- *CytB* region shown
- Color indicates SNP variation from reference
- Indicative of multiple individuals

Conclusions

Environmental DNA has potential

- Able to obtain whole mitogenome DNA from eDNA
- SNPs show eDNA samples likely contain DNA from multiple individuals
- Good non-invasive alternative to quickly sampling a location if you have enough eDNA
- Likely a broad-scale tool for identifying common genetic variation
  - But could grow to a tool for the genetic toolbox

Let’s Connect!

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Currently seeking collaborations and grant-writing opportunities

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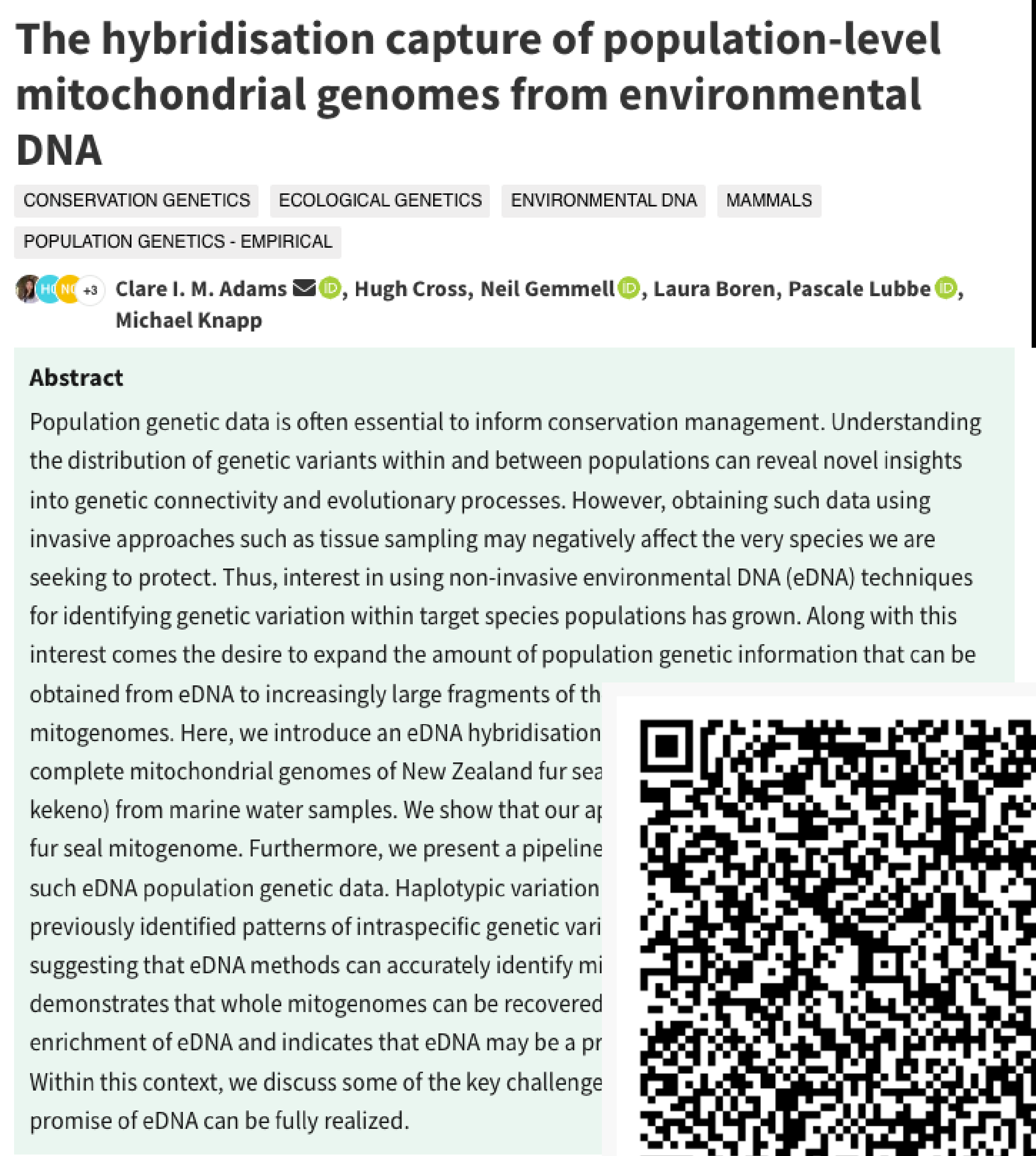
(in revision, see preprint here)



The hybridisation capture of population-level mitochondrial genomes from environmental DNA

CONSERVATION GENETICS · ECOLOGICAL GENETICS · ENVIRONMENTAL DNA · MAMMALS · POPULATION GENETICS - EMPIRICAL

Clare I. M. Adams, Hugh Cross, Neil Gemmell, Laura Boren, Pascale Lubbe, Michael Knapp

Abstract

Population genetic data is often essential to inform conservation management. Understanding the distribution of genetic variants within and between populations can reveal novel insights into genetic connectivity and evolutionary processes. However, obtaining such data using invasive approaches such as tissue sampling may negatively affect the very species we are seeking to protect. Thus, interest in using non-invasive environmental DNA (eDNA) techniques for identifying genetic variation within target species populations has grown. Along with this interest comes the desire to expand the amount of population genetic information that can be obtained from eDNA to increasingly large fragments of th
mitogenomes. Here, we introduce an eDNA hybridisation
complete mitochondrial genomes of New Zealand fur sea
kekeno) from marine water samples. We show that our a
fur seal mitogenome. Furthermore, we present a pipeline
such eDNA population genetic data. Haplotypic variation
previously identified patterns of intraspecific genetic vari
suggesting that eDNA methods can accurately identify mi
demonstrates that whole mitogenomes can be recovered
enrichment of eDNA and indicates that eDNA may be a pr
Within this context, we discuss some of the key challenge
promise of eDNA can be fully realized.

Seal Mitogenome Capture

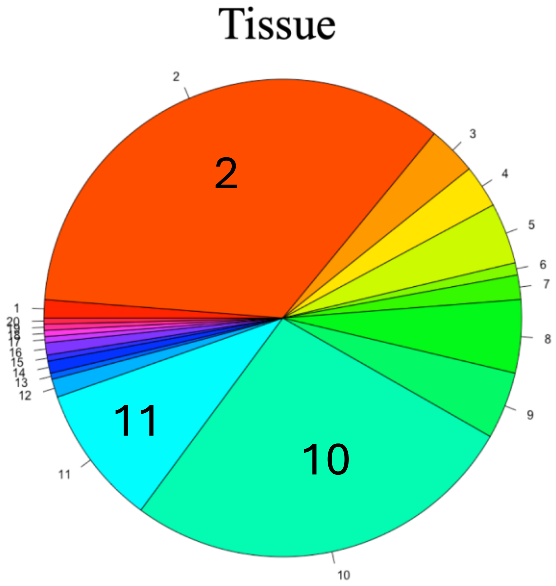
- Successful for some samples
- Some sites worked better than others

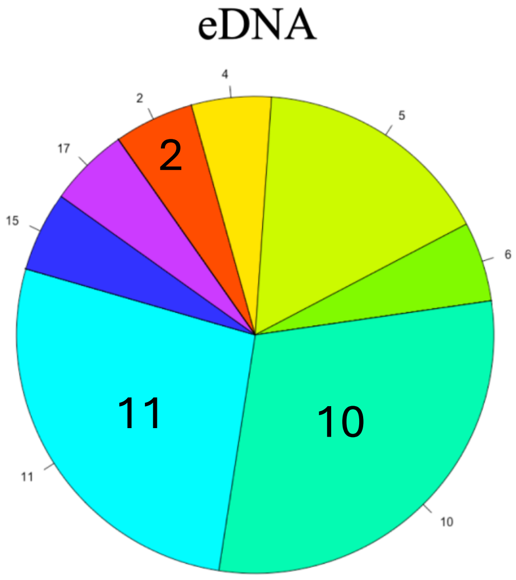
	Average Number of Reads Mapped (±St. Dev)	Average Coverage (±St. Dev)	Average Read Depth (±St. Dev)
Cape Foulwind	21,963.89 ± 16,941.58	99.18 ± 2.05	115 ± 92.04
Moeraki Esplanade	840.44 ± 404.14	73.52 ± 18.80	3.93 ± 2.08
Ohau Point	11,151.78 ± 6272.15	99.81 ± 0.10	58.04 ± 33.00
Sandfly Bay	2,852.56 ± 1149.71	94.92 ± 8.68	14.15 ± 5.15
Total	9,202.17 ± 12,088.75	91.86 ± 14.76	47.87 ± 64.65

Cytochrome B Results

Cytochrome B

- → Able to identify SNPs
- → Three major haplotypes identified with previous tissue samples were also identified with our eDNA





Cytochrome B – Estimated Haplotypes/Sample

Sample	Estimated Minimum	Included Haplotypes	Other Possible Haplotypes
Cape Foulwind 1	1	11	
Cape Foulwind 2	4	4,5,11,10	1,2
Cape Foulwind 3	3	5,10,11	1,2
Cape Foulwind 4	2	10,11	1,2
Cape Foulwind 5	4	4,5,11,10	1,2
Cape Foulwind 6	1	2	none
Cape Foulwind 7	3	5,11,10	1,2
Cape Foulwind 8	3	2,5,11	unclear
Ohau Point 1	2	10 [1 or 2]	1,2
Ohau Point 2	2	10 [1 or 2]	1,2
Ohau Point 3	2	[1 or 2], [8 or 10]	1,2,8,10
Ohau Point 4	2	6,17	1,2,8,10
Ohau Point 5	4	6,10,11,15	1,2,7
Ohau Point 6	3	5,10,11	1,2
Ohau Point 7	2	10,11	1,2,7
Ohau Point 8	4	2,10,15,17	1,7

Cytochrome B – Consistent presence of haplotypes across sampling sites

	Haplotype	Cape Foulwind - Historic Presence	Ohau Point - Historic Presence	Cape Foulwind - eDNA presence	Ohau Point - eDNA presence
	1		Yes	Possible	Possible
✳	**2**	Yes	Yes	Yes	Yes
	4		Yes	Yes	
	5		Yes	Yes	Yes
	6		Yes		Yes
	8		Yes		Possible
✳	**10**	Yes	Yes	Yes	Yes
✳	**11**	Yes	Yes	Yes	Yes
	15				Yes
	17				Yes

Cytochrome B – Haplotypes 15 and 17?

- Haplotypes 15 and 17 had previously only been found in Otago
- We find Haplotypes 15 and 17 at Ohau Point
- Would help support a more northward distribution of NZ fur seals
  - Gene flow?

NOT ENOUGH EVIDENCE
MORE TESTING NEEDS TO BE DONE