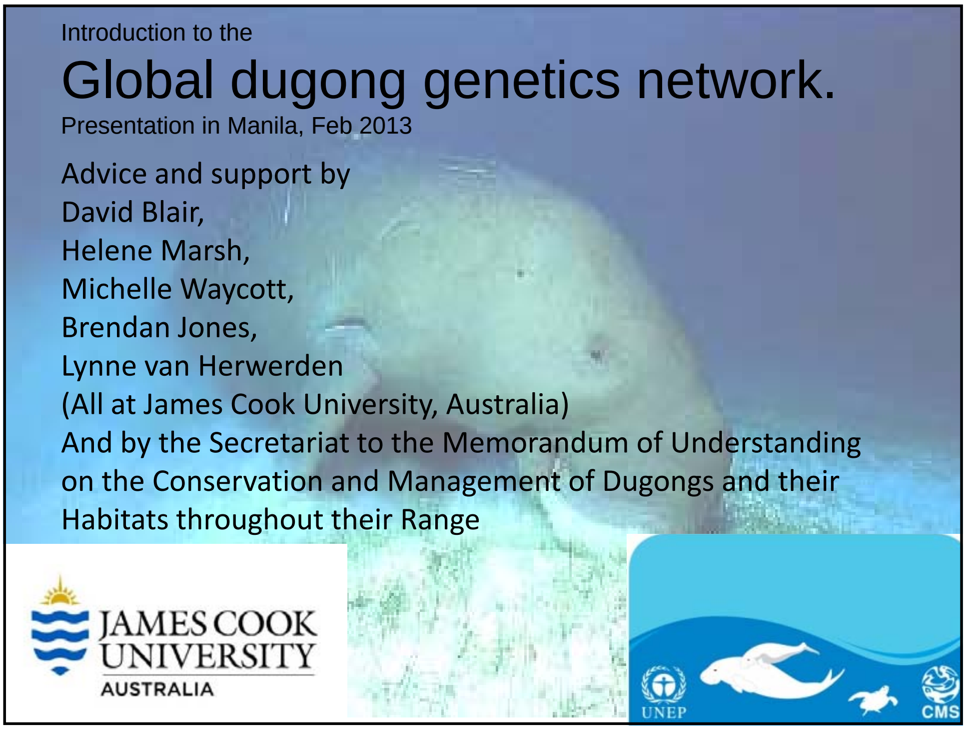

Introduction to the

# Global dugong genetics network.

Presentation in Manila, Feb 2013

Advice and support by
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Lynne van Herwerden
(All at James Cook University, Australia)
And by the Secretariat to the Memorandum of Understanding on the Conservation and Management of Dugongs and their Habitats throughout their Range

JAMES COOK UNIVERSITY
AUSTRALIA

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## Why do we want to study genetics of dugongs, and how will this help dugong conservation?

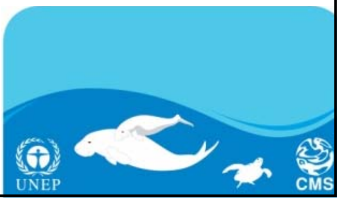
- Genetic history of all animal species (and of people) is recorded in their DNA,
- Sampling can often be relatively non-invasive;
- Genetic data can provide;
  - insights into the evolutionary history and biogeography of the species.
  - estimates of population sizes through evolutionary time,
  - estimates of the extent to which dugongs travel between populations (i.e. gene flow),
  - indications of inbreeding and “genetic health”,
  - information about “mating systems”,

From a management point of view, such information can…

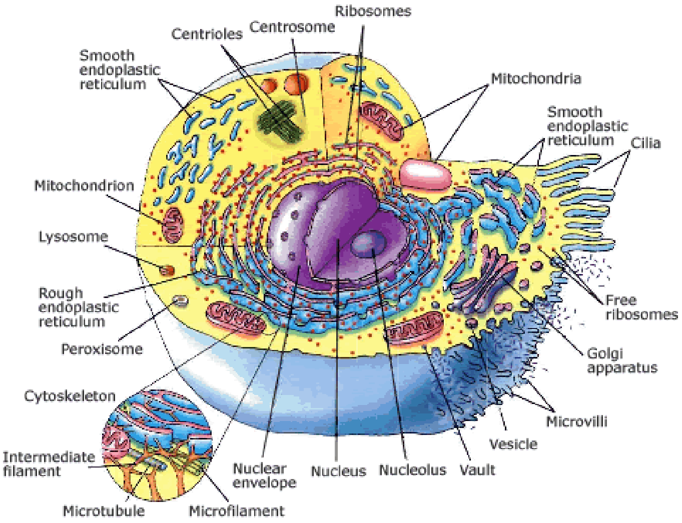
- Indicate whether reduced local populations might be replenished by dugongs from elsewhere,
- indicate whether there are distinct “stocks” of dugongs in different parts of the species’ range,
- provide insights into environmental circumstances, such as glacial cycles and sea-level changes, that have influenced dugong populations in the past. This might allow us to predict future changes.
- indicate whether inbreeding might be a problem in reduced populations.

Recognising this, the dugong MoU Secretariat is supporting the development of a network of scientists in range states who can obtain samples suitable for this work (usually small pieces of skin) and who are willing to contribute information to a range-wide study.

Although the lead institution is James Cook University in Australia, any person wishing to do genetic analyses is their own country is provided with the necessary technical information to produce compatible and comparable data.



Now for some technical stuff. We use DNA from two different parts of each cell.

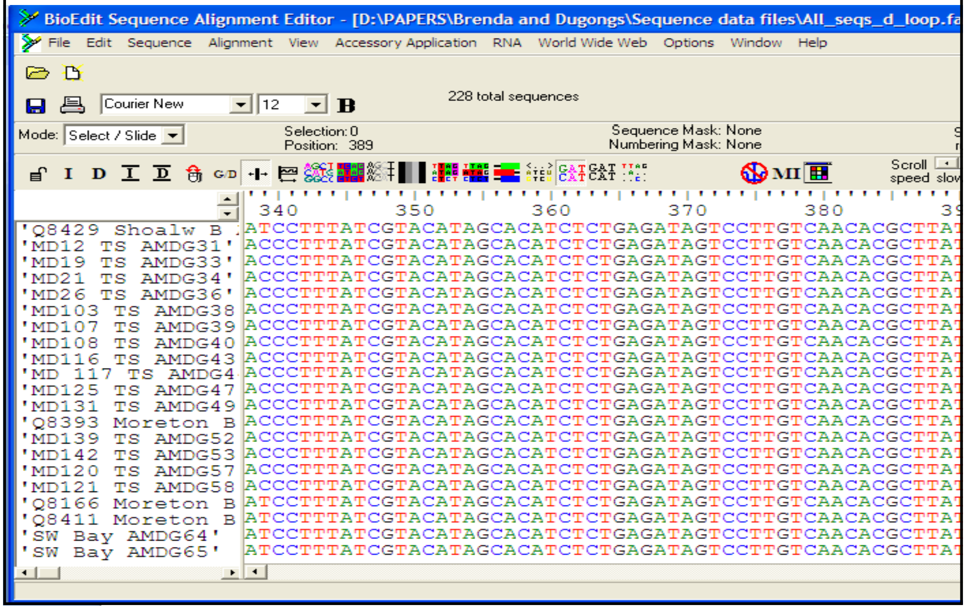


Mitochondria (mt) have their own genome which is maternally inherited (inheritance analogous to transmission of surnames).

We obtain DNA sequence from part of the mitochondrial genome for each individual dugong and compare the sequences with each other to obtain information on:

- Historical processes due to range changes, barriers etc,
- Estimates (rough) of historical population sizes,
- Gene flow
- Genetic diversity

This is what the mitochondrial sequence data looks like…



228 total sequences

Mode: Select / Slide

Selection: 0
Position: 389

Sequence Mask: None
Numbering Mask: None

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                  340          350          360          370          380
'Q8429 Shoalw B  ATCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD12 TS AMDG31' ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD19 TS AMDG33' ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD21 TS AMDG34' ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD26 TS AMDG36' ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD103 TS AMDG38 ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD107 TS AMDG39 ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD108 TS AMDG40 ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
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'MD131 TS AMDG49 ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'Q8393 Moreton B ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'MD139 TS AMDG52 ACCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
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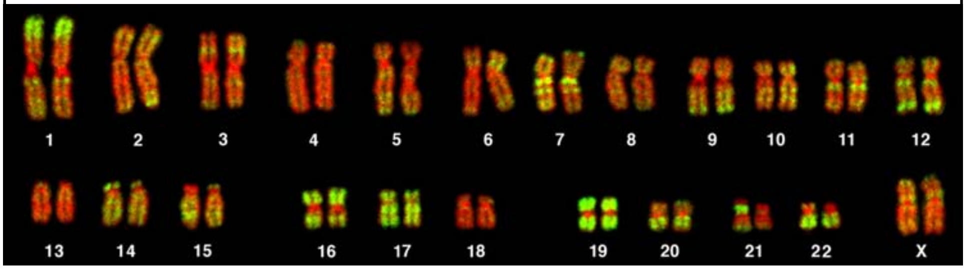
'Q8411 Moreton B ATCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'SW Bay AMDG64'  ATCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
'SW Bay AMDG65'  ATCCTTTATCGTACATAGCACATCTCTGAGATAGTCCTTGTCAACACGCTTA
```

Nuclear genomes:

- Are huge, complex and still not fully understood,
- Contain many genes and gene families,
- Are inherited bi-parentally (each individual has two complete sets of chromosomes, one inherited from each parent. Genes on these are shuffled and then one copy of each chromosome is passed into each egg or sperm.



Nuclear genomes:
- Many genes differ slightly from individual to individual,
- For about 10 genes, we identify which variant is present in each individual,

From the nuclear gene information, we can obtain:
- estimates of the extent to which dugongs travel between populations (i.e. recent and ongoing gene flow),
- indications of inbreeding and "genetic health",
- information about "mating systems",

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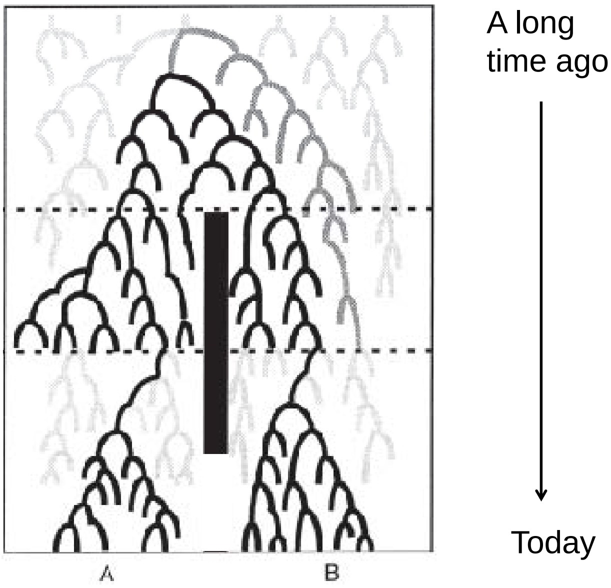
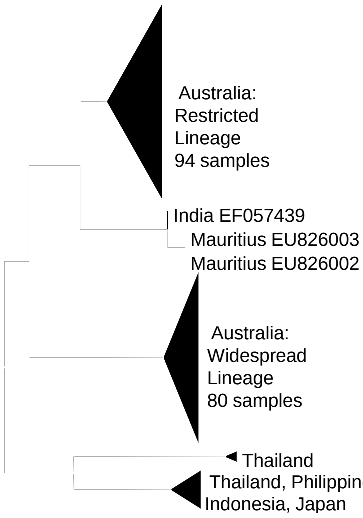
**Examples:**

Mt sequences in populations separated by barriers will eventually form distinct clusters (mutation and random extinction of lineages). If the barrier disappears, the pattern we see in mtDNA tells us that it used to be there: Phylogeography.

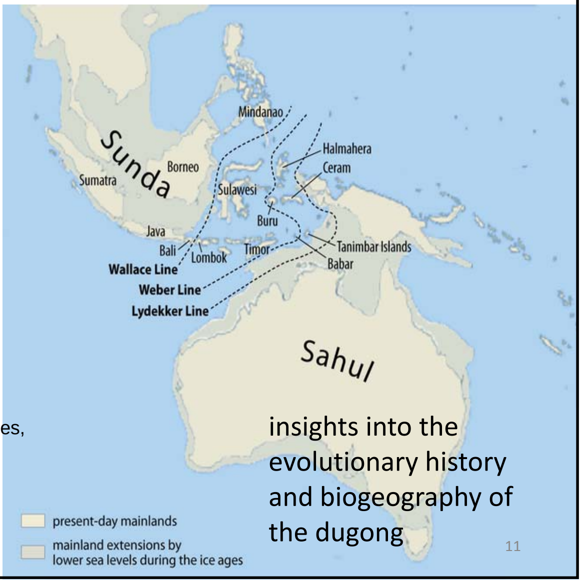


Based on Schaal B A , Olsen K M PNAS 2000;97:7024-7029

## Mitochondrial sequences inform us about past processes

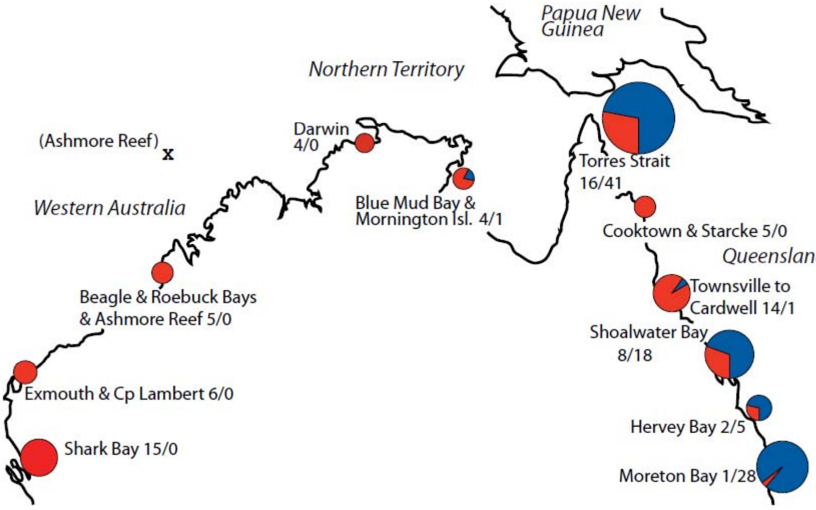


Phylogenetic tree based on 200 mitochondrial DNA sequences.



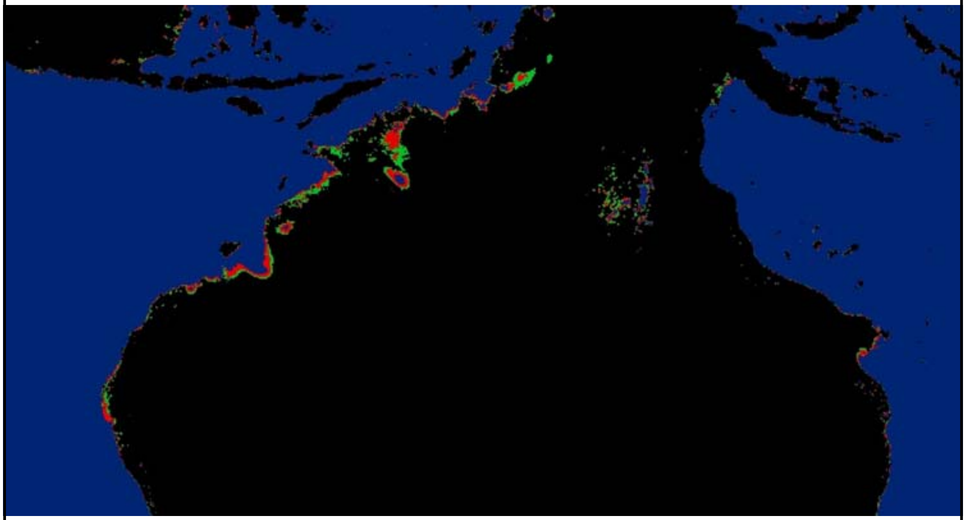
insights into the evolutionary history and biogeography of the dugong

## Two “mitochondrial lineages” in Australia



## Sea-level changes, 18,000 ybp–present day

Maps provided by J. Guinotte



**Green (0-15m) , Red (15-40m), Blue (>40m), Black (terrestrial)**

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## Sea-level changes, 18,000 ybp–present day

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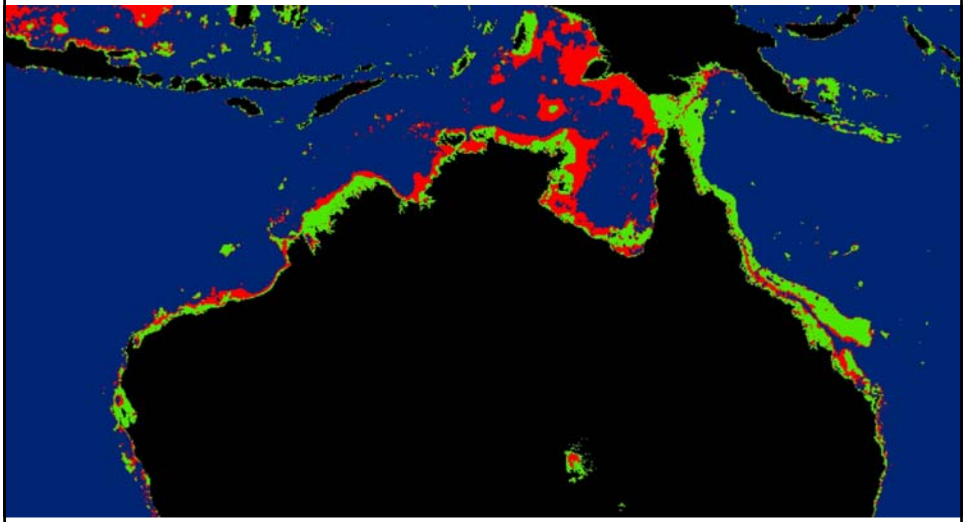

**Green (0-15m) , Red (15-40m), Blue (>40m), Black (terrestrial)**

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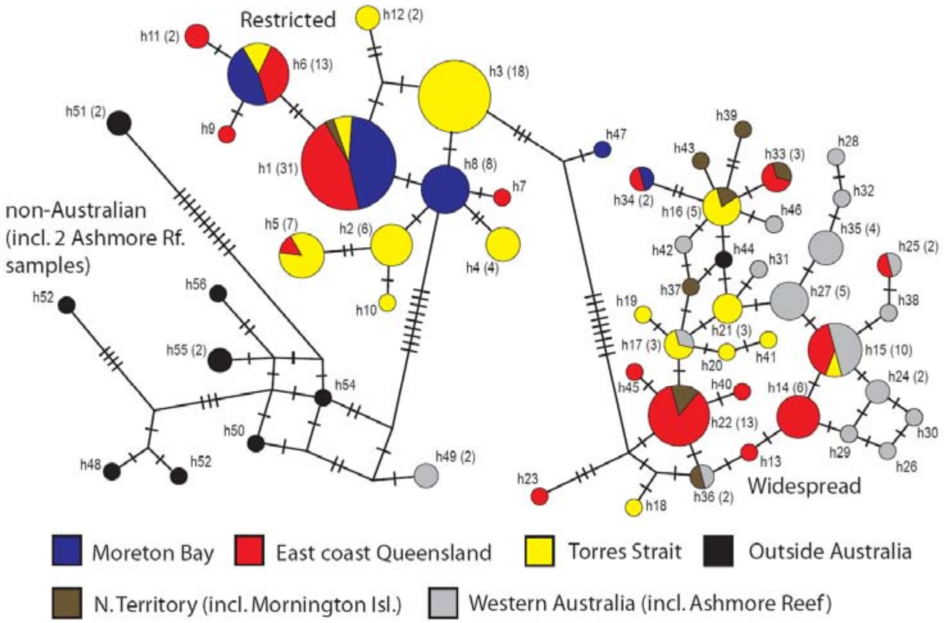
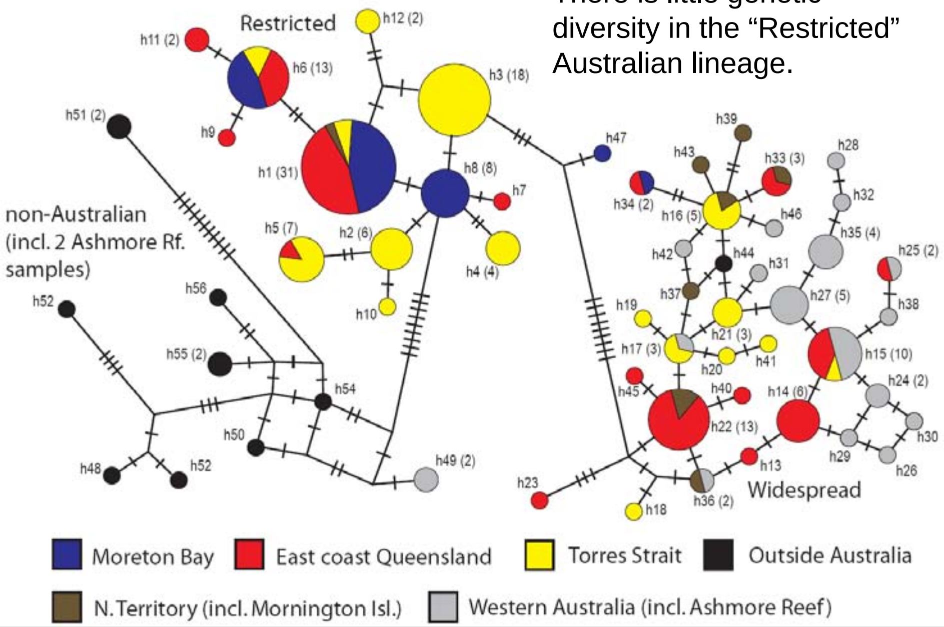
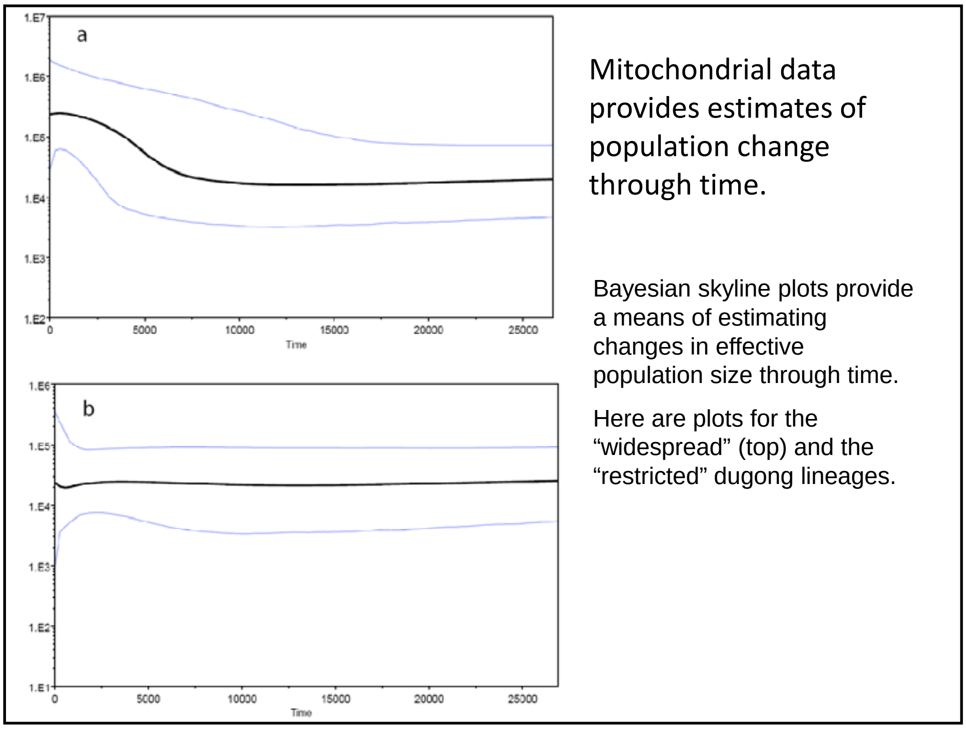


There is little genetic diversity in the “Restricted” Australian lineage.

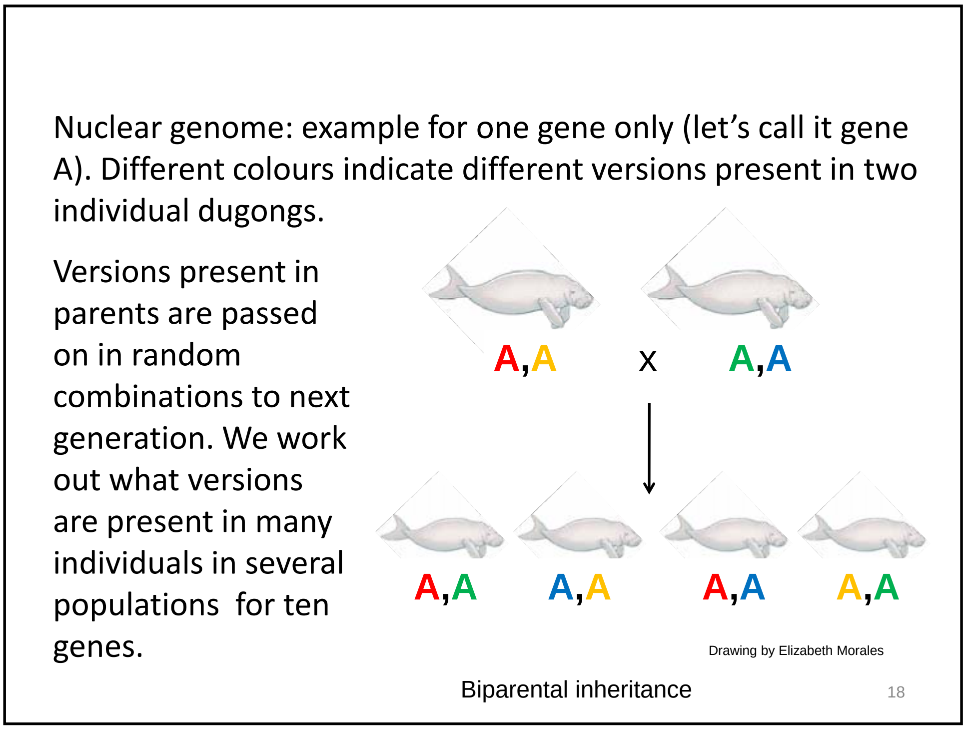




Mitochondrial data provides estimates of population change through time.

Bayesian skyline plots provide a means of estimating changes in effective population size through time.

Here are plots for the "widespread" (top) and the "restricted" dugong lineages.

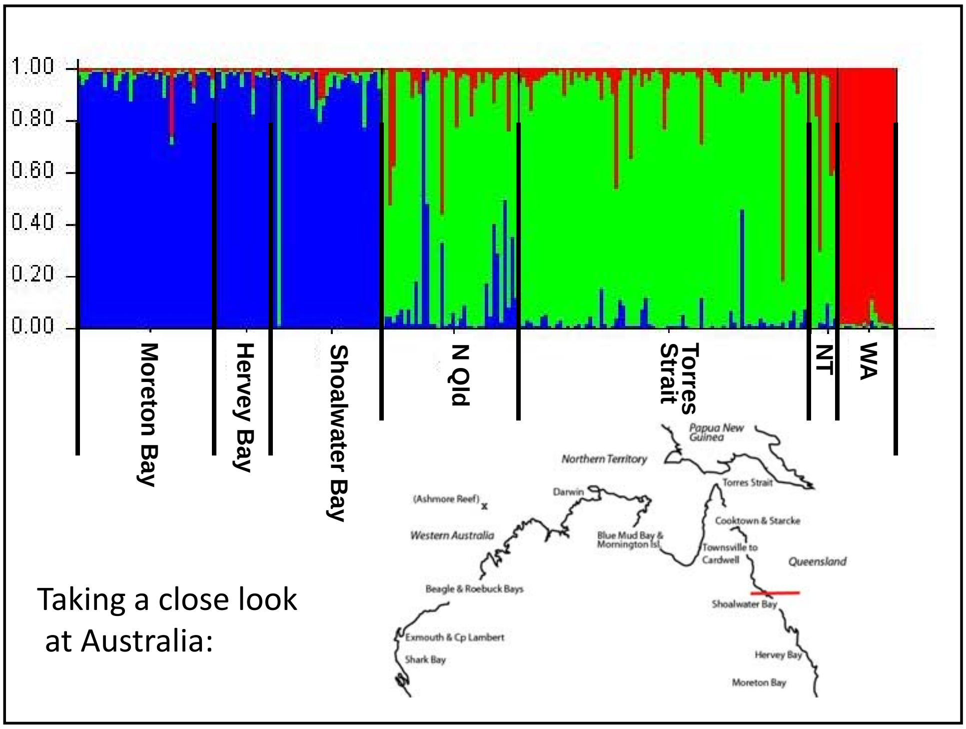


Nuclear genome: example for one gene only (let's call it gene A). Different colours indicate different versions present in two individual dugongs.

Versions present in parents are passed on in random combinations to next generation. We work out what versions are present in many individuals in several populations for ten genes.

Drawing by Elizabeth Morales

Biparental inheritance



Taking a close look at Australia:

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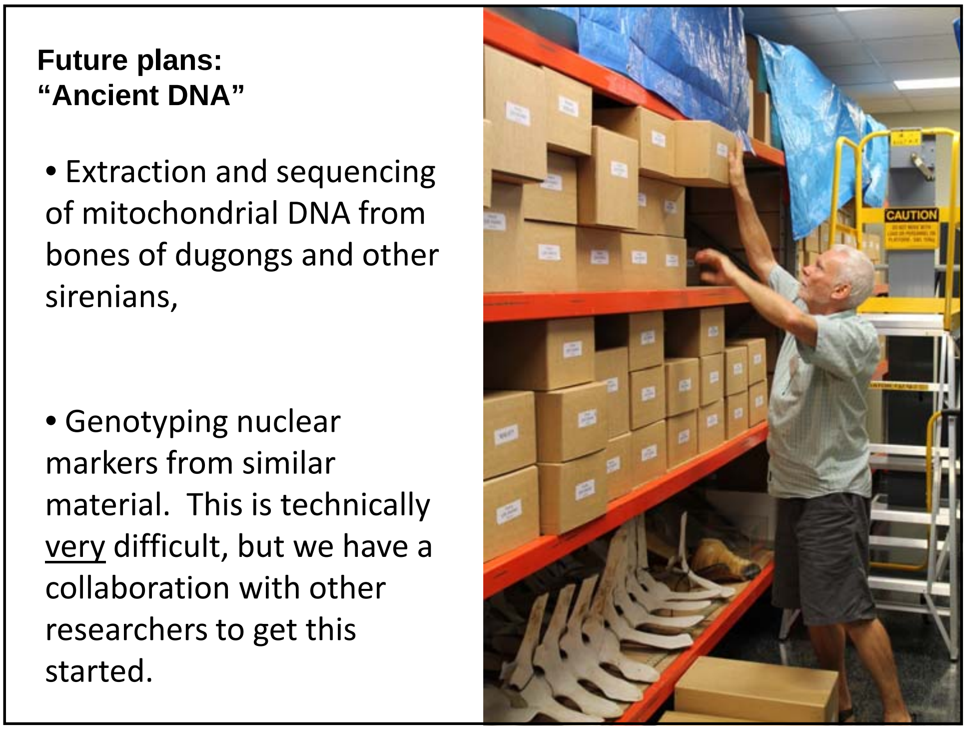
Some difficulties with genetic approaches;

- Time-scales
  - mitochondrial data can give little or no information on recent events (perhaps within 1000 years – depends on mutation rates),
  - nuclear markers can give information on more recent events, but probably not within the last few generations,
- Estimates of effective population size must be within very broad confidence limits,
- Sample sizes for robust inference of gene flow,
- Cost and technical expertise,
- The “CSI factor” and unrealistic expectations.



**Future plans:**
**"Ancient DNA"**

- Extraction and sequencing of mitochondrial DNA from bones of dugongs and other sirenians,

- Genotyping nuclear markers from similar material. This is technically very difficult, but we have a collaboration with other researchers to get this started.

Thank you