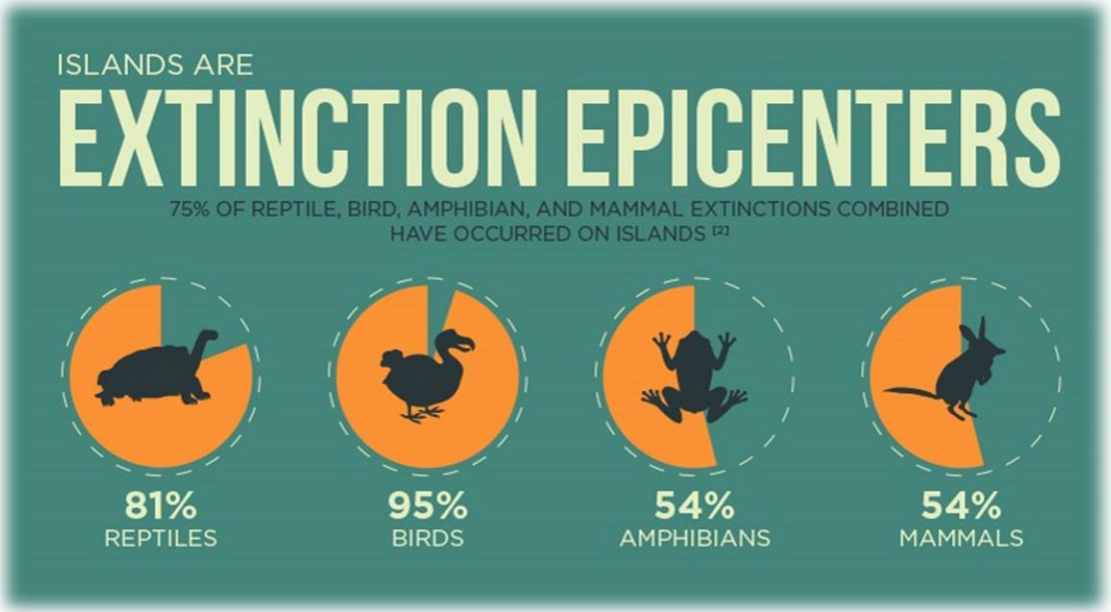
Saving Nature Faster:
the Power of People

Dr Sally Bryant
Friends of TMAG
15 Nov 2023

Islands all over the world are centers of species extinction.

Tasmania is one of those islands.



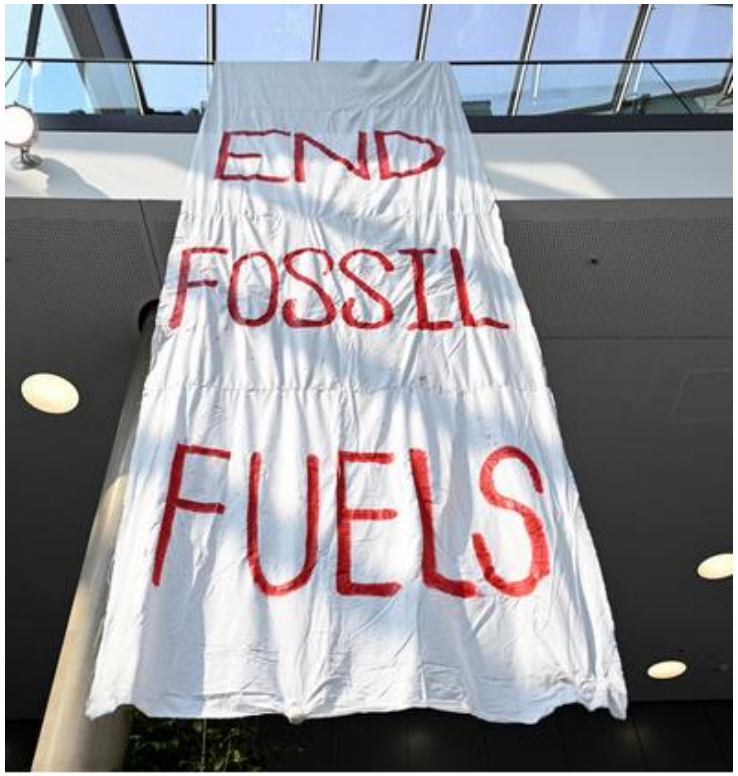
THREATENED VALUES IN TASMANIA
493 plant species
226 animal species
39 vegetation communities
14 Key National Threatening Processes

CONSERVATION STRATEGIES
Threatened Species Strategy 2000
17 Flora Recovery Plans – 129 species (26%)
12 Fauna Recovery Plans – 54 species (23%)

It’s not what nature can do for you –

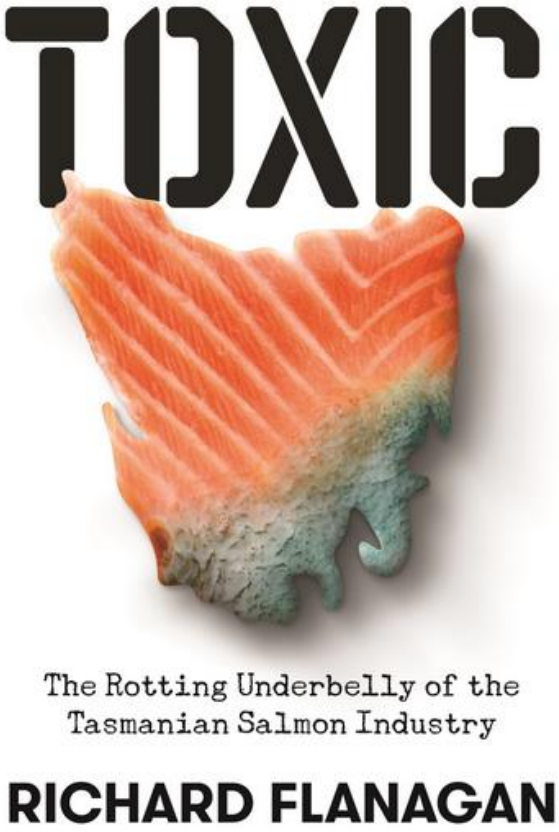
but what you can do for nature

Global Issues



Local Issues

Brand Issues



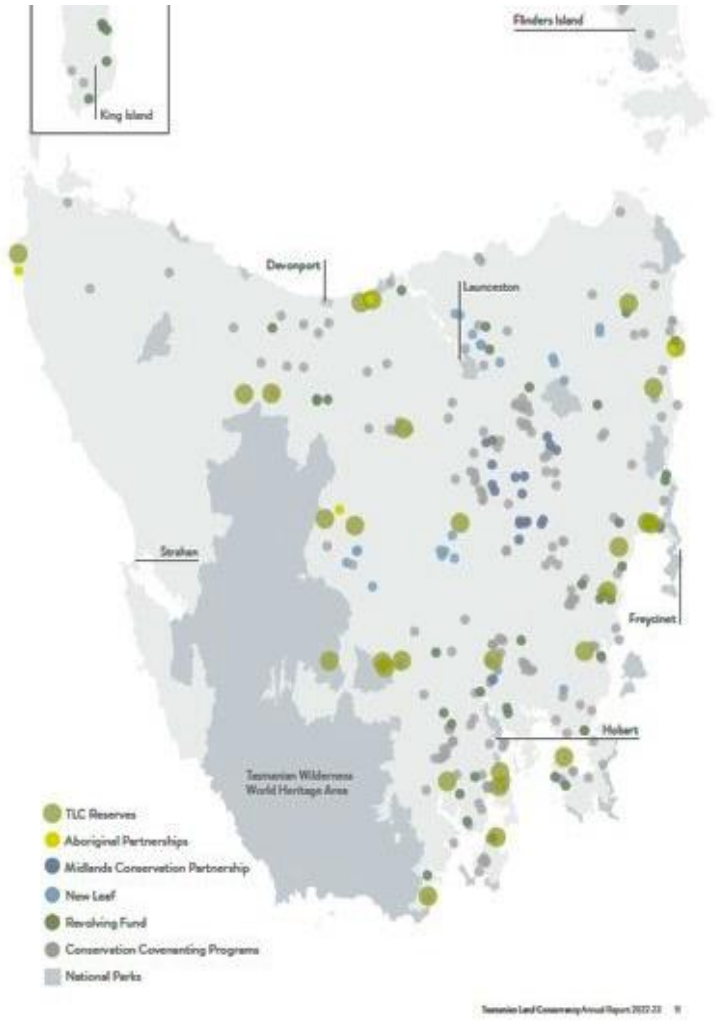
Resource Issues

Fearless Science

WELL-DIRECTED SCIENCE IS ESSENTIAL IN NAVIGATING A PATH FORWARD AT THIS TIME OF CLIMATE, BIODIVERSITY & EXTINCTION CRISES. HOW DO WE ENSURE THAT RESEARCH IS RELEVANT AND CLEARLY COMMUNICATED, AND THAT IT FORMS THE FOUNDATION OF TASMANIAN ENVIRONMENTAL POLICY. 5 GREAT MINDS DISCUSS.

- *Eloise Carr - The Australia Institute*
- *Eve Lazarus - Landscape Recovery Foundation*
- *Charley Gros - Bob Brown Foundation*
- *Sally Bryant AM- Wildlife Ecologist*
- *Eric Woehler OAM- Shore- and Sea-bird Ecologist*

Tasmanian Land Conservancy



WORKING WITH LANDHOLDERS

Land for Wildlife	WildTracker
769 Properties	312 Properties
26,731 HA Managed for conservation	5,166 HA Registered for WildTracker
148 Participants in workshops 22/23	213 Participants in 22/23
Land for Wildlife program achievements at a glance:	153,896 images tagged, top three threatened species:
63 New properties registered in 22/23	01 Tasmanian devil
09 Volunteer assessors across the state	02 Eastern barred bandicoot

Bequests and Philanthropy

Do Something Now

If Not You – Who ?

If Not Here – Where?

If Not Now – When ?

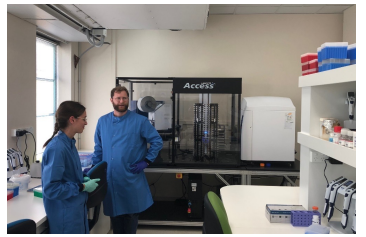
THANK YOU

Biological collections
as research infrastructure for Conservation Science

Andrew Young

CSIRO National Research Collections






Collections – early tools for biological science

ROYAL SOCIETY OPEN SCIENCE

royalsocietypublishing.org/journal/rsos

Research

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Botanical memory: five centuries of floristic changes revealed by a Renaissance herbarium (Ulisse Aldrovandi, 1551–1586)

Fabrizio Buldrini[1,2], Alessandro Alessandrini[3], Umberto Mossetti[2], Enrico Muzzi[4], Giovanna Pezzi[1], Adriano Soldano[5] and Juri Nascimbene[1]

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[5]Independent Researcher, Largo Brigata Cagliari 6, 13100 Vercelli, Italy

- Species discovery
- Taxonomy
- Medicines
- Food and fibre
- Environmental indicators

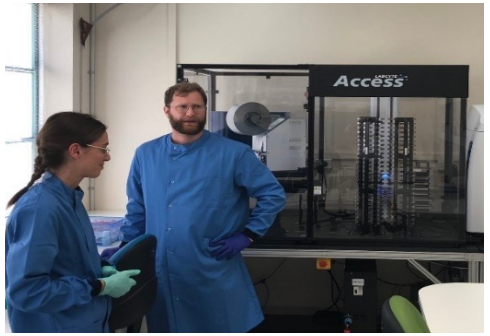
Ulisse Aldrovandi’s herbarium (1551–1586)

Biological collections today

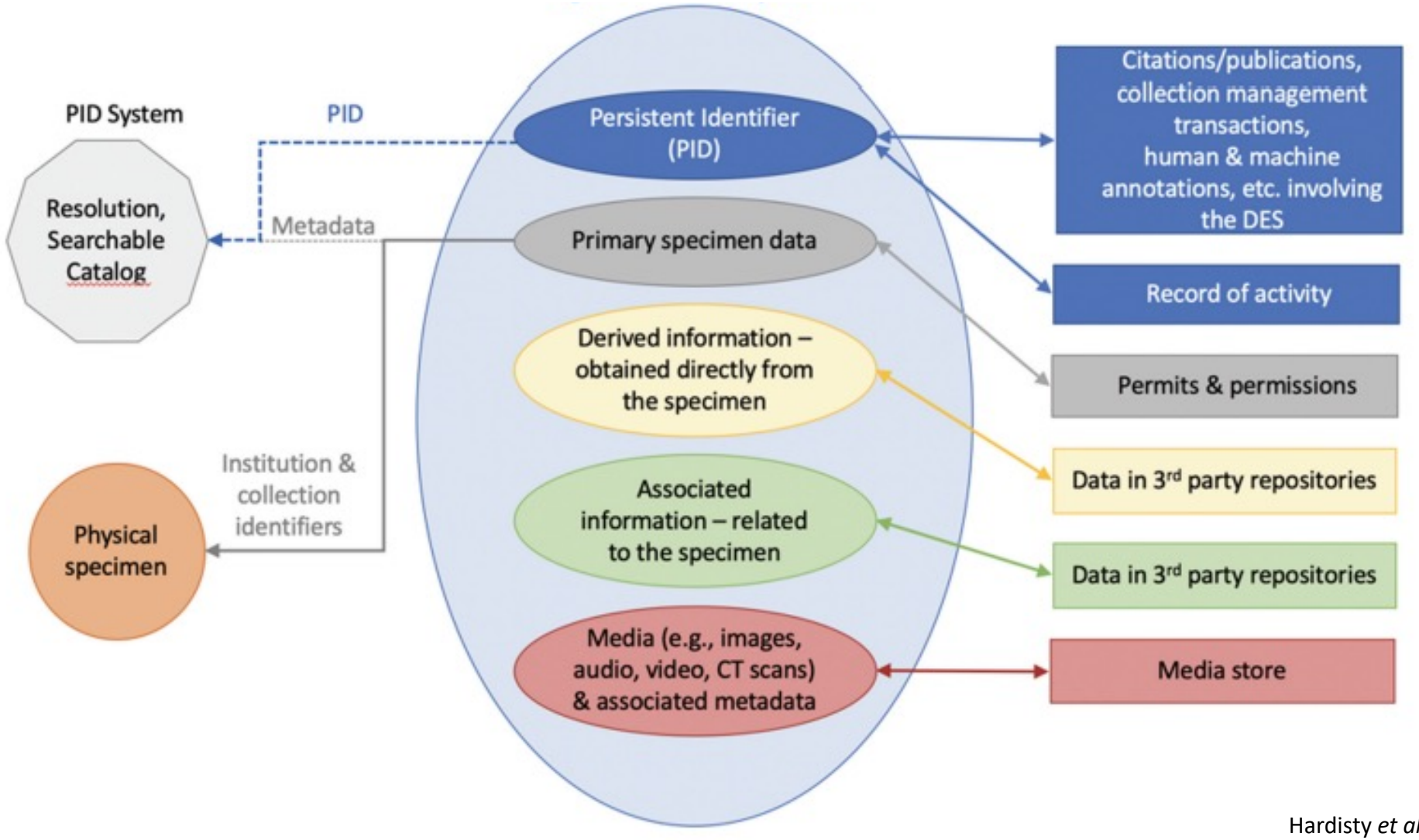
- 1000+ natural history collections
- 2+ billion specimens globally
- Biological breadth
- Environmental scope
- Temporal depth
- Taxonomic certainty
- Object-based point of truth

Transformational science and technology

1. Digital mobilisation & integration of specimen data
    - iDigBio, DiSSCo, ALA, GBIF
    - “Digital Extended Specimen” concept
2. New analytical tools & data layers
    - High resolution 2D & 3D images
    - Genomics, transcriptomics & meta-barcoding
    - AI/ML-based digital trait extraction
3. New types of collections
    - Tissues, blood, DNA
    - Environmental samples



The “Extended Digital Specimen” concept



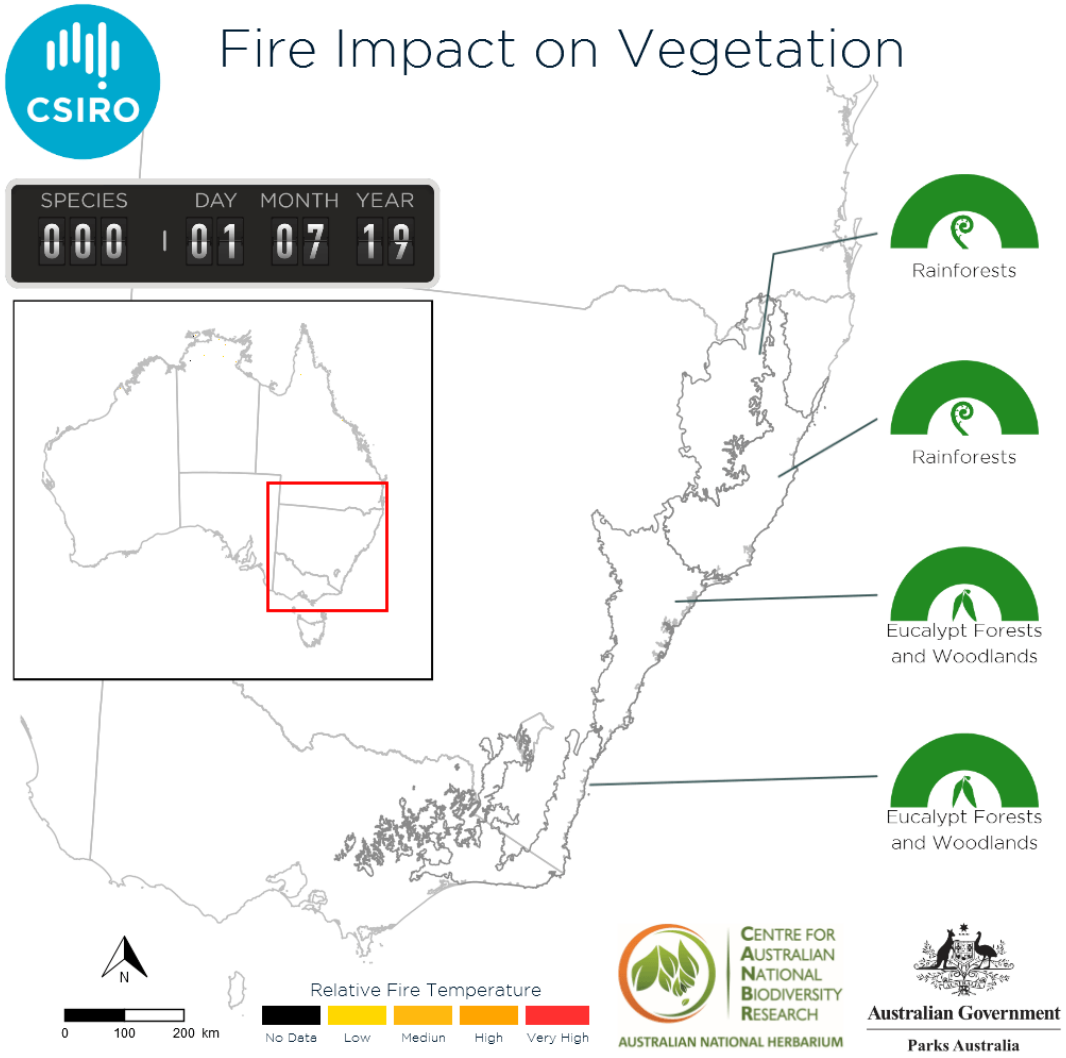
Hardisty *et al.* 2022 Bioscience 72:10

Applications in conservation science

- **Catastrophic events** - occurrence and distribution data
- **Measuring ecological processes** - reference sequences for eDNA analysis
- **Climate change response** - time series trait information
- **Cryptic species management** - genomic data for molecular ecology

Catastrophic events- Black Summer bushfires

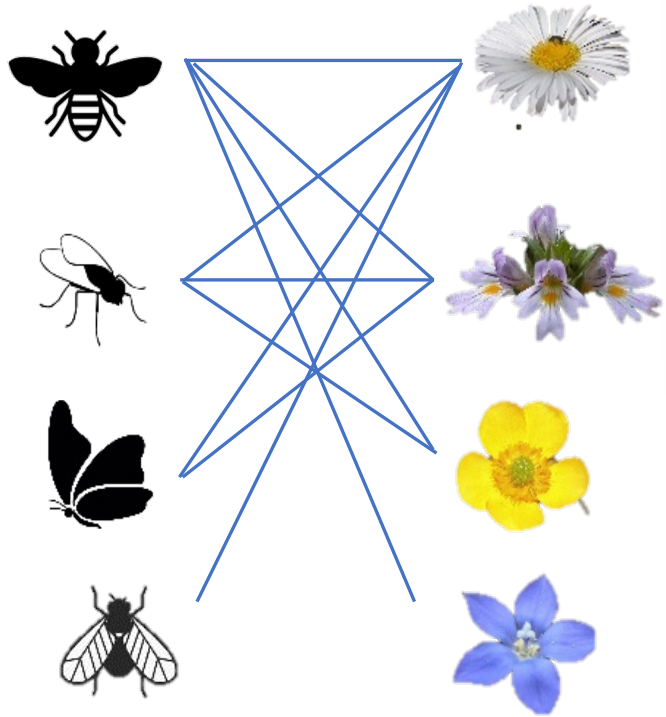
- 2019-2020 bushfires burned 8 million hectares of vegetation across the south-east
- Unprecedented in the last 200 years – what's the impact, how will it recover?
- Intersected fire intensity models with geocoded herbarium specimen data
- Fire affected > 50% of known locations for 816 species of vascular plants
- 11 Australian bioregions, 17 major native vegetation groups
- Relictual Gondwanan rainforests particularly susceptible to regeneration failure



Godfree, R.C., Knerr, N., Encinas-Viso, F. *et al. Nat Commun* **12**, 1023 (2021). https://doi.org/10.1038/s41467-021-21266-5

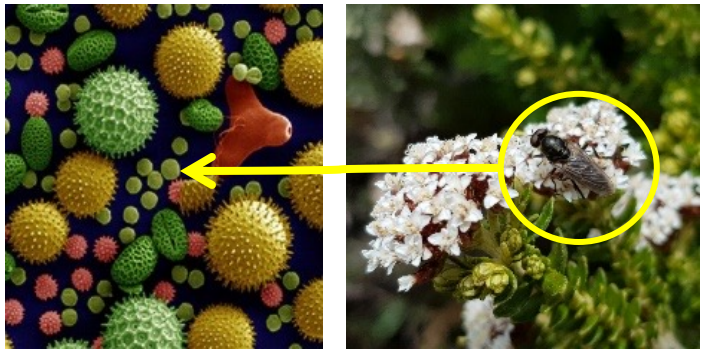
Ecological processes – alpine pollination networks

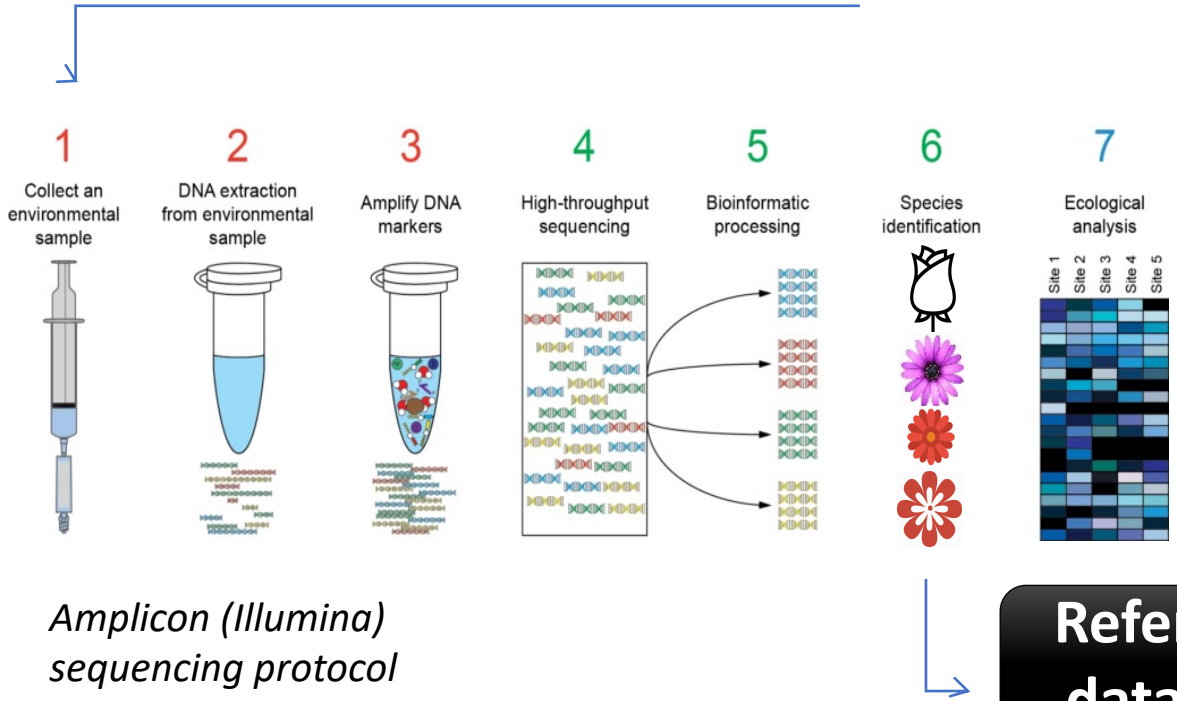
- Critical ecological process affected by climate change
- Pollination networks difficult to measure and monitor using human observations
- Herbarium specimens used as DNA reference libraries for Victorian alpine species
- Genetic metabarcoding of pollen loads on field caught insects provide data on plant-pollinator interactions



Encinas-Viso *et al*. Mol. Ecol (2022) https://doi.org/10.1111/mec.16682

Pollen metabarcoding





Amplicon (Illumina) sequencing protocol

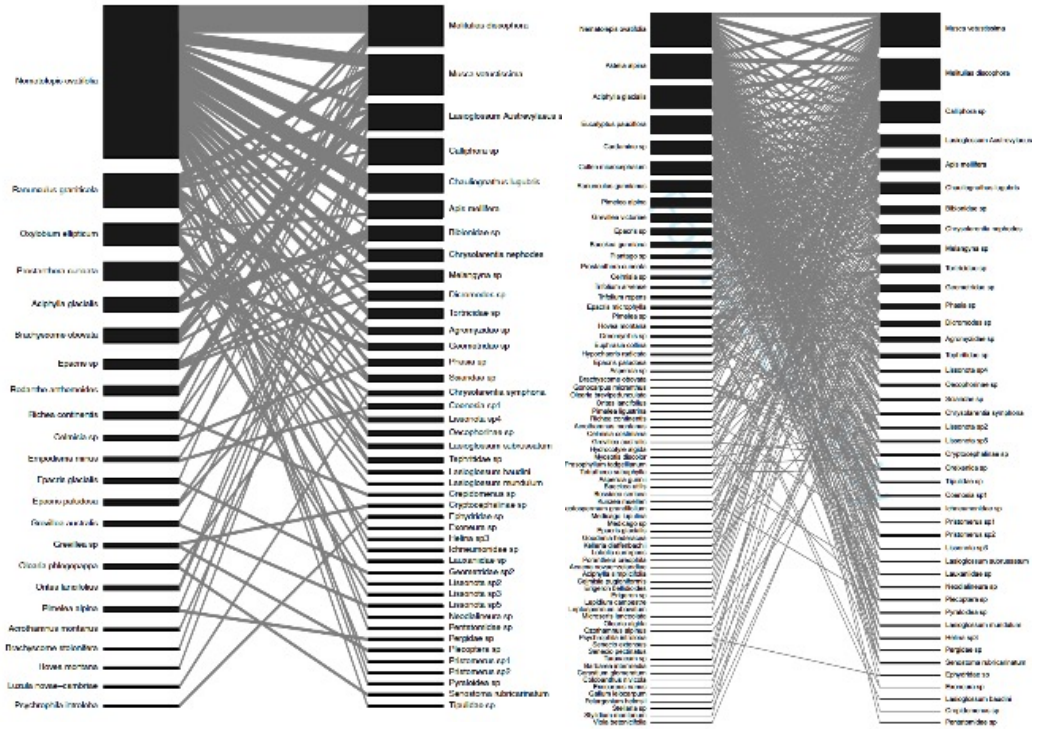
Reference database

Plant molecular markers :

- ***trnL***: plastid marker
- ***ITS2***: Nuclear ribosomal region

Environmental monitoring – alpine pollination networks

- Metabarcoding revealed 3 x more plant species and 5 x as many plant-pollinator interactions than human observations
- Exploring use of preserved insect specimens to reconstruct historical plant communities and pollination networks

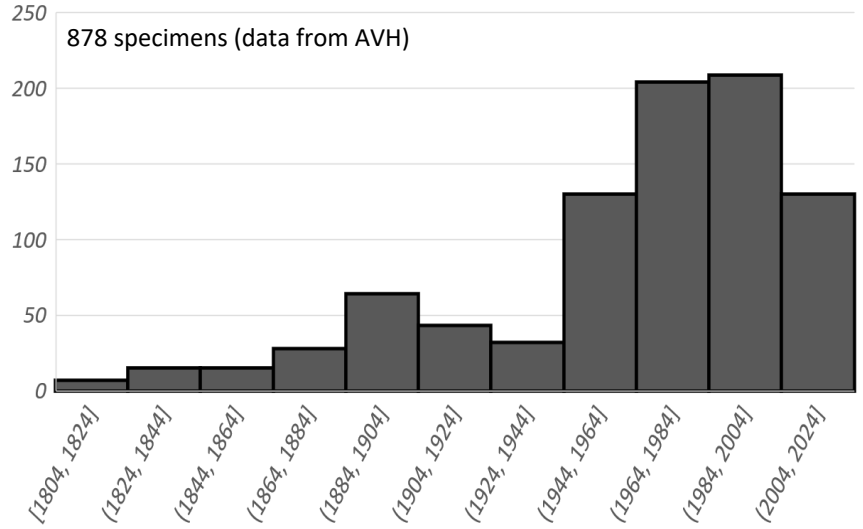


Encinas-Viso *et al*. Mol. Ecol (2022) https://doi.org/10.1111/mec.16682

Climate response – reproductive phenology

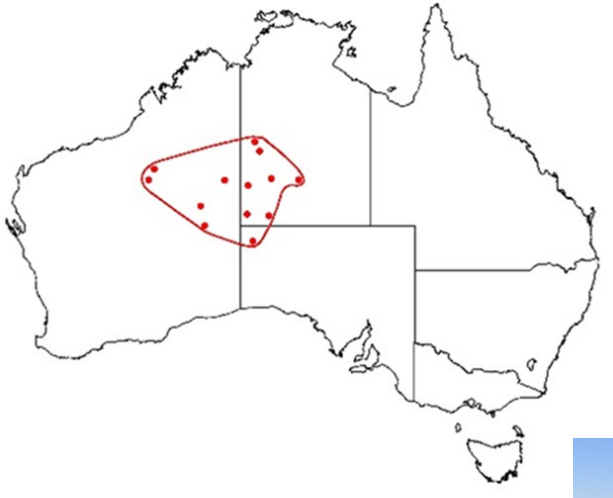
- Reproductive phenology important trait that determines fitness
- Also determines timing of local resource availability e.g. seeds
- Subject to environmental cues that are changing with climate warming
- Historical herbarium specimens track changes in flowering time
- AI-based digital trait extraction dramatically upscales these analyses

Leucochrysum albicans



Cryptic species management – Tjakuṟa ecology

- Large skink in the genus *Lopholis*
- Significant cultural value as an Aboriginal food source and a tjukupra (creation law) species
- Only known from 15 populations in and around Uluṟu Kata-Tjuṯa National Park
- IUCN listed as vulnerable
- Lives in communal burrows
- Little is known about movements, diet, community structure
- Genetic data from museum Tjakura specimens provided genomic information



David Thuo CSIRO, David.thuo@csiro.au – unpublished data

Cryptic species management – Tjakura ecology

- Working with Anangu people and Tjakura Rangers
- Sampled soil, latrines and scats around burrows
- DNA analysis is providing data on numbers of individuals, burrow structure and diet
- This information will be combined with local indigenous knowledge (two-way science) to inform Tjakura management

David Thuo CSIRO, David.thuo@csiro.au – unpublished data

Old dead rats… even more valuable than anticipated

MOLECULAR EVOLUTION

Old dead rats are valuable

Jared M. Diamond

THE polymerase chain reaction (PCR) has made it feasible to extract, amplify and sequence DNA from museum and archaeological specimens. In previous studies the technique has been used for taxonomic purposes by comparing DNA of extinct taxa (such as the thylacine and quagga) with that of putatively related extant taxa. W. K. Thomas, S. Paabo, F. X. Villablanca and A. C. Wilson (*J. molec. Evol.* **31**, 101–112; 1990) have now taken this approach a step further. They compare modern and historical specimens of the same extant species with respect to individual and geographical variation in mitochondrial DNA, and thereby directly measure the historical trajectory of genotype frequencies.

Thomas *et al.* used the Panamint kangaroo rat (*Dipodomys panamintinus*), a small rodent of the Californian and Nevadan deserts. They analysed mitochondrial DNA from dried skin of 43 study skins belonging to three subspecies of the rat, collected between 1911 and 1937 and preserved in the University of California (Berkeley) Museum of Vertebrate Zoology. In 1988 they collected 63 modern rats of the same subspecies from the same three sites and obtained DNA from liver. They then sequenced 225 base pairs from regions coding for two transfer RNA genes and an adjacent noncoding region.

Among the 106 individual rats, variation appears in 19 out of the 225 base positions. As would be expected for samples from three closely related populations, most of the variation involves transitions, with few transversions and no length differences. Most variable sites are in one portion of the noncoding region.

The 106 rats yield 23 mitochondrial genotypes: twelve, seven and five in subspecies A, B and C respectively. Only one individual each of B and C shares the same genotype; otherwise, each genotype is confined to a single subspecies. Both the number and the diversity of genotypes are greatest in subspecies A, the one with the widest geographical range, highest population density and hence largest population size. This is quite as expected: larger population translates into higher probabilities that a lineage will survive.

When one compares historical and modern samples of the same subspecies, the two samples of subspecies A share only two of twelve genotypes; those of B share two of six, those of C, three of five.

W. K. Thomas

Museum collections of flora and fauna may now be at the forefront of research in molecular evolution.

So… what's the future vision?

To position Australia's collections as digitally mature, scientifically enabled and impact-focused research infrastructure delivering solutions to our future environmental, economic and social challenges

National Research Infrastructure Roadmap: National approach to collections step-change