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Understanding ecosystem responses to environmental disturbances with sedimentary microbial DNA

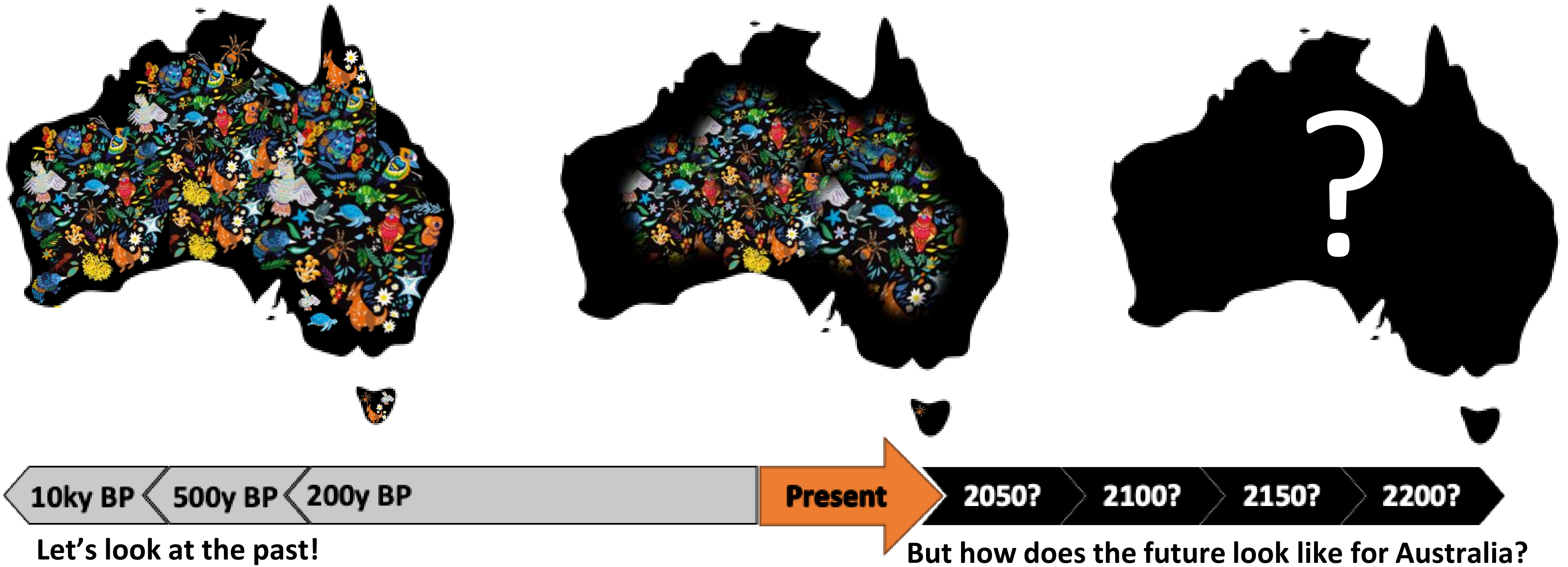
Vilma Pérez Godoy

University of Adelaide

Australia

I acknowledge the Traditional Owners of the land where we stand today and where this study is taking place, Kaurna country, - and recognise their continuing connection to land, waters and culture. I pay respect to their Elders past and present.

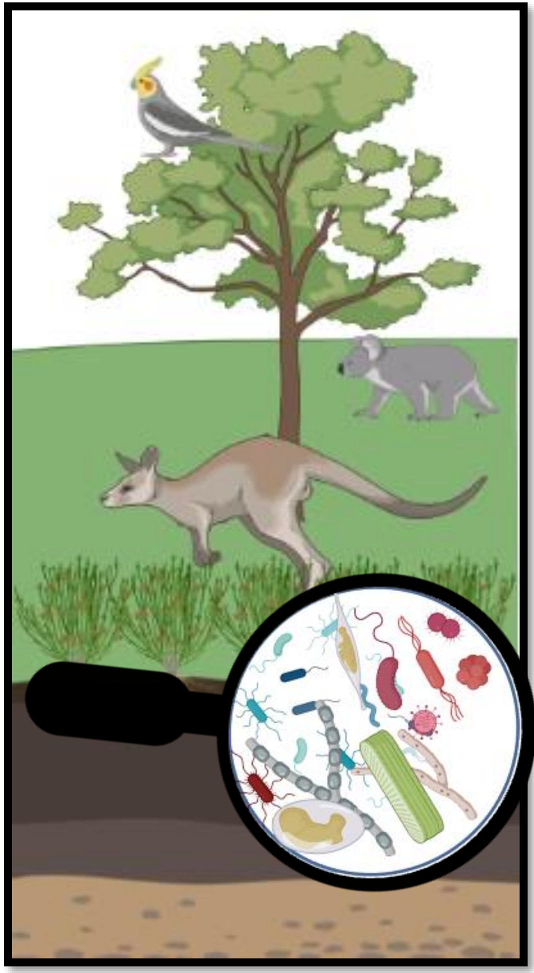
Anthropogenic impact and climate change

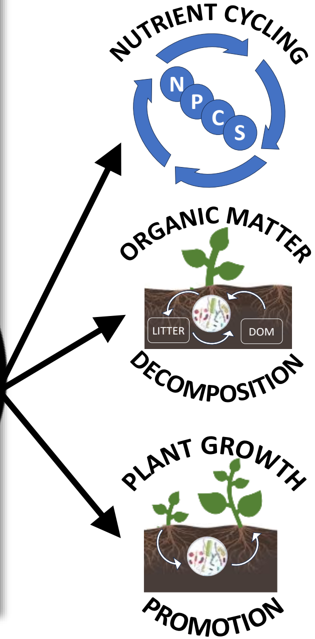


Let’s look at the past!

But how does the future look like for Australia?

BACKGROUND





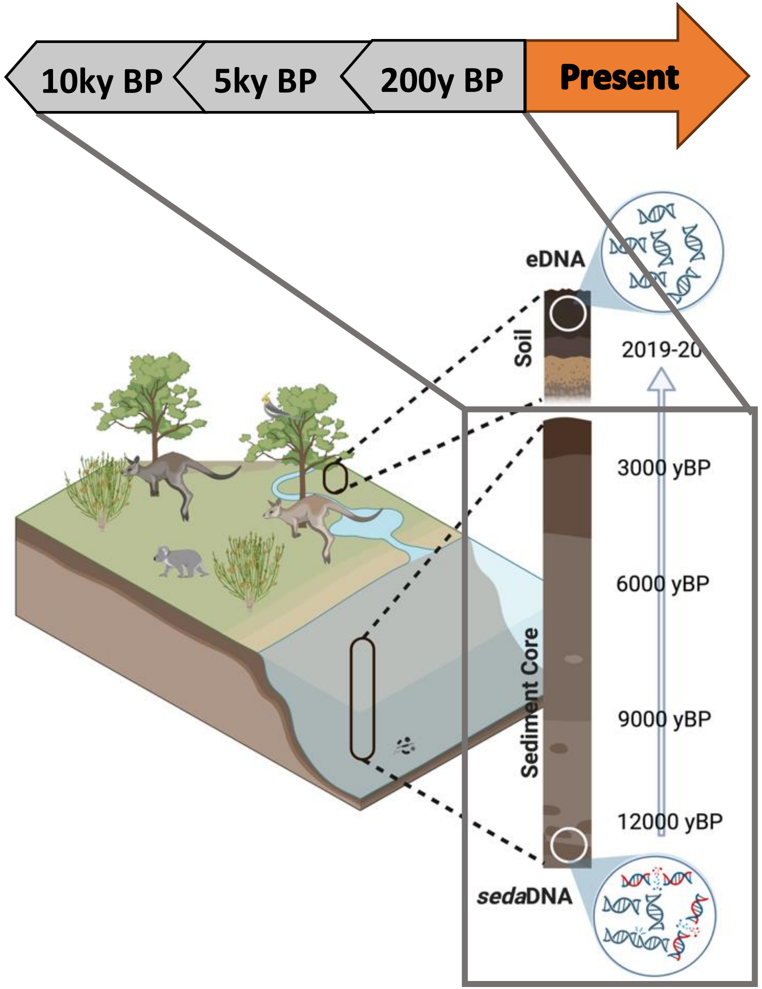
WHAT DO WE KNOW?

- Microorganisms perform essential ecological functions
- They are the foundation of long-term ecosystem health and resilience.
- The trajectory of ecosystem recovery is strongly linked to the taxonomic and functional succession of microbial communities.

WHAT IS MISSING?

But what happens to these microorganisms over extended temporal ecological scales after environmental changes remains unclear.

HOW DO WE FILL THIS GAP?

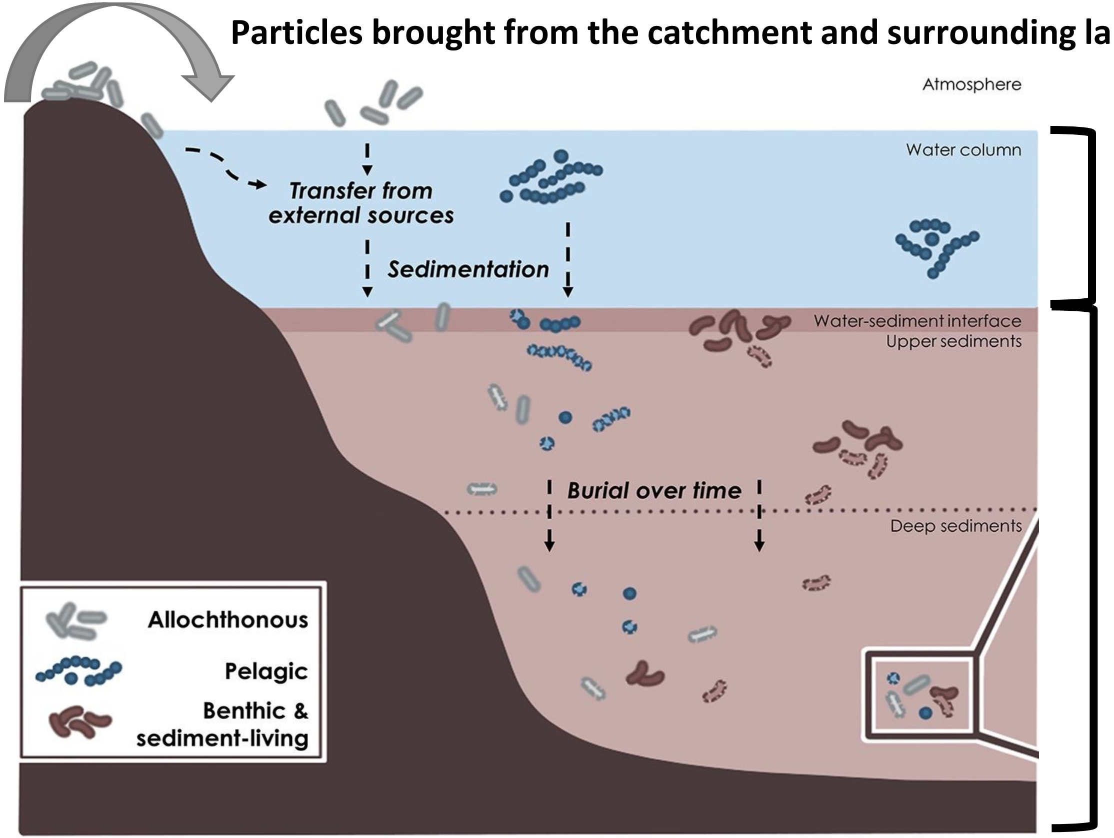


Build a long-term record of the impact of environmental changes on microbes in Australian environments

- Sedimentary ancient DNA (sedaDNA): environmental ancient DNA preserved in sediments.
- Powerful tool for reconstructing long-term ecological histories.
- Sediments accumulate over time creating a natural archive that enables us to examine ecosystem changes from decades to millennia.

Sedimentary record

Particles brought from the catchment and surrounding landscape



Microorganisms from within the water column

Microorganisms living in the sediment

Capo et al., 2022. E*nvironmental Microbiology*

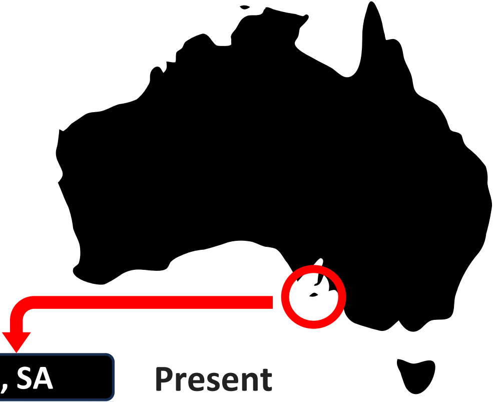
BACKGROUND

Dr Jonathan Tyler
University of Adelaide

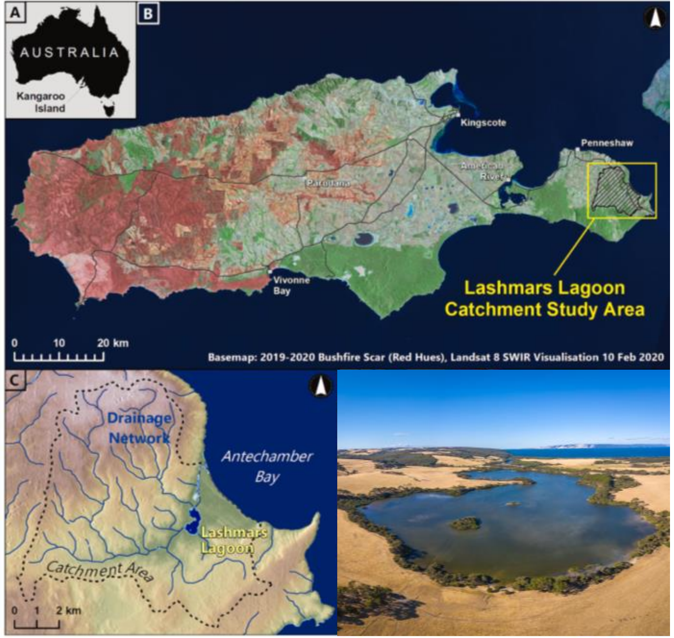
Lucinda Duxbury MSc, PhD(c)
University of Tasmania

Dr Haidee Cadd
University of Wollongong

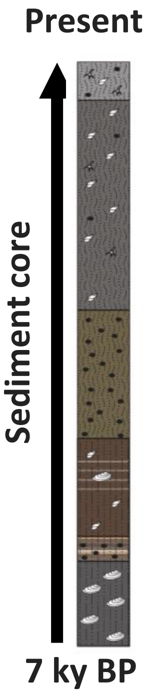
To **improve the reconstruction of ecological responses to bushfires** in the past in Southeastern Australia, to build **better predictive models** to determine how biological systems will respond to ongoing and future climate change.



Lashmars Lagoon, Kangaroo Island, SA



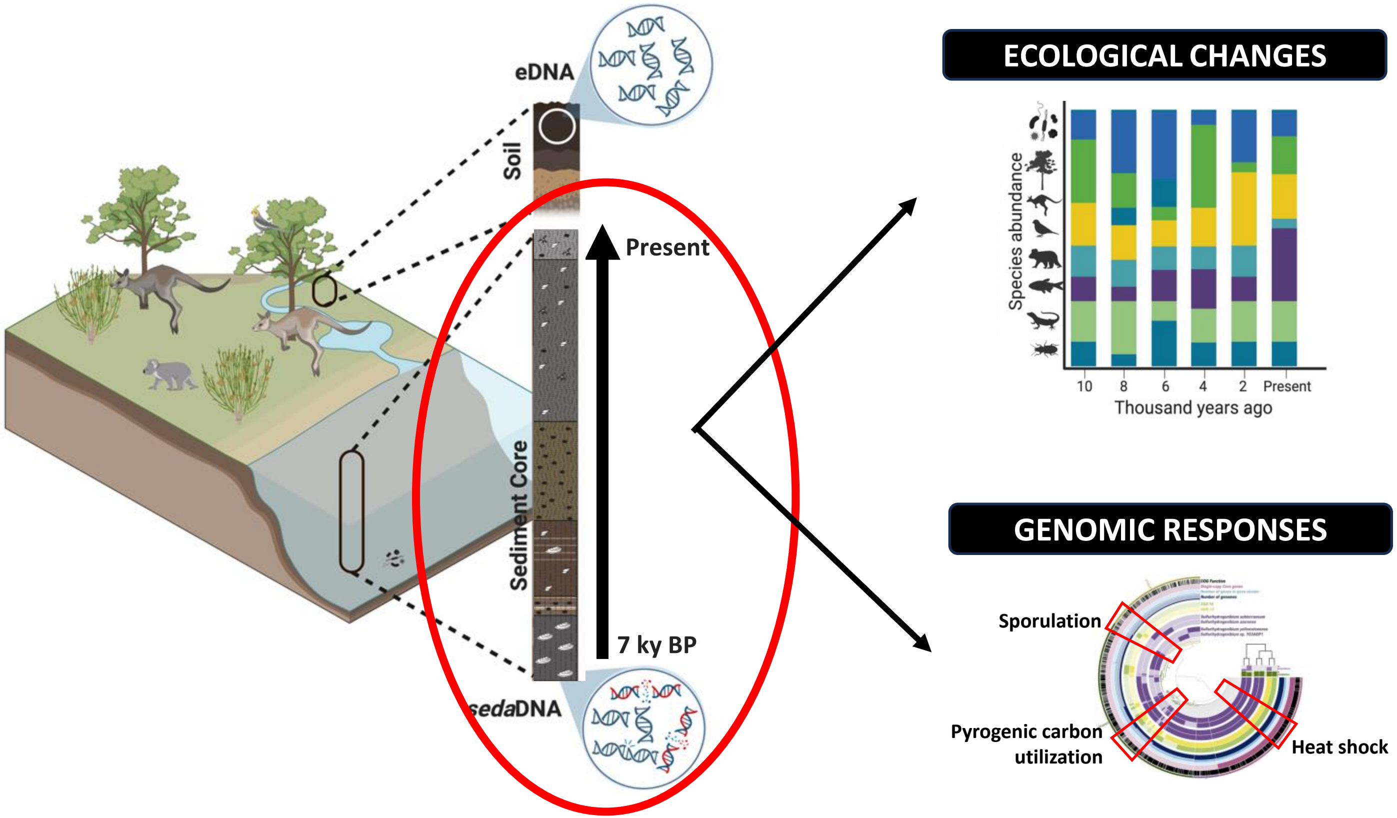
Modified from Duxbury et al., 2024. Palaeogeography, Palaeoclimatology, Palaeoecology



Traditional proxies:
- **Pollen**
- **Geochemistry**
- **Geochronology**

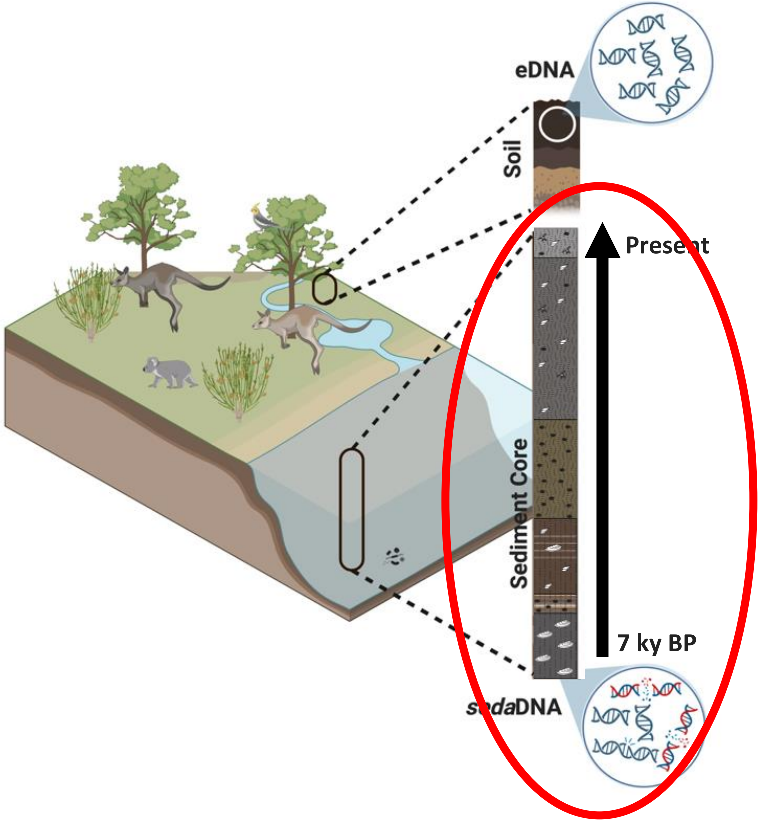
AIMS

Apply molecular techniques (i.e., sedaDNA) to study the biological adaptations of this ecosystem to changing environmental conditions.

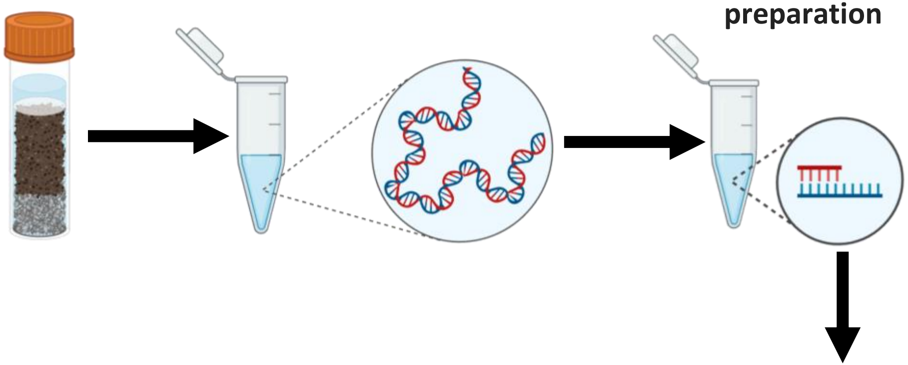


Identify genomic changes in microbial communities in response to environmental disturbances over the last 7,000 years in Lashmars Lagoon.

METHODS



Ultra-clean ancient DNA facility



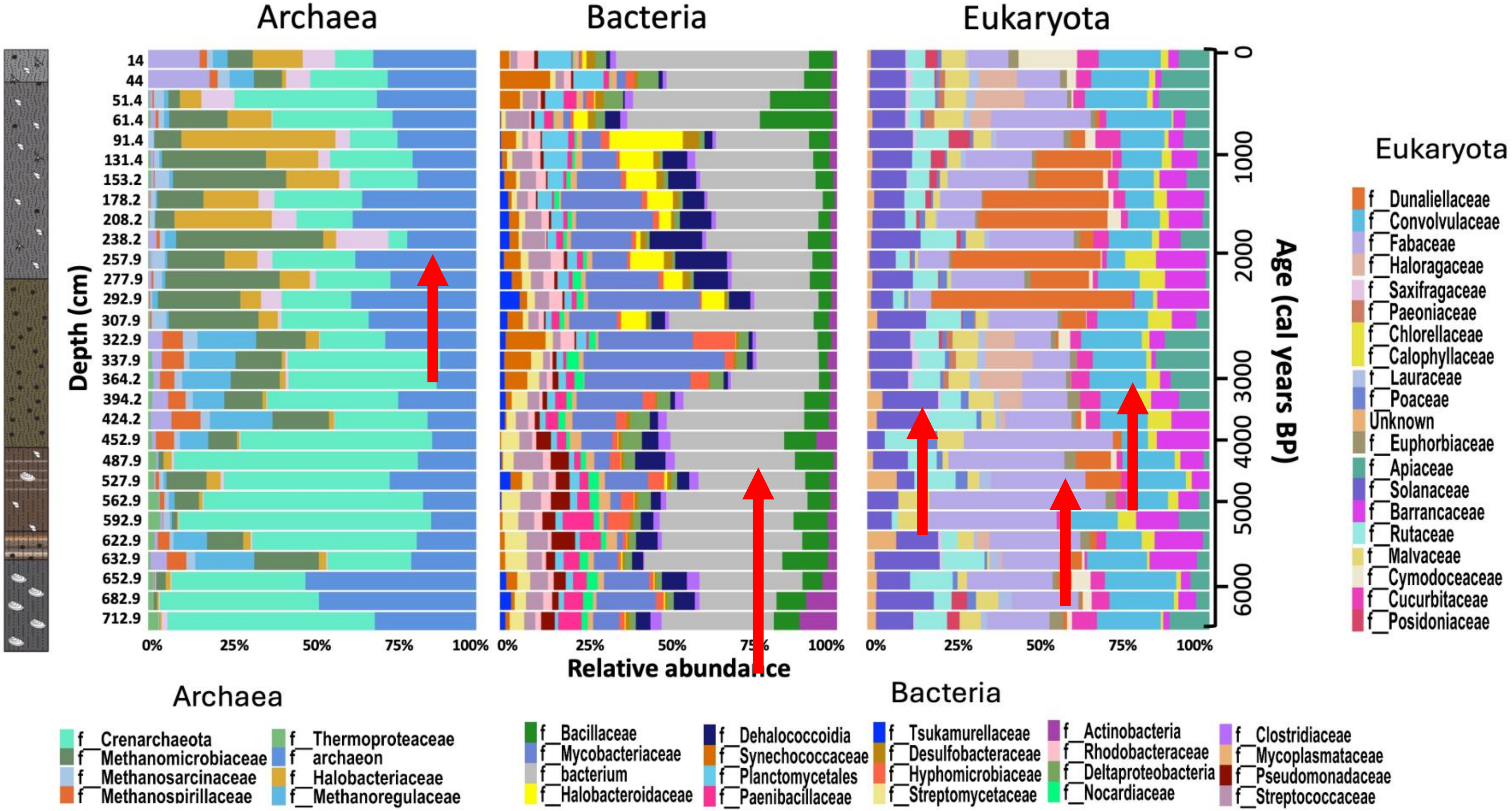
Sub-sample collection

DNA extraction

Sequencing library preparation

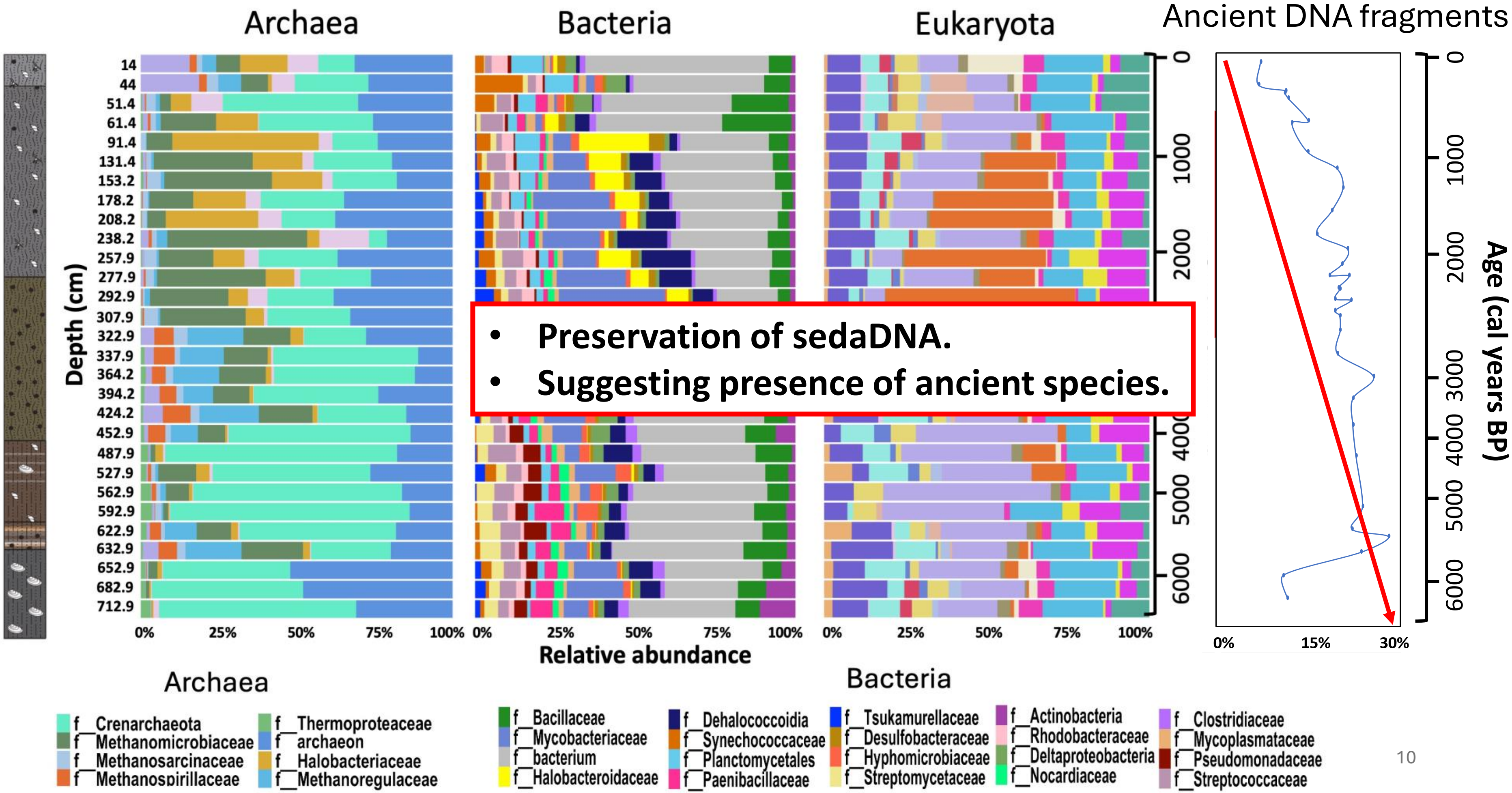
Shotgun metagenomics: gold standard for analysing short (<100 bp) and degraded DNA fragments

Taxonomic composition: most abundant families



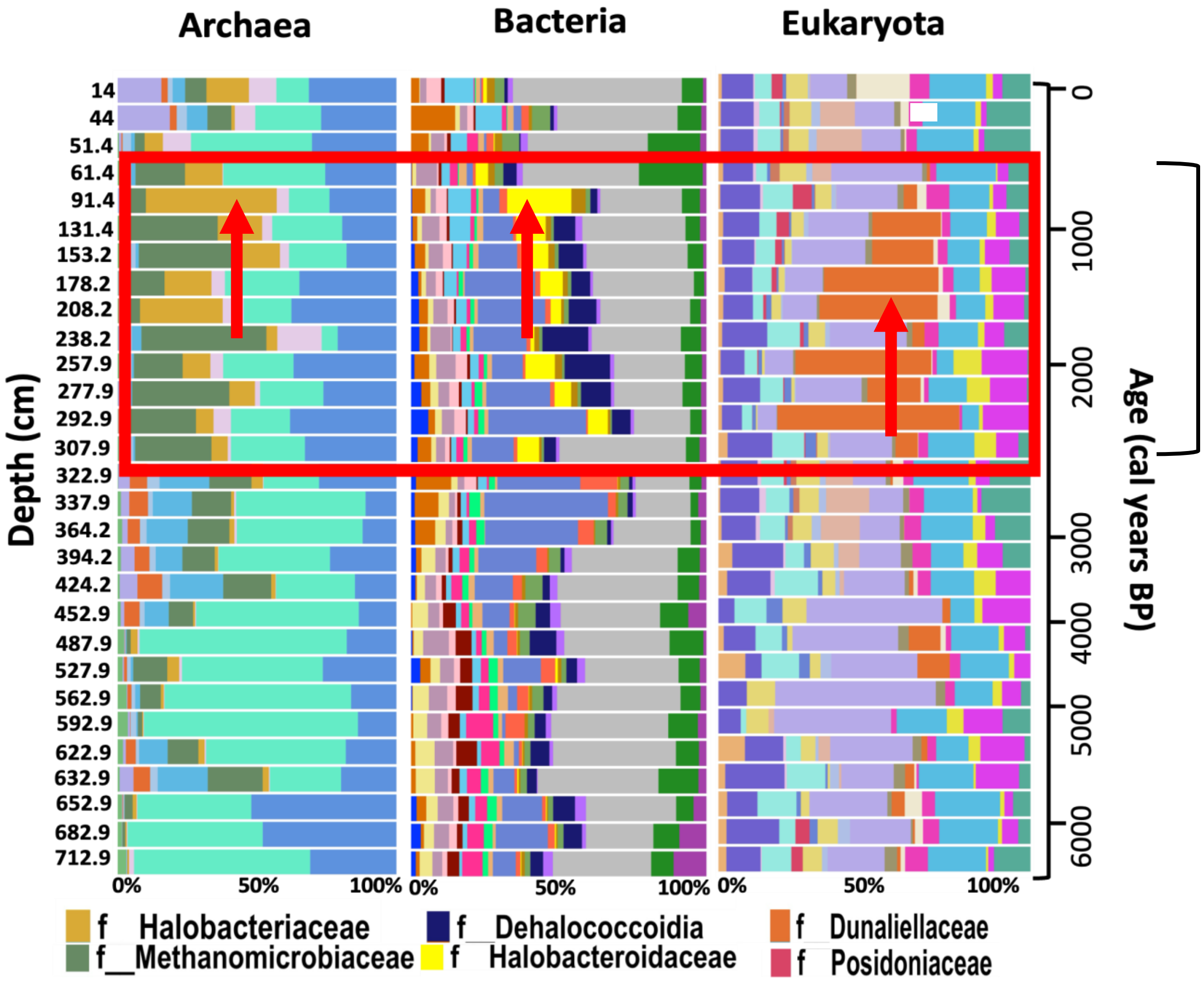
RESULTS

Increasing aDNA proportion along the sediment core



- **Preservation of sedaDNA.**
- **Suggesting presence of ancient species.**

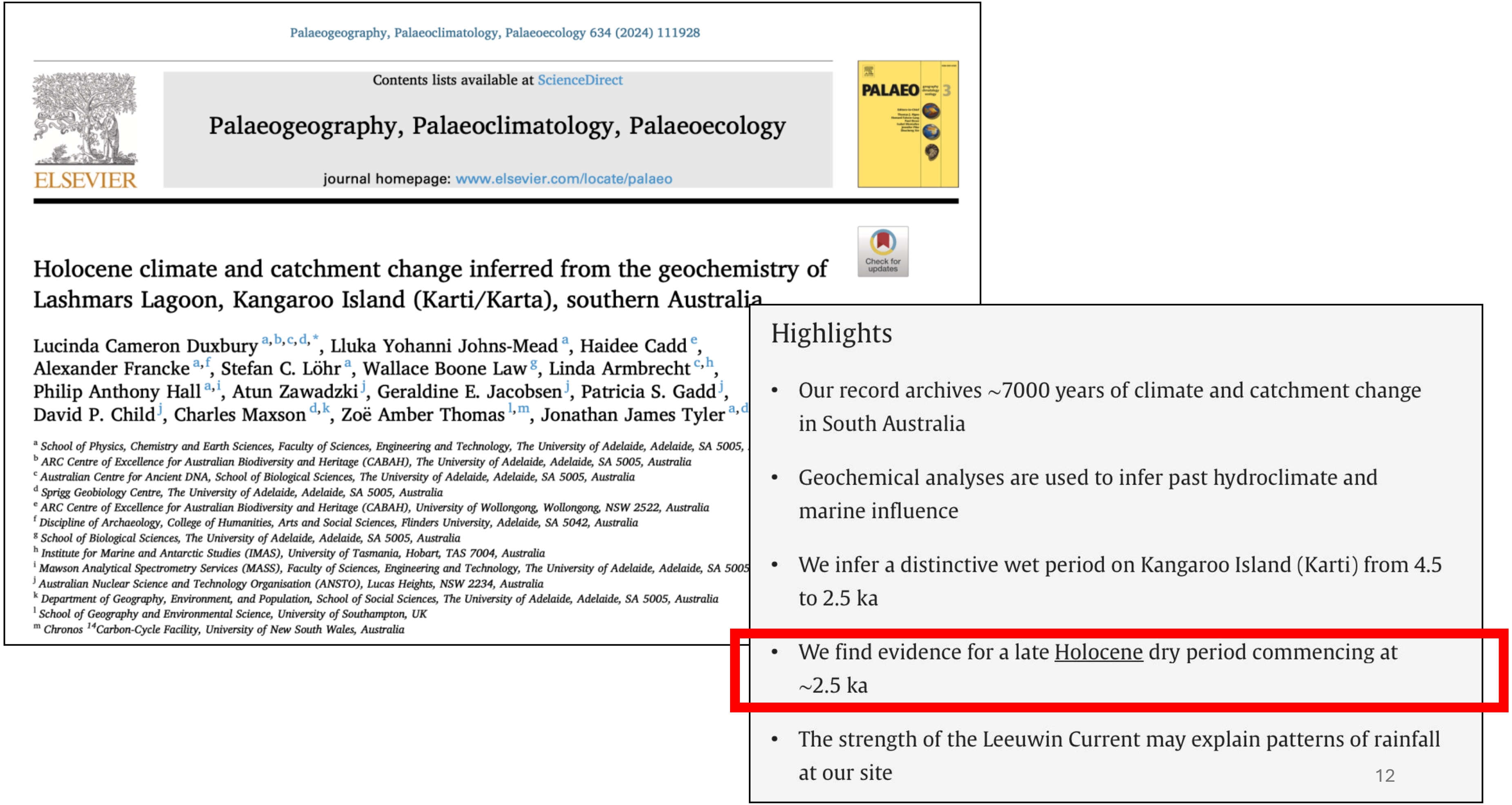
RESULTS



700 years BP

2500 years BP

BACKGROUND



Palaeogeography, Palaeoclimatology, Palaeoecology 634 (2024) 111928

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journal homepage: www.elsevier.com/locate/palaeo

Holocene climate and catchment change inferred from the geochemistry of Lashmars Lagoon, Kangaroo Island (Karti/Karta), southern Australia

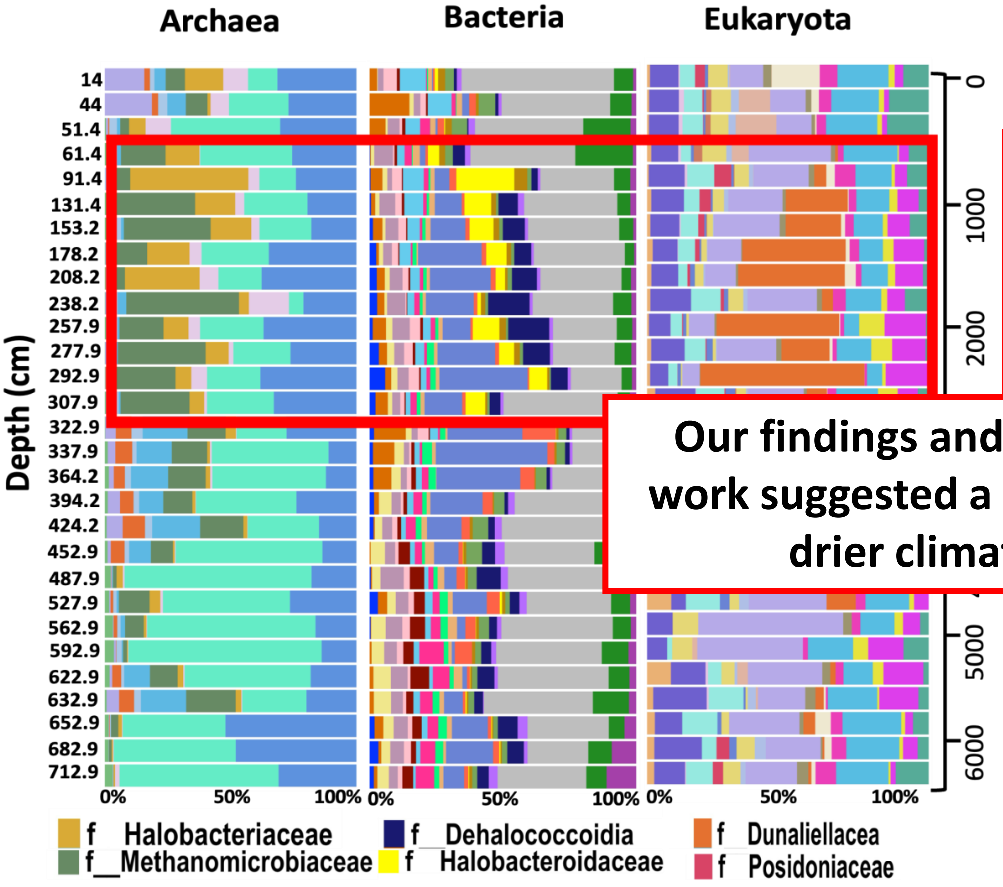
Lucinda Cameron Duxbury[a,b,c,d,*], Lluka Yohanni Johns-Mead[a], Haidee Cadd[e], Alexander Francke[a,f], Stefan C. Löhr[a], Wallace Boone Law[g], Linda Armbrecht[c,h], Philip Anthony Hall[a,i], Atun Zawadzki[j], Geraldine E. Jacobsen[j], Patricia S. Gadd[j], David P. Child[j], Charles Maxson[d,k], Zoë Amber Thomas[l,m], Jonathan James Tyler[a,d]

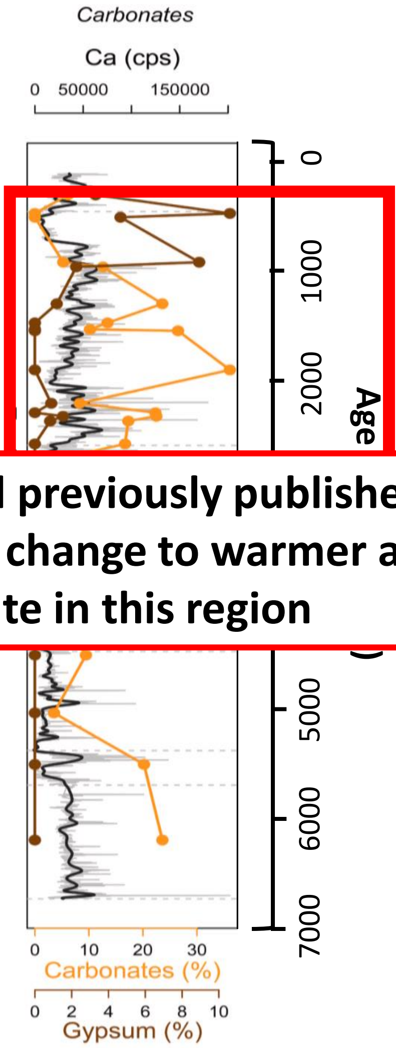
[a] *School of Physics, Chemistry and Earth Sciences, Faculty of Sciences, Engineering and Technology, The University of Adelaide, Adelaide, SA 5005,*
[b] *ARC Centre of Excellence for Australian Biodiversity and Heritage (CABAH), The University of Adelaide, Adelaide, SA 5005, Australia*
[c] *Australian Centre for Ancient DNA, School of Biological Sciences, The University of Adelaide, Adelaide, SA 5005, Australia*
[d] *Sprigg Geobiology Centre, The University of Adelaide, Adelaide, SA 5005, Australia*
[e] *ARC Centre of Excellence for Australian Biodiversity and Heritage (CABAH), University of Wollongong, Wollongong, NSW 2522, Australia*
[f] *Discipline of Archaeology, College of Humanities, Arts and Social Sciences, Flinders University, Adelaide, SA 5042, Australia*
[g] *School of Biological Sciences, The University of Adelaide, Adelaide, SA 5005, Australia*
[h] *Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, Hobart, TAS 7004, Australia*
[i] *Mawson Analytical Spectrometry Services (MASS), Faculty of Sciences, Engineering and Technology, The University of Adelaide, Adelaide, SA 5005*
[j] *Australian Nuclear Science and Technology Organisation (ANSTO), Lucas Heights, NSW 2234, Australia*
[k] *Department of Geography, Environment, and Population, School of Social Sciences, The University of Adelaide, Adelaide, SA 5005, Australia*
[l] *School of Geography and Environmental Science, University of Southampton, UK*
[m] *Chronos ^{14}Carbon-Cycle Facility, University of New South Wales, Australia*

Highlights

- Our record archives ~7000 years of climate and catchment change in South Australia
- Geochemical analyses are used to infer past hydroclimate and marine influence
- We infer a distinctive wet period on Kangaroo Island (Karti) from 4.5 to 2.5 ka
- We find evidence for a late Holocene dry period commencing at ~2.5 ka
- The strength of the Leeuwin Current may explain patterns of rainfall at our site

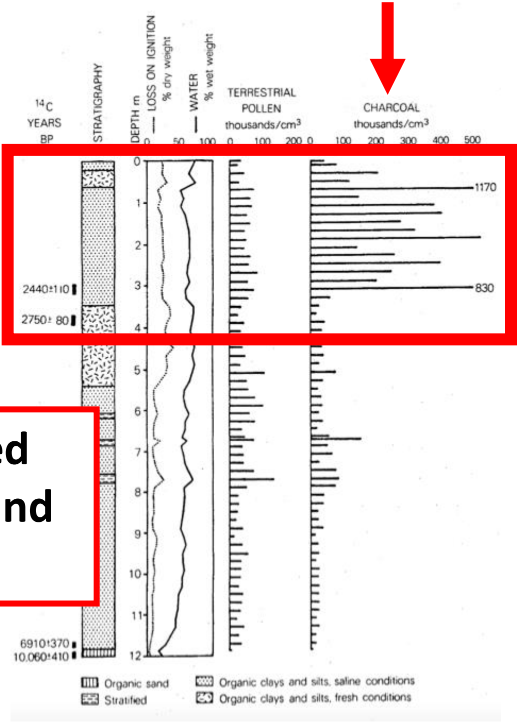
RESULTS





Modified figure 6 from Duxbury et al., 2024.

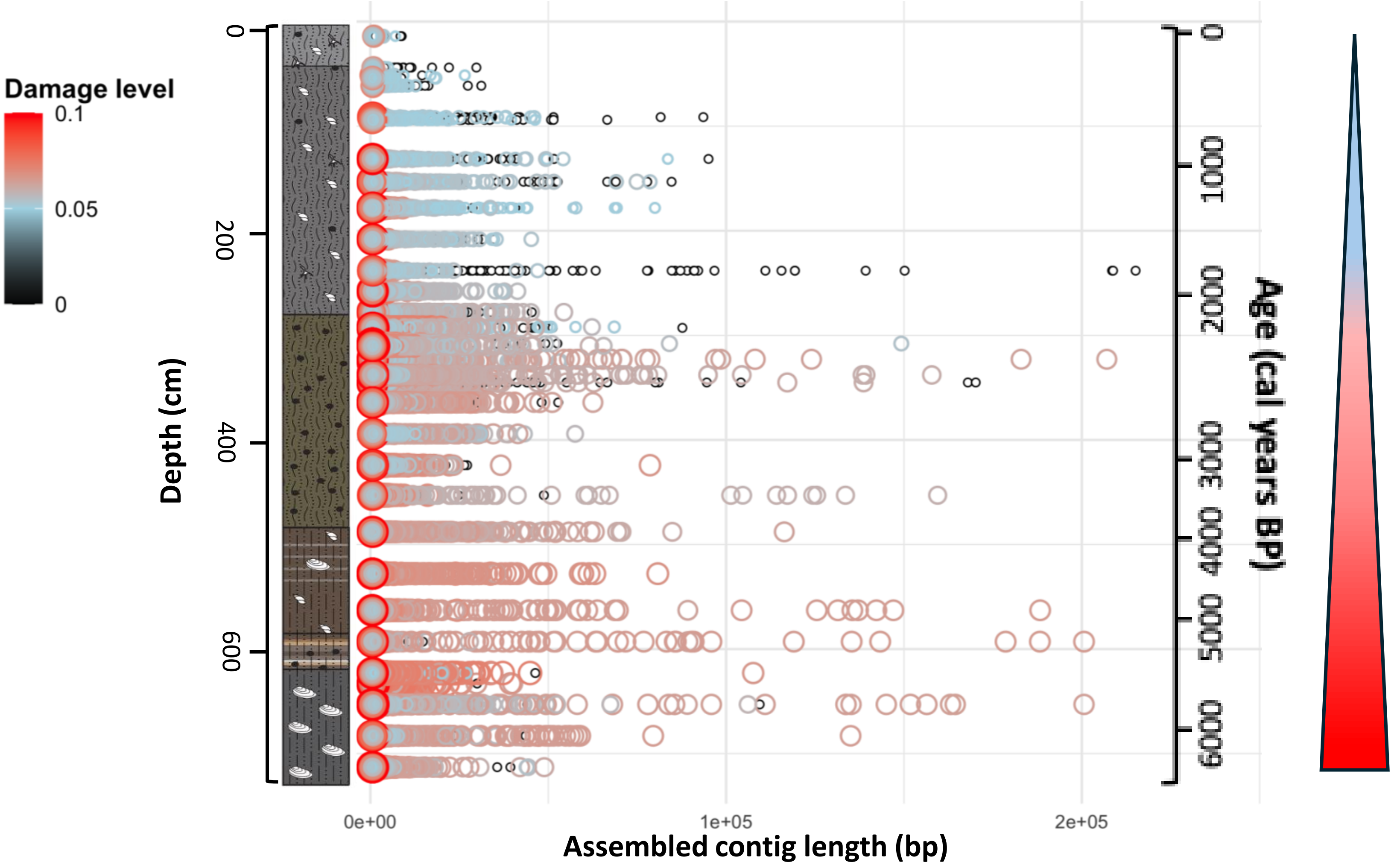
Our findings and previously published work suggested a change to warmer and drier climate in this region



Modified figure from Clark, 1983

Increased microcharcoal indicating high intensity fires or more frequent fires in this region

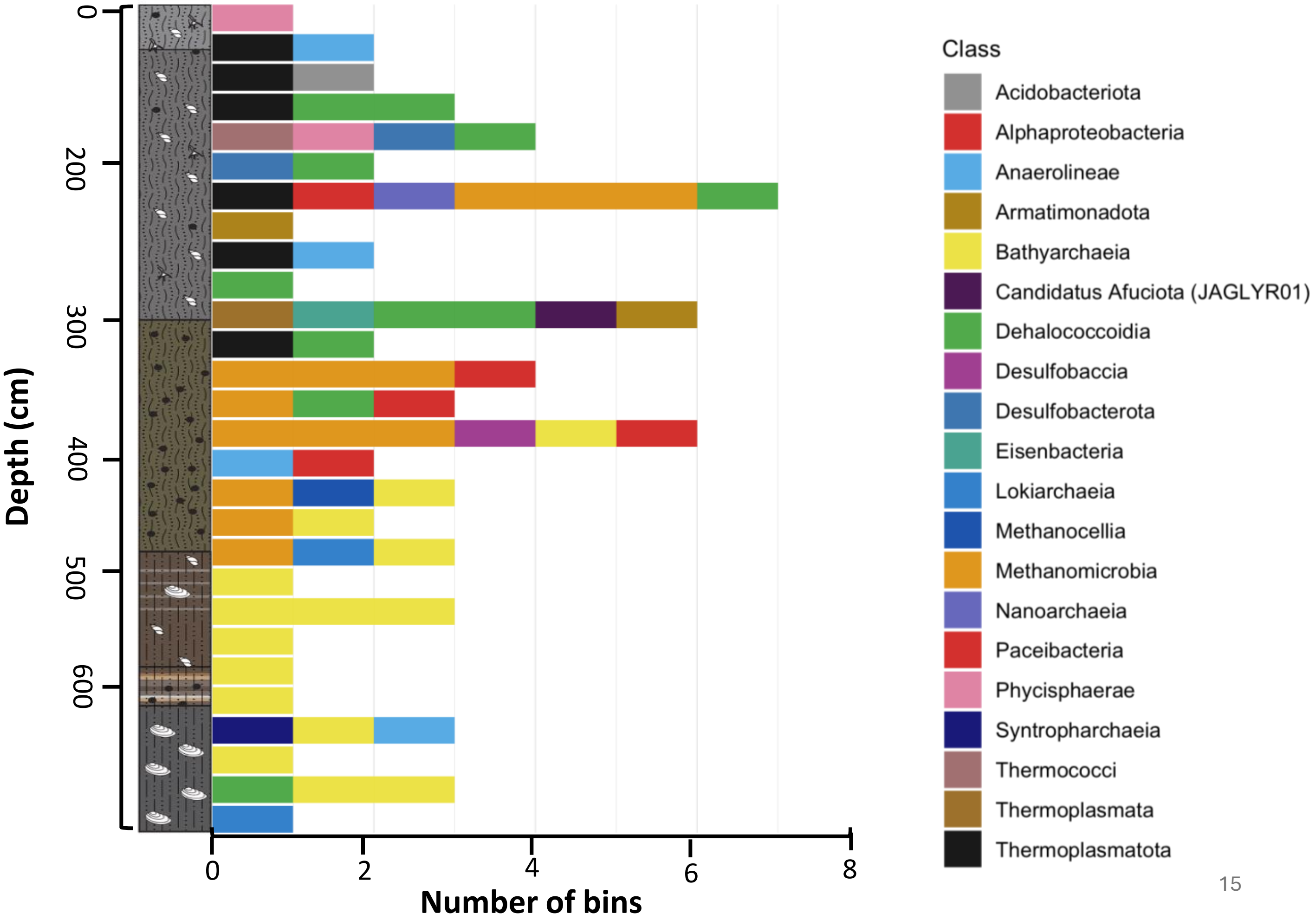
Increasing damaged contigs (>500 bp) along sediment core



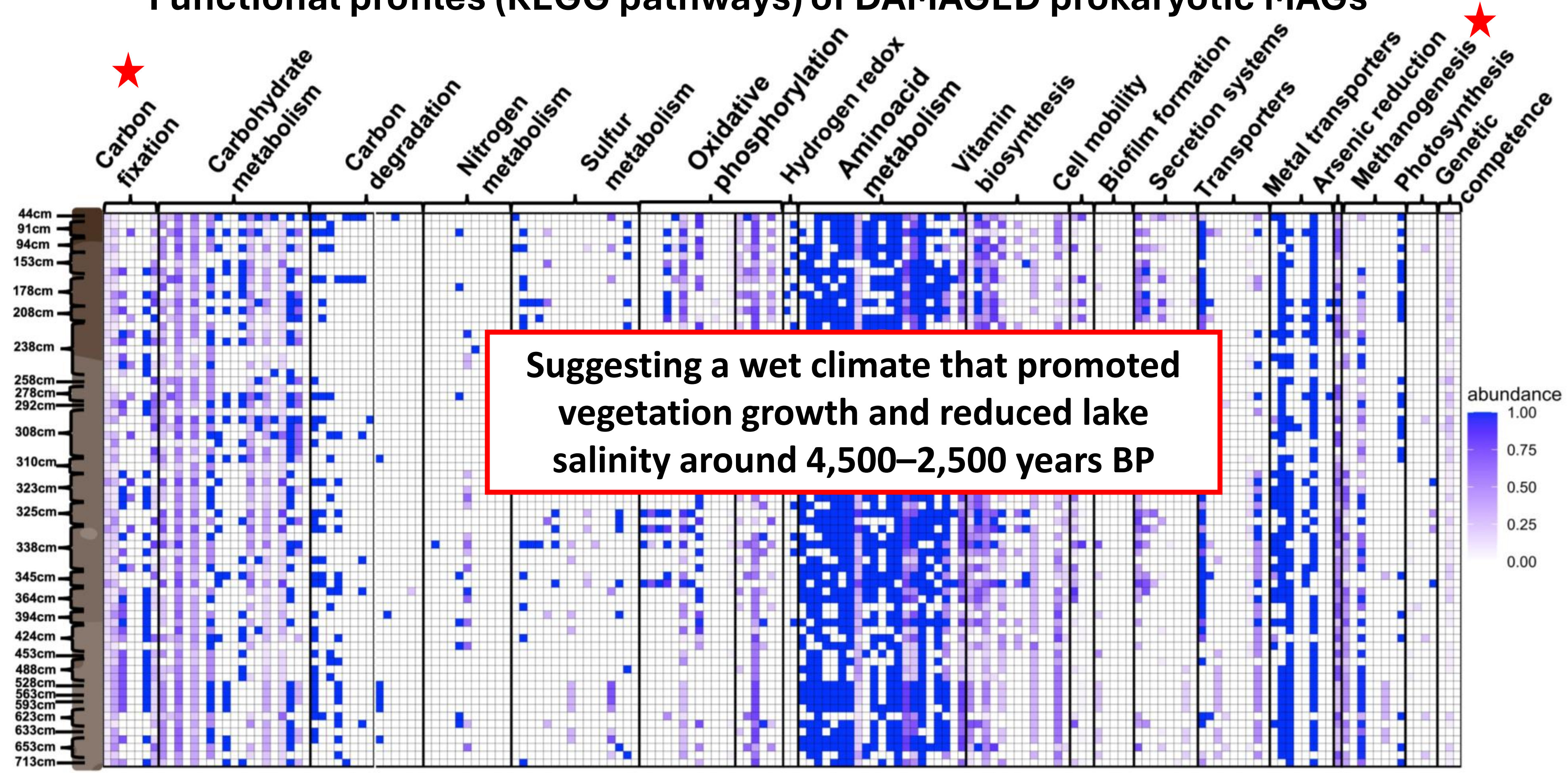
Recovered medium- and high-quality prokaryotic MAGs

Total 71 MAGs:

- **67 damaged MAGs, potentially ancient.**
- **4 non-damaged MAG, potentially modern. (Phycisphaerae, Paceibacteria, Dehalococcoidia, Desulfobaccia)**



Functional profiles (KEGG pathways) of DAMAGED prokaryotic MAGs



Suggesting a wet climate that promoted vegetation growth and reduced lake salinity around 4,500–2,500 years BP

Take home messages so far..

- Our results showed **vertical changes in sedimentary microbial communities correlated to environmental change proxies** (e.g., Ca-salinity, fire-microcharcoal).
- The **sedimentary microbial communities** in the sediment cores in the Lashmars Lagoon **showed authentic ancient DNA signal.**
- **Microbial communities likely responded** to **past environmental conditions** and **geochemical changes** of the sediment during burial.
- These observations suggest that microbial communities are **useful paleo-bioindicators of environmental change over time**.
- **More optimisation is needed for this type of complex environmental ancient DNA data.**

Thank you!!
Acknowledgements

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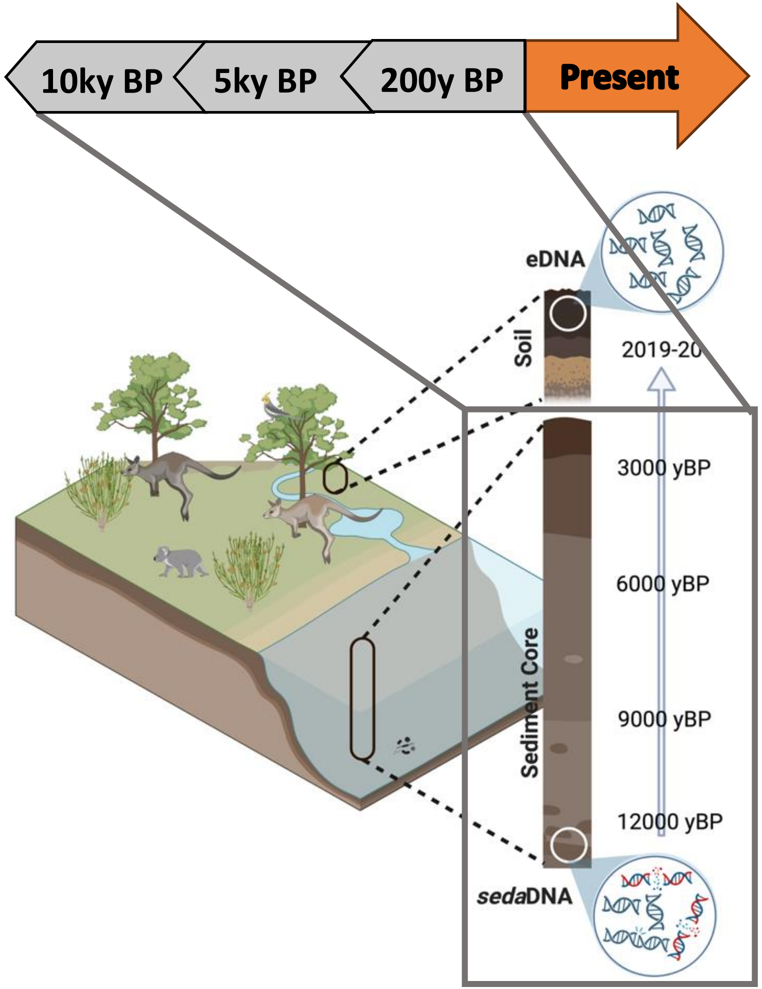
- Associate Professor Laura Weyrich, The Pennsylvania State University, USA
- Dr Linda Armbrecht, University of Tasmania
- Dr Alexander Francke, University of Adelaide

HOW DO WE FILL THIS GAP?

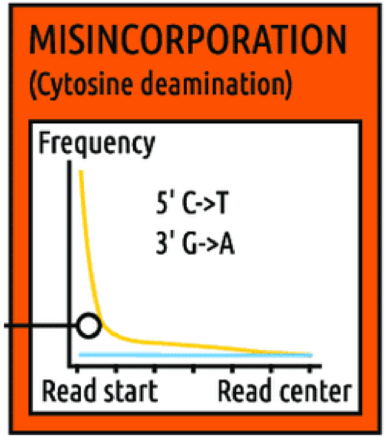


Build a long-term (Holocene) record of the impact of environmental changes on microbes in Australian environments

- Most studies in ancient microbial research use short-read sequencing.
- Limits findings to known taxa and their close relatives.
- Functional annotation more challenging and inaccurate.

”ancient” microbial metagenome-assembled genomes

RESULTS



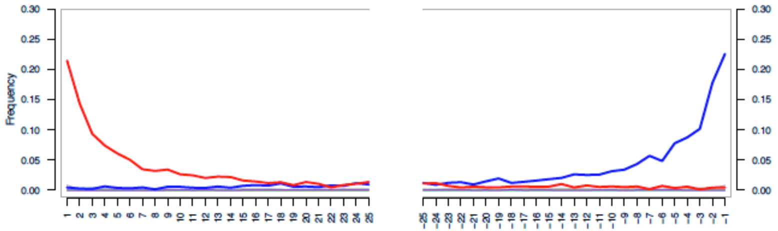
LEGEND

🟨 Ancient DNA

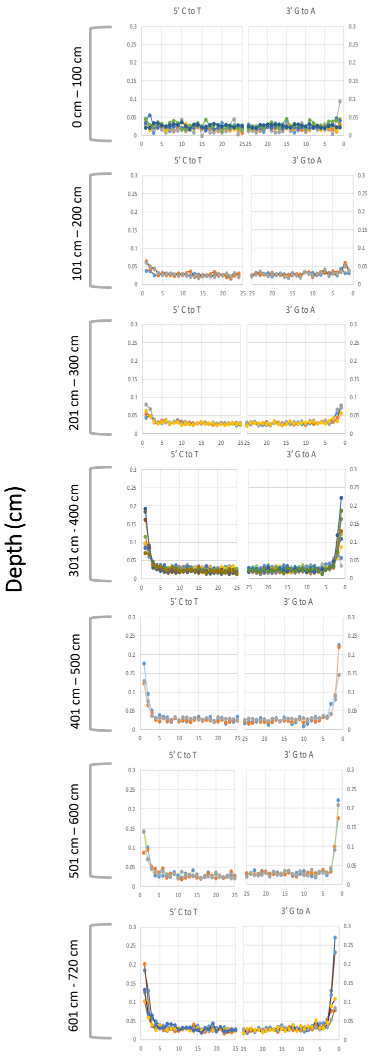
🟦 Modern DNA

🟧 Change from reference

All emojis designed by OpenMoji. CC BY-SA 4.0



Der Sarkissian et al., 2021



Chloroflexi sp.

Core figure from Duxbury et al., 2024