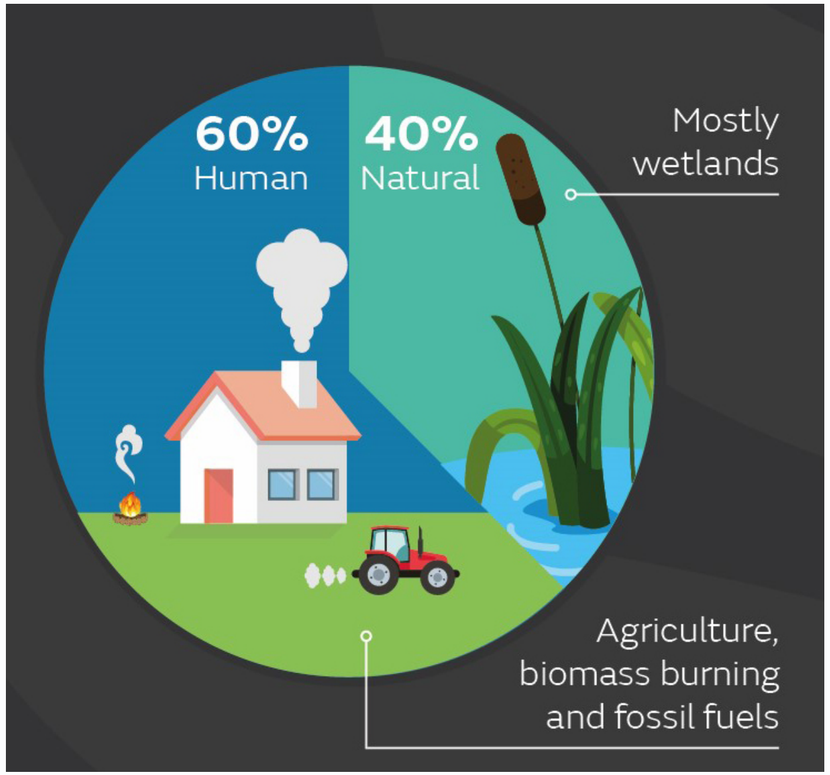
Microbial Ecology and Methane Production in a Hypersaline Coastal Lagoon

Chris Keneally
PhD Candidate - School of Biological Sciences
The University of Adelaide

Supervisors
Dr. Steven Kidd, Dr. Virginie Gaget,
Prof. Justin Brookes

Image: The Coorong's North Lagoon (from Parnka Point)

Methane in coastal wetlands

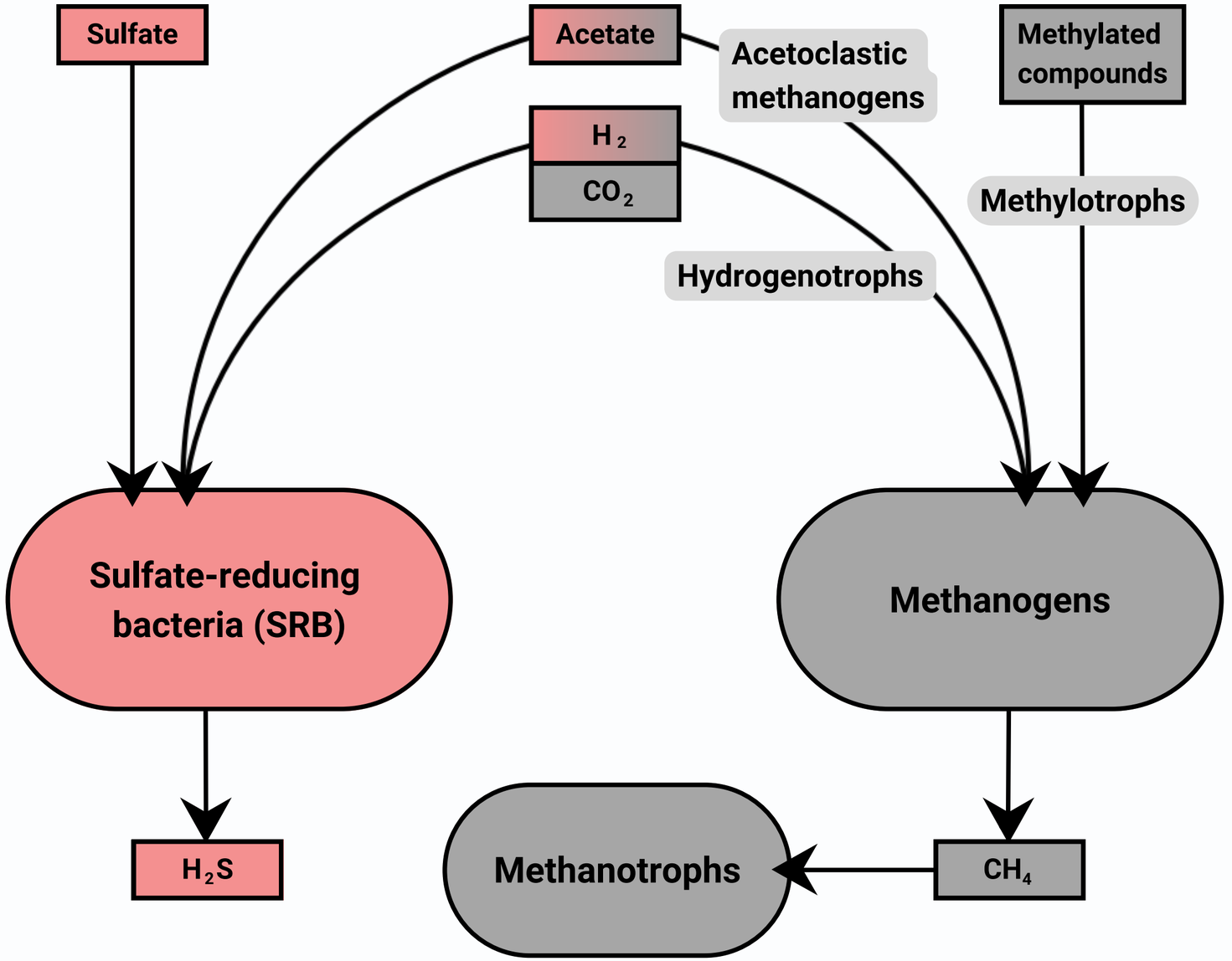


- Methane (CH_4) is a greenhouse gas with ~28 times the warming potential of CO_2
- Wetlands: up to 33% of emissions (Jackson *et al* 2020)
- Coastal wetlands are considered to have minimal emissions (Poffenbarger *et al* 2011)
- Promising 'Blue Carbon' sink, but requires more understanding of processes
- Often dependent on freshwater flows

Image: Met Office UK

Relevance of microbes

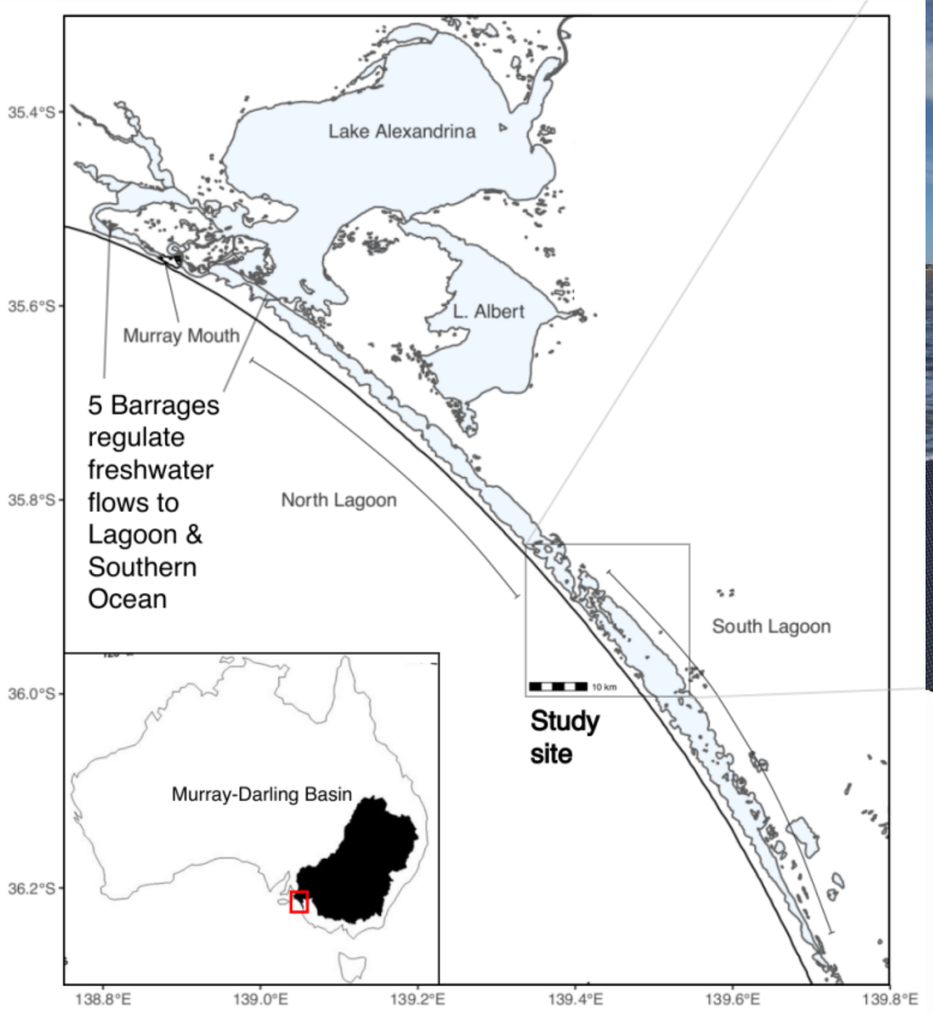
- Microbial ecology underpins carbon cycling
- Coastal methanogens compete with sulfate reducing bacteria for Acetate and H_2
- Methylotrophic methanogens use non-compatible solutes, including osmolytes:
  - Methylamines (Betaine)
  - Methyl sulfonium
- Methanotrophs metabolise methane



Study Site: The Coorong Lagoon

- Ramsar-listed wetland
- Estuary of Murray-Darling Basin
- Important habitat for migratory birds
- Decrease in biodiversity since 1980s
- Degraded due to high salinity, nutrients, organic matter, and reduced freshwater flushing
- Drought, water extractions, land uses upstream

Study Site: The Coorong Lagoon



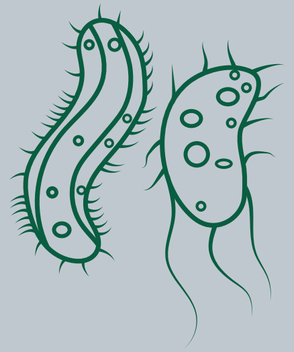
- South Lagoon: heavily degraded
- Max depth: 2 metres
- Fine monosulfidic black ooze at 'depositional zones' (DZ) where sediment focusing occurs
- High methane readings observed in sediment resuspension plumes during pilot study

- What drives this mysterious methane?

Aims

1 - Environmental factors & methane?

Determine how sediment characteristics, organic matter, & salinity influence porewater & water column methane concentrations



2 - Who's there?

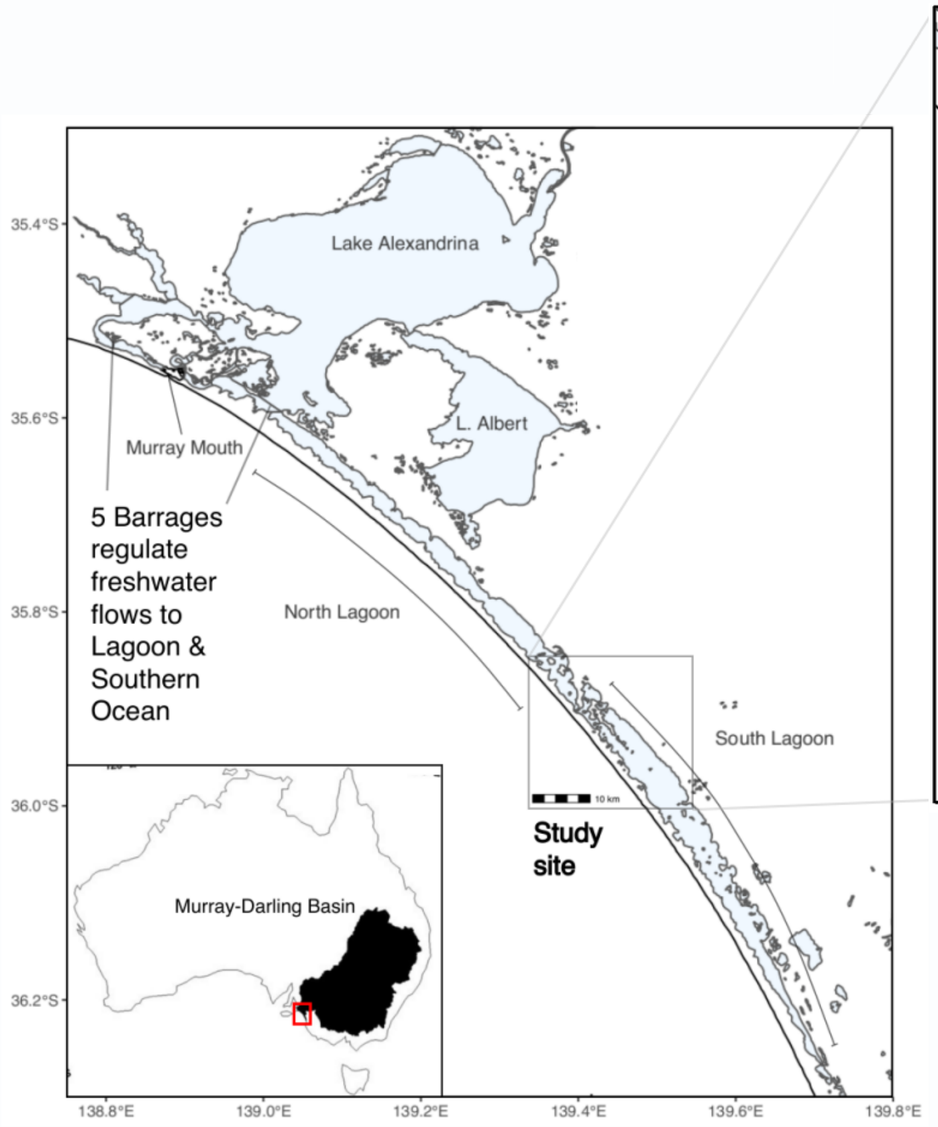
Understand if & how methanogens & associated microbial communities shift as a result of these variables

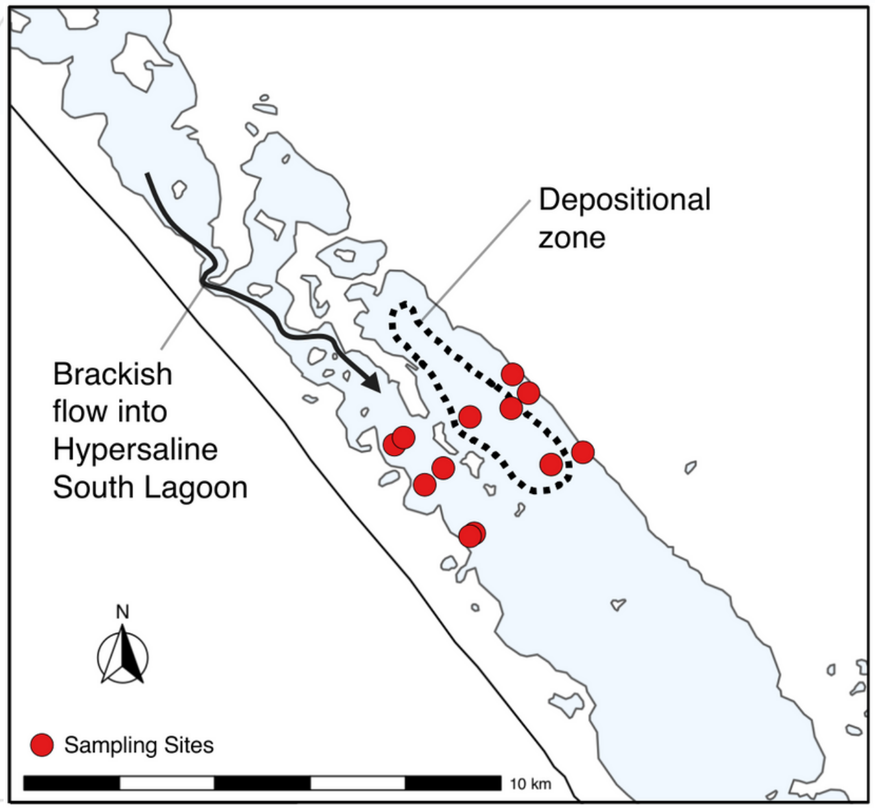
3 - What are they doing?

Quantify associated changes in functional genes

PICRUSt functional gene prediction to generate further hypotheses

Study Design

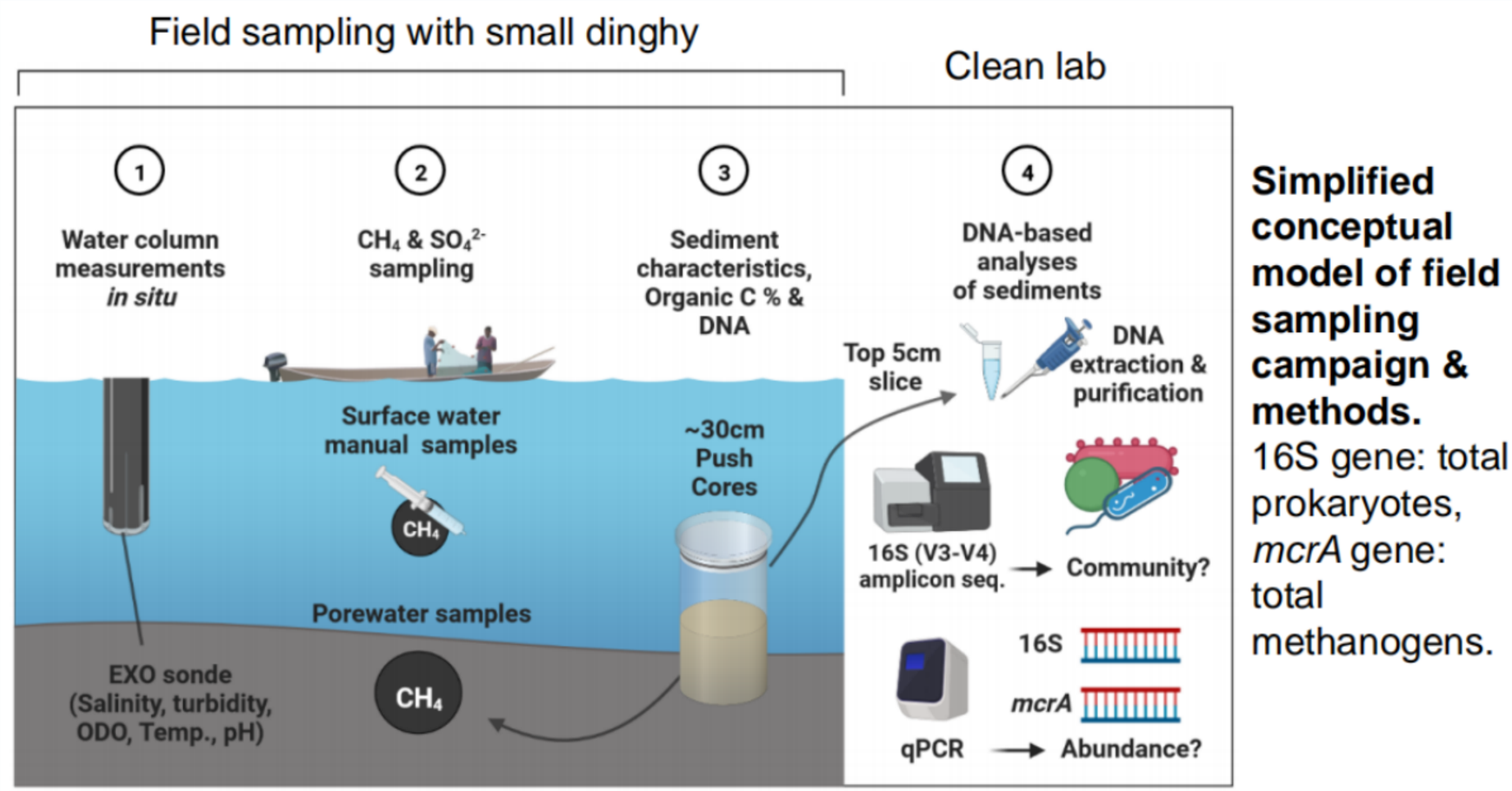




Villa Dei Yumpa

- Twelve sites
  - (3 transects)
  - Bank and centre on either side of island chain
  - Replication over 3 days
- Capture range of sediments
- West-East salinity gradient
    - 70 g/L - 85 g/L

Methods



Simplified conceptual model of field sampling campaign & methods.
16S gene: total prokaryotes, *mcrA* gene: total methanogens.

- Field sampling over 3 days
- Genetic assays in clean lab
- Also used PICRUSt to predict community functions from 16S data

Results

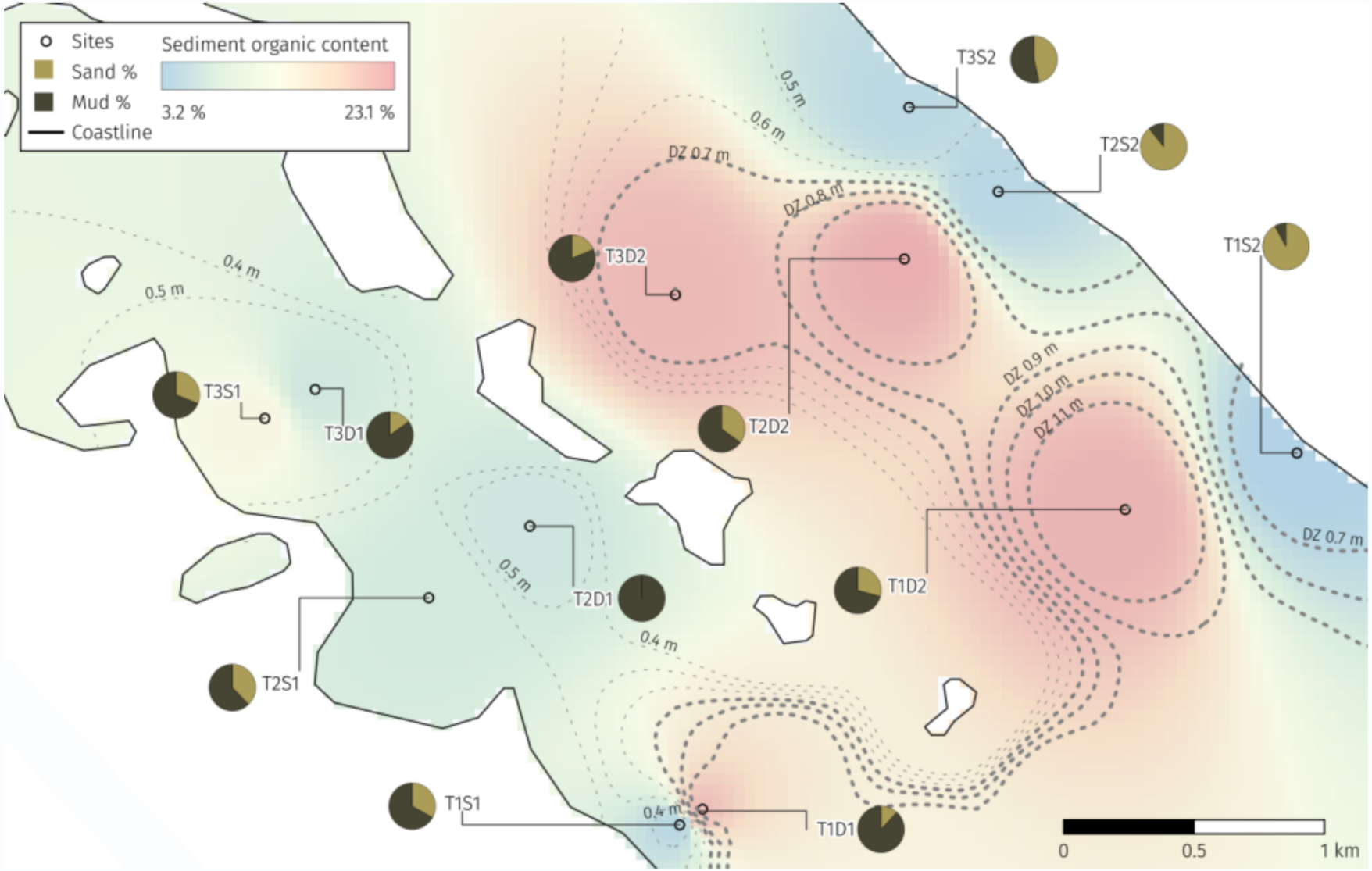
Environmental factors & Methane

Aim 1

Methane was highly correlated (>0.6) with:

- Organic content
- Salinity
- Water depth

These factors are all significantly increased in the DZ



Aim 2

Increased in the DZ:

- Taxa richness
- Phylogenetic diversity α-diversity indicies

Methanogen orders in DZ

Methylotrophs

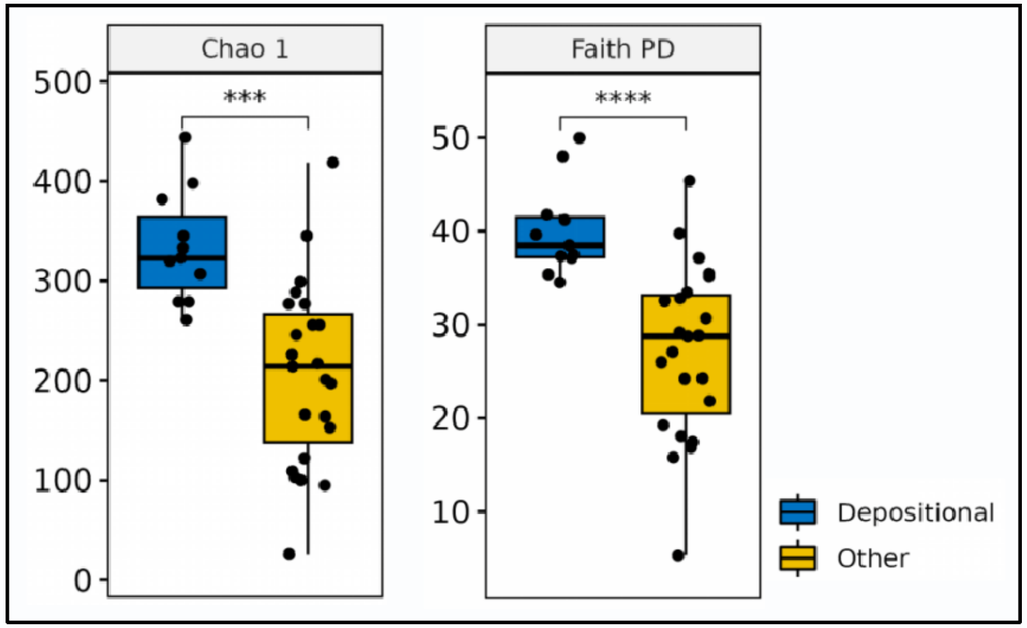
- **Methanofastidiosales ↑↑↑**
- Methanomassiliicoccales ↑

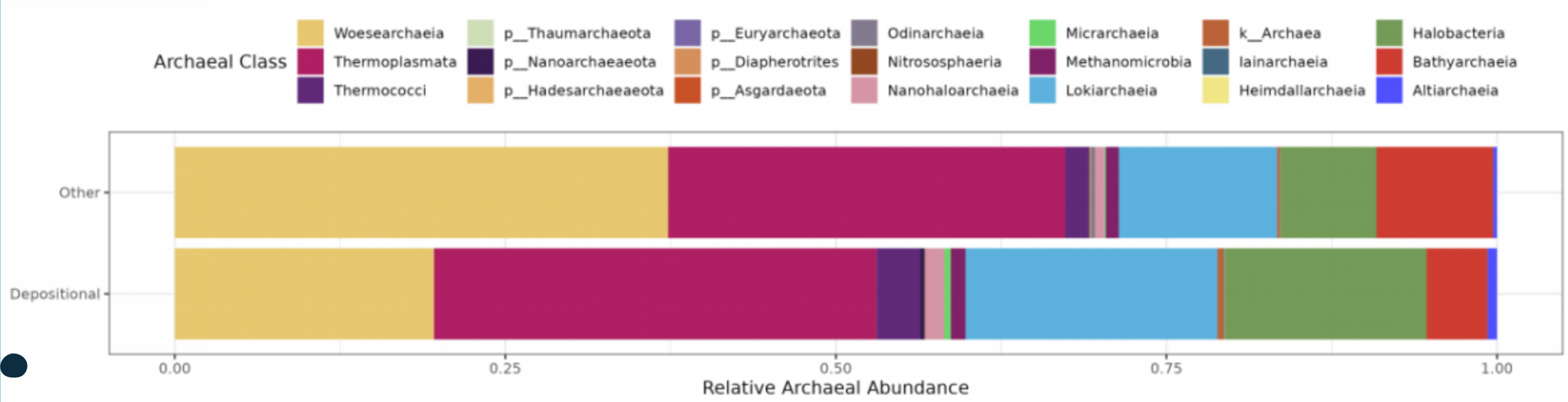
Acetoclastic/Hydrogenotrophic

- Methanosarcinales ↓

Results

Who's there- Archaea?





Aim 2

Results

Who's there - Bacteria?

Decreased in the DZ:

- Taxa richness
- Phylogenetic diversity

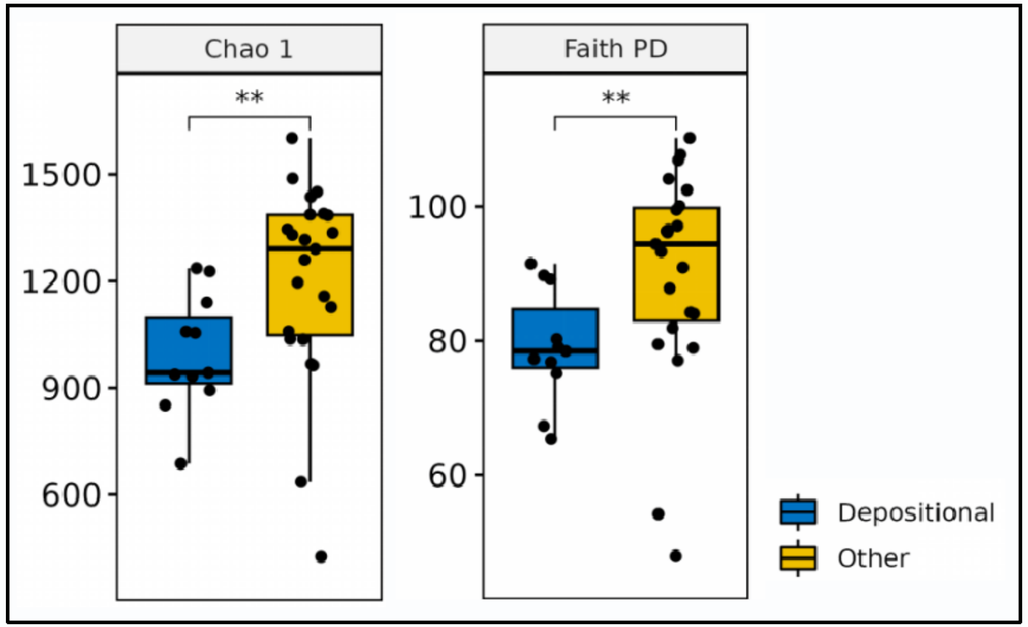
Methanotrophs ↓ in DZ

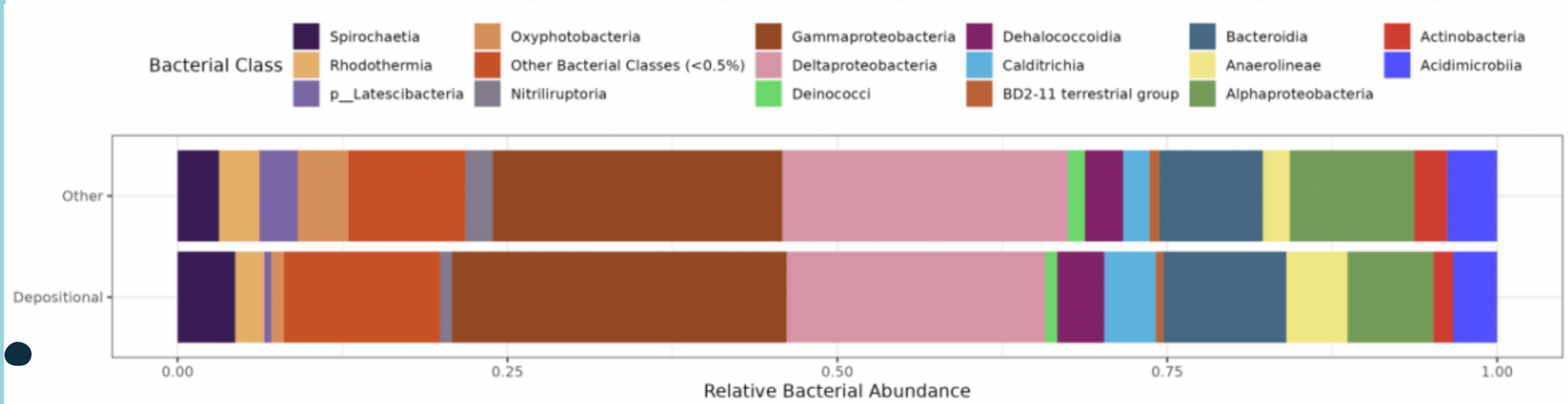
- Methyloacidiphilaceae
- Methyloligellaceae

Some SRB ↑ in DZ

- Desulfarculales

Overall, SRBs not significantly different





Results

What are they doing?

Aim 3

qPCR Results

↑ *mcrA:16S* ratio in DZ

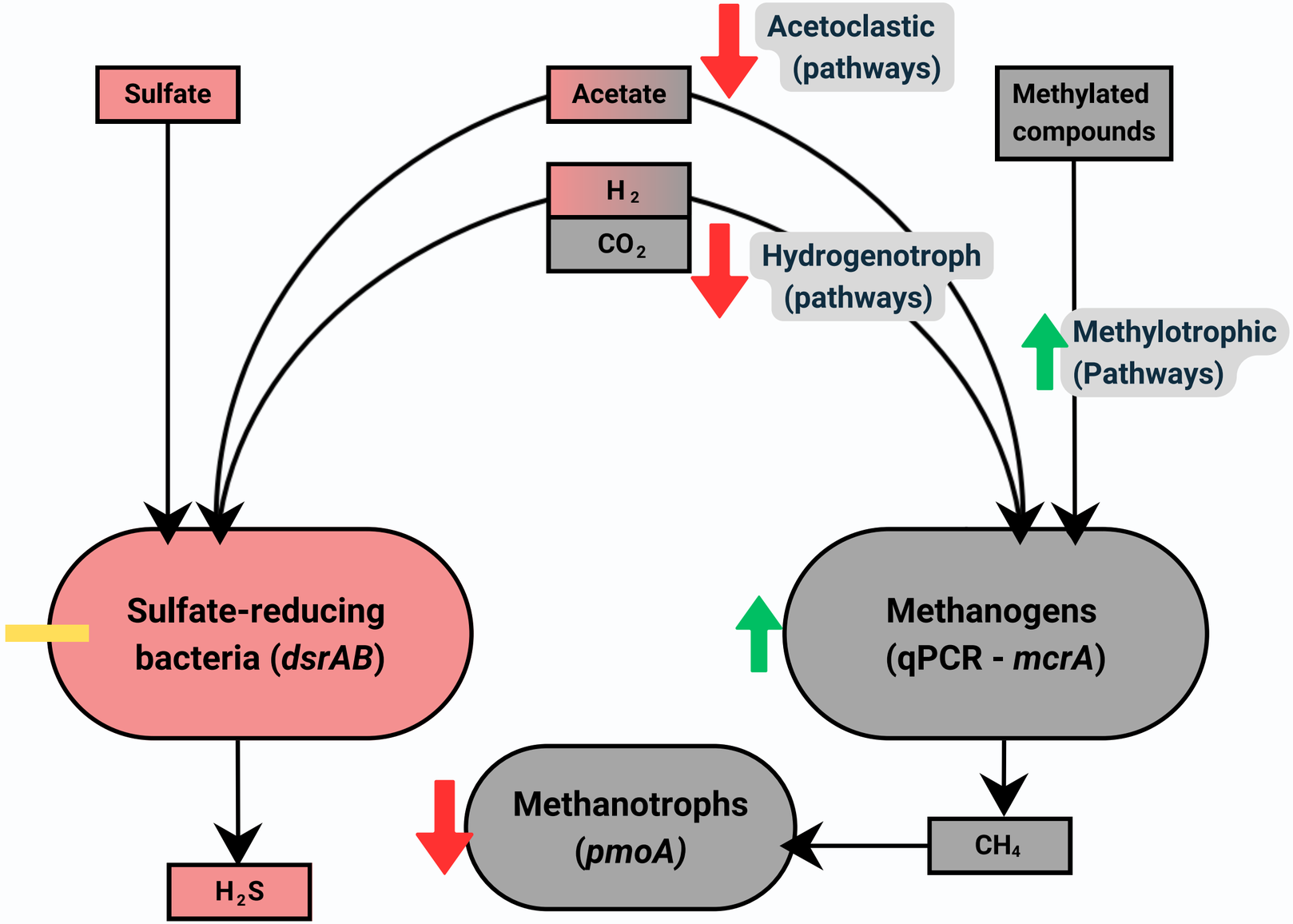
- Increased methanogenic functional potential

PICRUSt Results

Predicted increases in methylotrophic pathways within the DZ

CO2 + H2 & acetate pathways ↓ in DZ, indicating that methylotrophs may drive increased methane

Methanotrophs ↓ in the DZ, may indicate methane can bypass methanotrophy in surface sediments

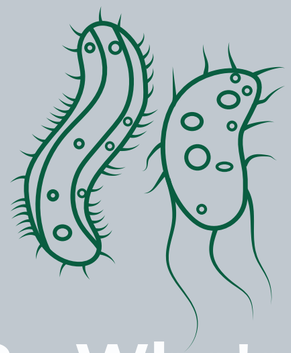


Key Findings

1 - Env. factors & methane?

Methane was high in the DZ, correlated with:

- Salinity
- Water depth
- Organic content

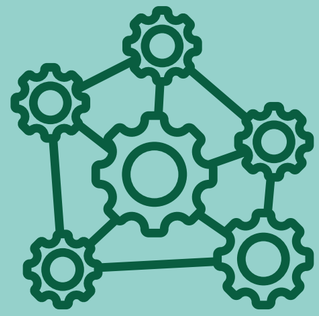


2 - Who's there?

Methanogens: Increased abundance and diversity in the DZ

Increased methylotrophic taxa

Methanotrophs: decreased abundance



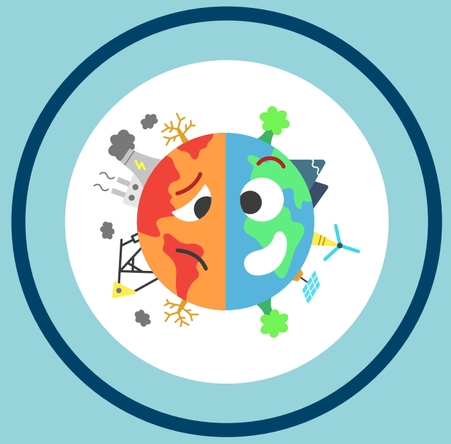
3 - What are they doing?

- Increased *mcrA:16S* ratio in the DZ
- PICRUSt predictions agree with qPCR data
- Predicted importance of methylotrophic pathways (potentially osmolyte-derived)
- Predicted decrease in methanotrophic function

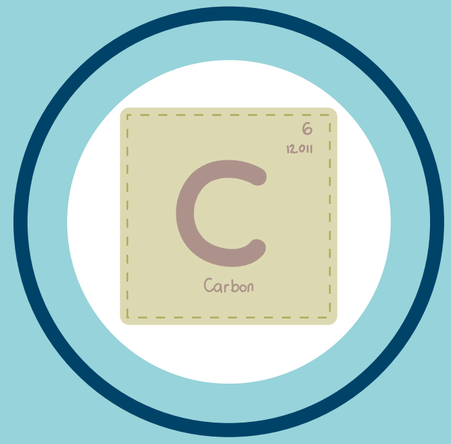
- Generated hypothesis should be confirmed with RNA sequencing to determine empirical activity

Significance

Freshwater flushing, and reduction in nutrients integral for healthy coastal wetlands



Climate change projected to drive ↑ in extent hypersaline conditions



Hypersalinity may offset Carbon sequestration in coastal wetlands

More research required to improve modelling and management

Thank you

Questions?

Acknowledgements

Ngarrindjeri people, on who's country sampling took place. Matilda Southgate (pictured left), Daniel Chilton, Stephen Kidd, Justin Brookes. Also Luke Mosley, David Welsh, Dirk Erler, Luke Vial, Tyler Dornan, Ashleigh Sharrad, and other members of the 'Healthy Coorong Healthy Basin' Goyder Institute inititative.

Contact me

christopher.keneally@adelaide.edu.au

Twitter:

@cckeneally

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GOYDER INSTITUTE FOR WATER RESEARCH

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