Global pattern of nitrogen metabolism in marine prokaryotes using metagenomics

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February 26th , 2026

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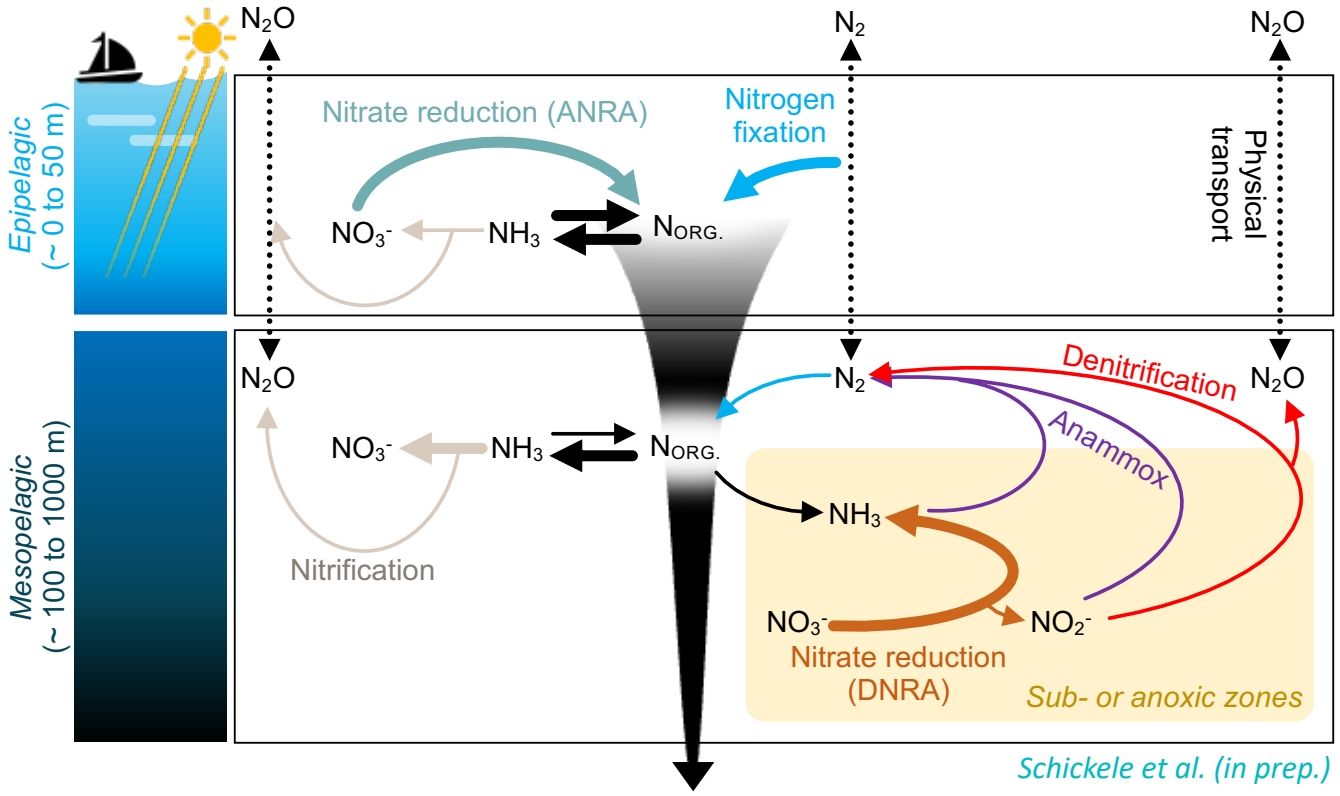
Scientific context

State of knowledge:
Prokaryotic plankton drive all major nitrogen transformations in the ocean

Knowledge largely based on:
- Net sampling
- Cultured bacteria

Research gap:
- Capture only a small fraction of prokaryotic diversity.
- Bias toward visible, abundant, or cultivable taxa (e.g. *Trichodesmium*)



Schickele et al. (in prep.)

Most bacteria and **archaea** driving nitrogen fluxes **remain overlooked**

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Motivation and questions

MOTIVATION

A new opportunity: *in situ* DNA observations
Metagenomic observations simultaneously provides:

- Taxonomic composition
- Functional potential (encoded metabolic pathways)

Unconstrained by *in vitro* culture or traditional sampling methods

Combined with **habitat modelling**, it enables direct links between:

- Microbial diversity
- Metabolic pathways
- Environmental conditions

RESEARCH QUESTIONS

Objective 1: How are nitrogen cycling enzymes distributed in the ocean metagenome?

- *Aerobic vs anaerobic pathways*
- *Bioavailable vs bio-unavailable*

Objective 2: What are the environmental drivers?

- *Temperature, oxygen, nutrients, productivity*

Objective 3: Which taxonomic group support these metabolic pathways?

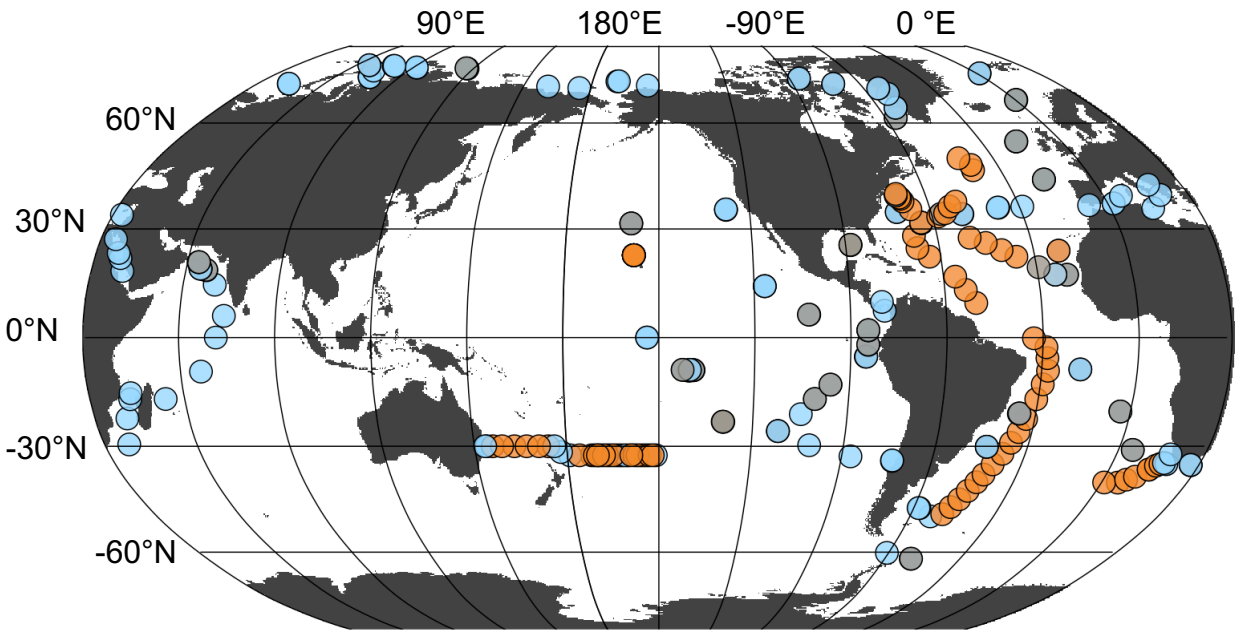
- *Cyanobacteria for nitrogen fixation*
- *Archea for nitrification*

Metagenomic observations

OCEAN MICROBIOMICS DATASET

- *35,000* ***genomes***
- *215 globally distributed* ***stations***
- *Enzymes and species* ***annotations***

Paoli et al. (2022)



Depth layer of the samples: 0 - 50 m both 100 - 1000 m

CONSIDERED PATHWAYS

Enzyme	Pathway
K02586 K02591 K02588	Nitrogen fixation
K00367 K00366	ANRA
K10944 K10945 K10946 K10535	Nitrification
K00362 K00363	DNRA
K04561 K02305 K00376	Denitrification

Schickele et al. (in prep.)

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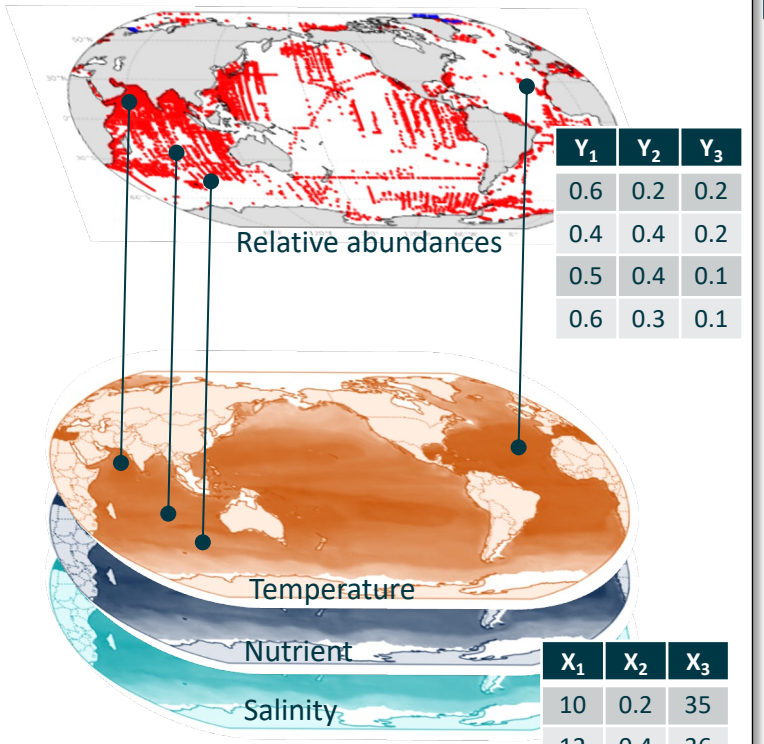
Habitat modelling for compositional data

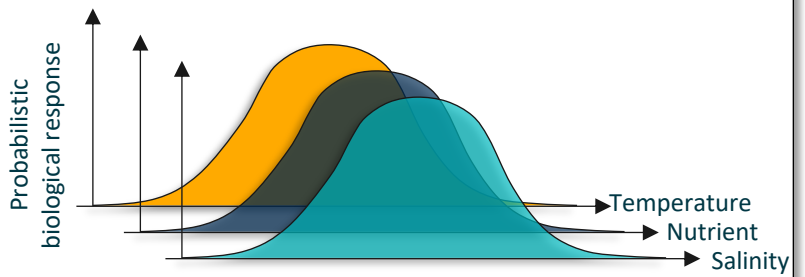
Data processing



Y_1	Y_2	Y_3
0.6	0.2	0.2
0.4	0.4	0.2
0.5	0.4	0.1
0.6	0.3	0.1

X_1	X_2	X_3
10	0.2	35
12	0.4	36
25	5	15
14	0.3	33

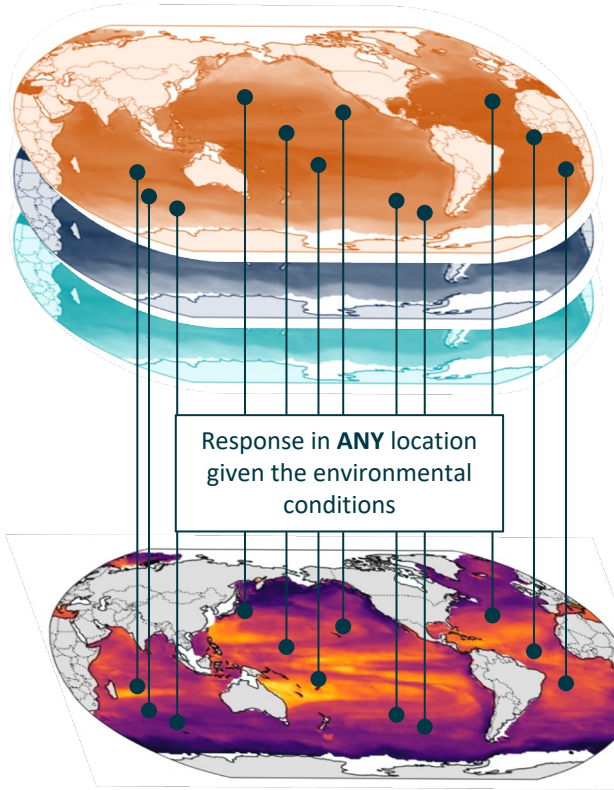
Model training & evaluation



At climatological scale:

The multi-dimensional space of environmental conditions and resources (e.g., temperature, nutrients, redox state) under which the genomic repertoire of an organism encodes the metabolic functions supporting the nitrogen cycle.

Spatial projections



Schickele et al. (2025.)

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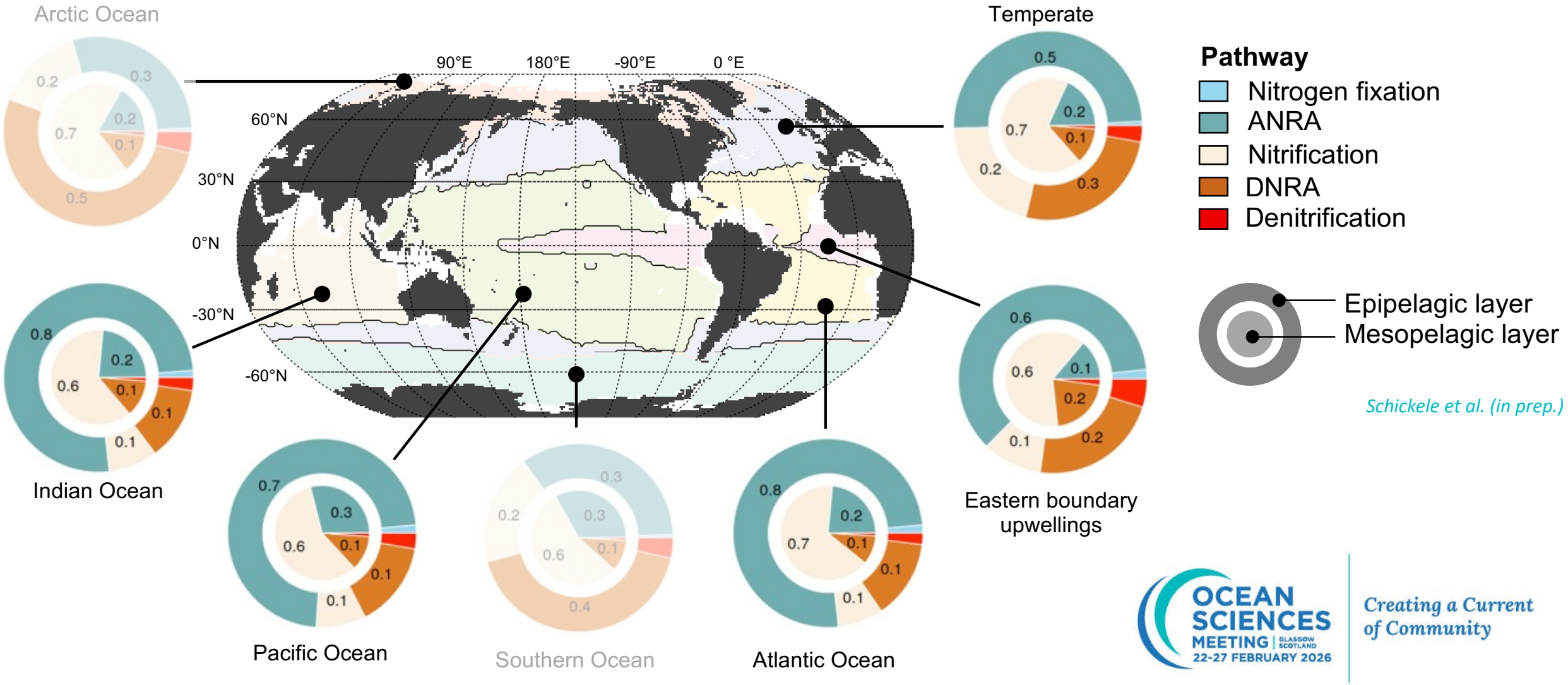
Overview of the genomic potential



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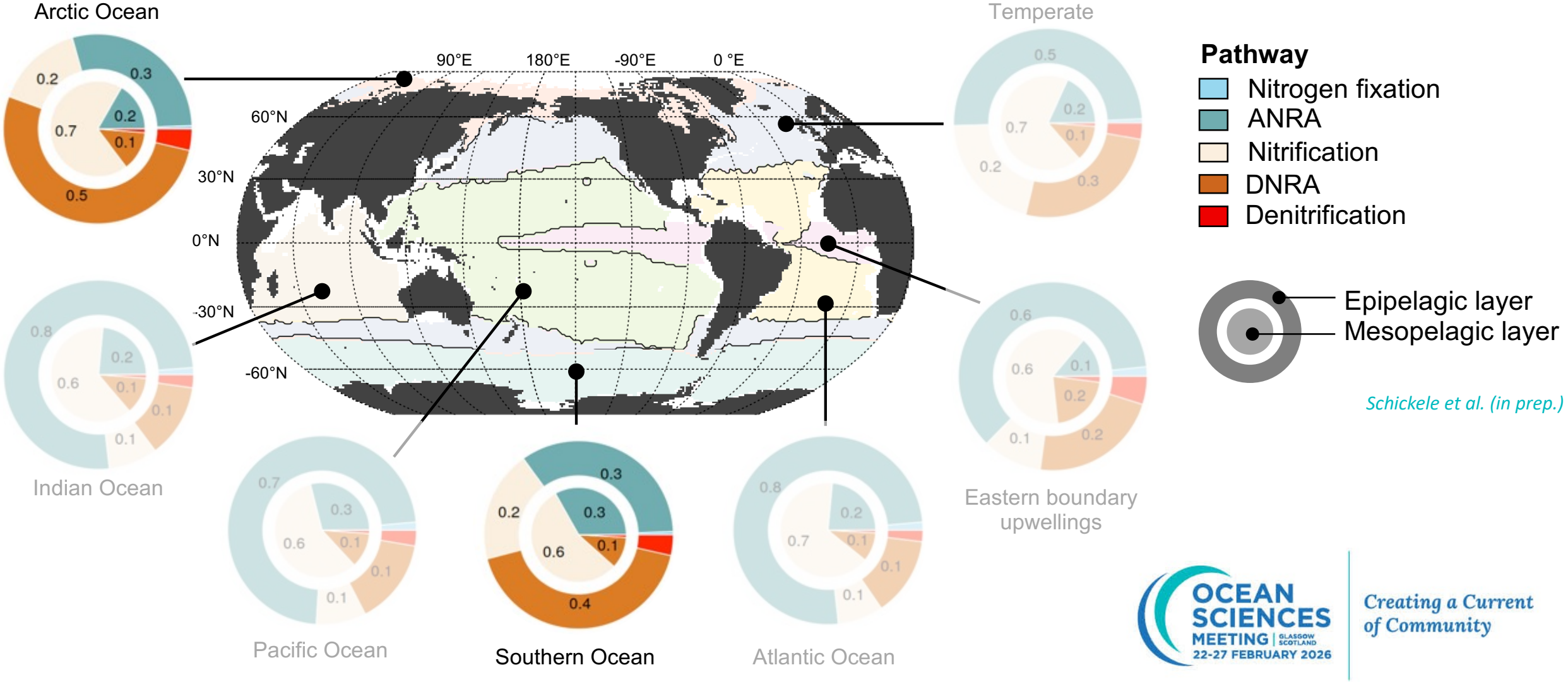

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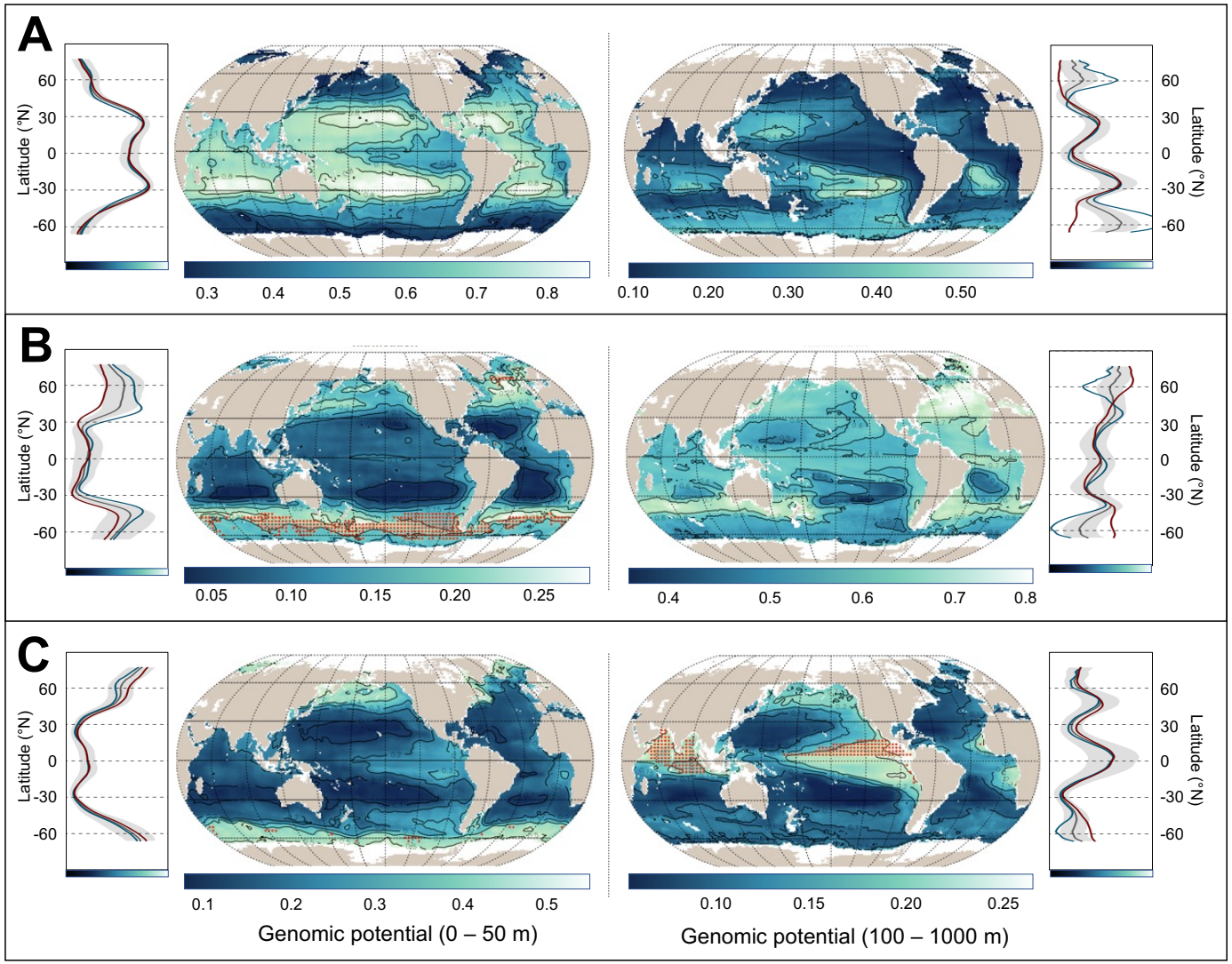
Bio-available nitrogen transformations



Schickele et al. (in prep)

Assimilatory Nitrate Reduction

- *Aerobic process*
- *Used for cellular biosynthesis*

Nitrification

- *Aerobic*
- *Light inhibited*
- *Dominates in the mesopelagic areas*

Dissimilatory Nitrate Reduction

- *Higher relative abundance in high latitudes and productive areas*
- *Used as electron acceptor from Nitrate*
- *Facultative anaerobe*

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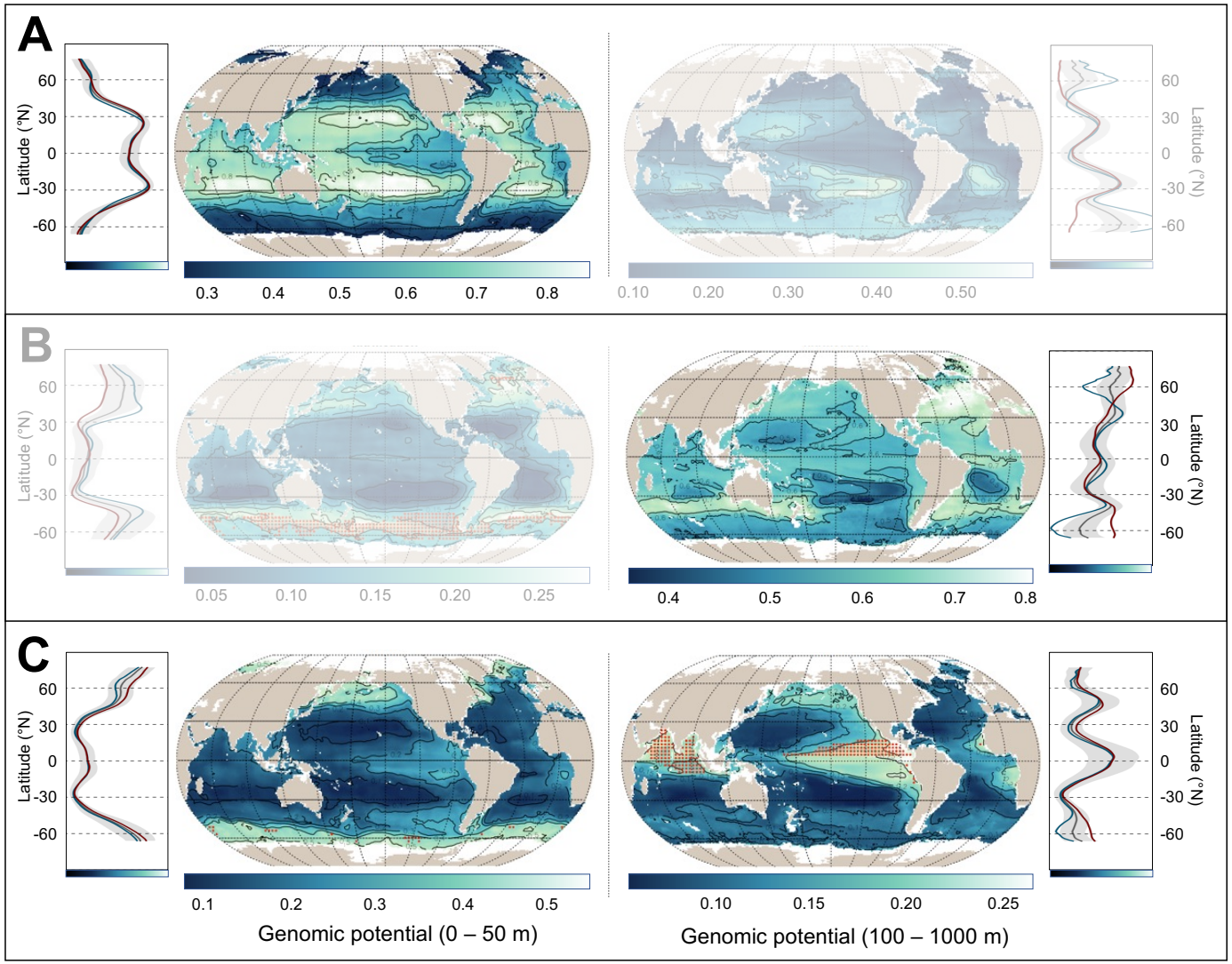

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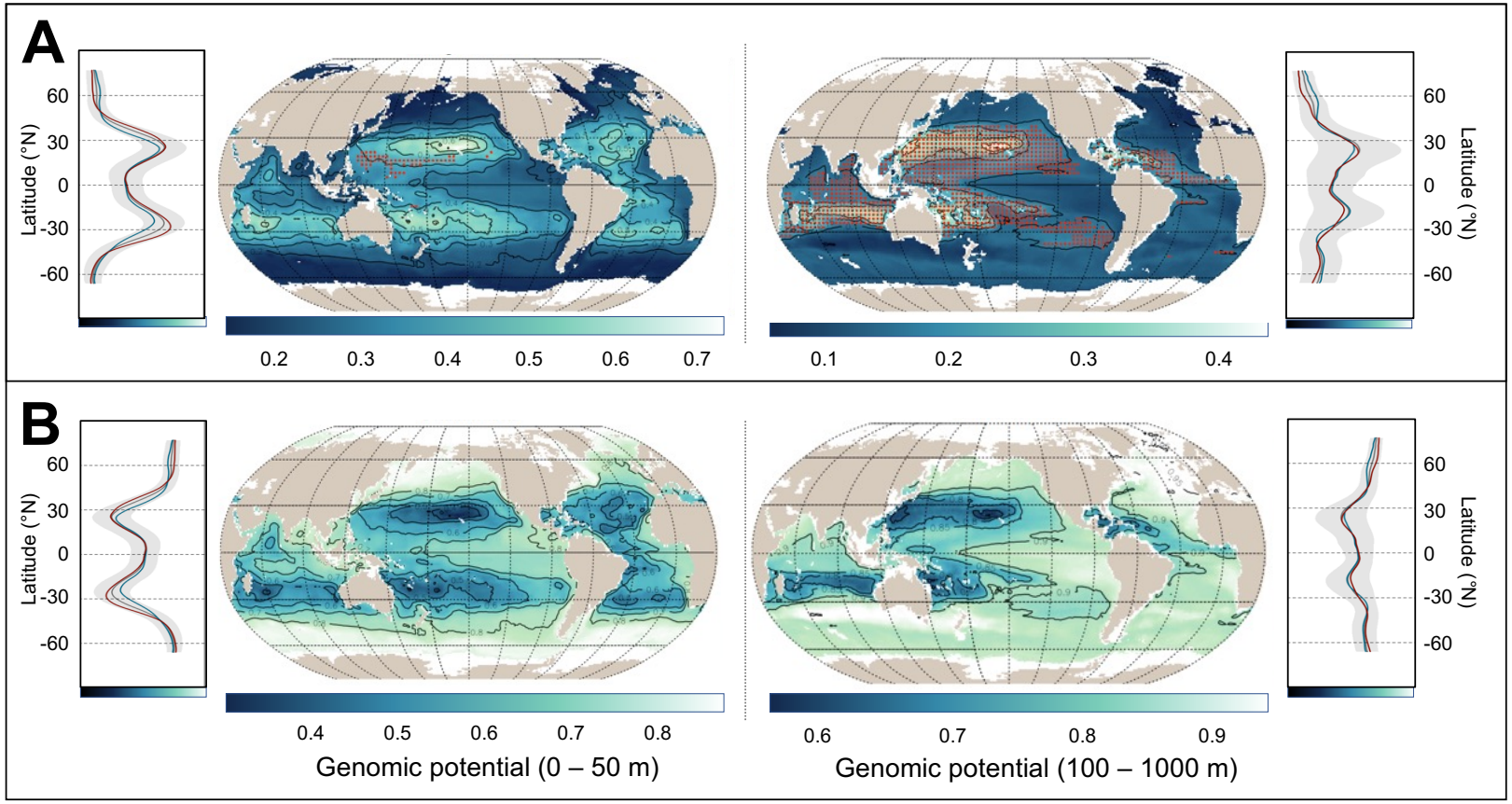
Bio-unavailable nitrogen transformations



Schickele et al. (in prep)

- ***Nitrogen fixation***
  - *Aerobic process*
  - *Used for cellular biosynthesis*

- ***Denitrification***
  - *Anaerobic process*
  - *Uses nitrogen as electron acceptor*

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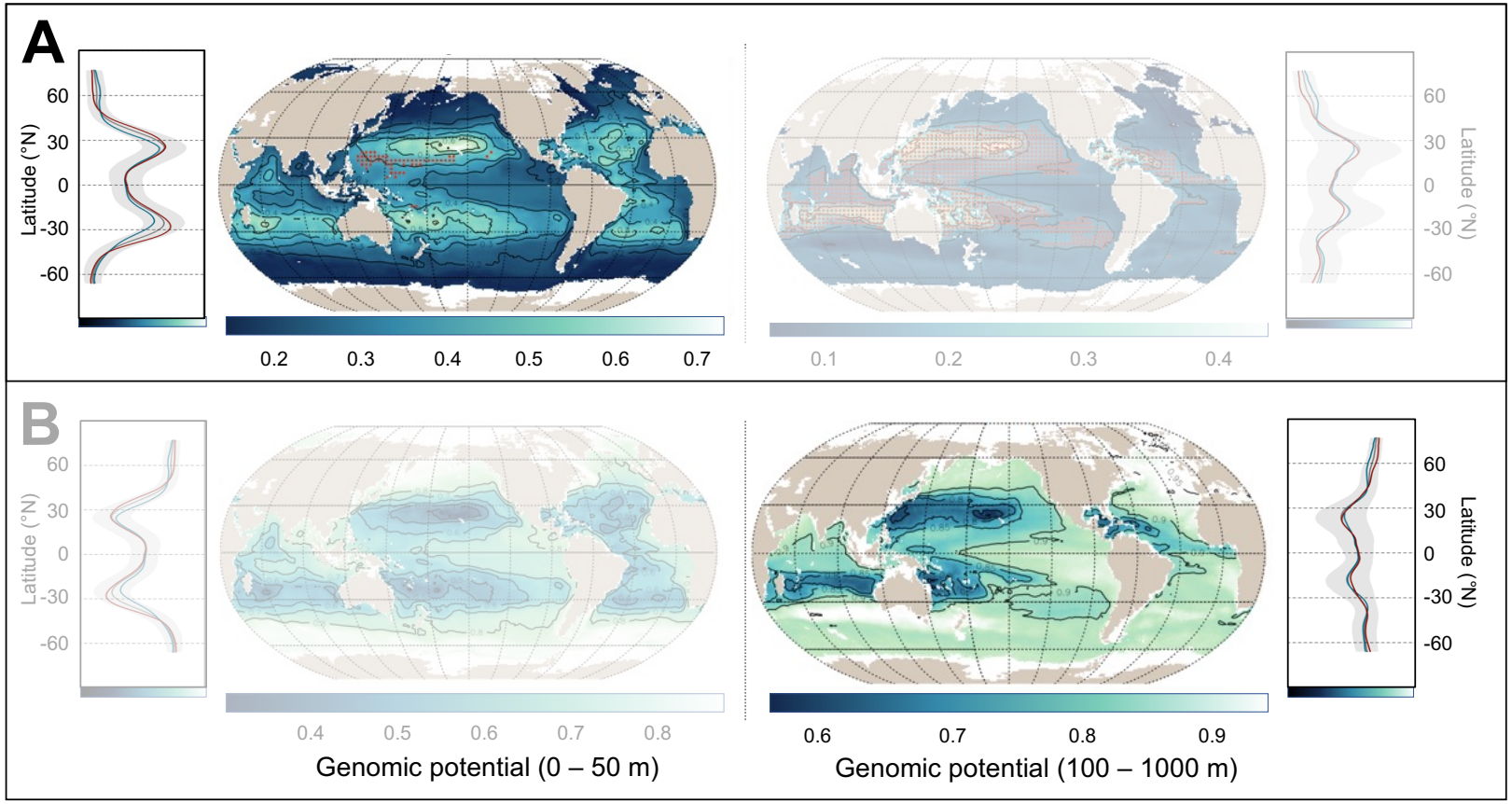

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Who supports these transformations ?

Nitrogen fixation (n = 90)

ANRA (n = 279)

Nitrification (n = 47)

DNRA (n = 841)

Denitrification (n = 560)

Nitrososphaeria
Cyanobacteriia
Gammaproteobacteria
Alphaproteobacteria
Bacteroidia
Planctomycetes
Nitrospinia
Leptospirae
Dehalococcoidia
Marinisomatia

Epipelagic layer (0 – 50 m)
Mesopelagic layer (100 – 1000 m)

Schickele et al. (in prep)

Taxonomic composition:

- *We find the main taxonomic classes known for nitrogen transformation*
- *Can go further and map their distribution, at class or species-level*

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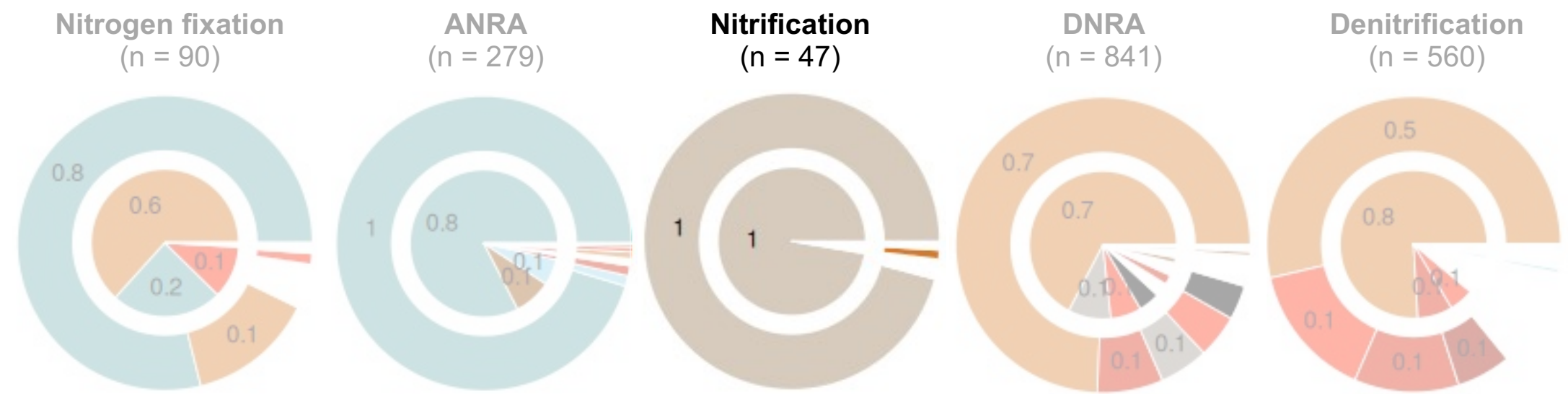

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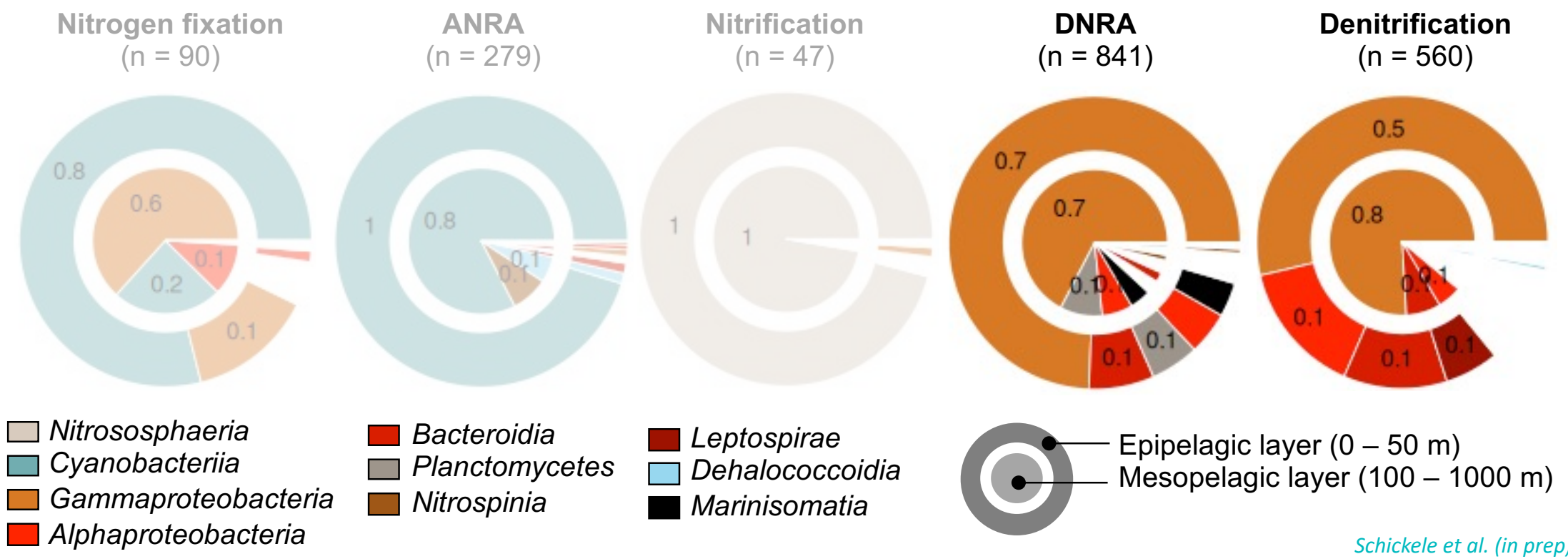

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Take home message(s)

Bio-unavailable transformations are rare

- *Nitrogen fixation and denitrification control the ocean nitrogen reservoir*
- *Yet they are only performed by a minority of organisms*

Environmental controls are depth dependant

- *Nitrogen concentration and temperature drive epipelagic nitrogen transformations*
- *Oxygen saturation drives mesopelagic nitrogen transformations*

To go further

- *Map the prokaryotic diversity supporting each nitrogen cycling pathways*
- *Move from metagenome towards transcriptome*
- *Links between diversity, gene presence, gene expression and fluxes*

THANKS FOR LISTENING !

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