南方海洋科学与工程广东省实验室（珠海）
Southern Marine Science and Engineering Guangdong Laboratory(Zhuhai)

croucher summer courses

Microbially-driven nutrient cycling and coupling mechanisms in mangrove sediments

Zhili He

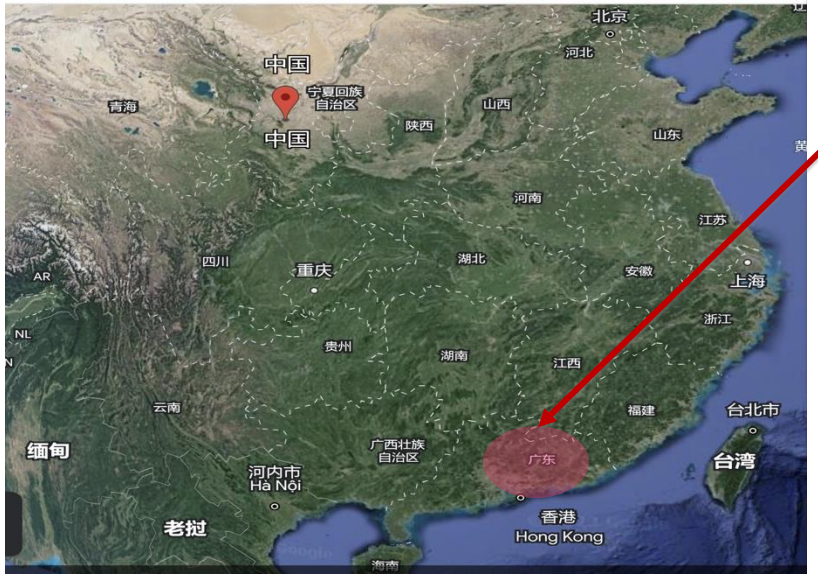
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Hong Kong University of Science and Technology

Hong Kong

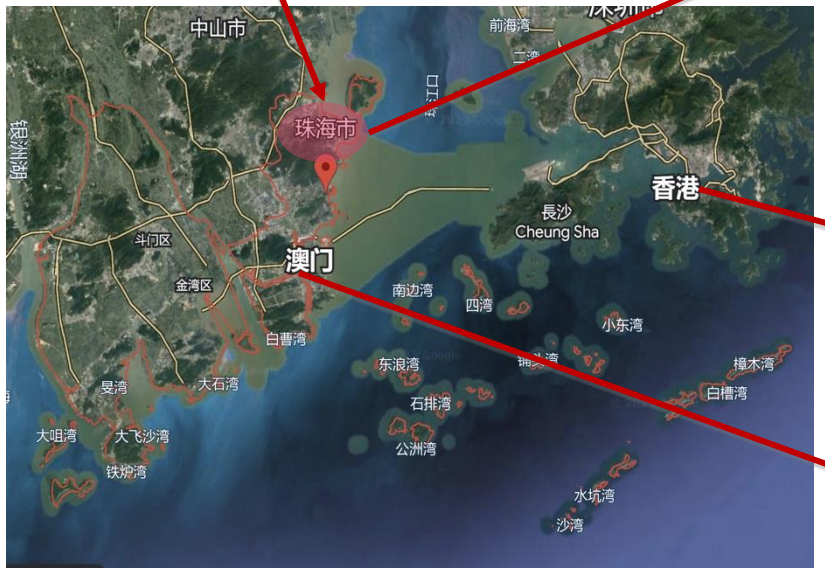
June 30, 2025



Guangdong province, China



Zhuhai



Hong Kong

Macau

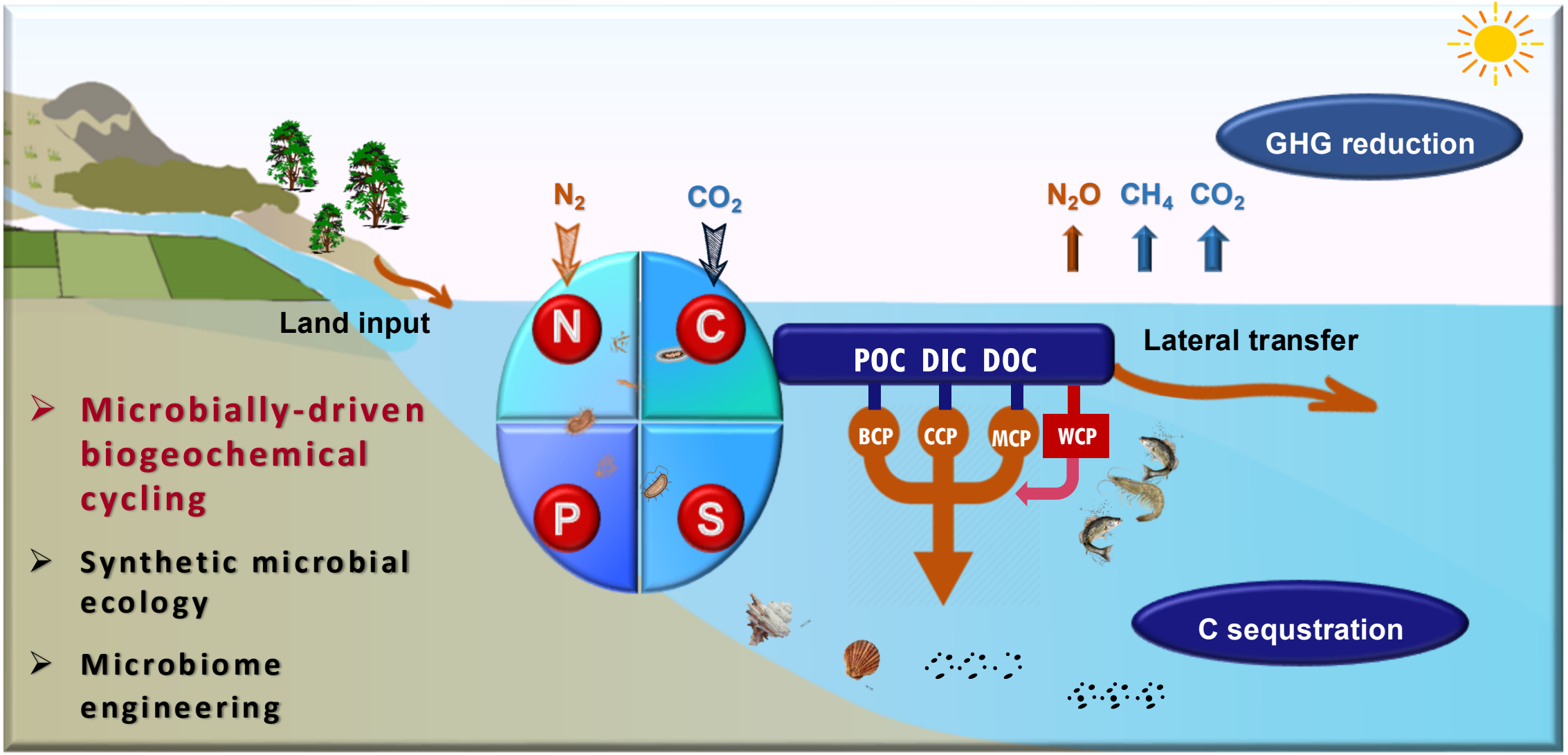
- Marine Microbiology Group
- Marine Synthetic Ecology Research Center (MSEC)

崇尚首创 力争最优

To be the first or the best

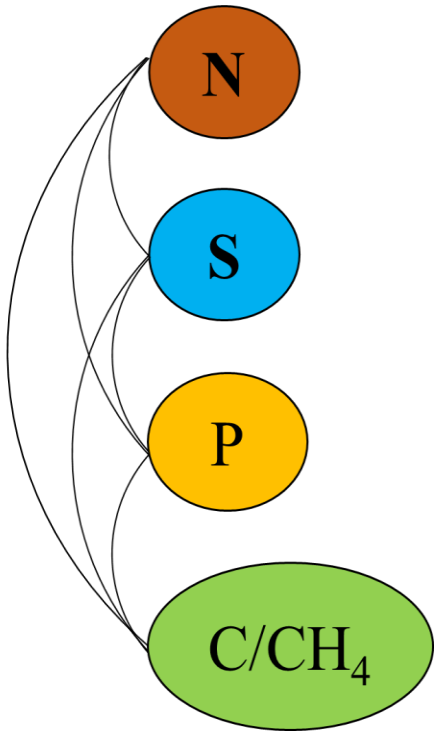
- Founded in 2018 for marine science and engineering
- Administrated by Sun Yat-sen University (SYSU)
- Affiliated with 43 institutions (e.g., SYSU, HKUST, MU)
- Eight public platforms for marine science and engineering
- ~1200 full-time or affiliated researchers and support staff
- Frontier Research Center for innovative research and development, including the Marine Microbiology Group, and the Marine Synthetic Ecology Research Center
- One journal: Ocean - Land - Atmosphere Research

Research directions in the Marine Microbiology group



WCP: waste carbon pump

C/N/S/P functional gene database construction



NCycDB (Tu et al., 2019, *Bioinformatics*)

- 68 gene families, 8 pathways and 219,146 representative sequences

SCycDB (Yu et al., 2021, *Mol Ecol Resour*)

- 207 gene families, 8 pathways and 585,055 representative sequences

PCycDB (Zeng et al., 2022, *Microbiome*)

- 139 gene families, 10 pathways and 863,513 representative sequences

MCycDB (Qian et al., 2022, *Mol Ecol Resour*)

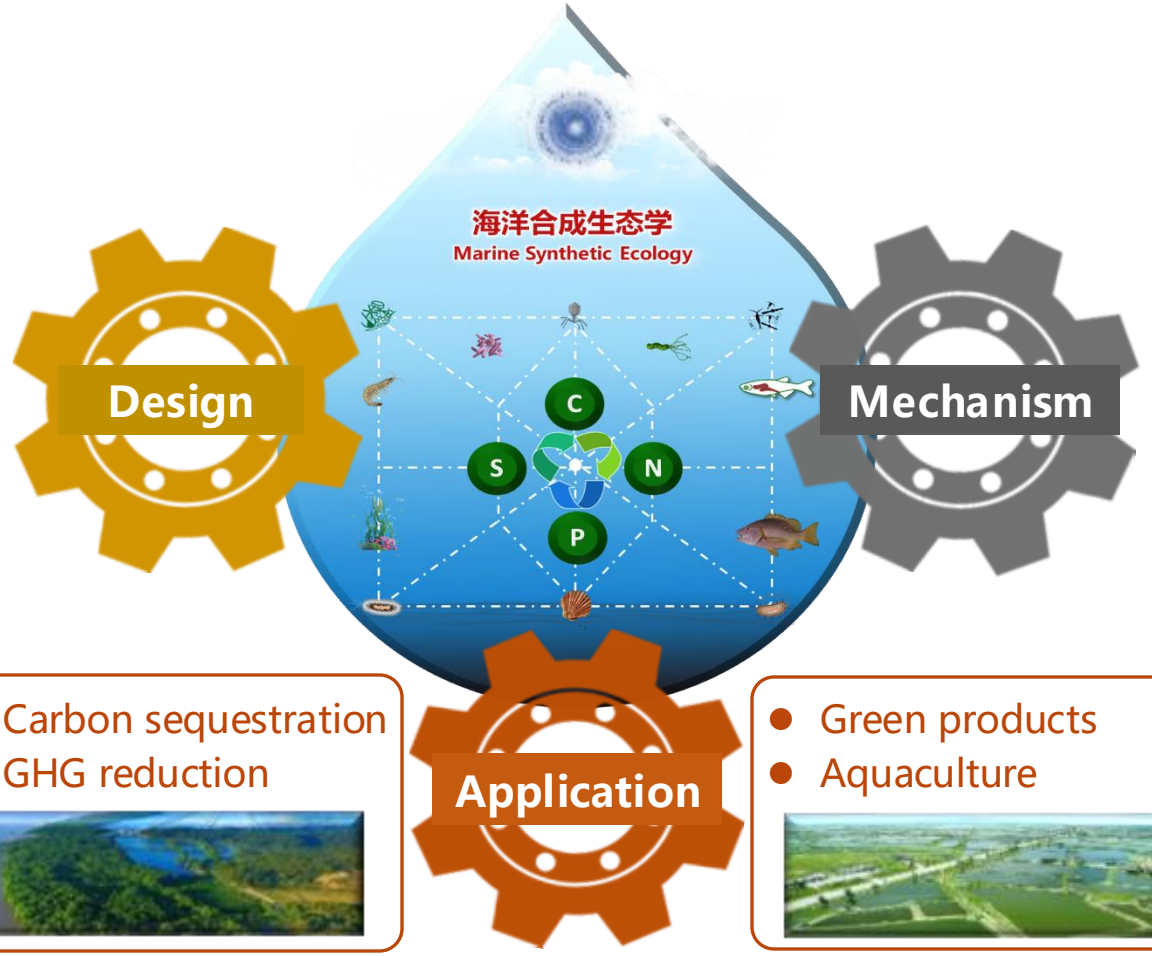
- 298 gene families, 10pathways and 651,098 representative sequences

CCycDB (Zhou et al., unpublished)

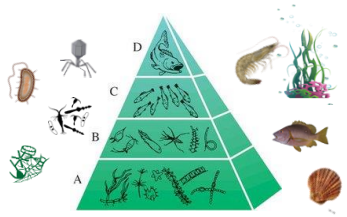
- 4572 gene families, 92 pathways, 6 modules, and 10,548,067 representative sequences

(https://ccycdb.github.io/)

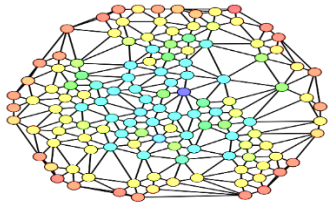
海洋合成生态学研究中心
Marine Synthetic Ecology Research Center (MSEC)



- Synthetic communities
- Synthetic ecosystems



- Interaction mechanisms
- Interactive networks

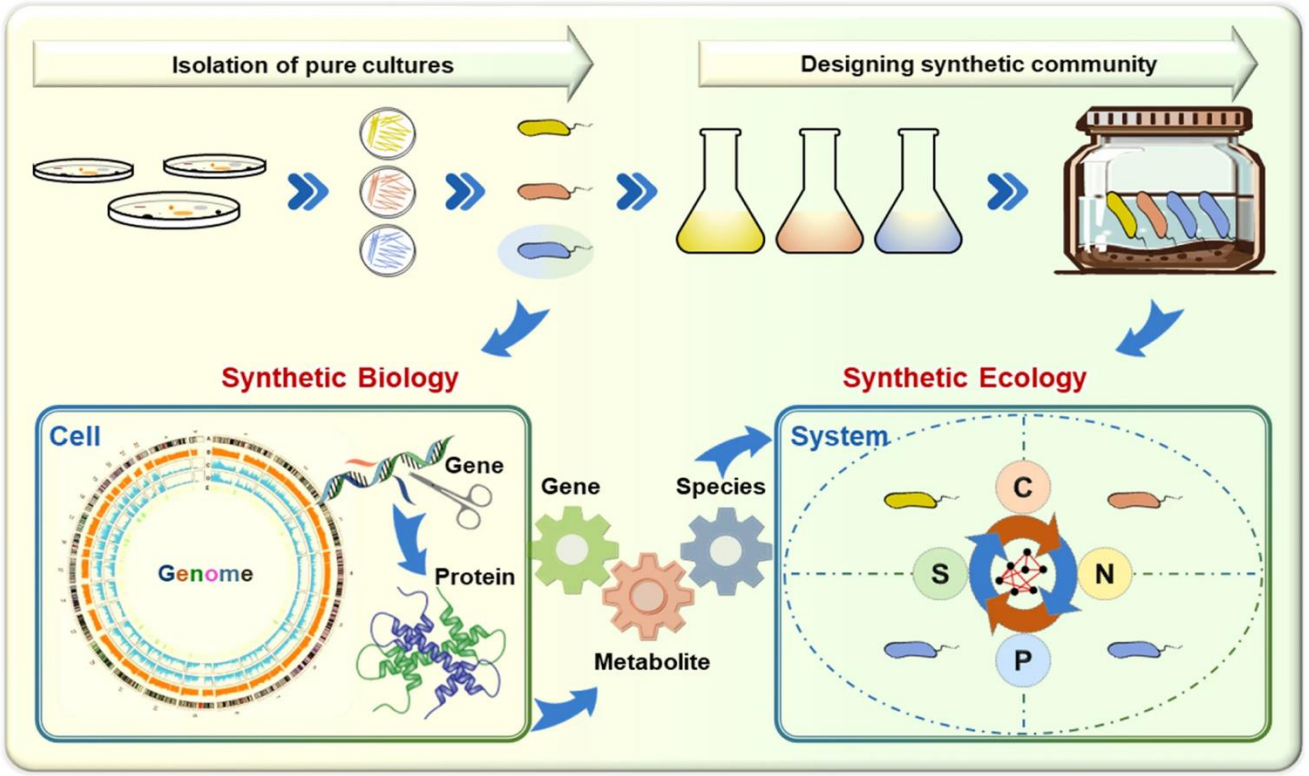


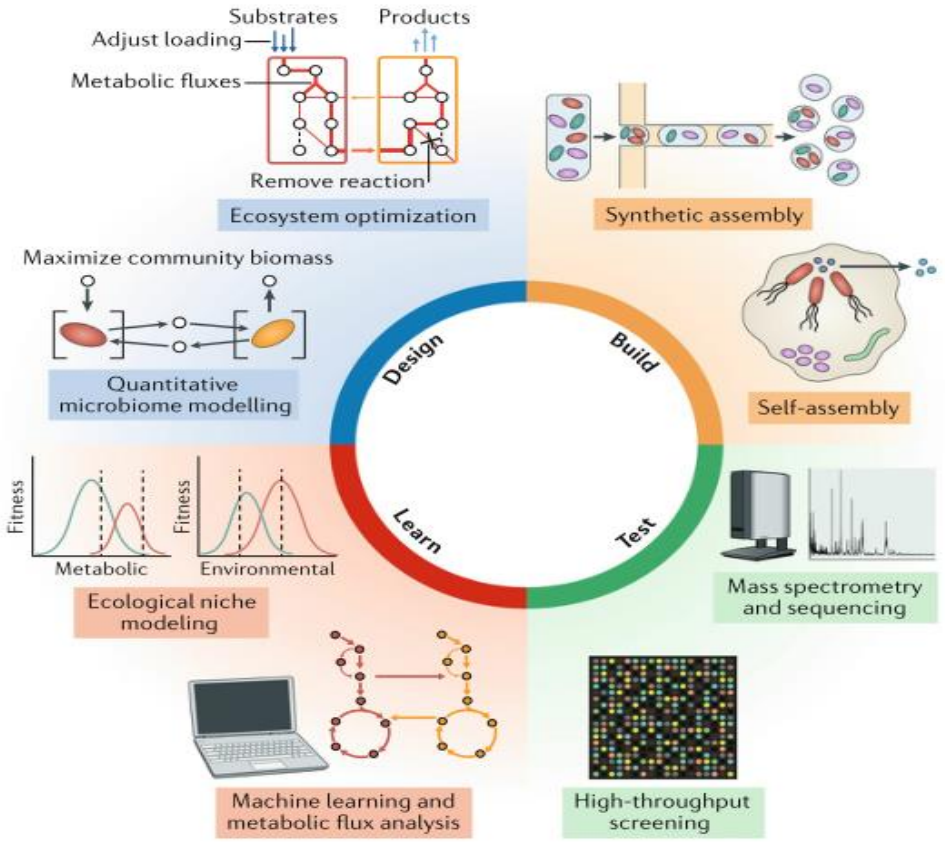
- Carbon sequestration
- GHG reduction

- Green products
- Aquaculture

Synthetic communities towards microbiome engineering

Microbial strains → Synthetic communities → Synthetic ecosystems





(Yan et al., 2025, *Adv Biotechnol*; Lawson et al., 2019, *Nat Rev Microbiol*)

Mangrove wetlands are unique coastal ecosystems









- High biodiversity/productivity
- Important carbon (C) sinks
- Filtering land pollutants
- Wave protection



(Kathiresan *et al*., 2001, *Adv Mar Biol*; Alongi, 2014, *Annu. Rev. Mar. Sci*; Lee *et al*., 2014, *Glob Ecol Biogeogr*)

High microbial diversity and functionality



- **High microbial diversity**
- **Co-existence of multiple electrons (e.g., O_2, NO_3^-, NO_2^-, Fe^{3+}, SO_4^{2-})**
- **Distinct element cycling features:**
  - High organic matter, decomposing fast
  - Low nitrogen, cycling efficiently
  - High sulfur, transforming quickly

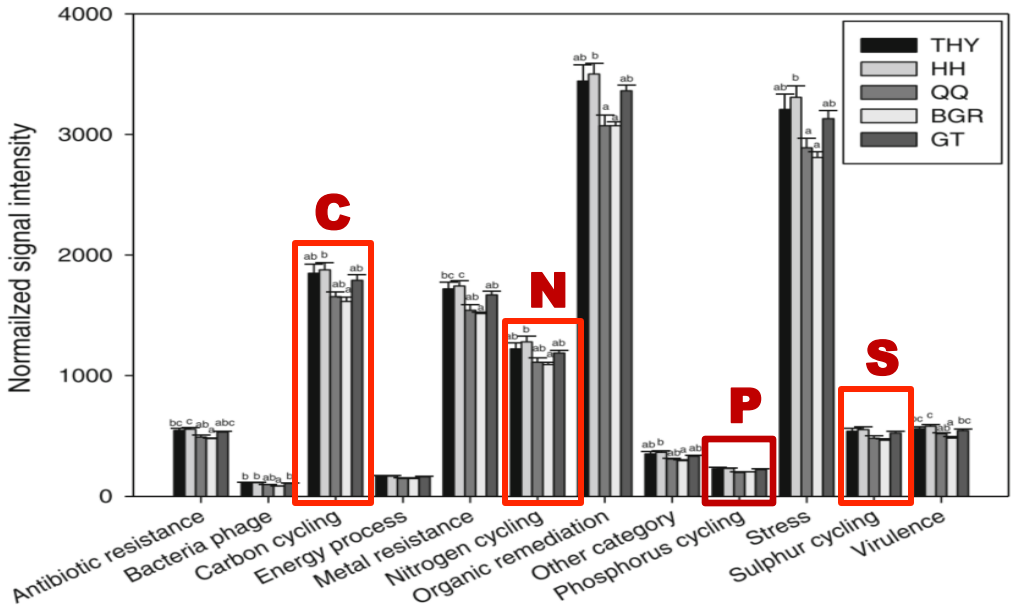


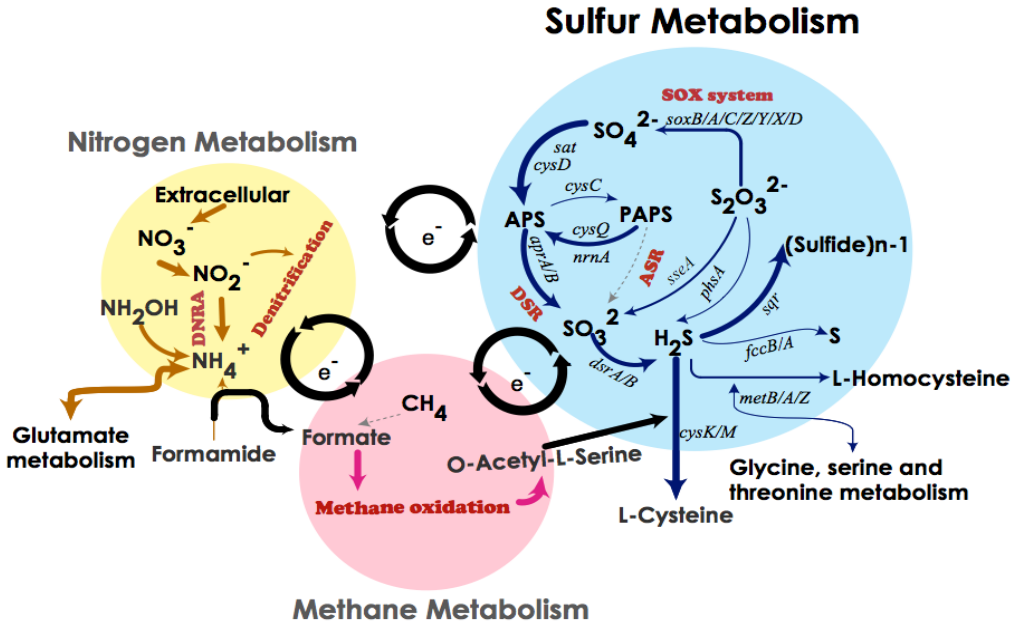






Microbially-driven C, N, S and P cycling processes

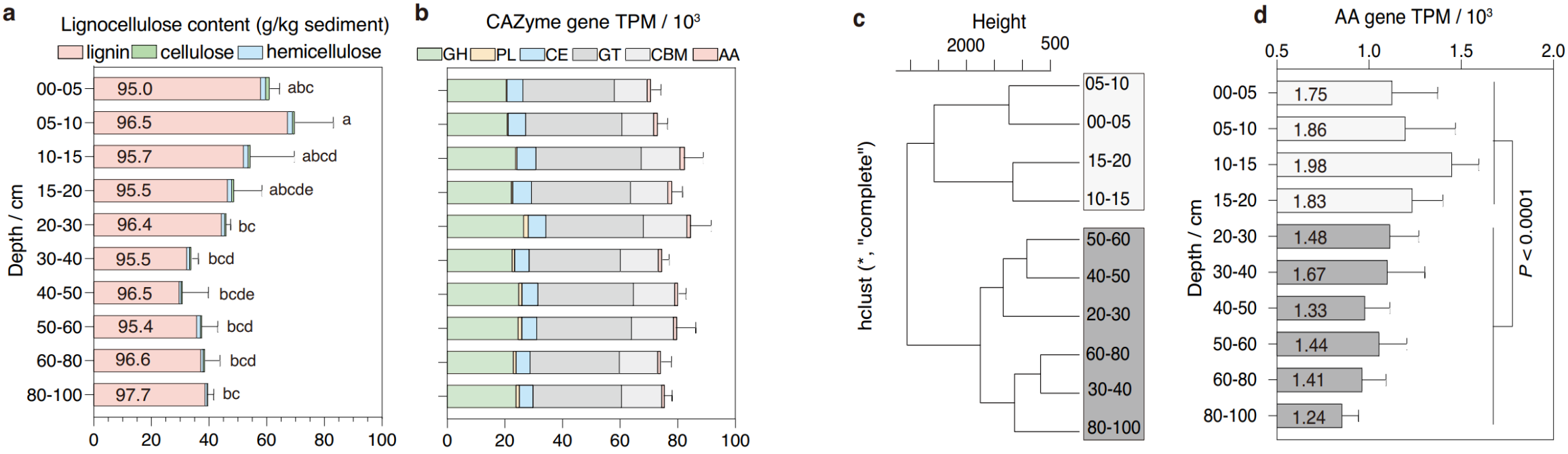




- High abundances of microbial C/N/S/P cycling genes
- Possible couplings of C/N/S/P cycling processes
- Methane metabolism as a bridge of C/N/S cycling

(Bai *et al.*, 2013, *Appl Microbiol Biotechnol*; Lin et al., 2019, *Microb Ecol*)

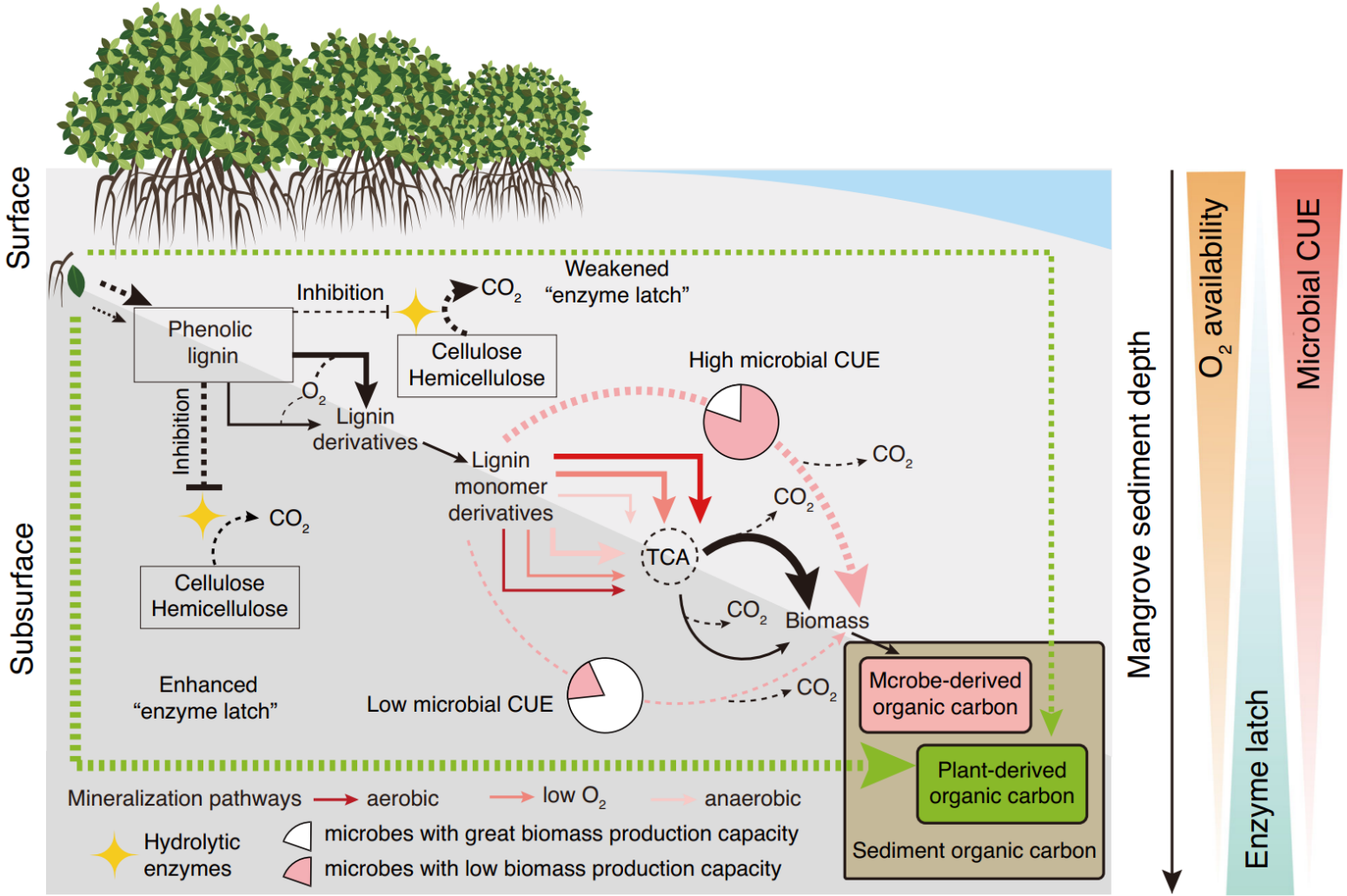
Lignocellulose and CAZyme-coding gene abundances



- Lignin is a main component of organic C in mangrove sediment
- Low abundances of lignin breakdown enzymes (e.g., auxiliary activity family genes)
- Accumulation of phenolic fragments and non-phenolic derivatives in deep sediments

(Ding et al., 2025, *npj Biofilms Microbiomes*)

C storage mechanisms in mangrove sediments

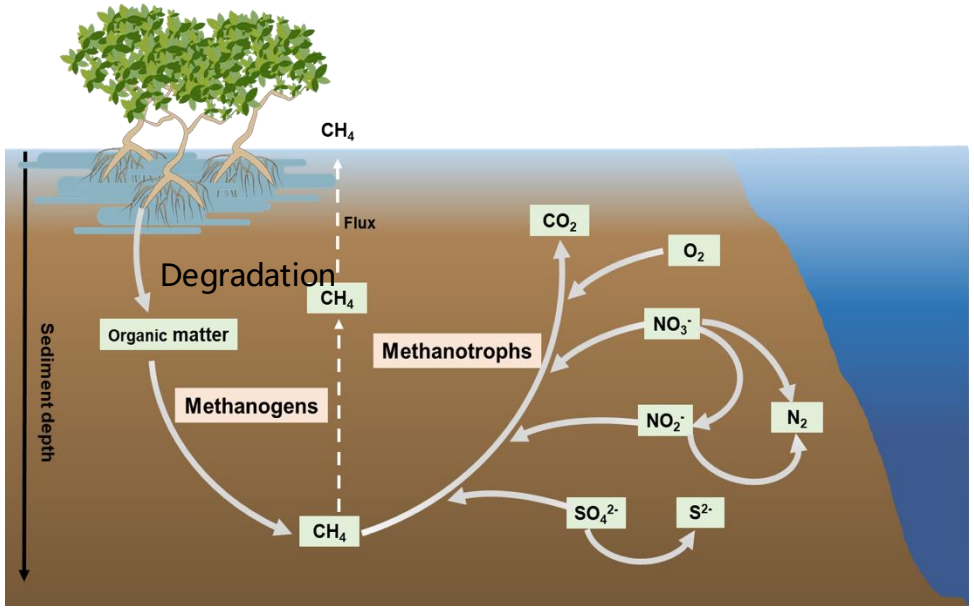


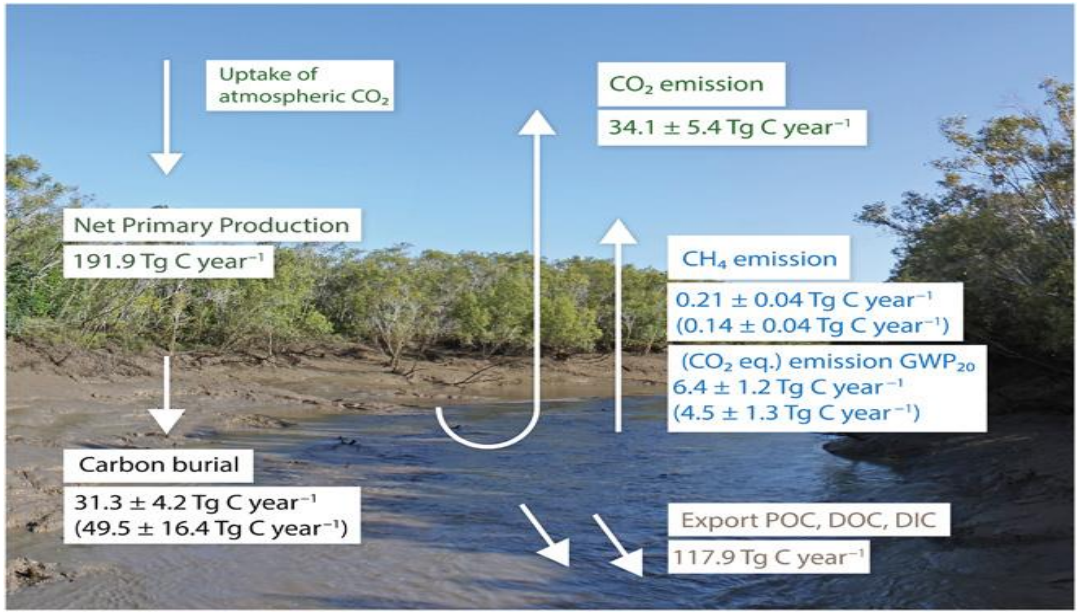
- **Low microbial CUE resulted in more plant-driven C storage in the deep sediment**
- **Weakened enzyme latch resulted in more microbial-derived organic C storage in the surface sediment**

(Ding et al., 2025, *npj Biofilms Microbiomes*)

Methane cycling in mangrove ecosystems

- 0.1% area
- 20% CH_4 emissions

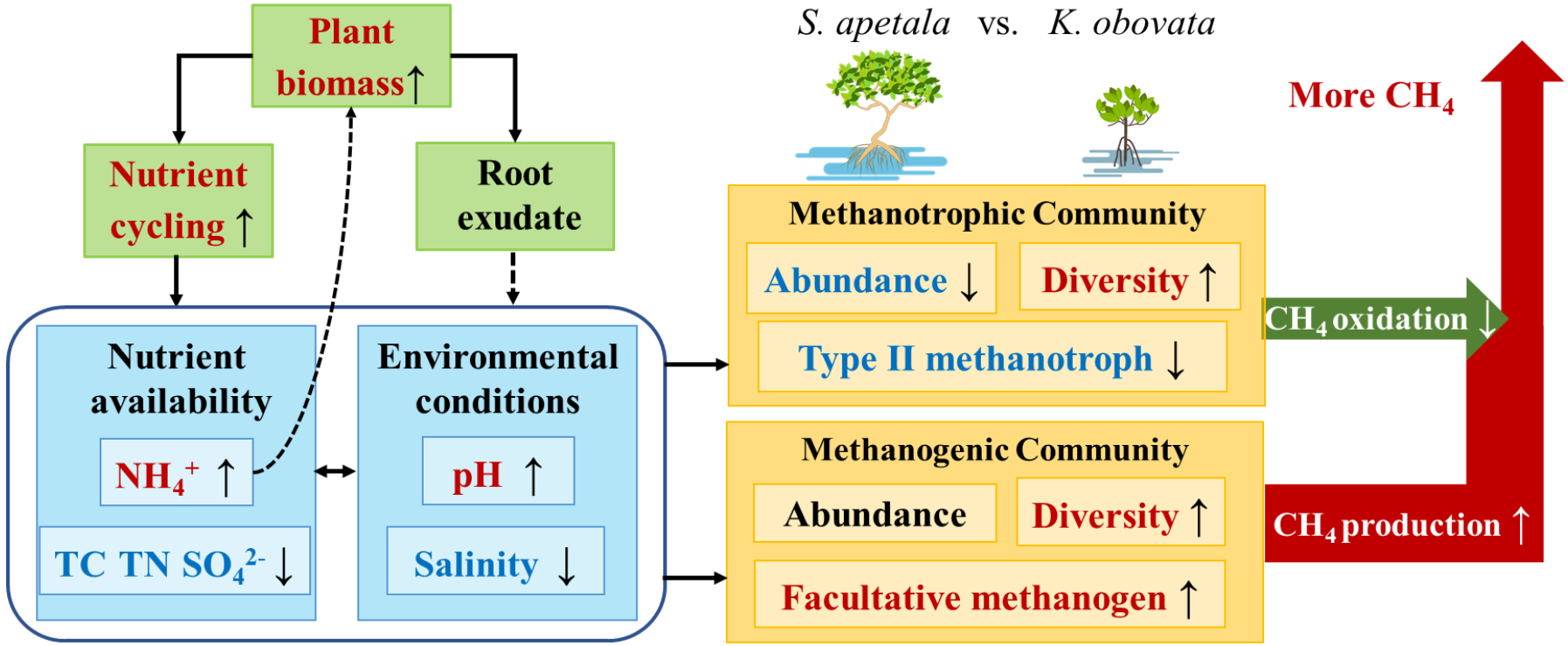




Methane emissions could offset 20% of the carbon storage in mangrove ecosystems

(IPCC, 2014; Zhang *et al*., 2017, *PNAS;* Cai et al., 2018, *ISME J*; Rosentreter *et al*., 2018, *Sci Adv*)

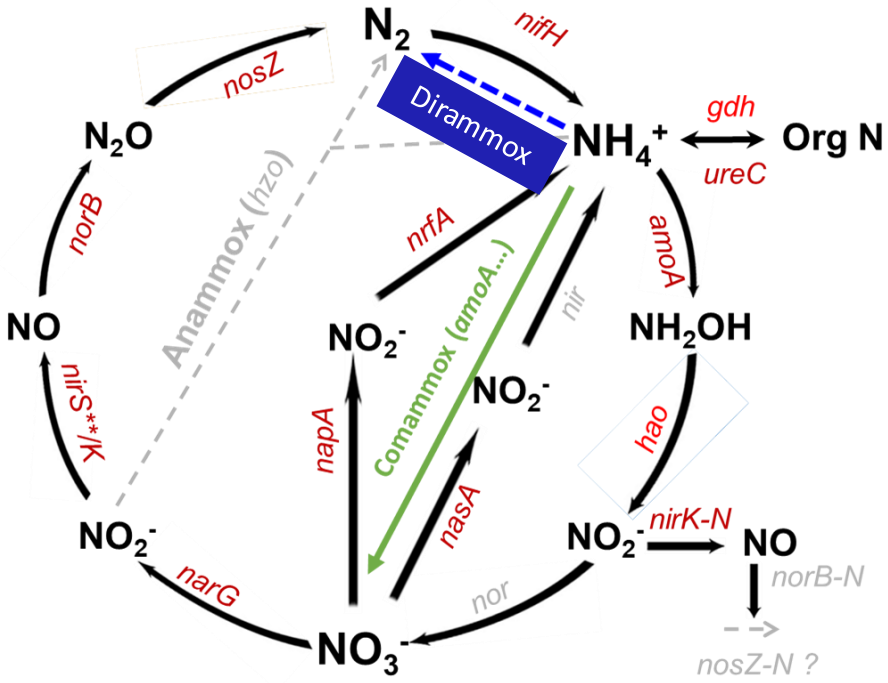
Introduced *S. apetala* increased methane emissions

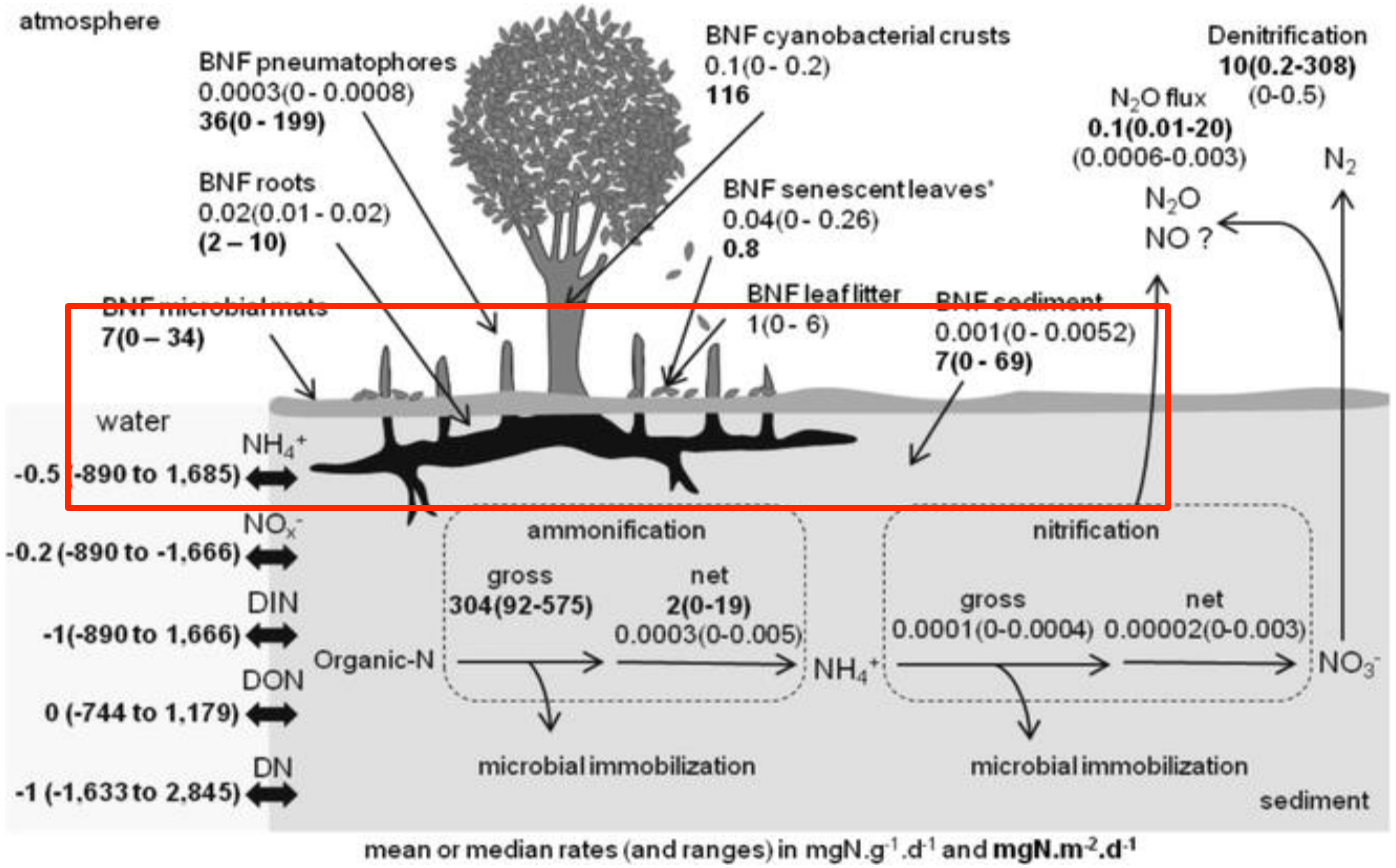


- *K. obovate* and *S. apetala* are popular native and introduced mangrove species
- Introduced *S. apetala* shifted methane cycling microbial communities, increased methane emissions, and decreased C sinks

(Yu et al., 2020, *Soil Biol Biochem*)

The N cycle in mangrove ecosystems



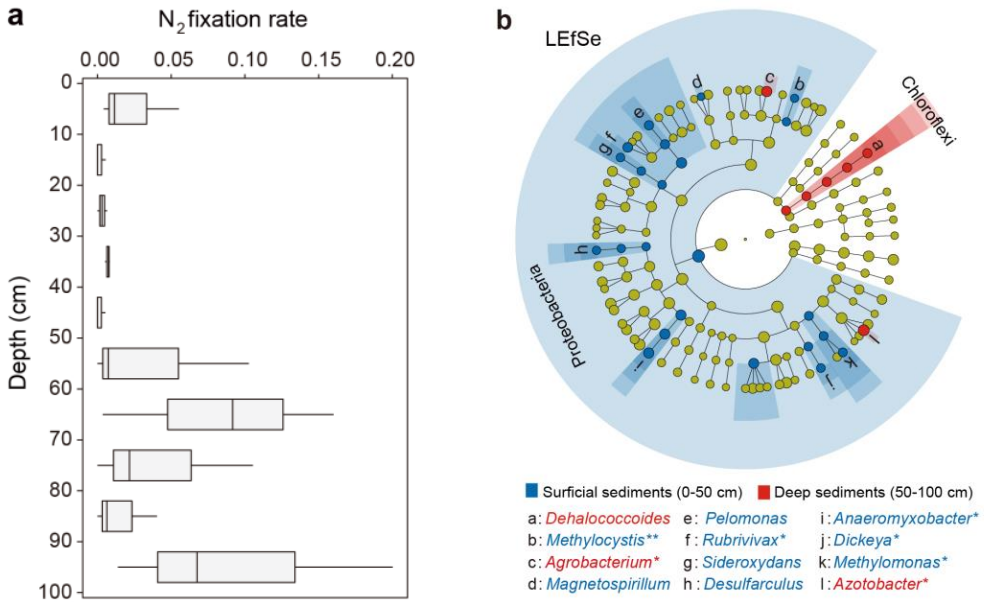


➢ **Microbial N_2 fixation is important N resources**

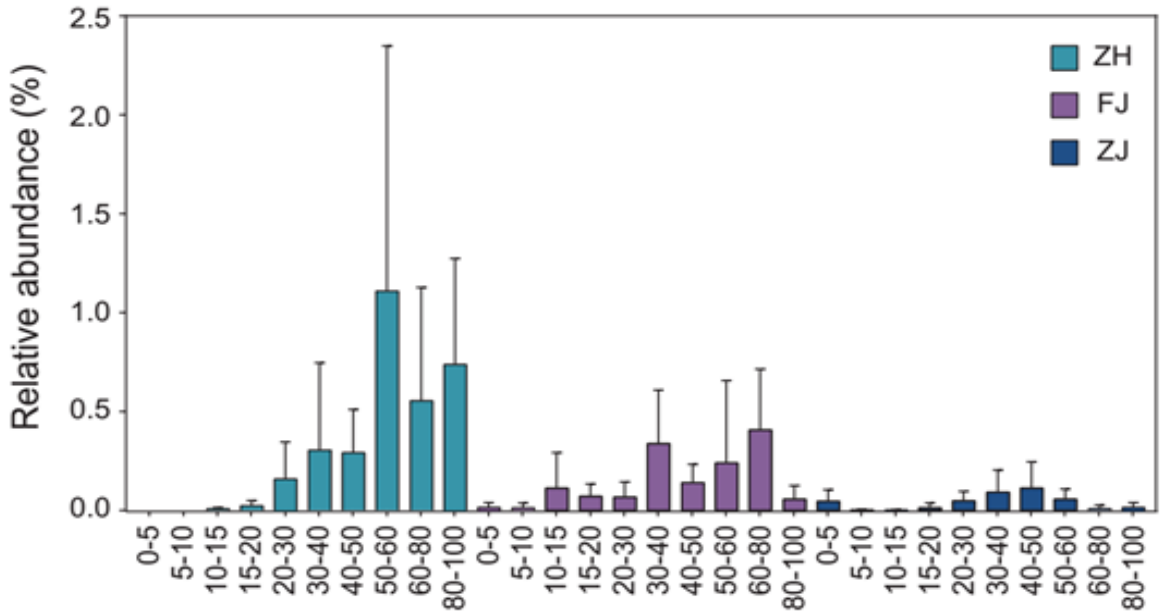
(He *et al.*, 2010, *Ecol Lett*; Reis *et al.*, 2017, *Plant Soil*)

N_2-fixing and methanogenic microbial communities

A. N_2-fixing microbial communities



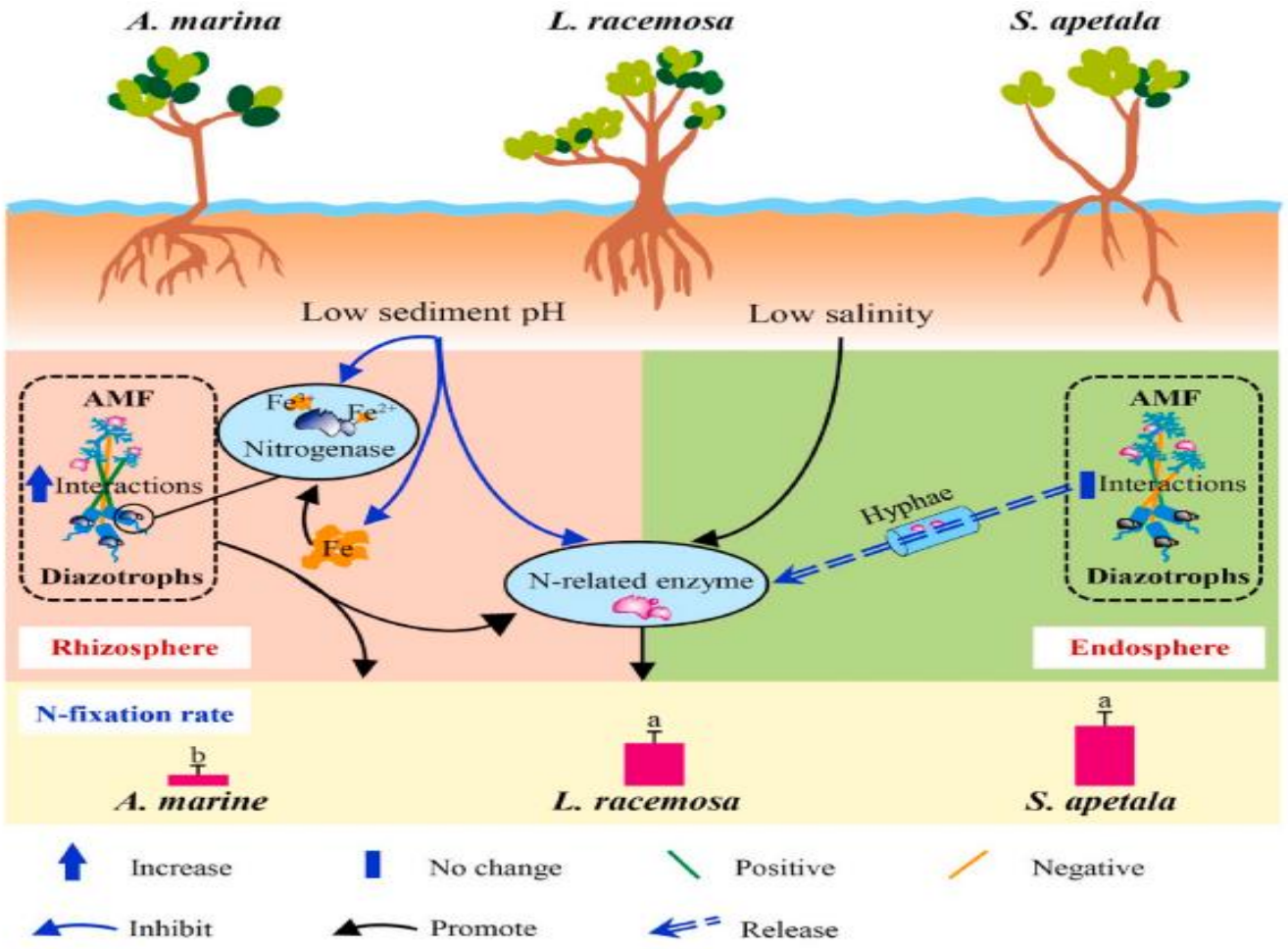
B. Methanomicrobia at different depths



- N_2-fixation increased with increasing depths
- N_2-fixing and methanogenic Methanomicrobia had high abundances at > 30 cm depths, probably as important N sinks in deep sediments

(Luo, et al., 2021, *Microbiome*)

Microbial N_2 fixation mitigated mangrove N-limitation

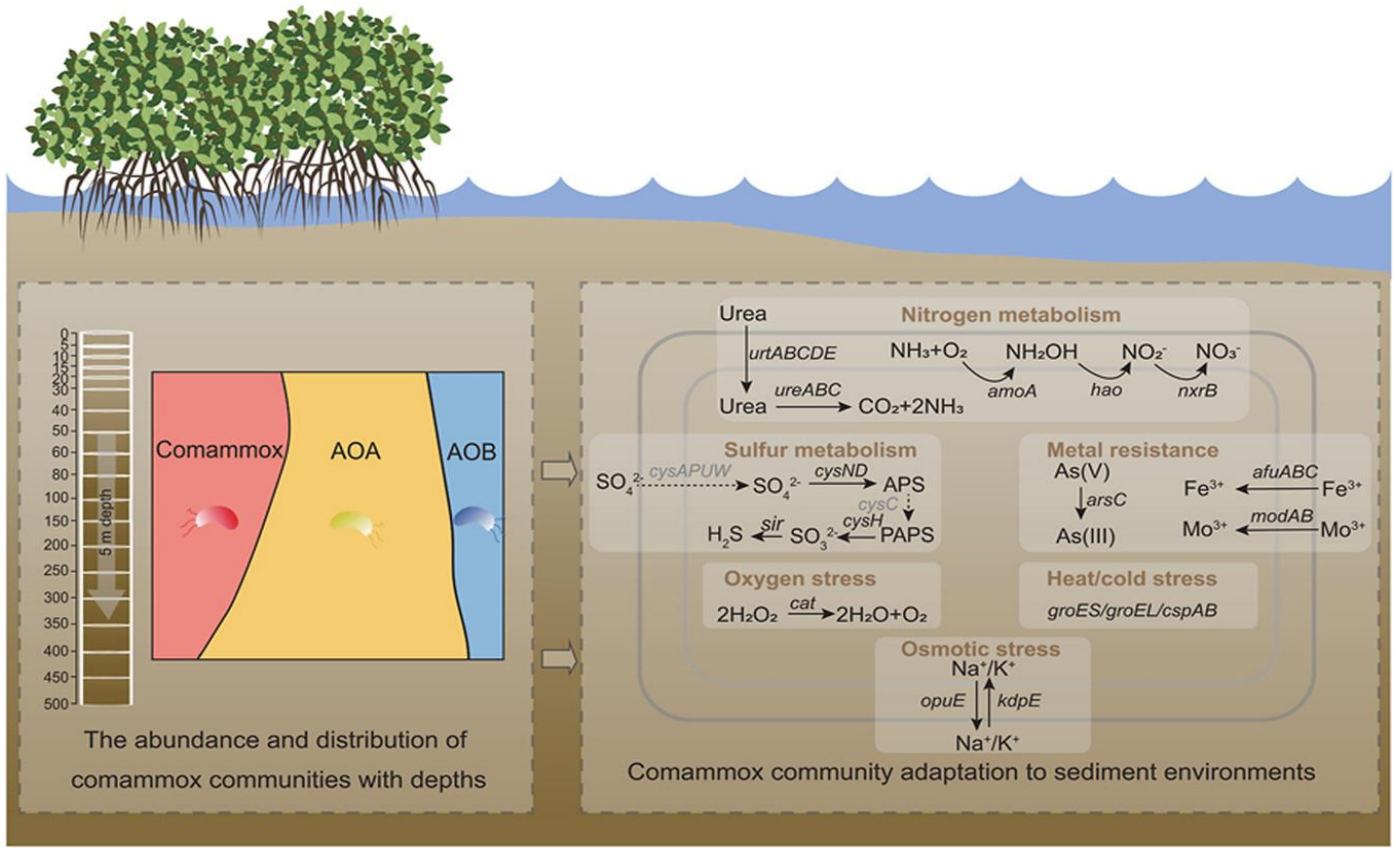


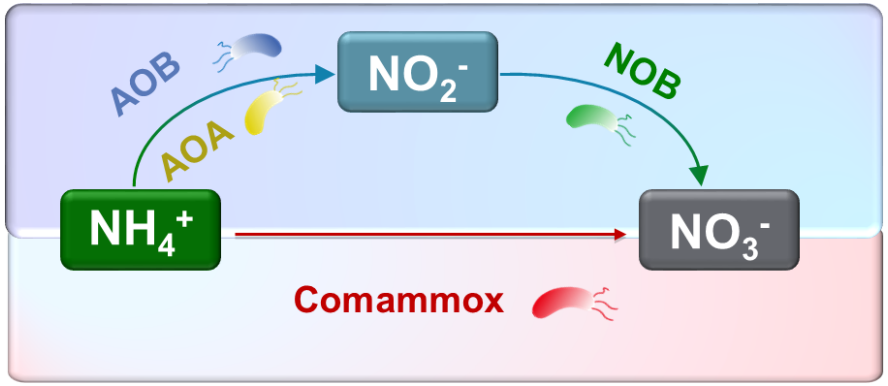
Arbuscular mycorrhizal fungi (AMF) and N_2-fixing bacteria could interact to mitigate mangrove N-limitation

(Yu et al., 2021, *Soil Biol Biochem*)

Comammox bacteria in mangrove sediments

AOA: ammonia oxidizing archaea
AOB: ammonia oxidizing bacteria
Comammox: complete ammonia oxidization





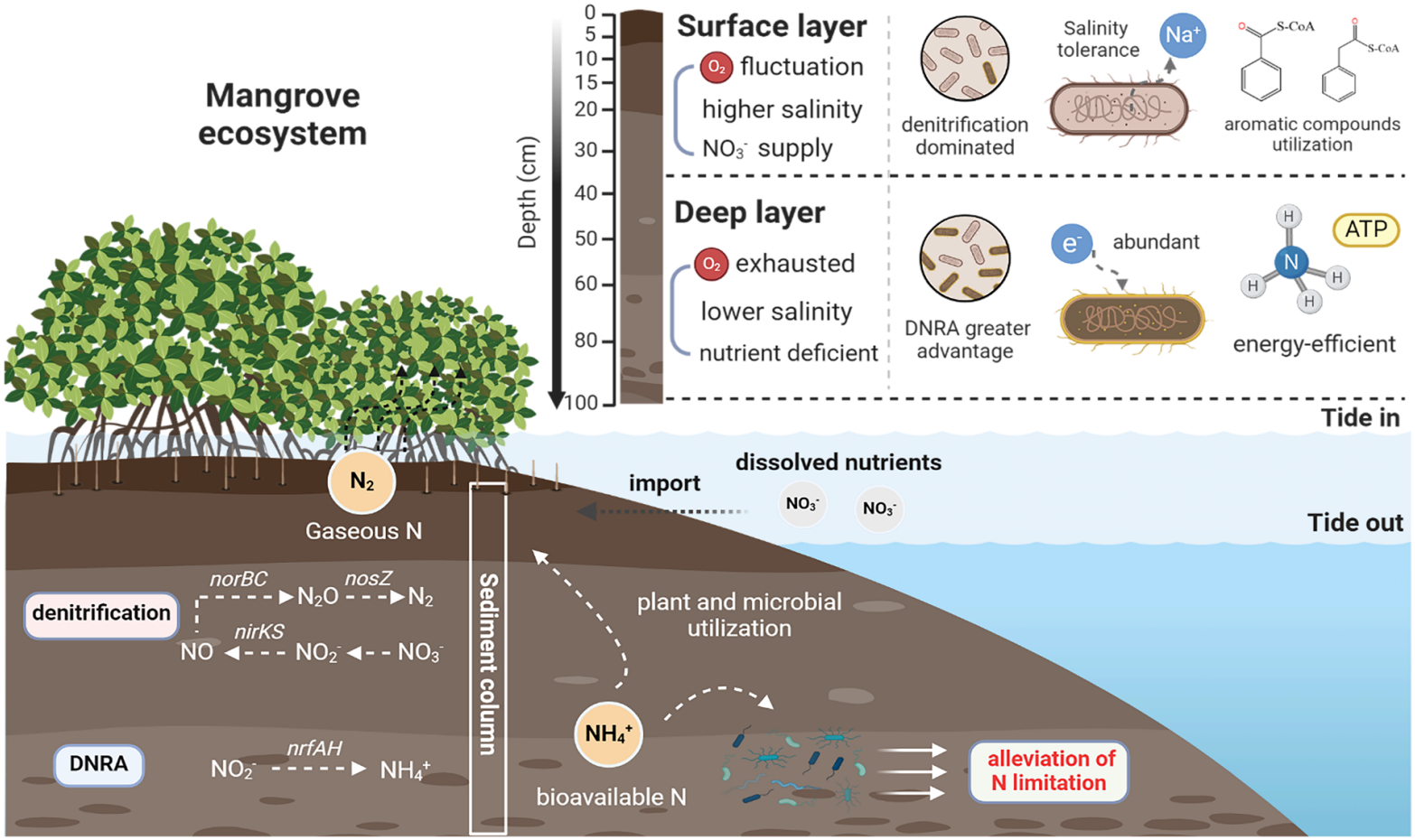
- **Comammox bacteria** were found in mangrove sediments
- **Metabolically diverse** genes in the C/N/S cycling
- **Adapted to sediment environments**

(Yang *et al.*, 2025, *Environ Res*)

Depth-dependent N transformation

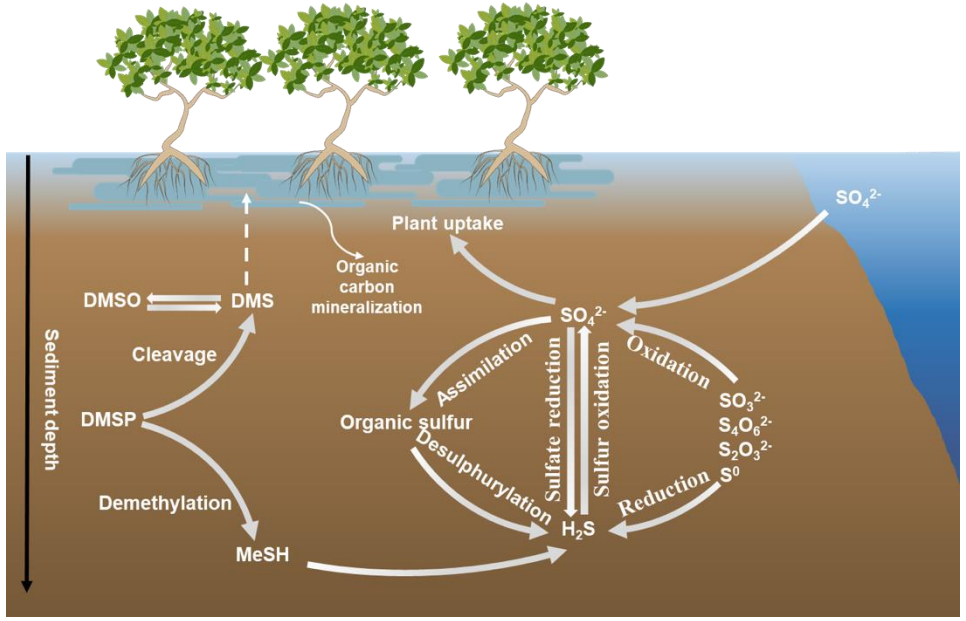
- **Vertical competition between DNRA and denitrification**
- **Alleviation of N limitation in mangrove sediments**

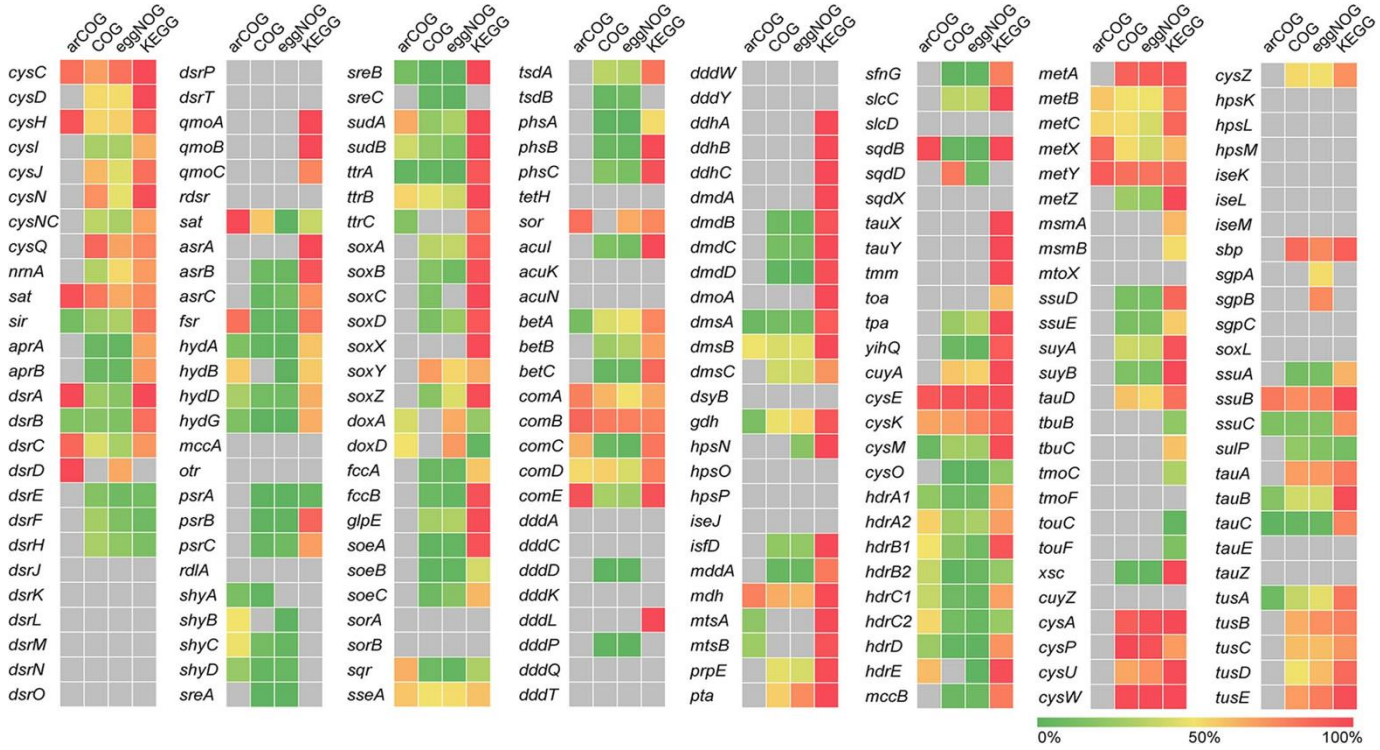
DNRA: dissimilatory nitrate reduction to annonium



(Fan et al., 2024, *Water Res*)

Sulfur cycling in mangrove ecosystems

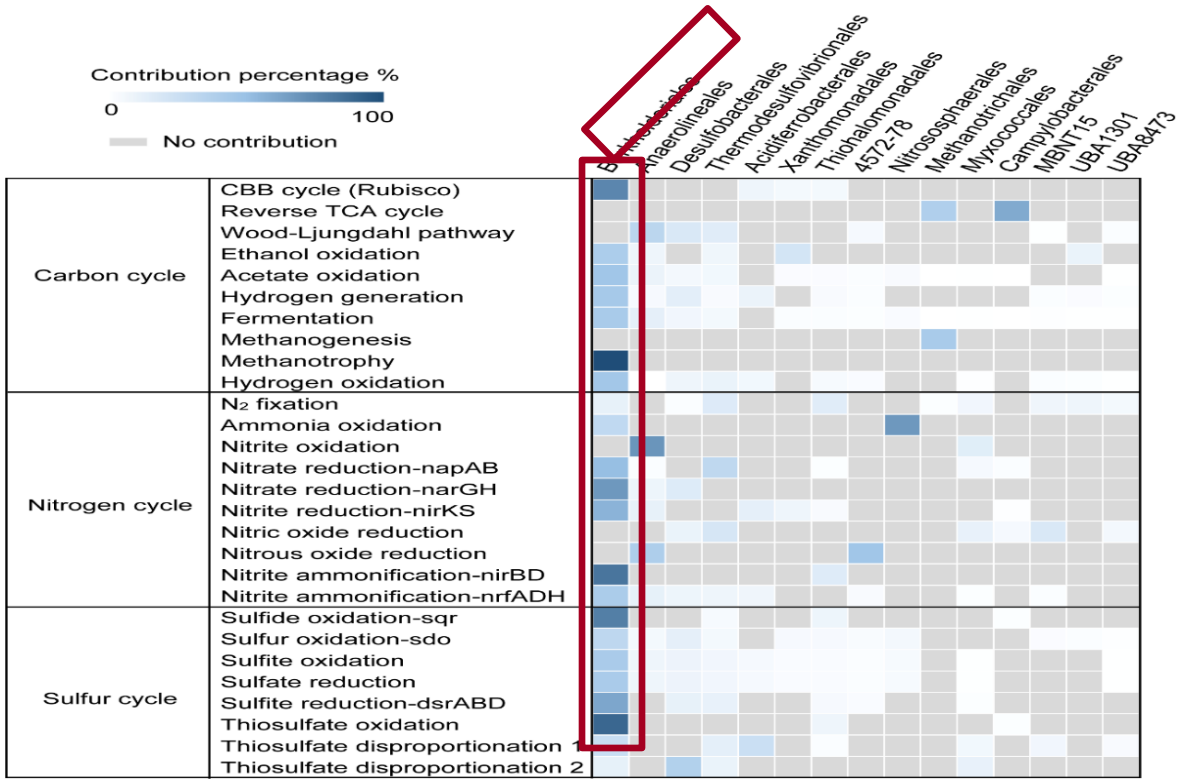




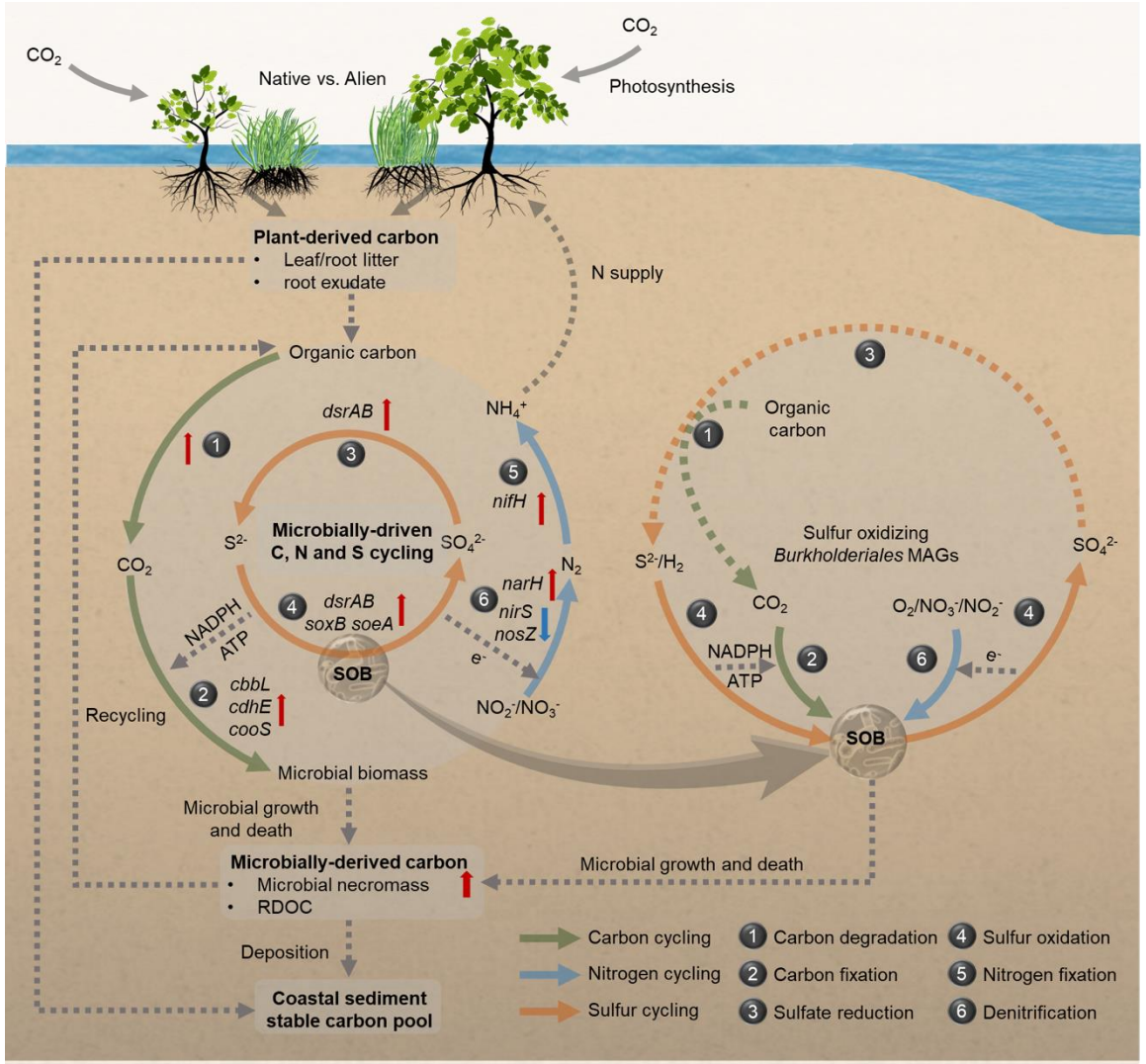
- **Various sulfur compounds and cycling processes in mangrove ecosystems**
- **S cycling plays an important role in the matter and energy transformation in mangrove sediments**

(Yu *et al*., 2021, *Mol Ecol Resour;* Varon-Lopez *et al*., 2014, *Environ Microbiol*)

Burkholderiales for microbial necromass C formation



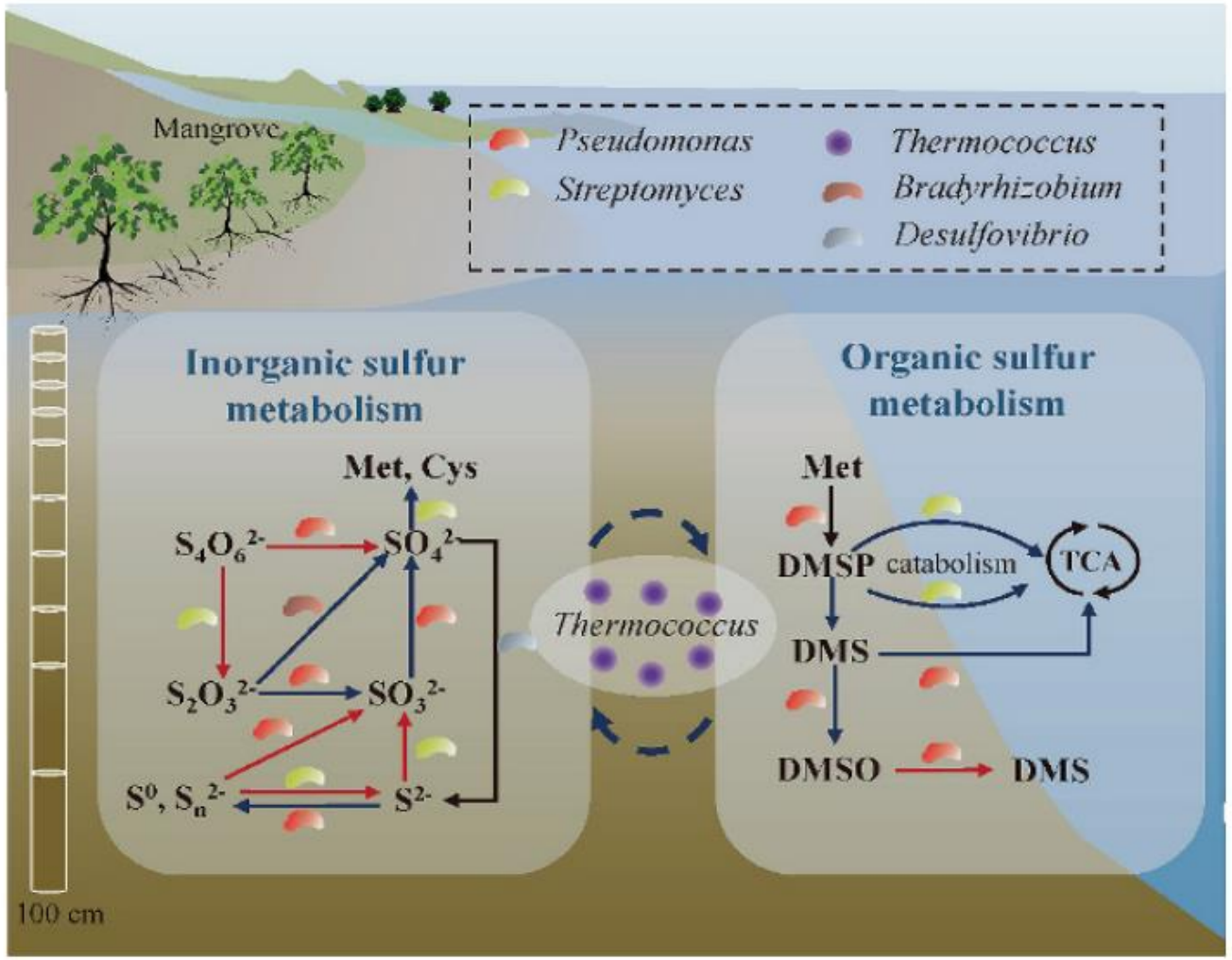
Chemoautotrophic sulfur oxidizers dominate microbial necromass C formation in coastal blue C ecosystems (e.g., mangrove, salt marsh)



(Yu et al., 2023, *Func Ecol*)

S cycling microbial groups in mangrove sediments

- **S oxidization** and **DMSP catabolism** dominated at the surface (0-20 cm) sediment
- **S reduction** and **DMS transformation** dominated at the deep (20-100 cm) sediment
- ***Pseudomonas*** and ***Streptomyces*** were S cycling microbial groups
- ***Thermococcus*** linked inorganic and organic S metabolisms



(Qian *et al.*, 2024, *Sci Total Environ*)

Key scientific questions

The vertical distribution and coupling mechanisms of microbially-driven C, N and S cycling processes in mangrove sediments

- The vertical distribution of microbial groups and functional genes
- Correlation analysis of CH_4/N/S cycling functional genes
- Possible couplings of microbial groups and functional processes
- Molecular ecological network analysis

Sampling the mangrove sediment





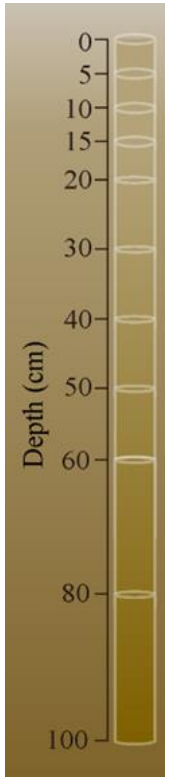




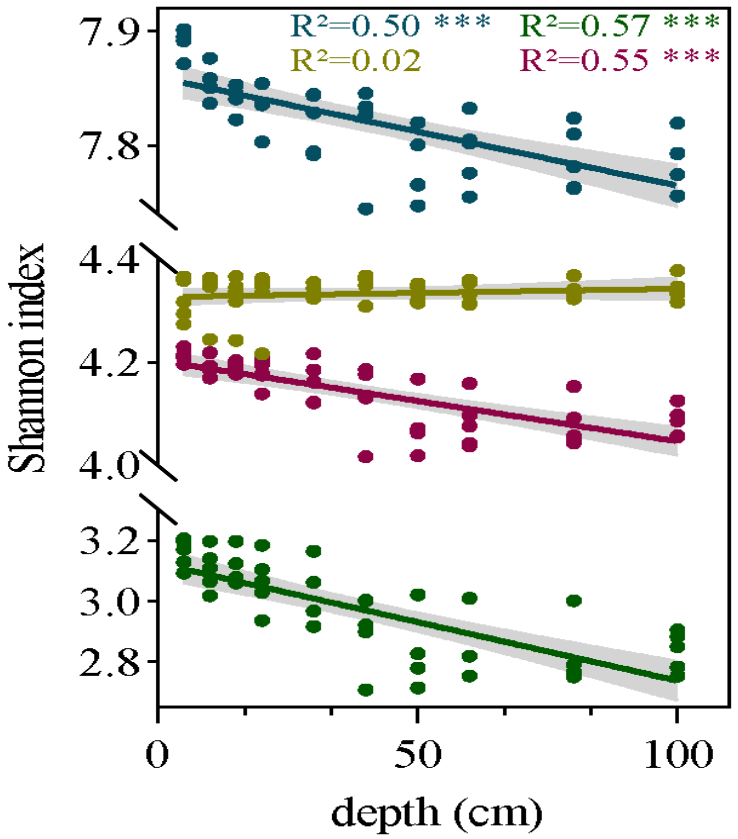


The study site is located at the Qiao Mangrove reserves, Zhuhai, China

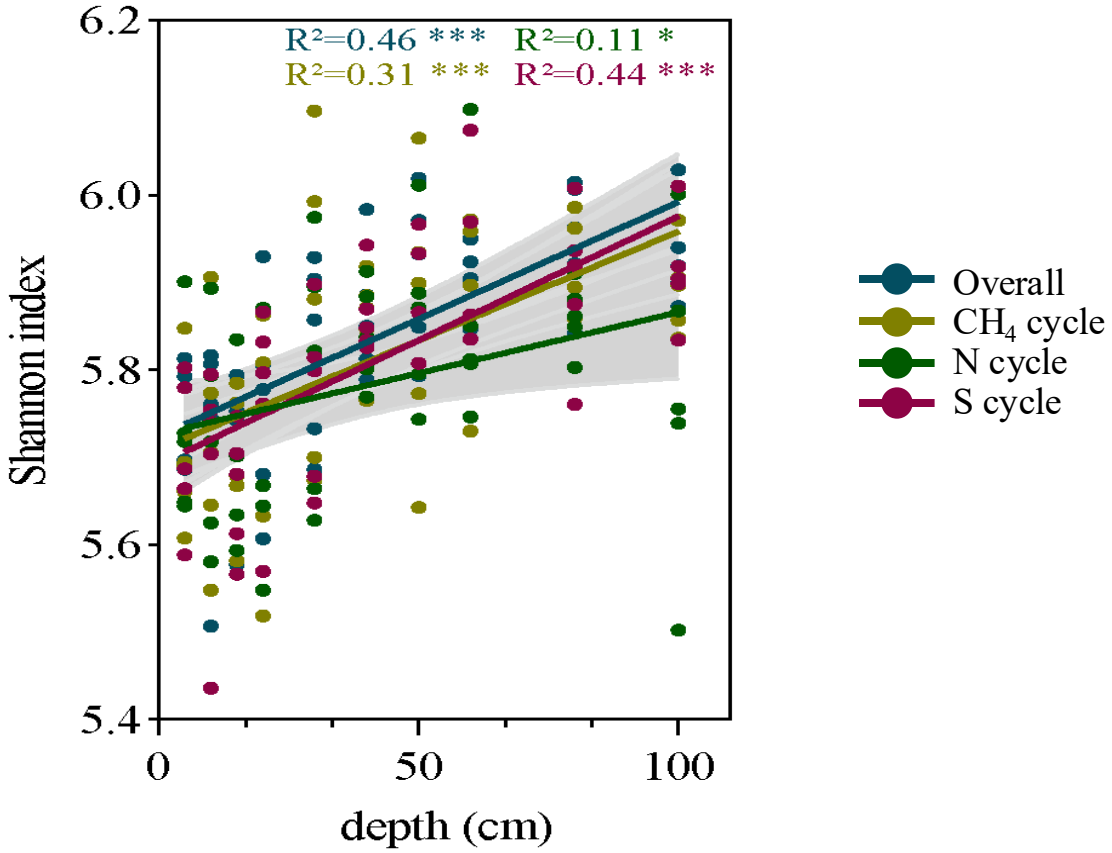
Microbial diversity changed with sediment depths



Functional diversity



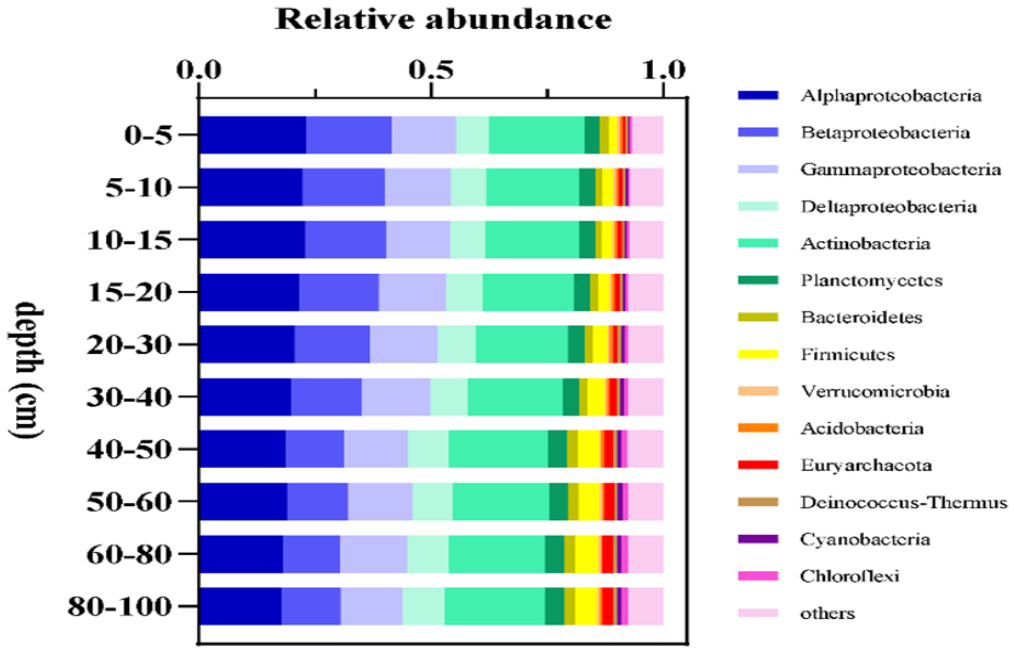
Taxonomic diversity



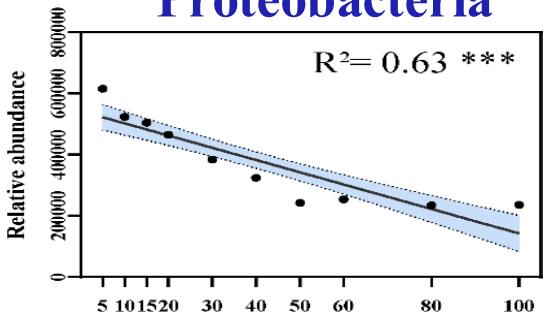
(Qian et al., 2023, *Microbiome*)

Main microbial groups of CH_4/N/S cycling

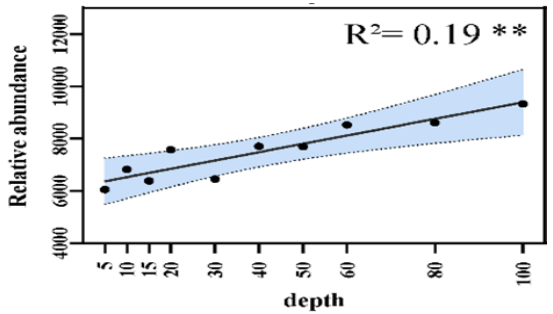
Taxonomic profiling of microbial communities



Proteobacteria

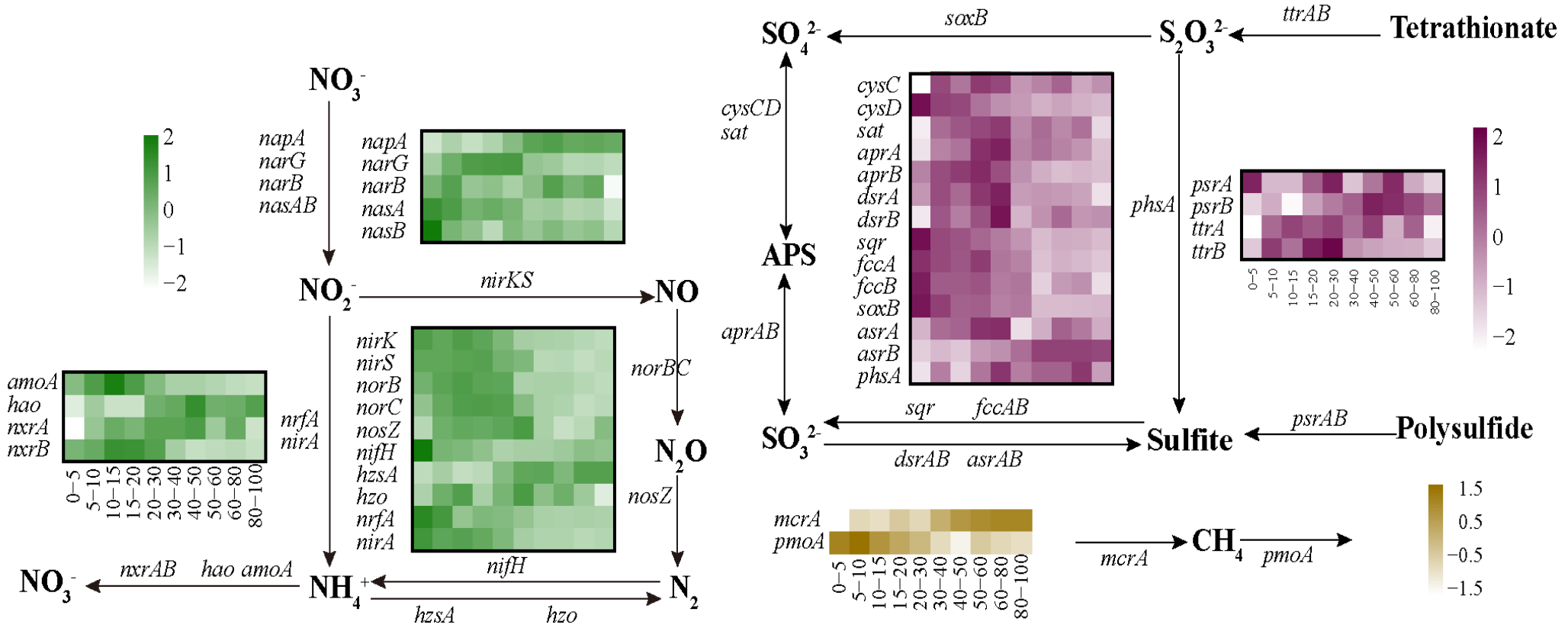


Euryarchaeota



- For N/S/CH_4 cycling bacteria and archaea, Proteobacteria was the major phylum and its abundance decreased with depths
- Euryarchaeota was the main phylum and its abundance increased with depths

Vertical distribution of key CH_4/N/S cycling genes

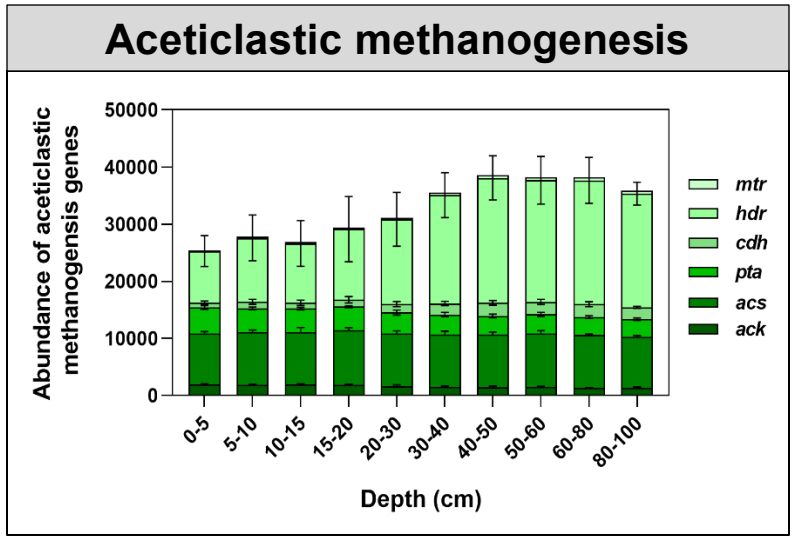


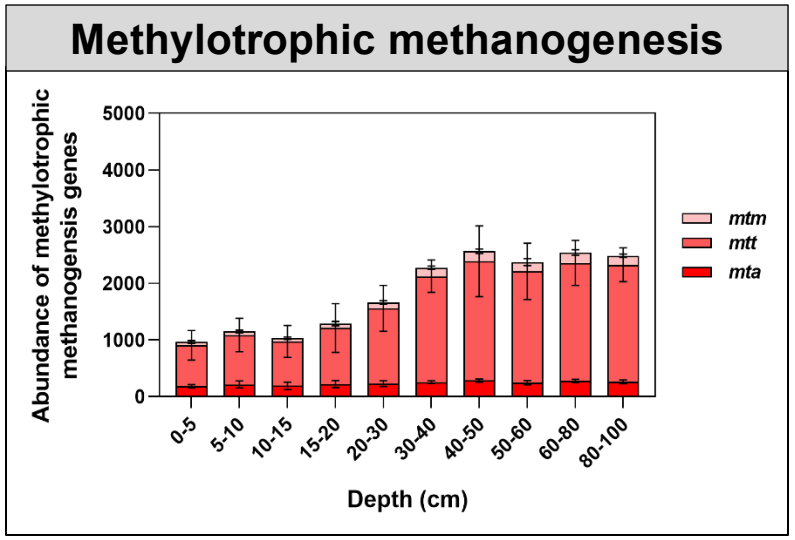
- **Denitrification and S-oxidation genes were mainly distributed at the surface sediment**
- **Methanogenic genes were mainly distributed at the deep sediment**

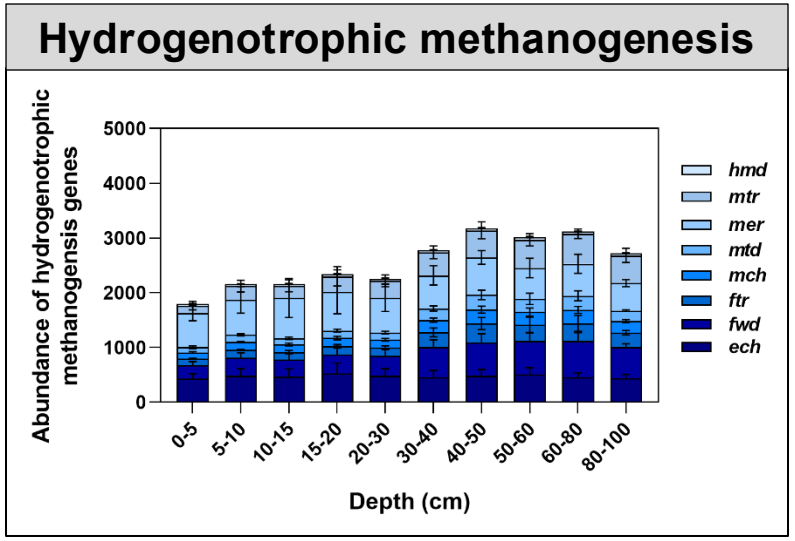
(Qian et al., 2023, *Microbiome*)

Aceticlastic methanogenesis was the main pathway

Abundances of methanogenic genes in mangrove sediments





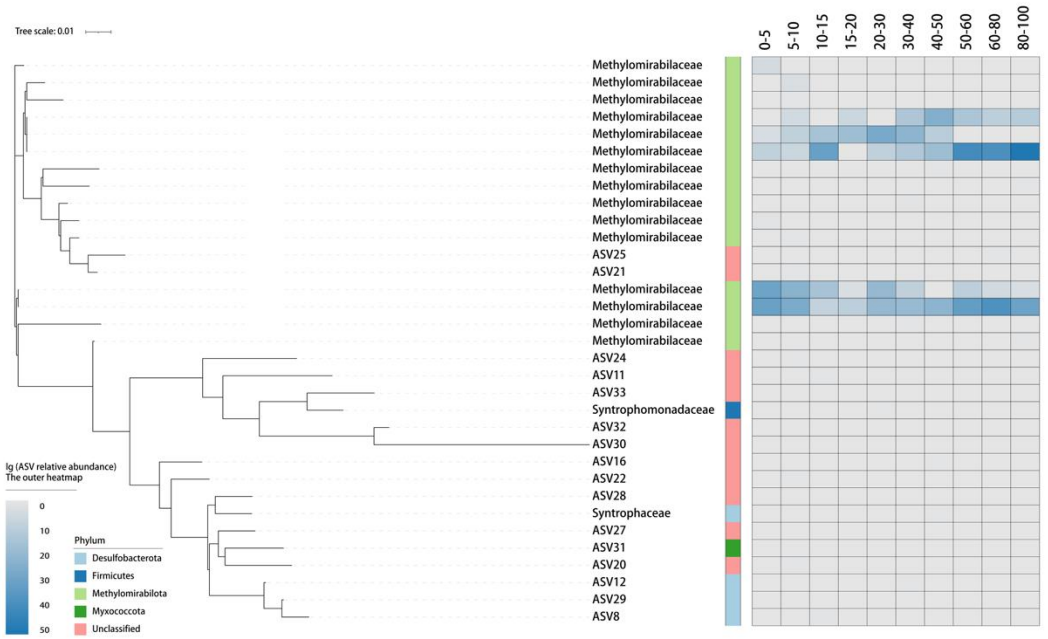


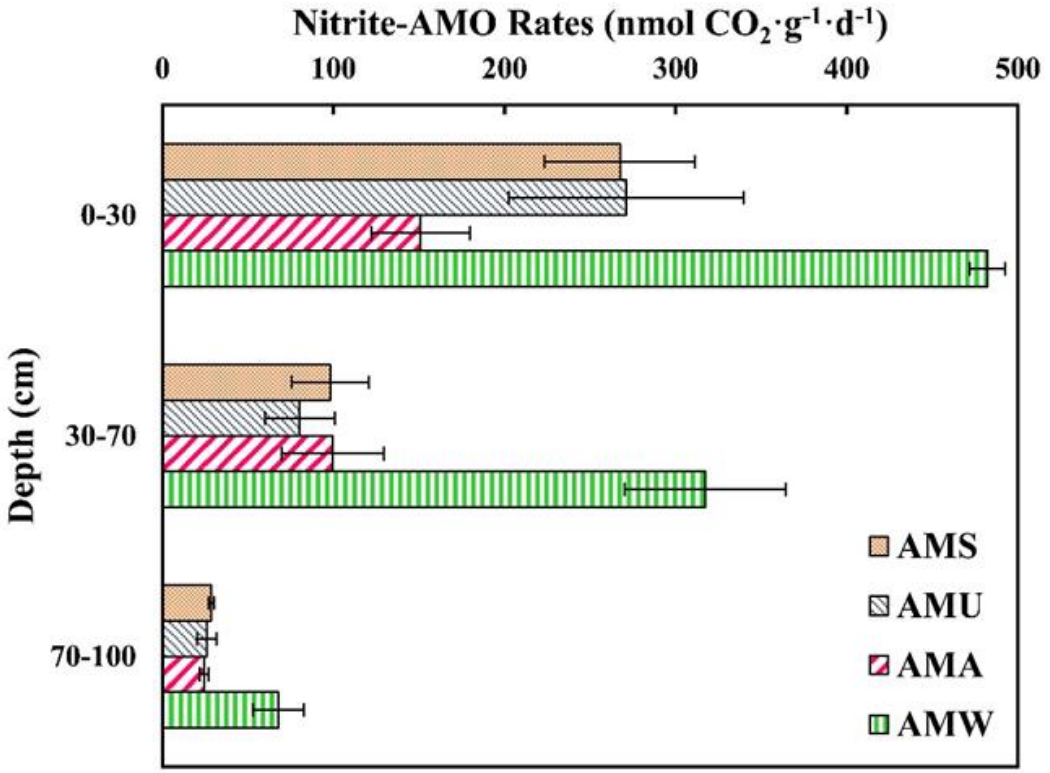
$$H_4MPT\text{-}CH_3 \xrightleftharpoons{mtr} CH_3\text{-}CoM \xrightleftharpoons{mcr} CH_4$$

- Aceticlastic methanogenic gene abundances were higher than methylotropic or hydrogenotropic methanogenic genes

NC10 bacteria widely distribute in mangrove sediments

Phylogenetic analysis of NC10 bacterial OTUs

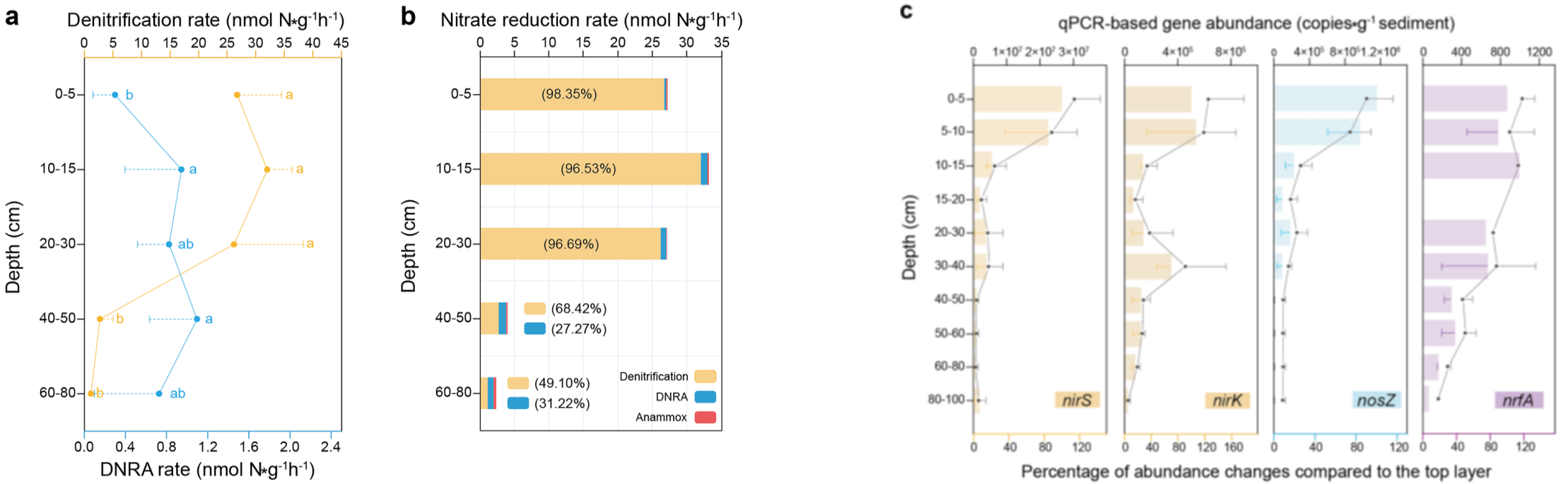




- **NC10 bacteria were involved in anaerobic methane oxidization (with nitrite as acceptor), and more active at the surface sediment**

(Provided by Prof. Tian at Xiamen University)

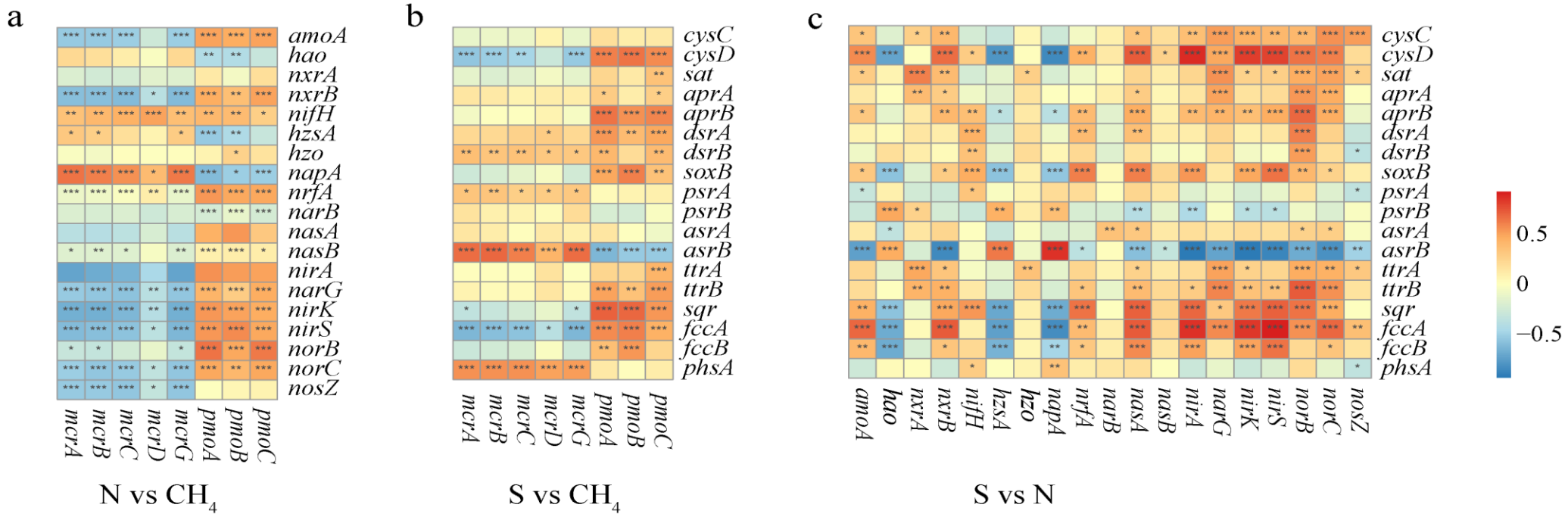
^{15}N-isotope analysis of N transformation rate



- Denitrification was high at shallow depths, while DNRA and anammox increased with the depth
- This is consistent with metagenome sequencing data

(Fan et al., 2024, *Water Res*)

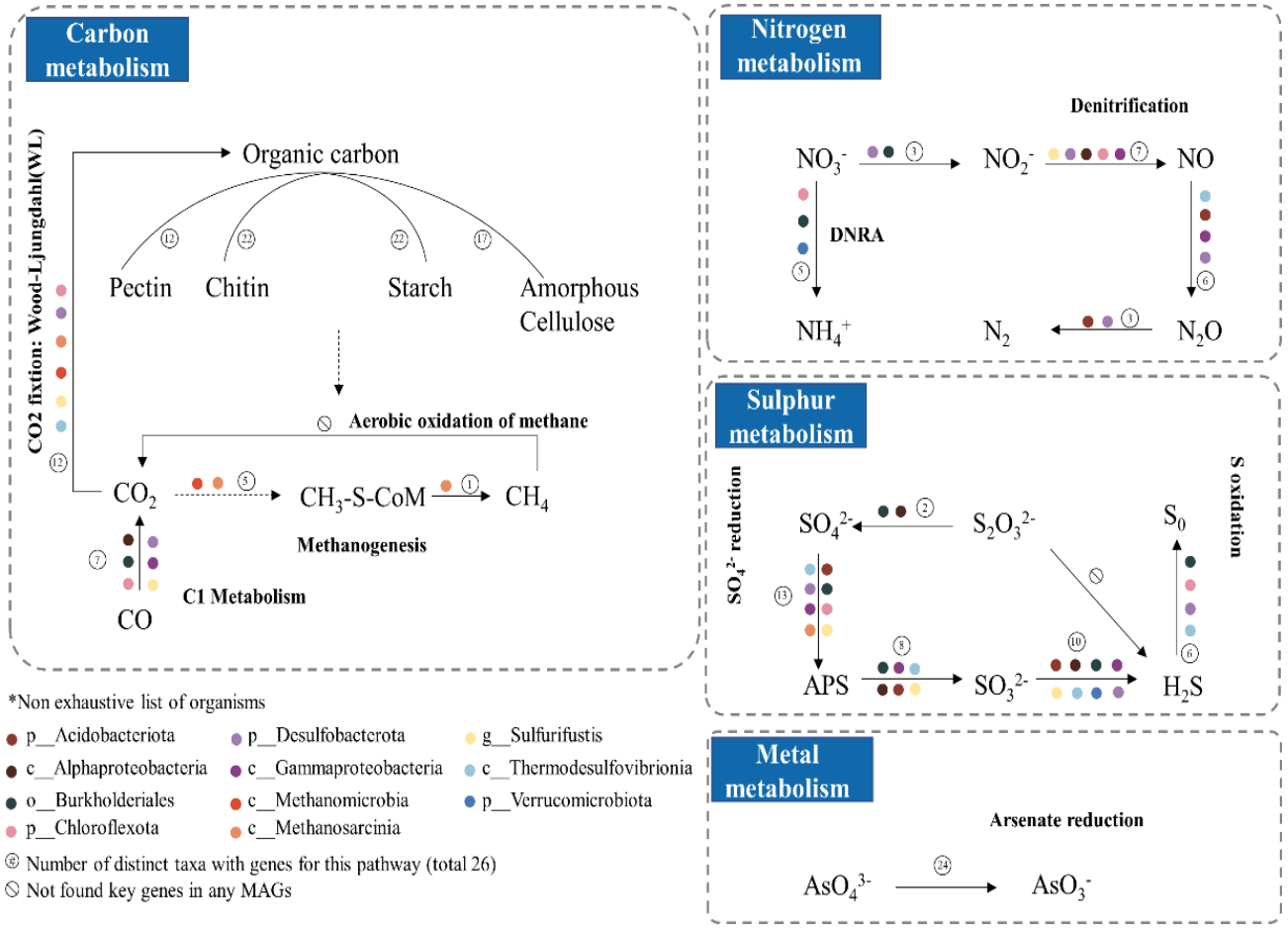
Co-relation analysis of key CH_4/N/S cycling genes



- Key denitrification genes and CH_4 oxidation genes
- S-reduction gene (*asrB*) and methanogenic genes
- S-oxidation genes and denitrification/nitrate-reduction genes

(Qian et al., 2023, *Microbiomes*)

Matagenome assembled genome analysis



26 Matagenome assembled genomes (MAGs) were obtained, including:

- Acidobacteriota
- Choroflexota
- Thermodesulfovibrionia
- Chloroflexota
- Burkholderiales
- Sulfurifustis
- Desulfobacterota

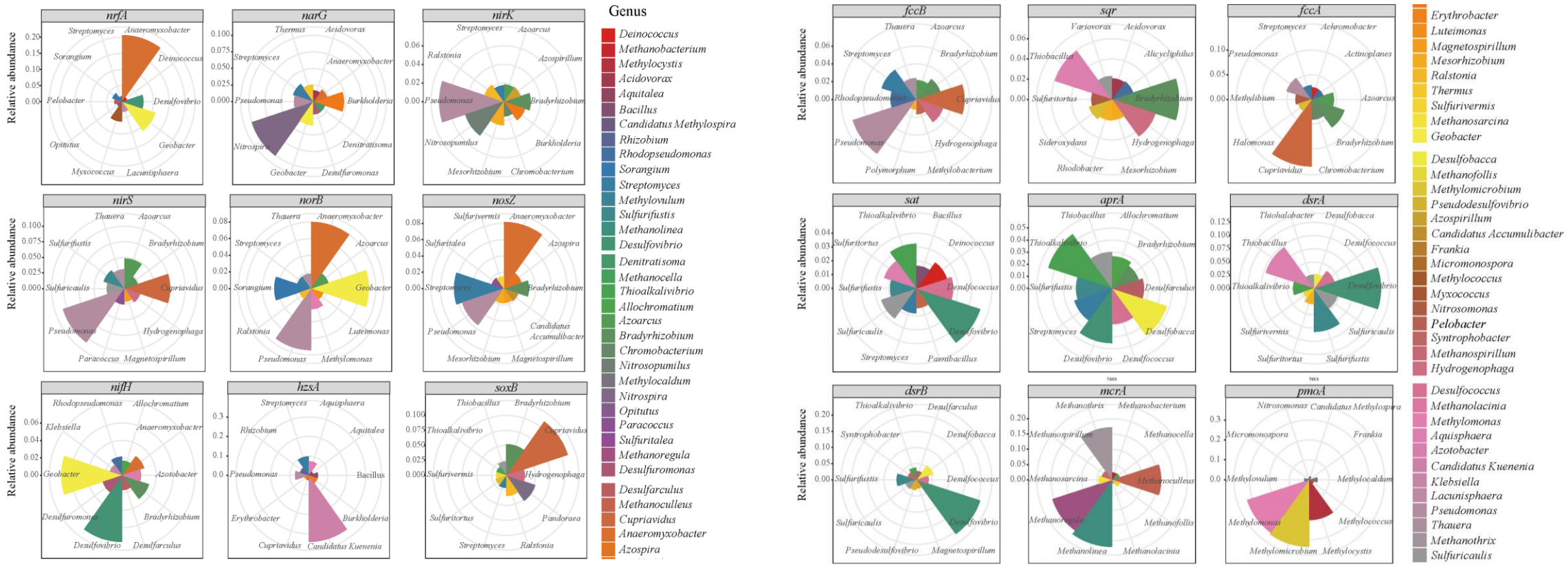
S- oxidation
Denitrification
Sulfate reduction

- Gammaproteobacteria
- Methanomicrobia
- Methanosarcina

Anaerobic CH_4 oxidation
Methanogenesis

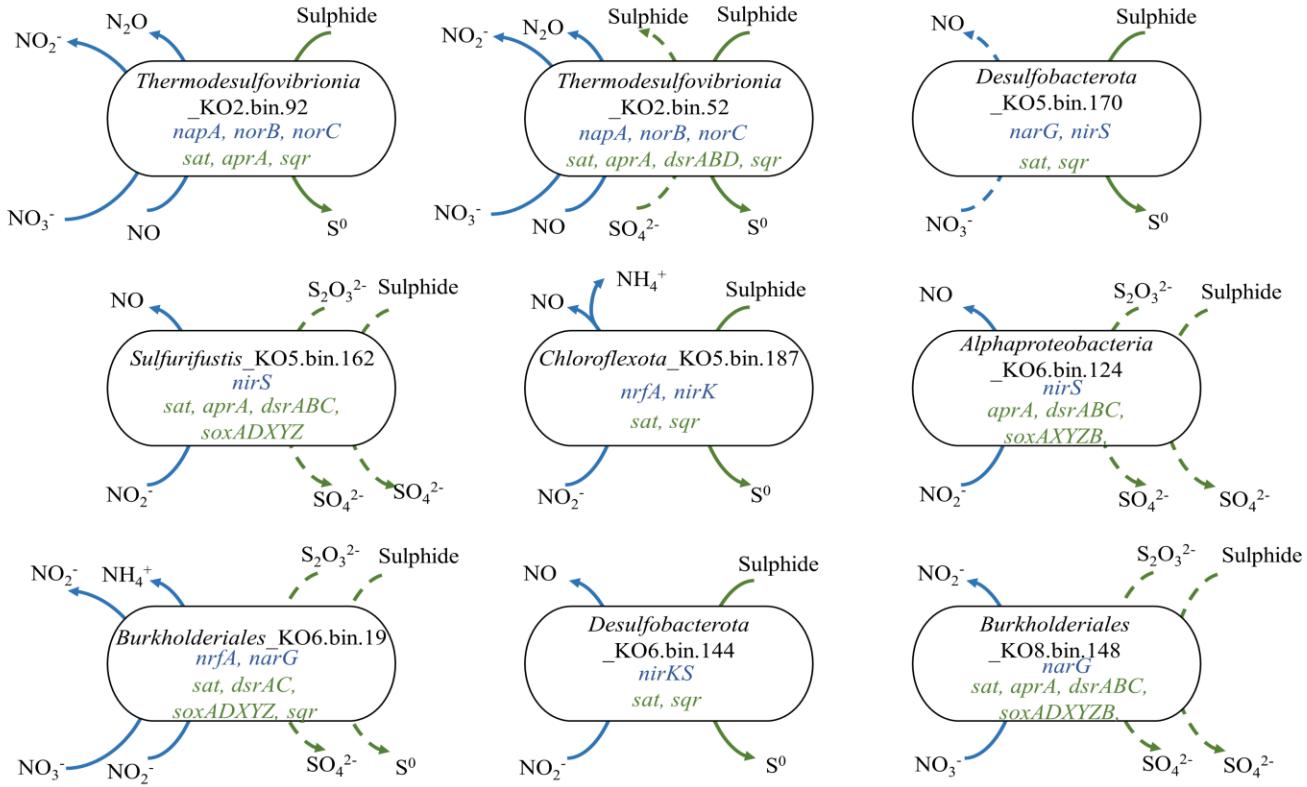
- Verrucomicrobiota
- Alphaproteobacteria

S-oxidizing and nitrate-reducing microbial groups are important in mangrove sediments



- S-oxidizers and nitrate-reducers had strong relationships with high abundances
- *Cupriavidus, Pseudomonasand* and *Sulfurifustis* could perform S oxidization and denitrification

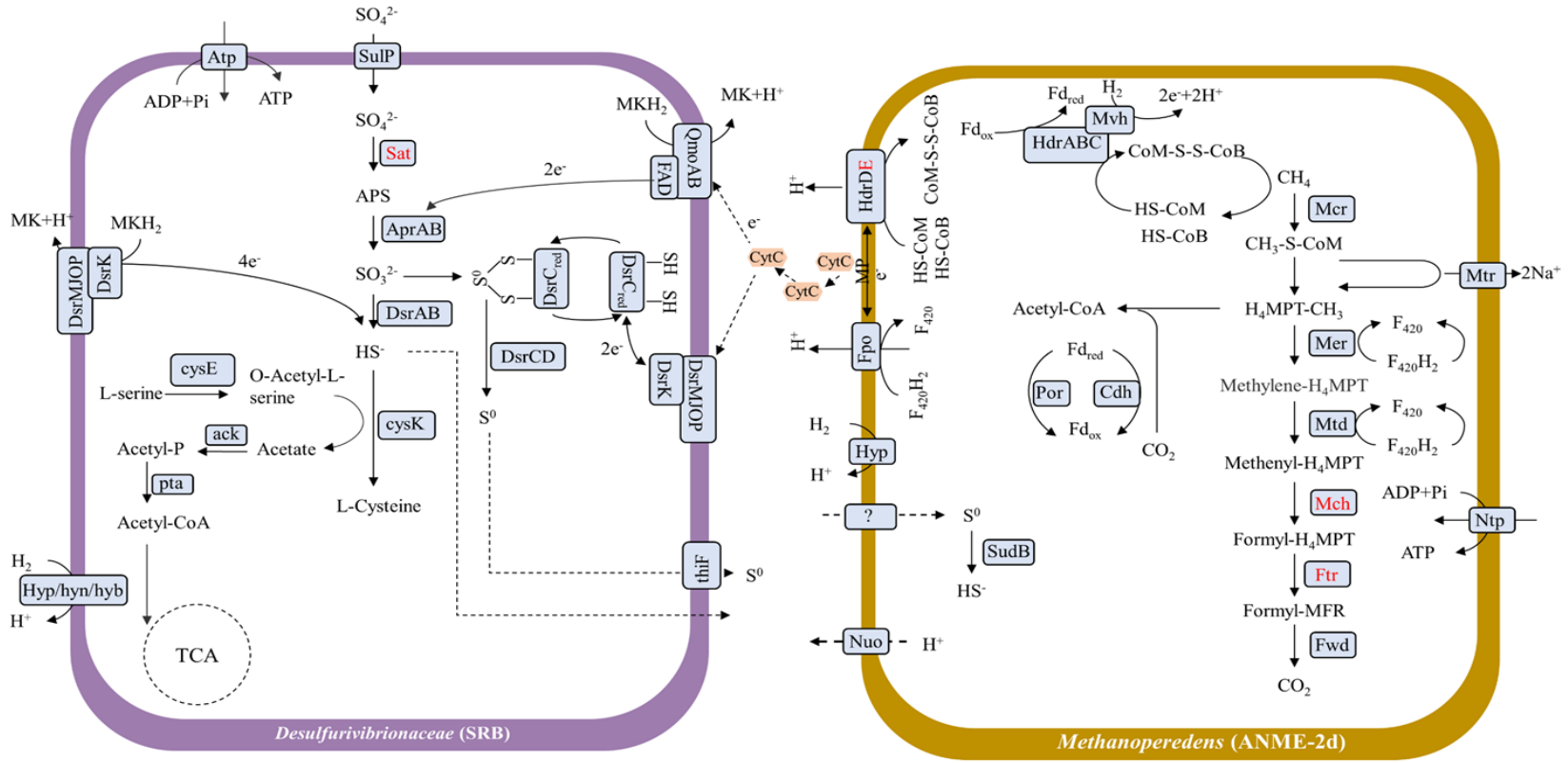
Nine MAGs with S oxidation and denitrification genes



- Six MAGs appeared to be able to oxidize sulfides to S^0
- S oxidation and denitrification processes could be coupled in mangrove sediments

(Qian et al., 2023, *Microbiomes*)

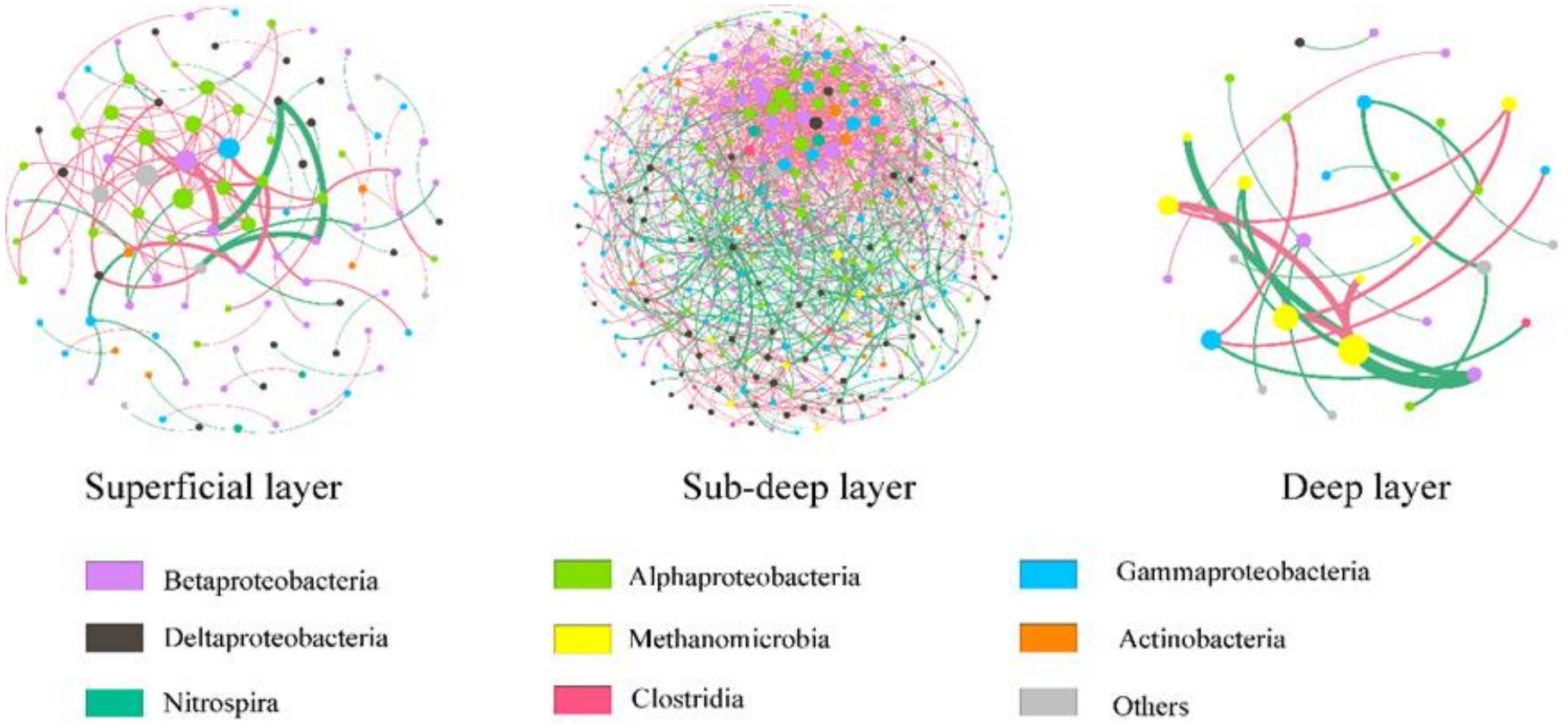
Associations between ANME and SRB MAGs



- Methanopereden MAG and Desulfobacterota MAG could interact as ANME and SRB representatives
- Both could form symbiotic relationships through extracellular electron transfer, or S^0 transfer, thus promoting anaerobic methane oxidation and reducing methane emissions

(Qian et al., 2023, *Microbiomes*)

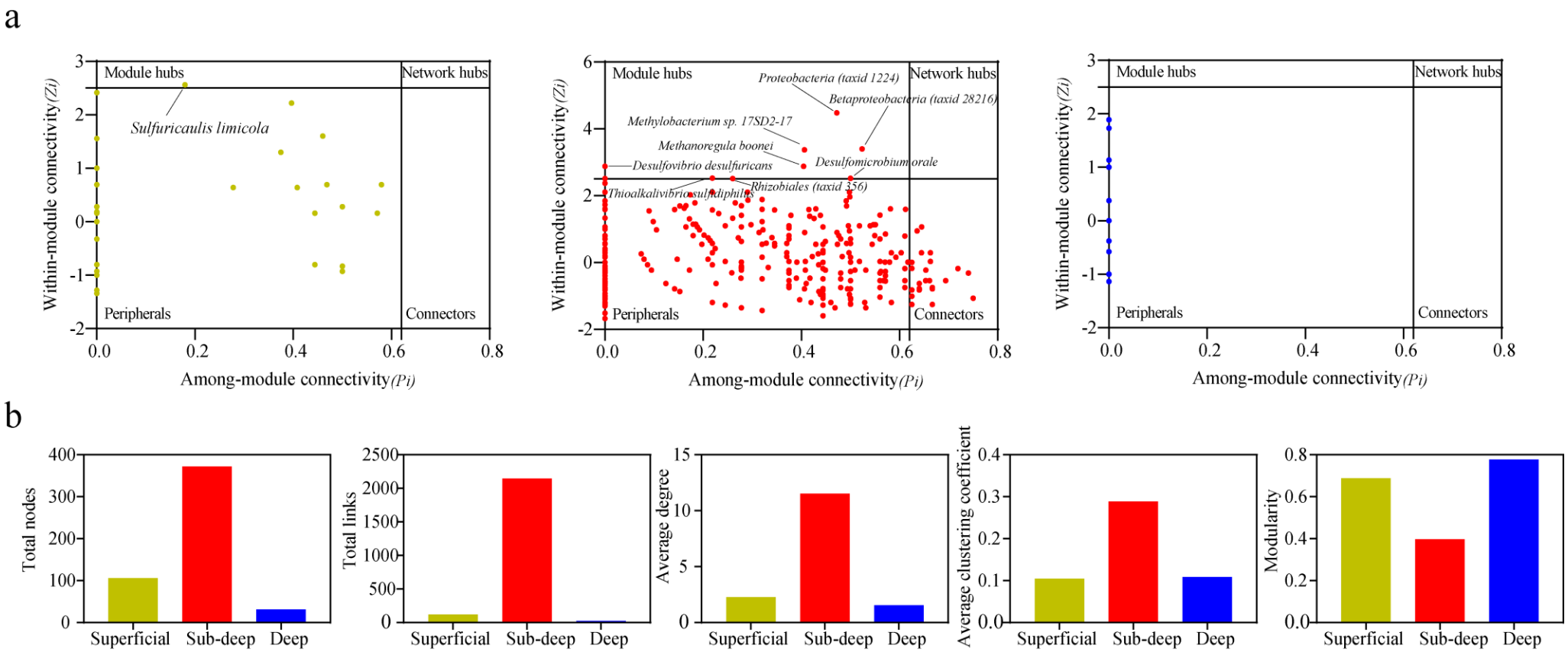
Molecular ecological network analysis of CH_4/N/S cycling microbial communities



More complex microbial interactions appeared to be at the middle layer (5-30 cm) of mangrove sediments than those at the surface (0-5 cm) or deep layer (30-100 cm)

(Qian et al., 2023, *Microbiomes*)

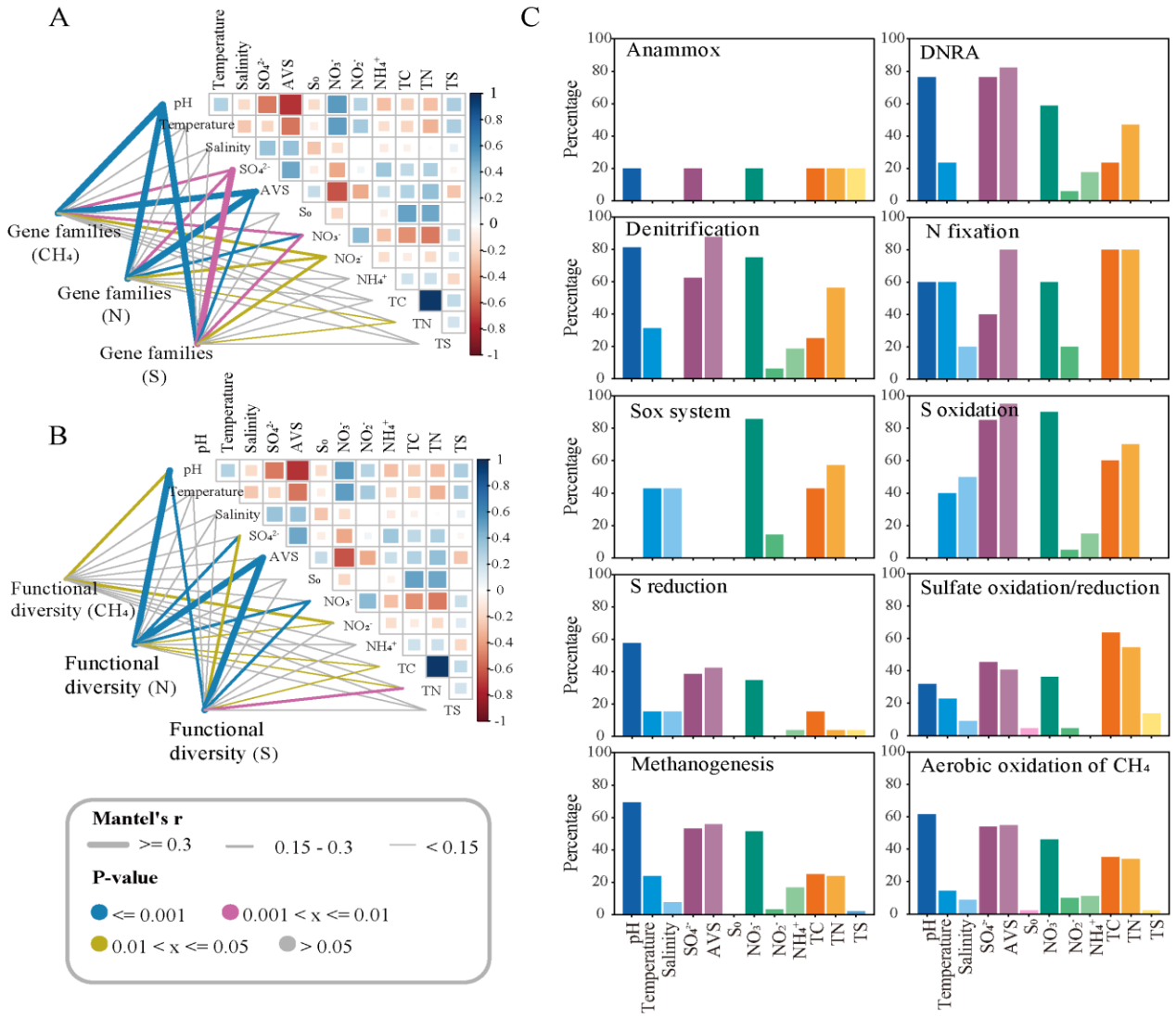
Possible interactive mechanisms between CH_4 and S cycling microbes



- ***Desulfovibrio desulfuricans*** **and** ***methanogens*** **were associated, while** ***Methanoregula boonei*** **and sulfate reducing bacteria (SRB) were closely related, suggesting methanogens may interact with SRB**

(Qian et al., 2023, *Microbiomes*)

Environmental factors for shaping C/N/S cycling microbial community structure

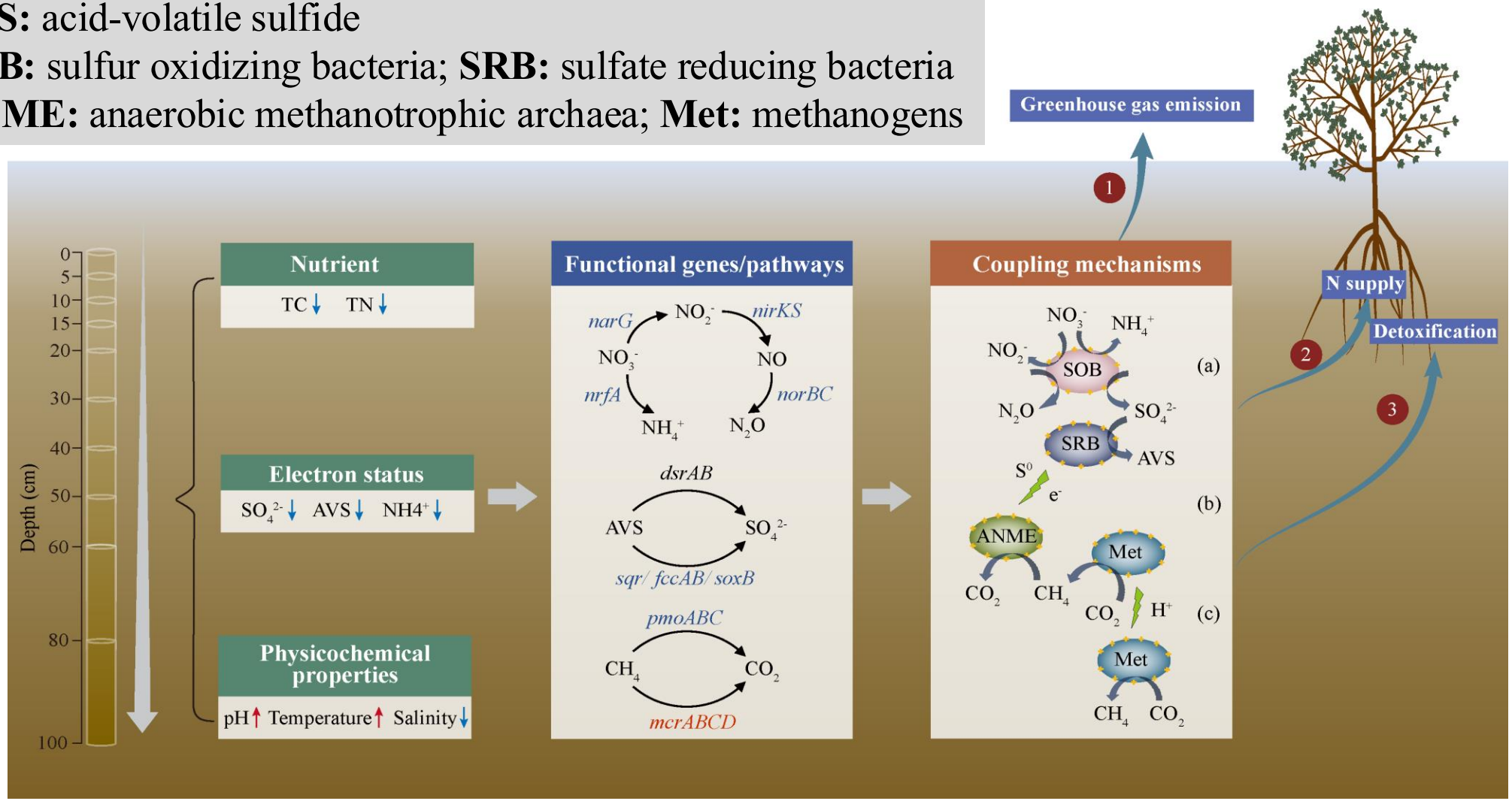


- pH and AVS significantly affected microbial community diversity at all depths
- AVS could explain denitrification and DNRA processes
- NO_3^- strongly affected S oxidation processes

(Qian et al., 2023, *Microbiome*)

A conceptual model for CH_4/N/S cycling microbial communities in mangrove sediments

AVS: acid-volatile sulfide
SOB: sulfur oxidizing bacteria; **SRB:** sulfate reducing bacteria
ANME: anaerobic methanotrophic archaea; **Met:** methanogens



(Qian et al., 2023, *Microbiome*)

Summary

- Environmental factors (e.g., AVS, pH) drive CH_4/N/S cycling microbial communities divergent at different depths, and AVS may be a key electron donor of S oxidization and denitrification in mangrove sediments
- The abundance of S oxidization and denitrification genes was high at the surface sediment (0-15 cm) , and Burkholderiales play important roles in their coupling processes
- SRB and methanogens had high abundances at the middle layer (15-30 cm) and deep layer (30-100 cm)， and SRB could interact with methanotrophs by electron transfer or S^0； SRB could also co-exist with methanogens at the middle and deep sediments

Thanks!



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