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

Microbial mechanisms of carbon sequestration in mangrove sediments

Zhili He

Email : hezhili@sml-zhuhai.cn

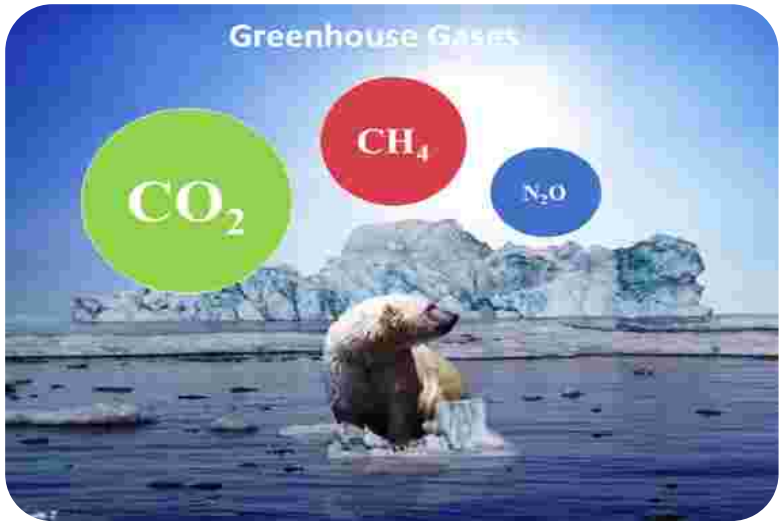
WeChat: zhilihe65

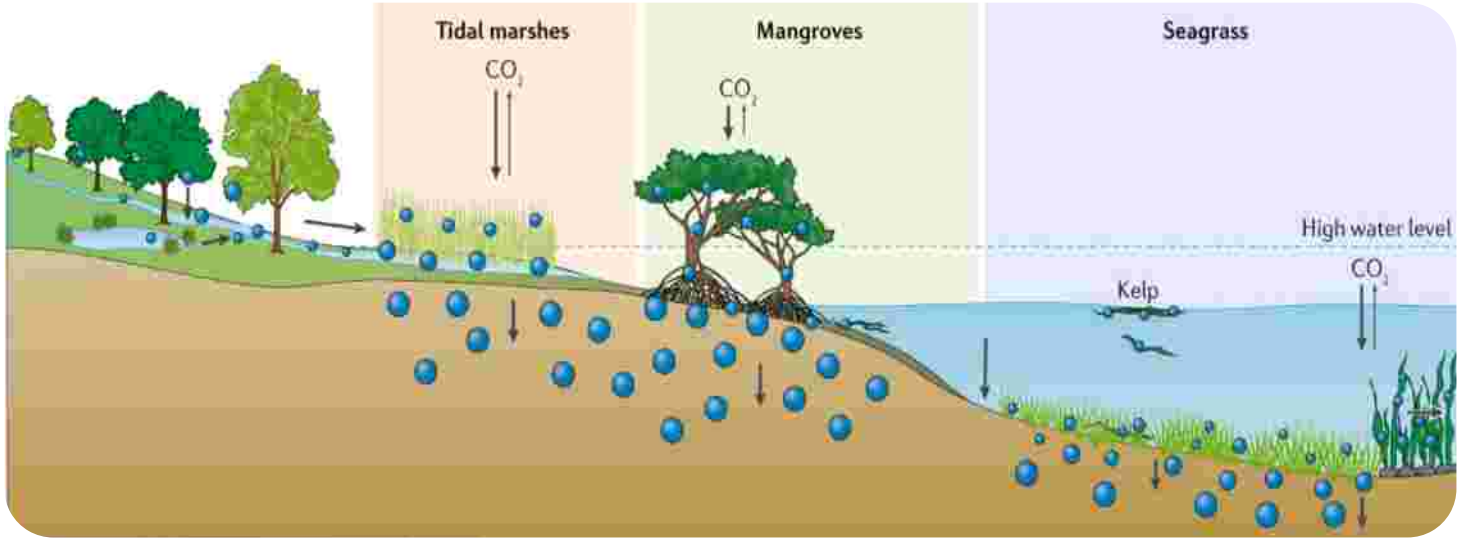
Hong Kong University of Science and Technology

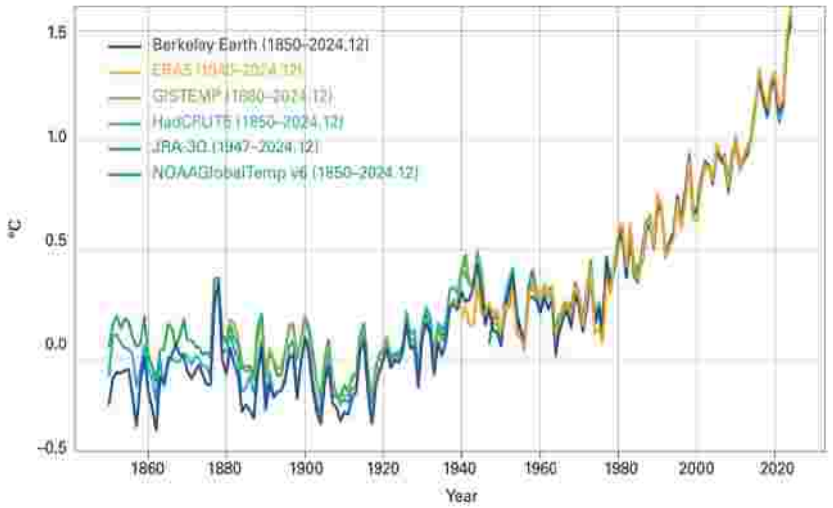
Hong Kong

July 3, 2025

Global climate warming is a challenge for humanity







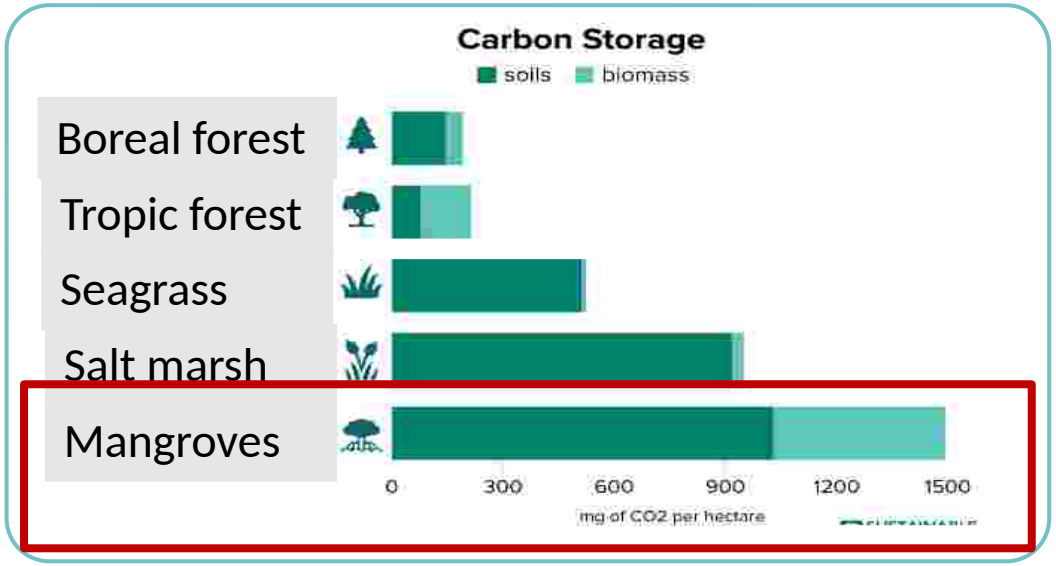
- **Human activities have led to a sharp rise in greenhouse gas concentrations and global average temperatures**
- **Blue carbon (C) ecosystems are suggested as a nature-based climate solution**

（Macreadie *et al*., 2021, *Nat Rev Earth Environ*; WMO 2024, *State of the Global Climate*）

Mangroves are important blue carbon ecosystems



- Land-sea interface
- Filtering contaminants
- High biodiversity
- High productivity
- **Carbon (C) sink**

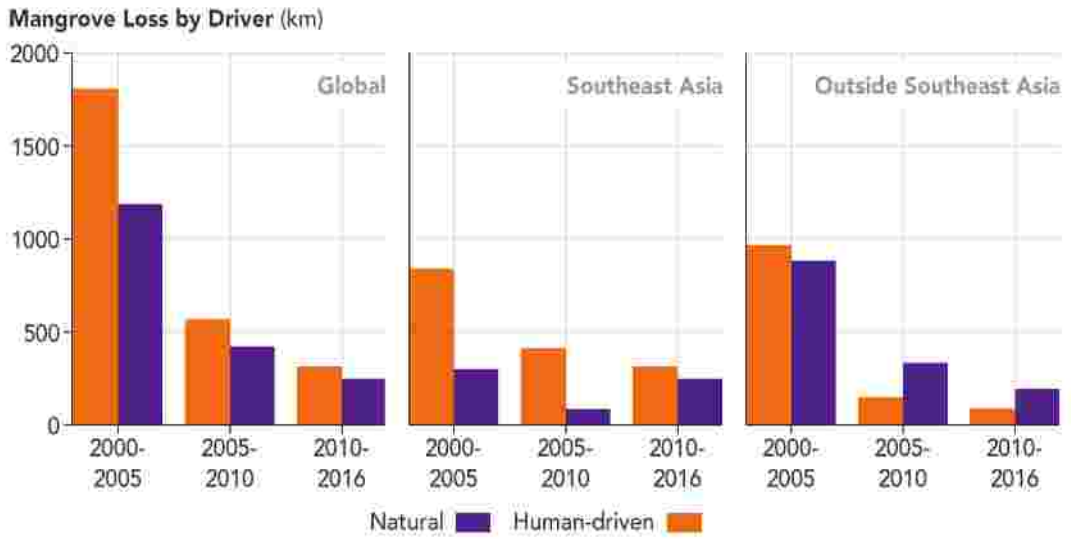


- Mangrove sediments store most of C in the ecosystem
- One of efficient ecosystems for C storage
- A key scientific question: microbially-driven carbon sequestration mechanisms？

（Daniel 2014, *Annu Rev Mar Sci*; Bourgeois *et al*., 2024, *Sci Adv*; Song *et al*., 2023, *Nat Commun*）

Non-native mangroves are used in reforestation

NASA's Earth Observatory



- High adaptability and fast growth
- High individual biomass
- **Low C storage ability**
- 11.0% area in China



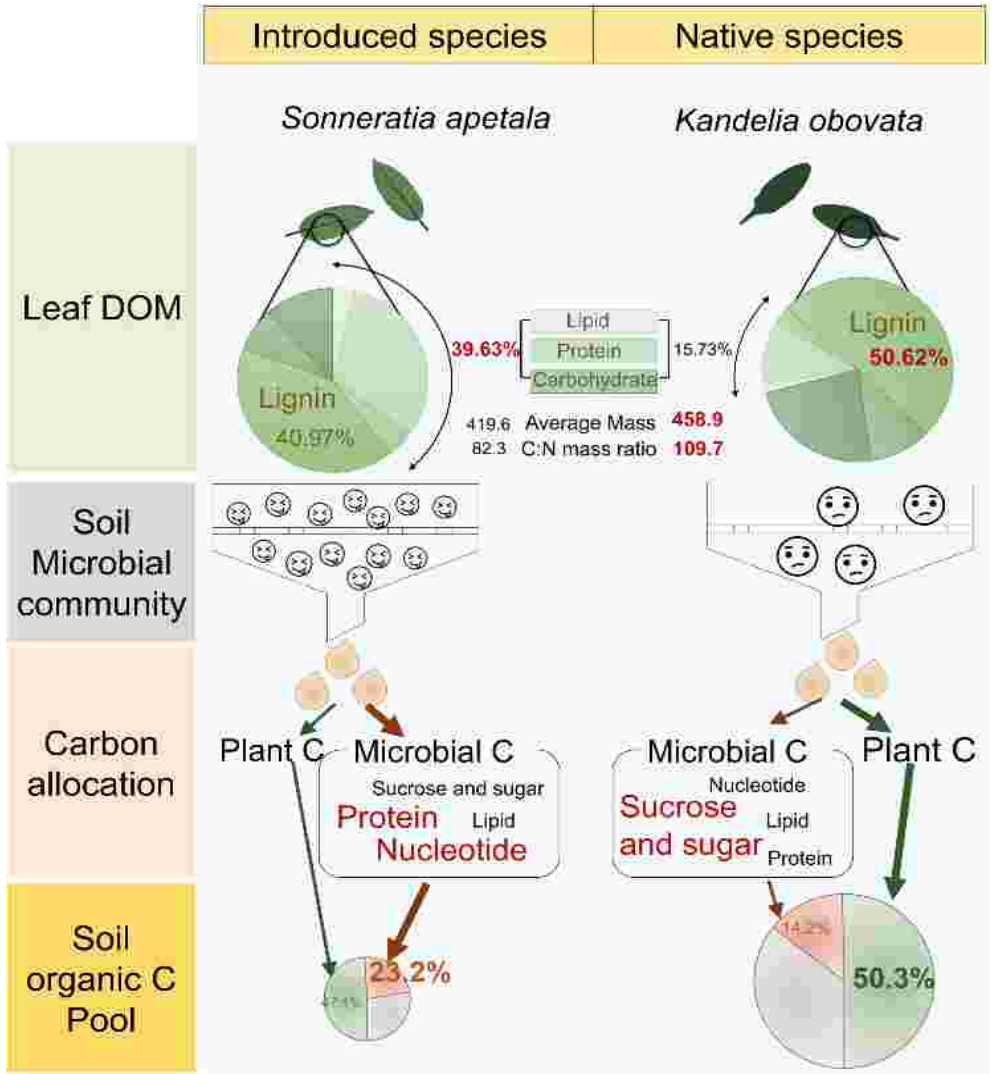


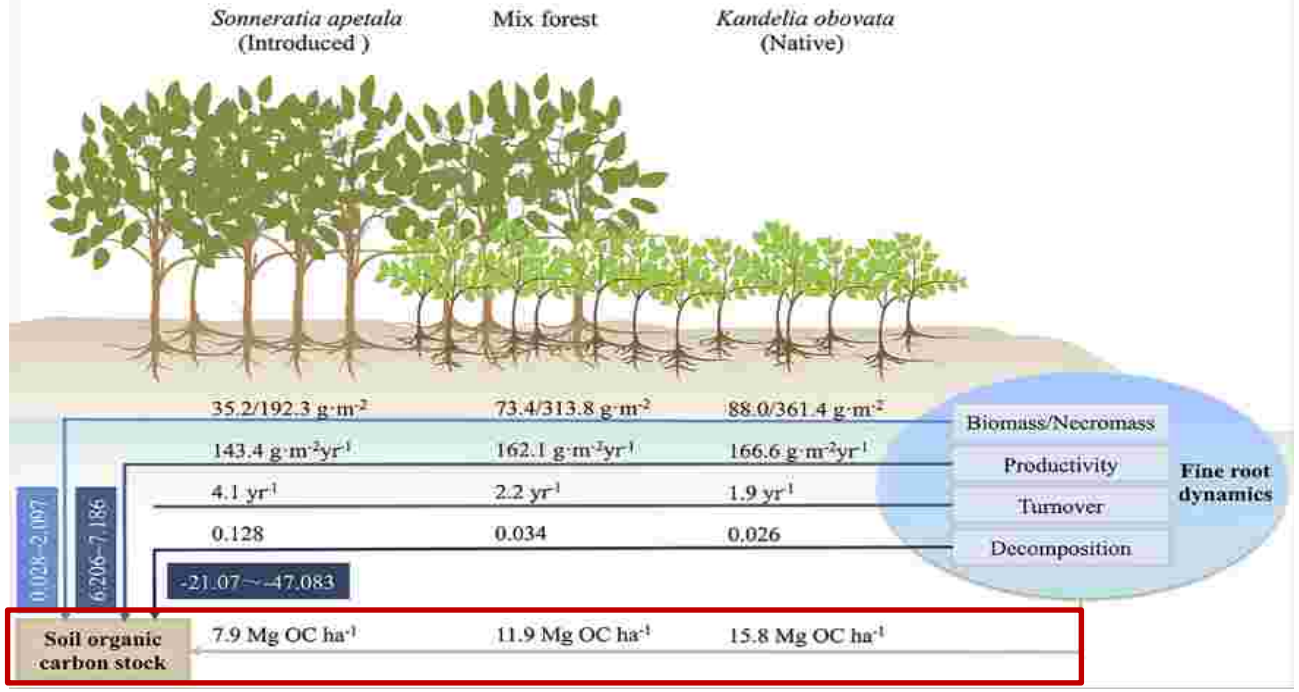


- **Human activities** are one of main drivers of mangrove loss
- **Reforestation** is important to restore mangrove ecosystems

(Ren *et al*., 2009, *Eco Eng*; He *et al*., 2018, *Plant Soil*; He *et al*., 2020, *Carbon Bal Manage*; He *et al*., 2021, *Front Mar Sci*)

Non-native mangroves showed low C storage



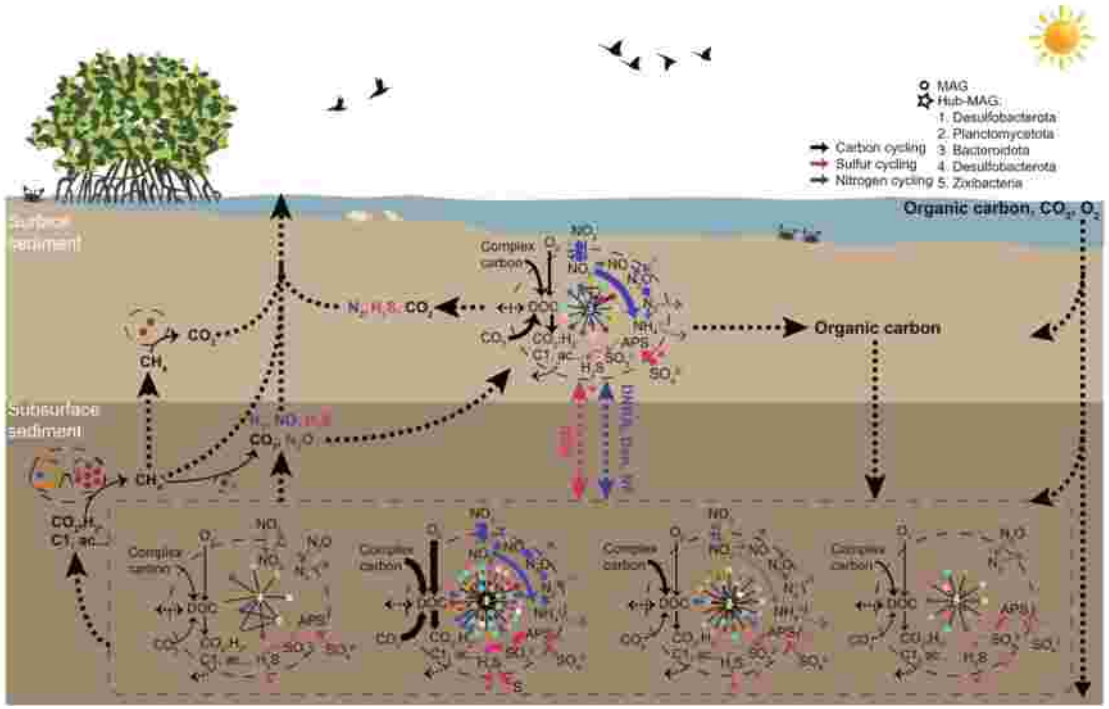


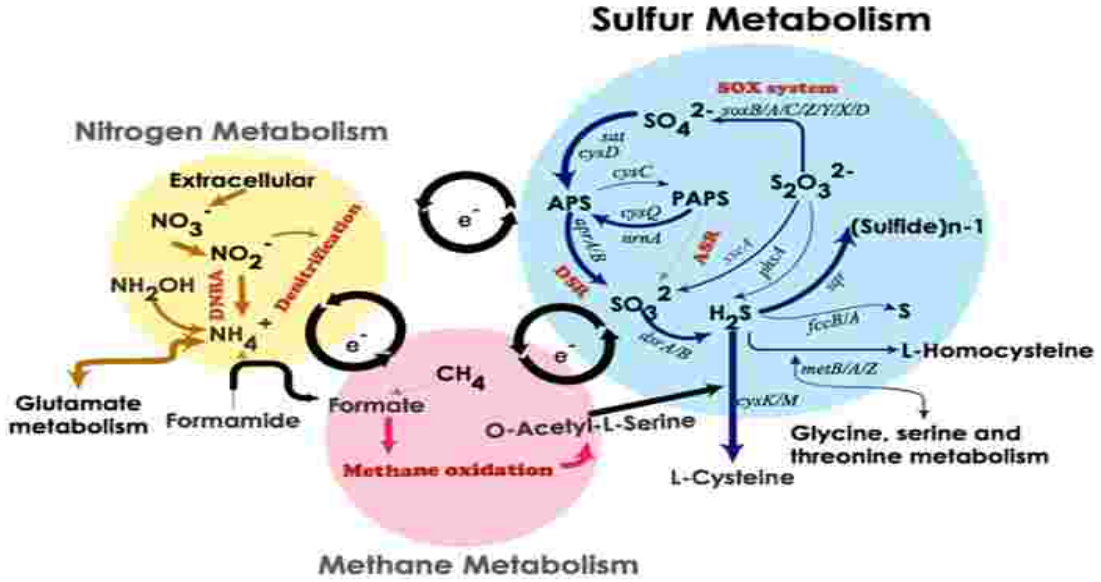
Key scientific question :

What are microbial mechanisms of C sequestration in mangrove sediments?

(He *et al*., 2020, *Carbon Bal Manage*; He *et al*., 2021, *Front Mar Sci*; Lu *et al*., 2024, *Global Change Biol*)

Features of microbially-driven nutrient cycling

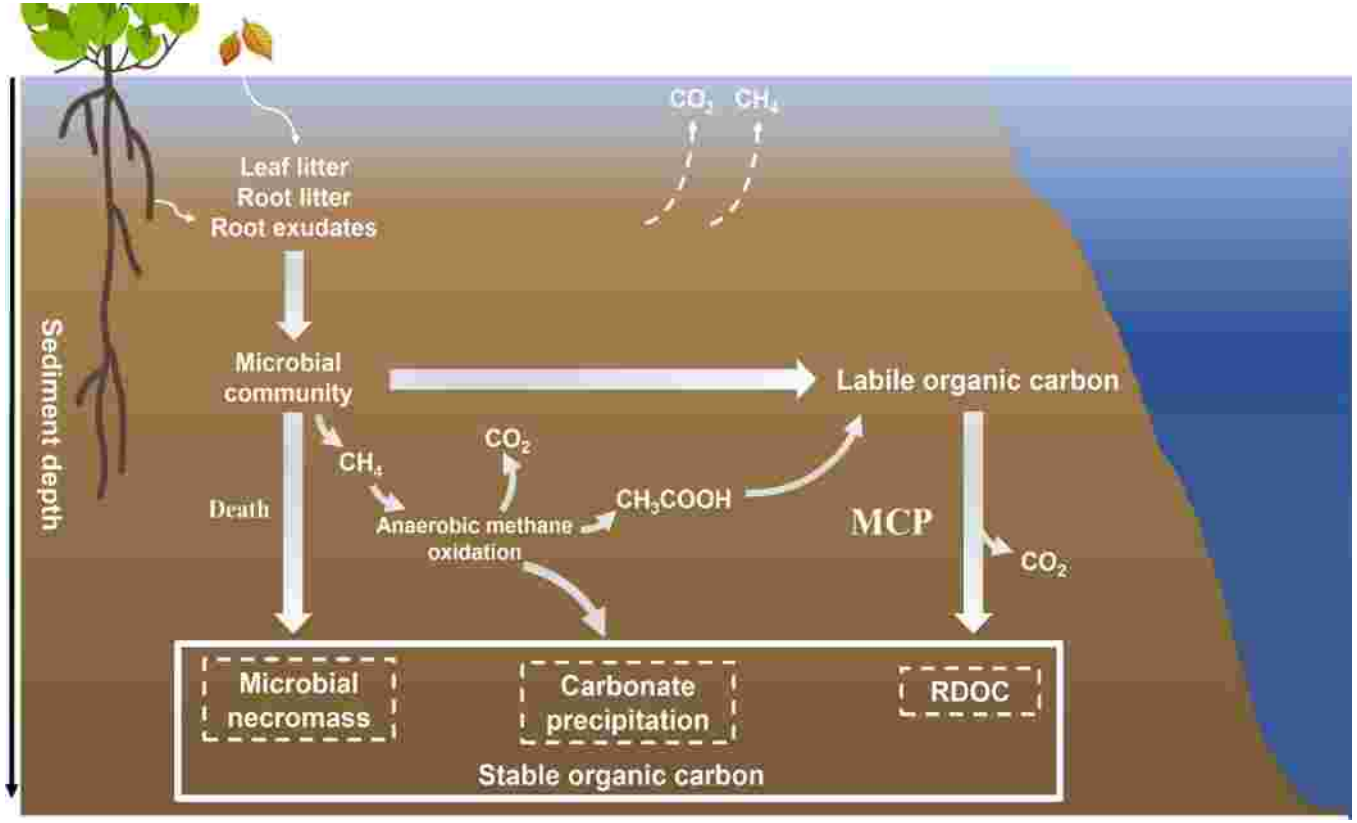




- **High** organic **C**, degrading fast
- **Low nitrogen (N)**, cycling efficiently
- **High sulfur (S)**, transforming quickly

(Tian, *et al*., 2016, *Nature*; Zhang *et al*., 2017, *PNAS*; Lin *et al*., 2019, *Microb Ecol* ; Du *et al*., 2022, *Microbiome*)

Microbially-driven C storage and transformation

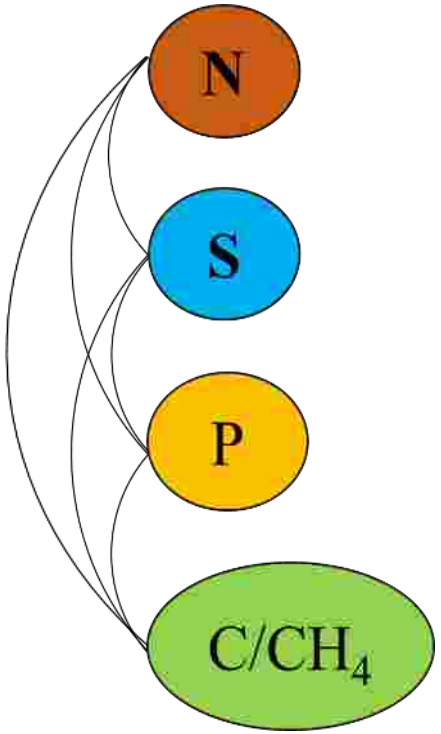


MCP: microbial carbon pump
RDOC: recalcitrant dissolved organic carbon

- **Microorganisms influence C storage** through C, nitrogen (N) and sulfur (S) cycling processes and their coupling mechanisms in mangrove sediments
- Microorganisms decompose mangrove litter and **form microbial necromass and RDOC**
- **Tides affect marine C storage** by horizontally transferring C compounds

(Zhang *et al.*, 2022, *Sci Bull*)

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)

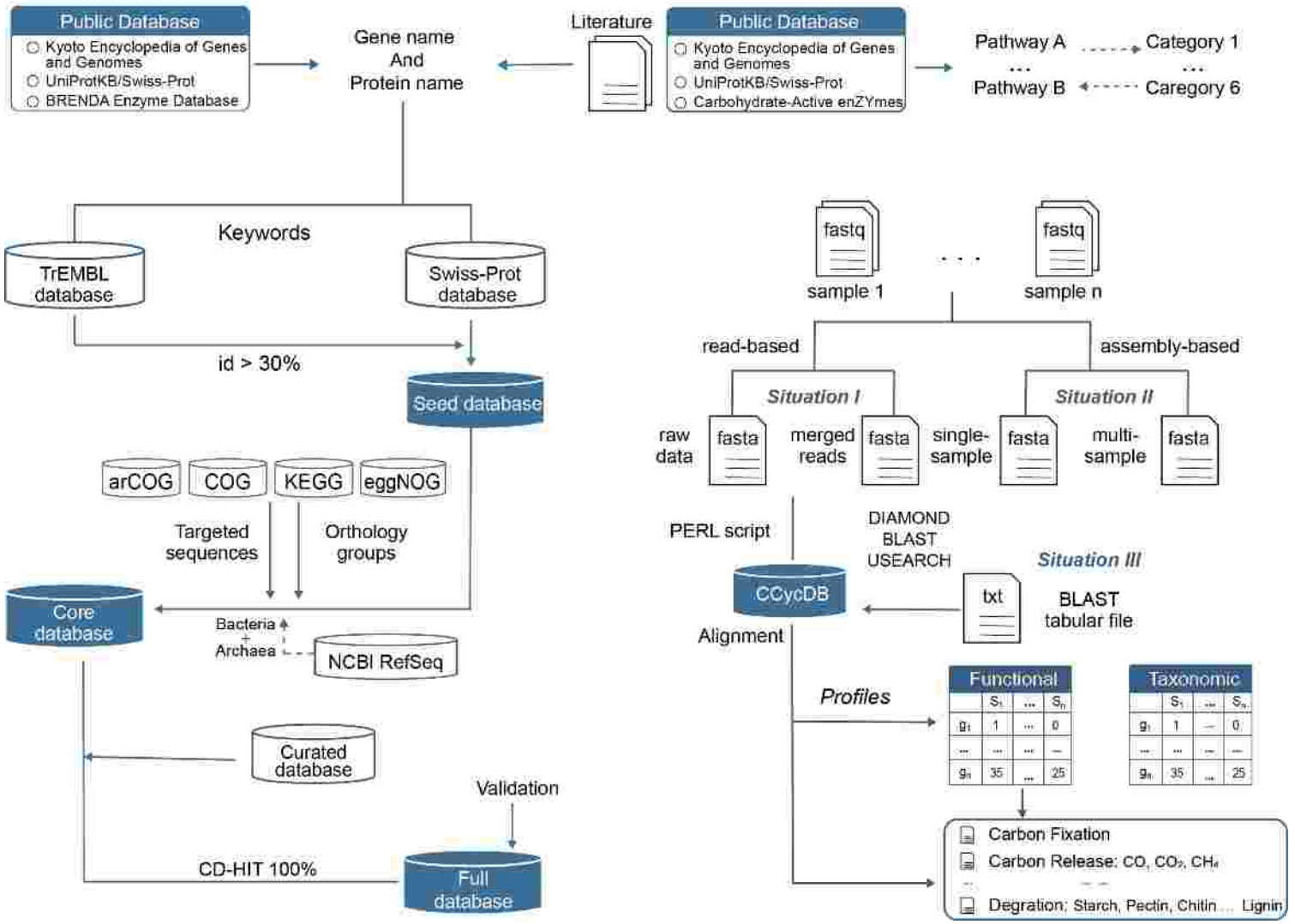
- 4572 gene families, 92 pathways, 6 modules, and 10,548,067 representative sequences

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

CCycDB construction and modules

CCycDB modules

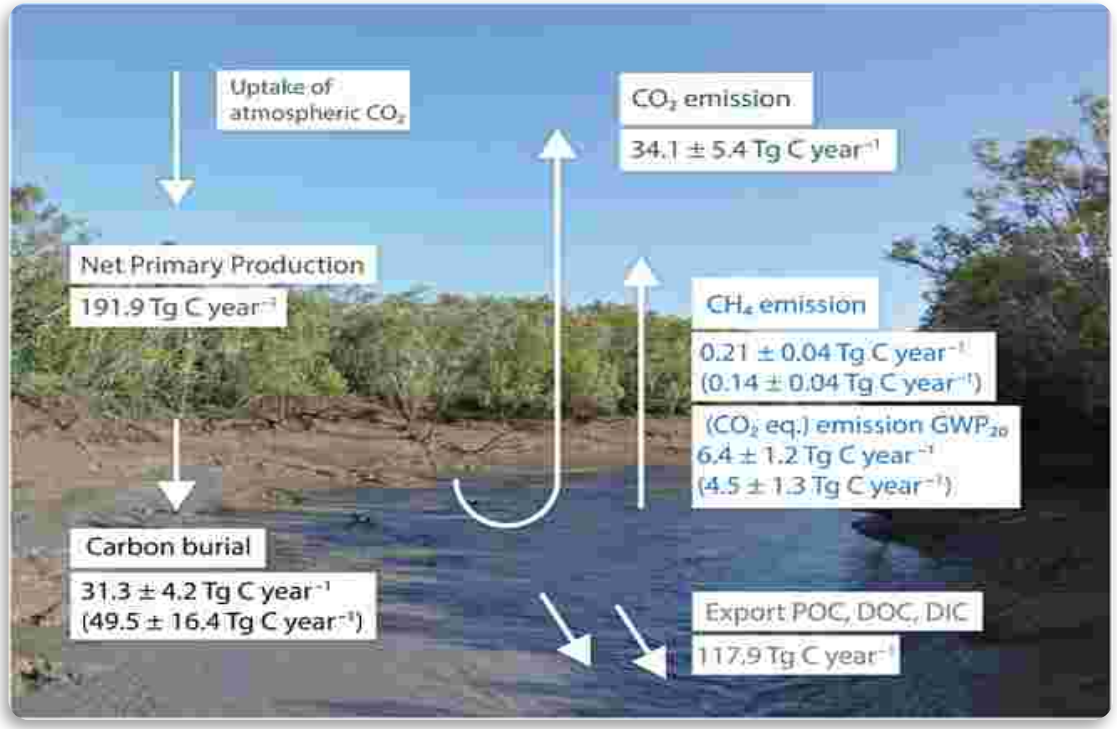
- Carbon fixation
- Carbon release
- Organic biosynthesis
- Organic degradation
- Organic transformation
- Transporters

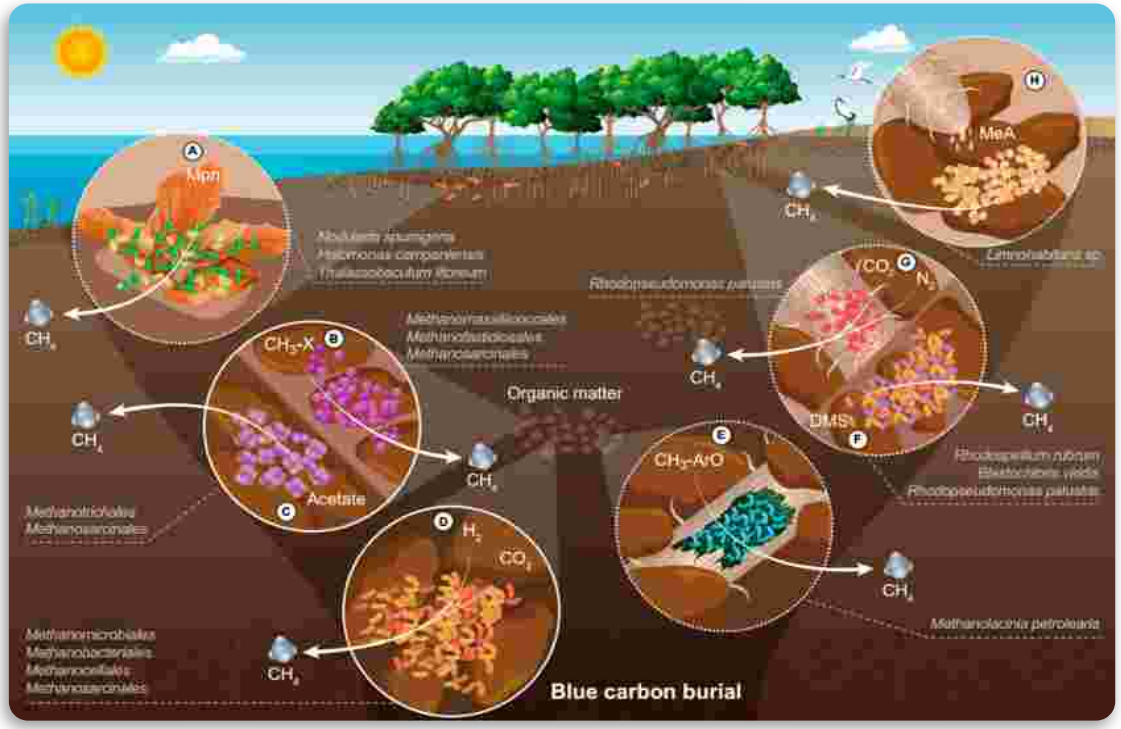


Microbial mechanisms of C sequestration

- Reducing CH_4 emissions
- Enhancing C storage
- Mediating mangrove-microbe interactions

Methane cycle in mangrove wetlands



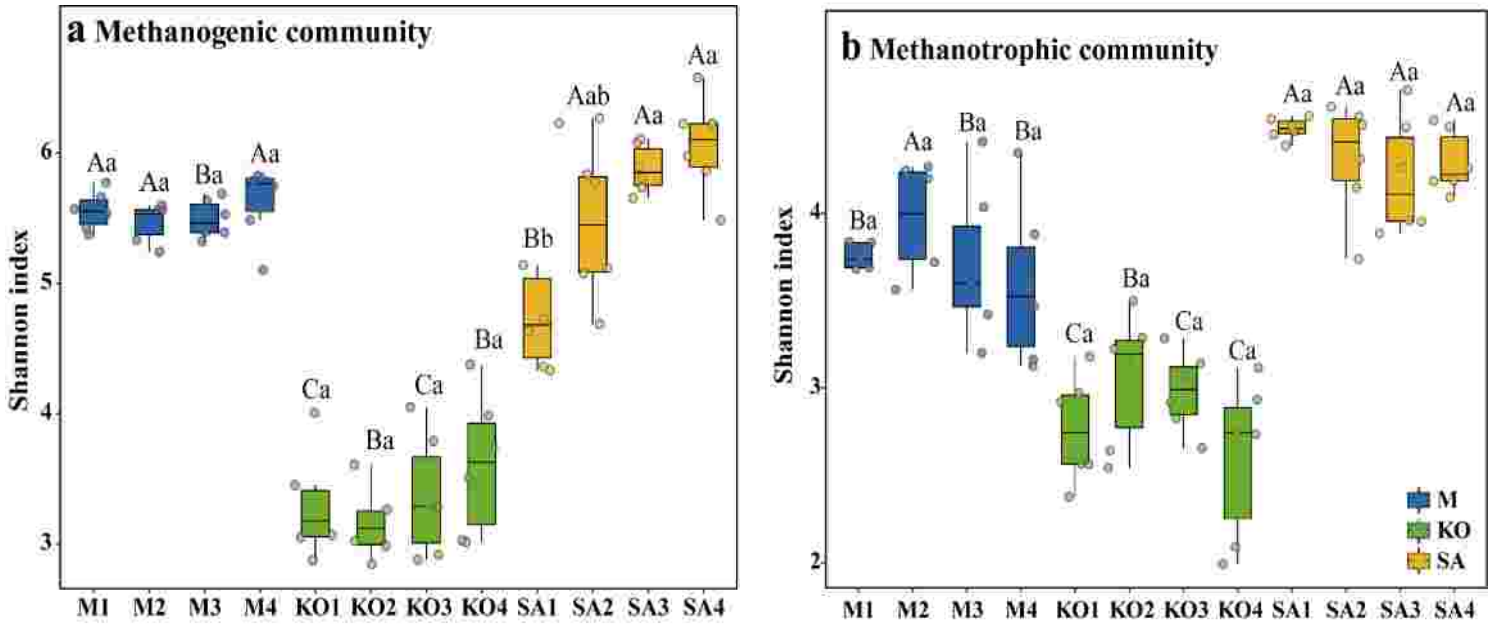


- CH_4 emissions can **offset 20% of C storage** in mangrove wetlands
- Microbially-driven CH_4 cycling is of great significance for reducing **CH_4 emissions** and increasing **C storage**

(Hu *et al*., 2024, *Trends Microbiol;* Cai et al., 2018, *ISME J*; Rosentreter *et al*., 2018, *Sci Adv*)

CH_4-cycling communities in mangrove sediments

Shannon indices of methanogenic (a) and methanotrophic (b) communities

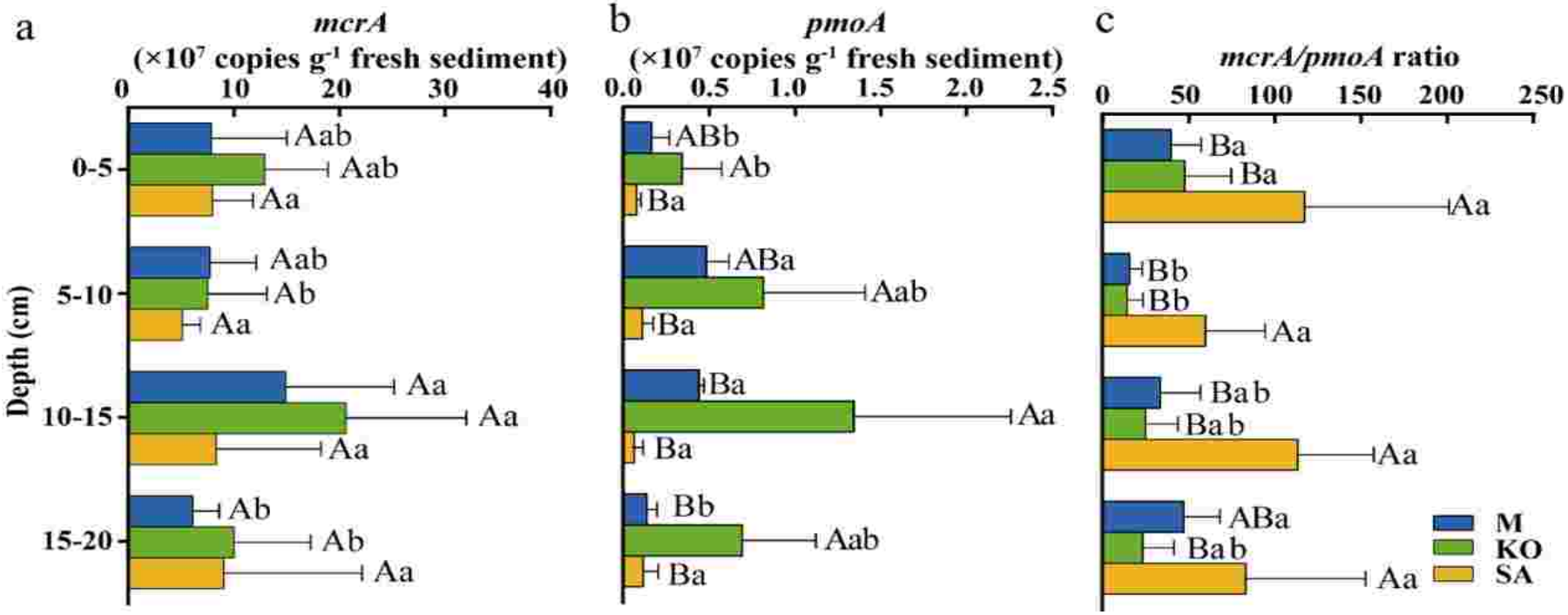


- **Higher alpha-diversity** of sediment CH_4-cycling communities was observed in *S. apetala* than in *K. obovata*

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

S. apetala sediments had lower abundances of *pmoA* genes

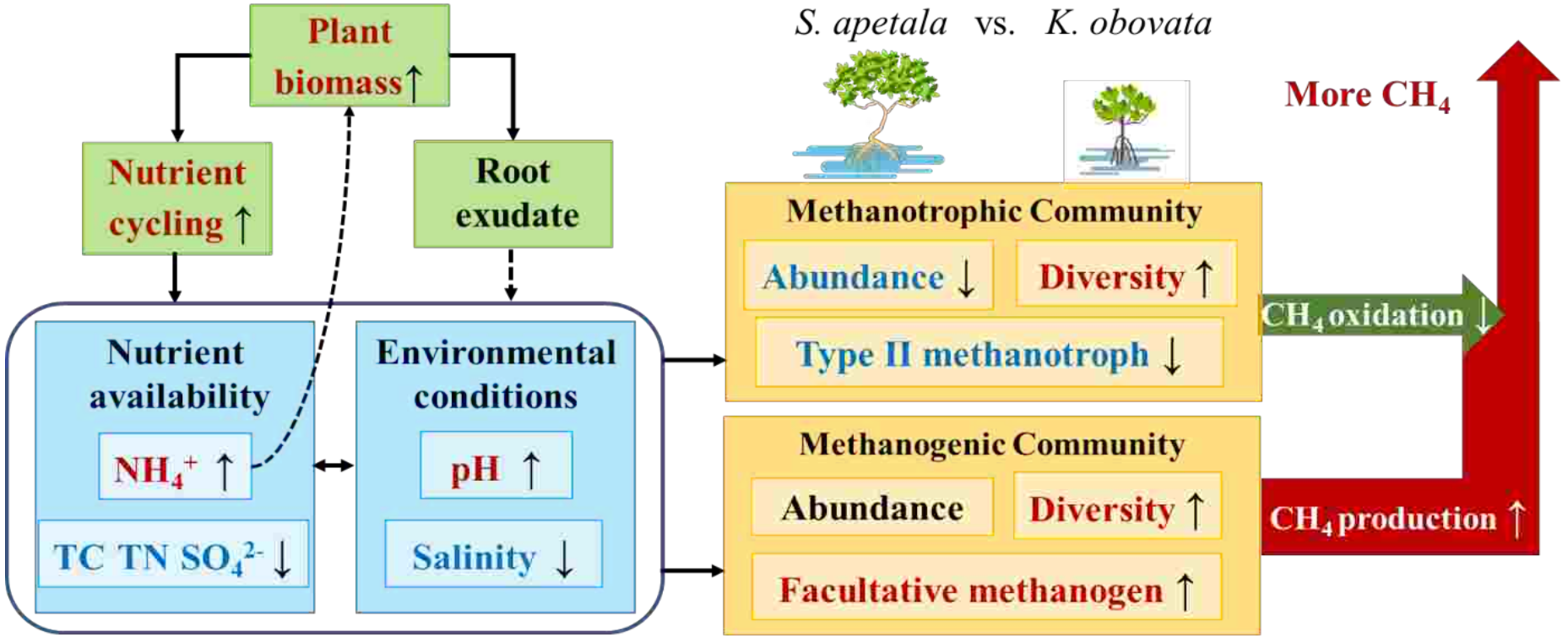
The abundance of *mcrA* (a), *pmoA* (b) and ratio of *mcrA/pmoA* (c)



- The *S. apetala* sediment had a significantly ($P < 0.05$) lower abundance of *pmoA* genes compared with the *K. obovata* sediment, which was possibly related to less CH_4 oxidized by methanotrophs

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

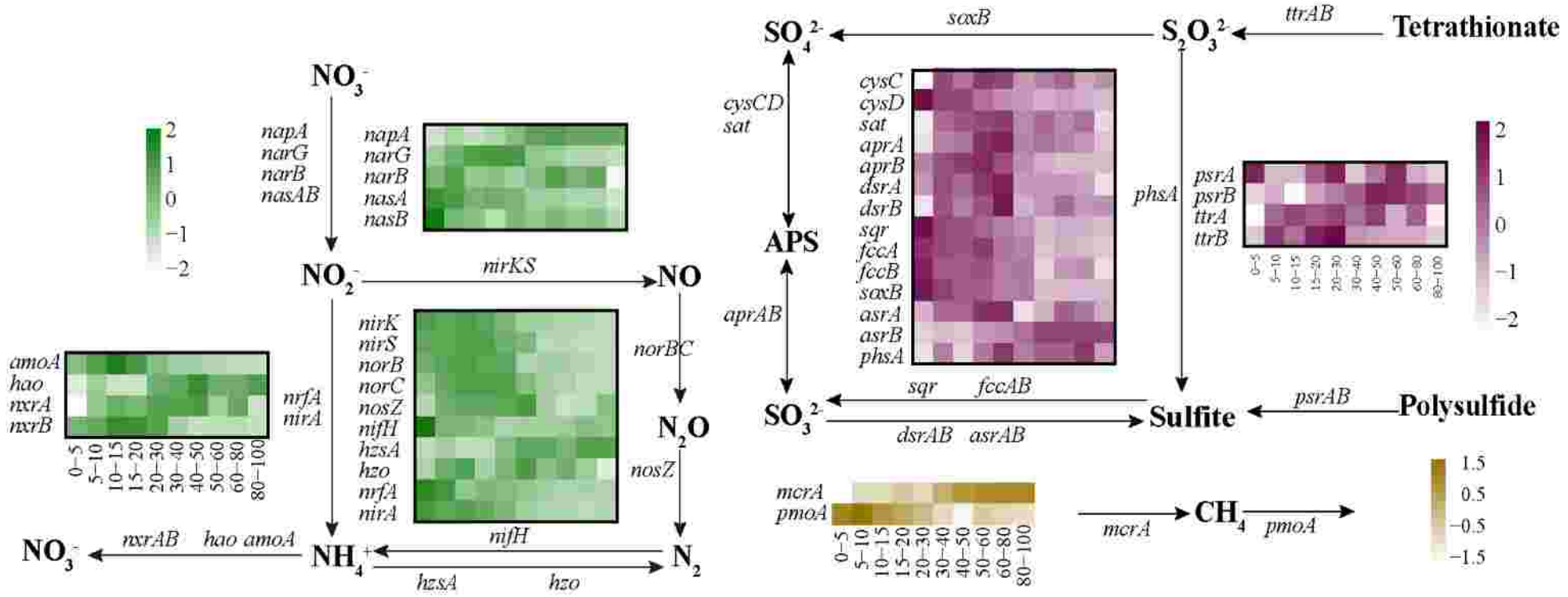
S. apetala introduction increased CH_4 emissions



- *S. apetala* introduction affected CH_4-cycling communities and **increased CH_4 emissions**, thus **decreasing its C sequestration ability**

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

Vertical distribution of CH_4/N/S cycling genes

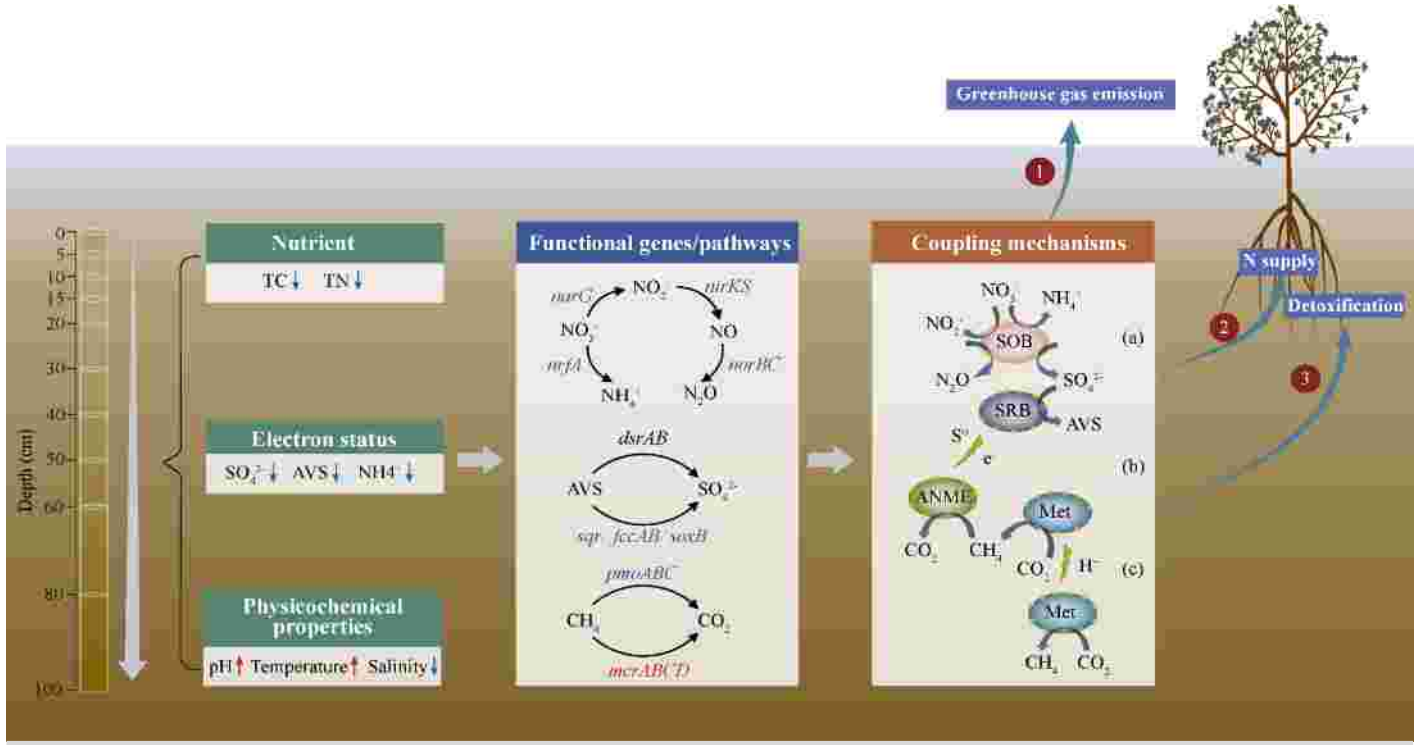


- **Denitrification and S oxidation genes** were mainly distributed in the surface sediments
- **Methanogenesis genes** were mainly distributed in the deep sediments

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

CH_4/N/S cycling and their coupling mechanisms

- S oxidation coupled with denitrification was found to be dominant in the surface mangrove sediments
- SRB could develop syntrophic relationships with ANME direct electron transfer or zero-valent S, thus **reducing CH_4 emissions** in the deep mangrove sediments



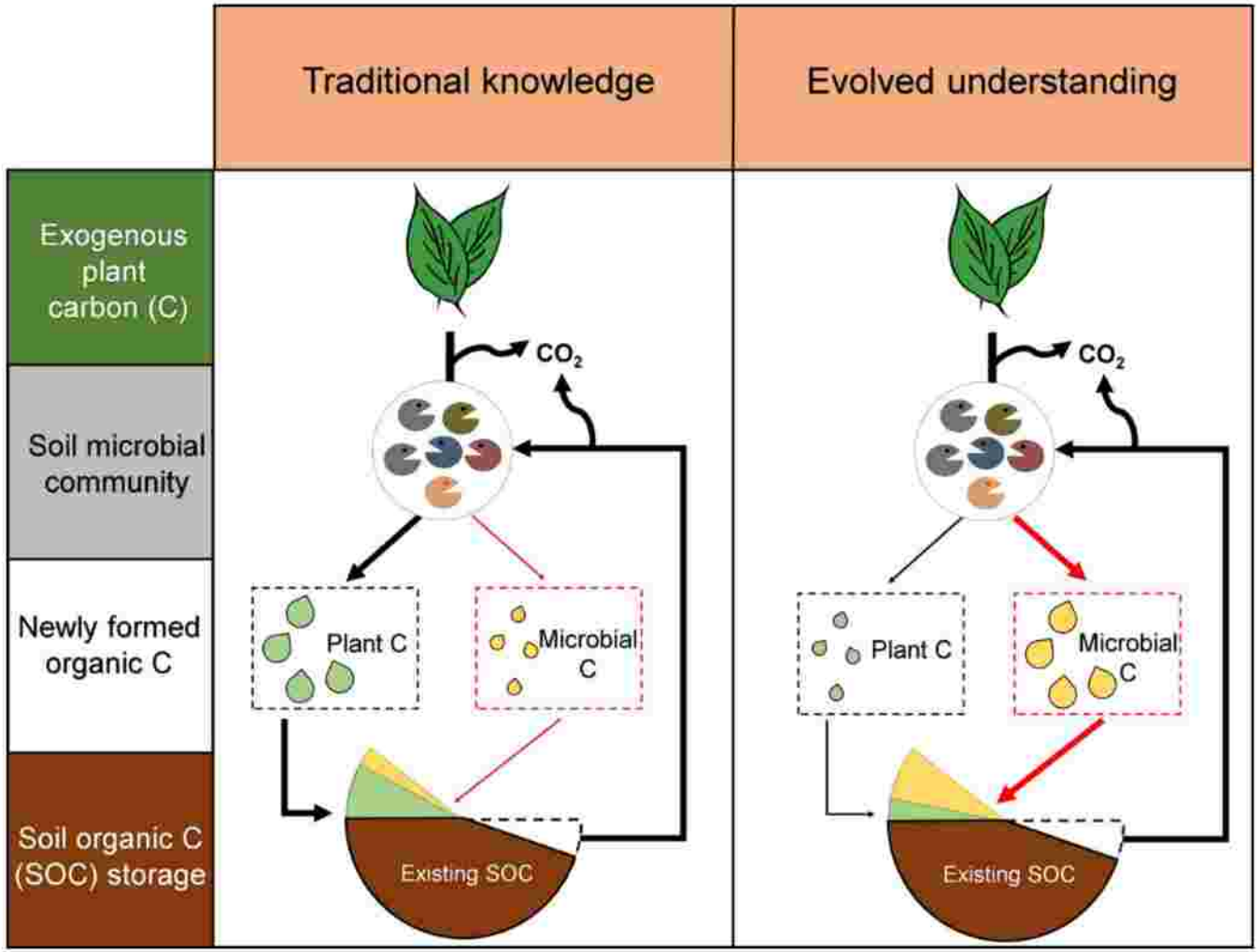
AVS: acid-volatile sulfide
SOB: sulfur oxidizing bacteria; **SRB:** sulfate reducing bacteria
ANME: anaerobic methanotrophic archaea; **Met:** methanogens

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

Microbial mechanisms of C sequestration

- Reducing CH_4 emissions
- Enhancing C storage
- Mediating mangrove-microbe interactions

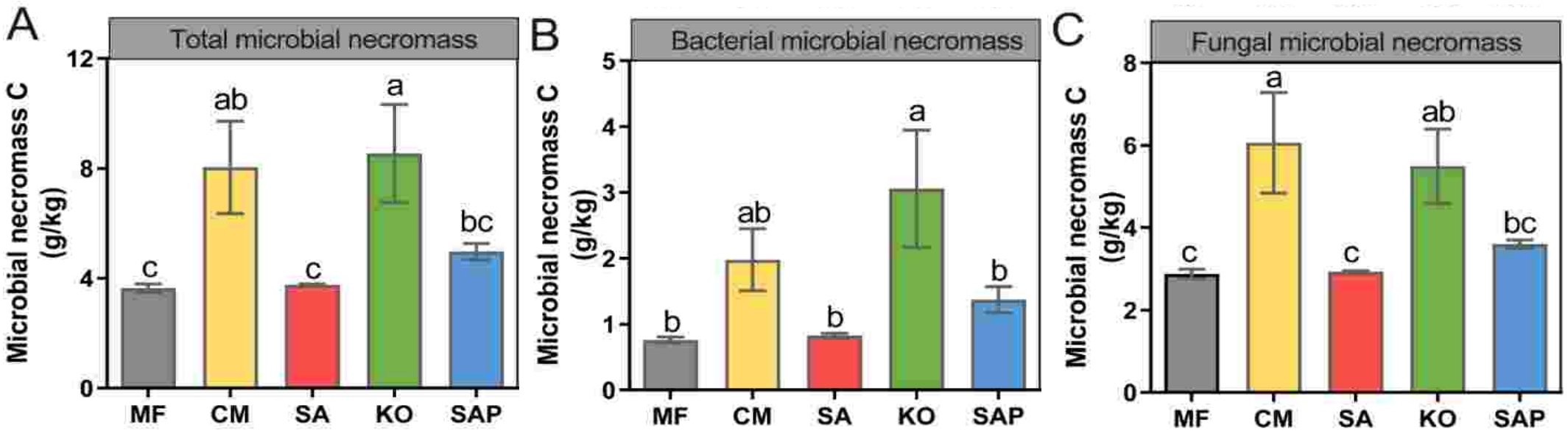
Microbial C plays an important role for C storage



- **Traditional knowledge:** Plant C is more important for soil C storage
- **Evolved understanding:** Most stable soil organic C comes from **microbial anabolic processes**

(Liang *et al*., 2017, *Nat Microbiol*; Basile-Doelsch *et al*., 2020, *Biogeosciences*; Zhu *et al*., 2020, *Global Change Biol*)

More microbial necromass in native-vegetated sediments

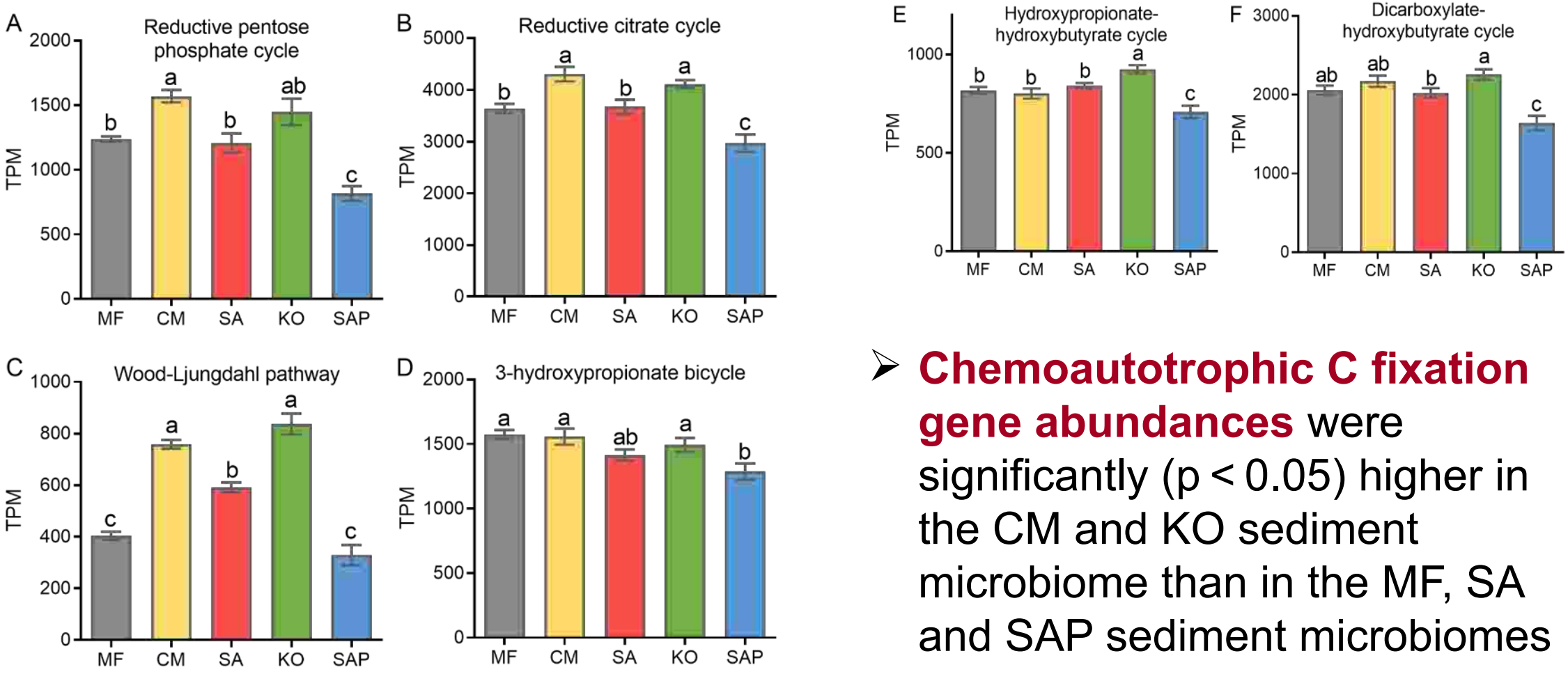


MF: Mudflat; **CM:** *Cyperus malaccensis*; **SA:** *Spartina alterniflora*; **KO:** *Kandelia obovata*; **SAP:** *Sonneratia apetala*

- **Total, bacterial and fungal microbial necromass C** were higher in native species (CM and KO)
- **High C storage of native species sediments** could be contributed by microbial necromass

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

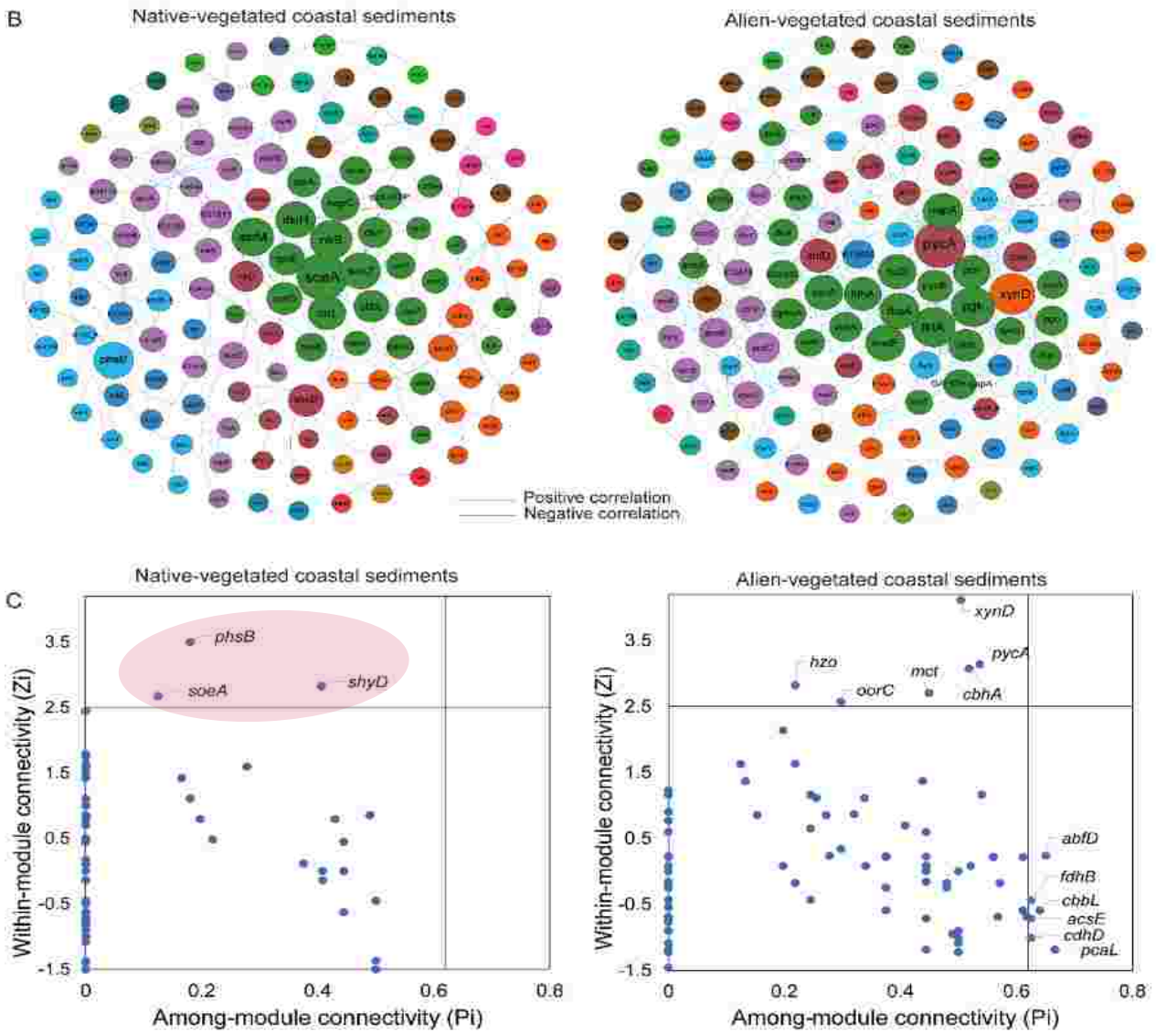
Higher C fixation potential in native-vegetated sediments



- **Chemoautotrophic C fixation gene abundances** were significantly ($p < 0.05$) higher in the CM and KO sediment microbiome than in the MF, SA and SAP sediment microbiomes

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

C fixation coupled with S oxidation and N reduction

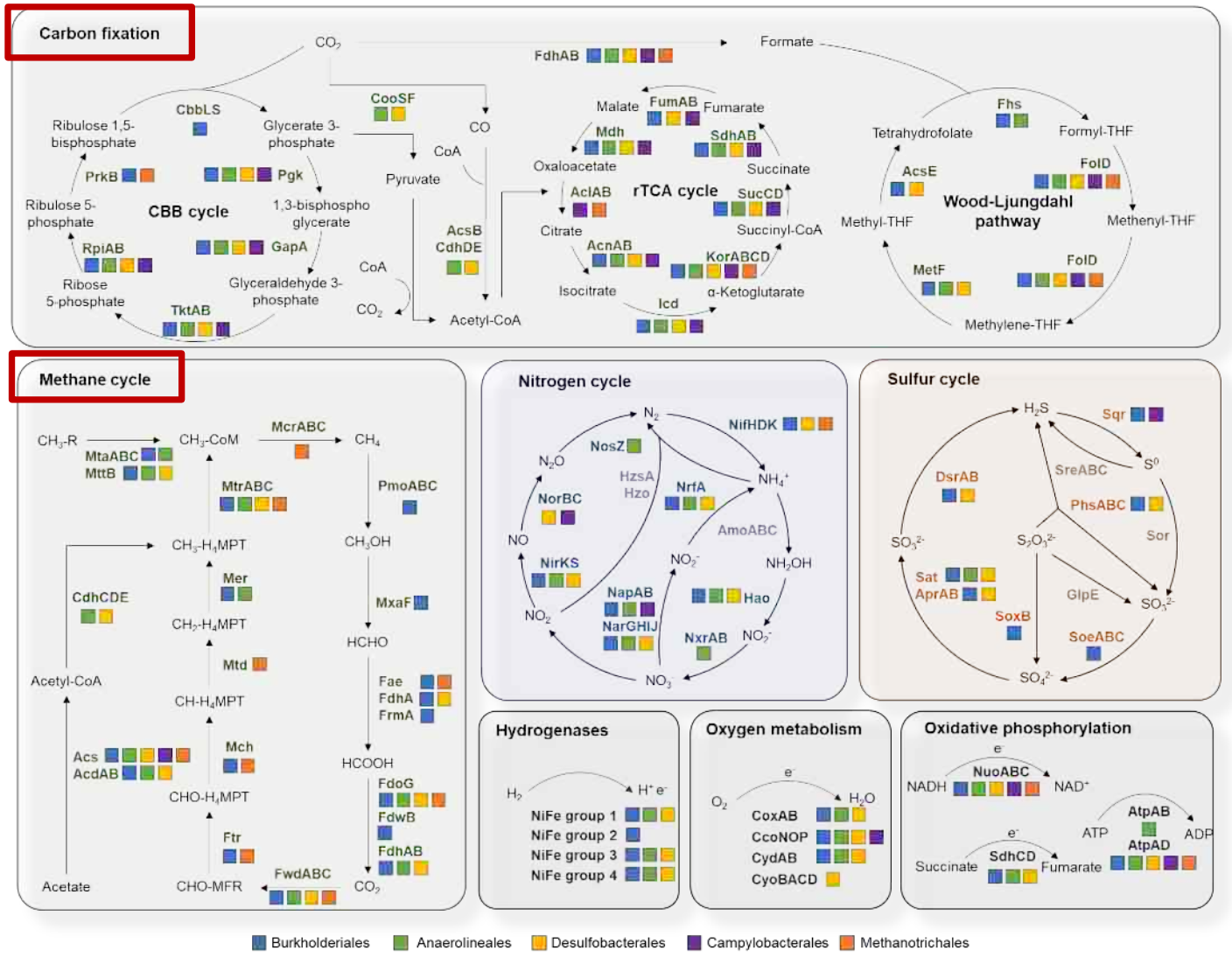


- **C fixation, S oxidation and nitrate/nitrite reduction genes** were clustered together and formed the largest functional module in the native-vegetated sediment microbiome
- S cycling gene families (e.g. ***soeA***, ***phsB***, ***shyD***) were found to be module hubs

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

Microbial mechanisms of *Burkholderiales* for C storage

- *Burkholderiales* could oxidize **reduced S compounds or hydrogen** as energy sources for CO_2 fixation with oxygen or nitrate/nitrite as electron acceptors
- An important group for **C sequestration** in coastal sediments

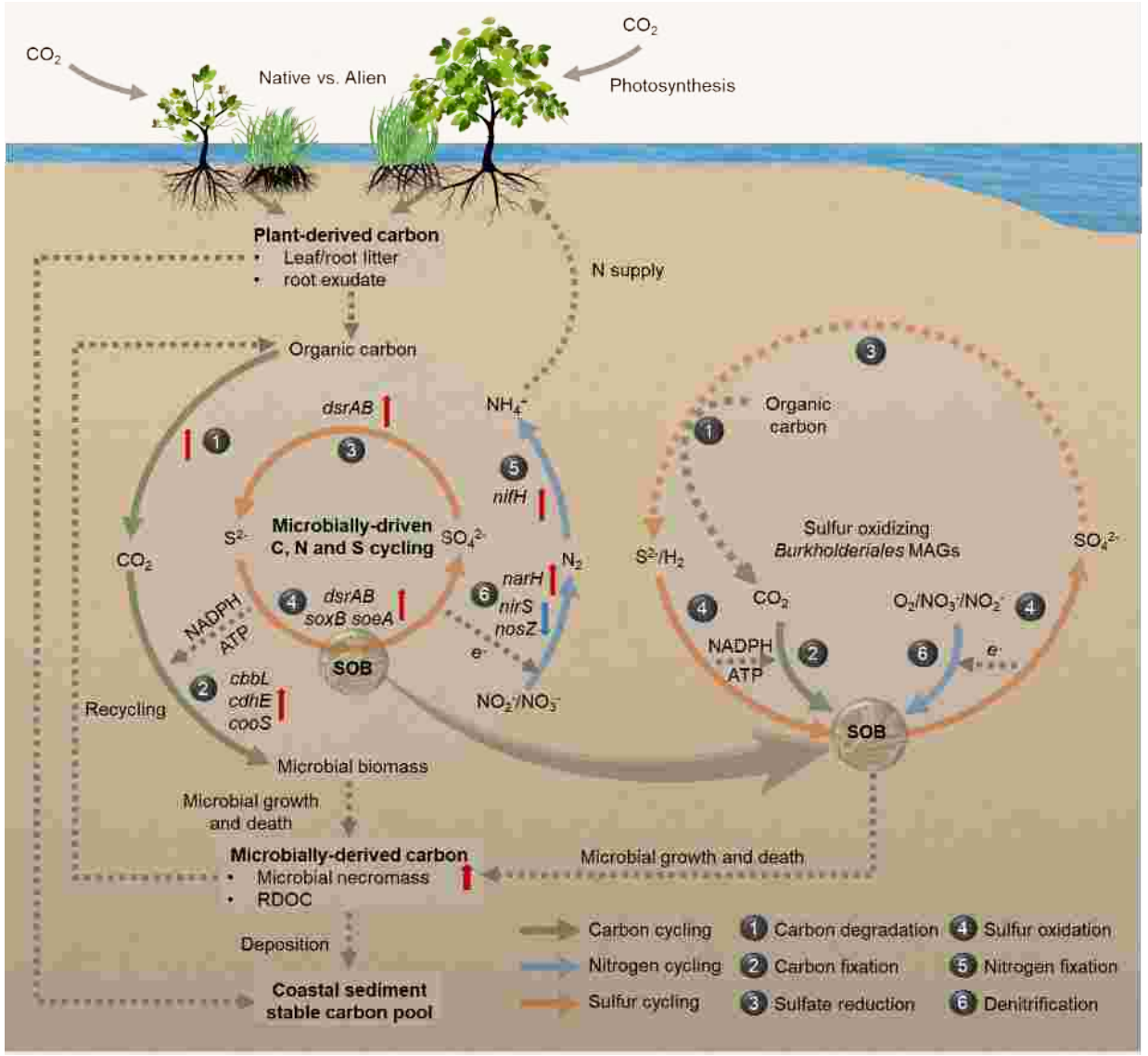


(Yu *et al*.,2023, *Func Ecol*)

Chemoautotrophic CO_2 fixation was important for C storage

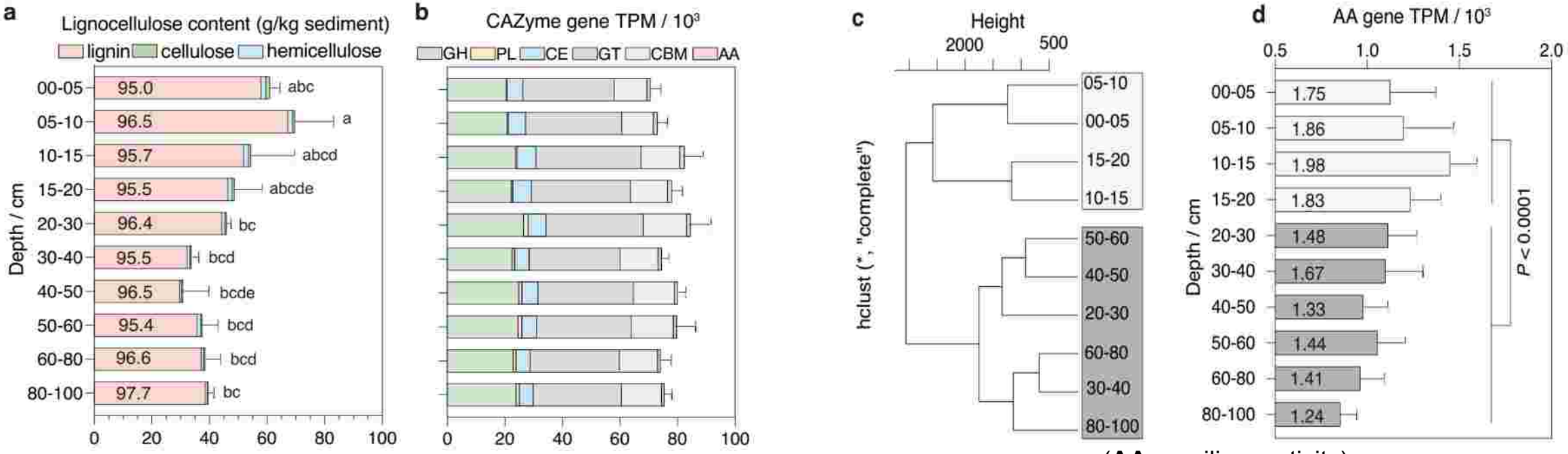
Three possible C sequestration mechanisms:

- Microbial anabolism
- Coupling of microbially driven C, N and S cycling processes
- Deposition of microbially derived C



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

Lignocellulose and CAZyme-coding gene abundances

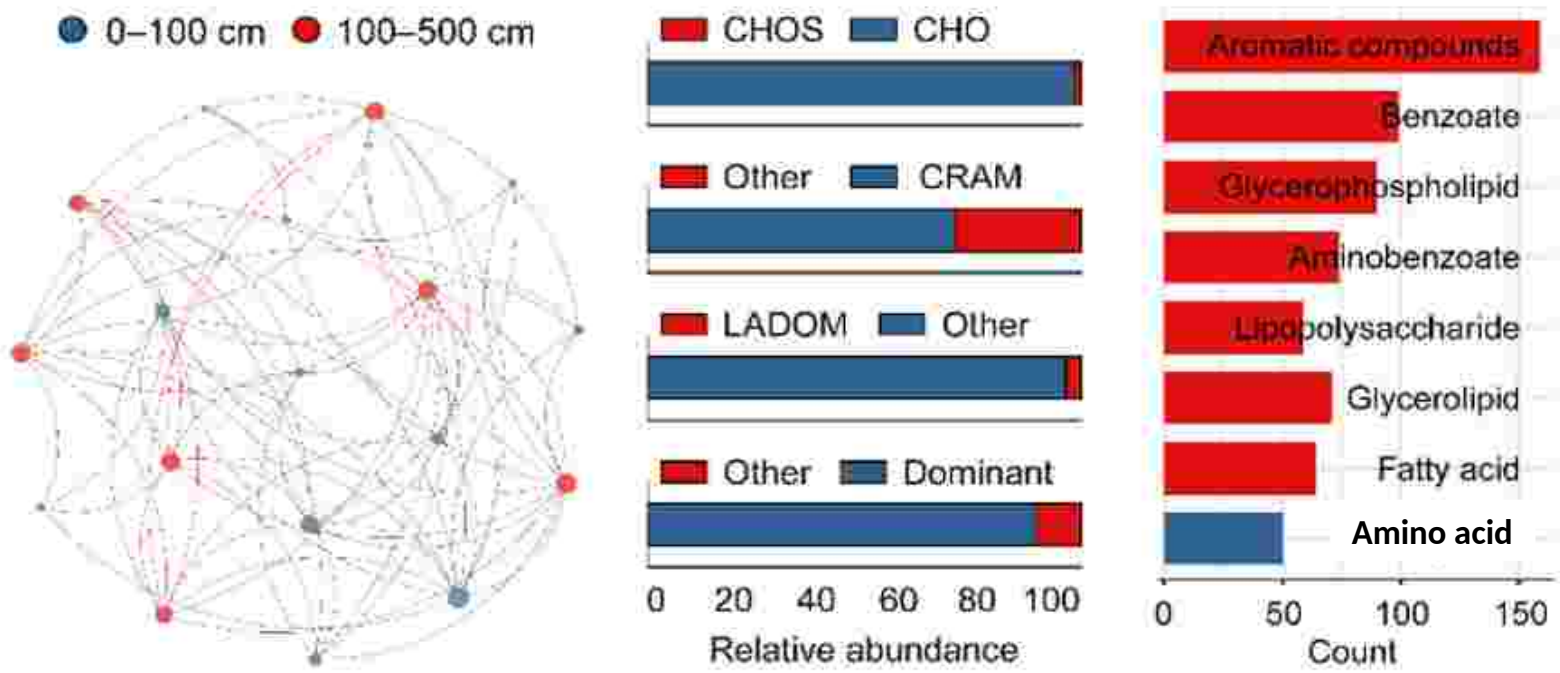


(**AA:** auxiliary activity)

- **Lignin is a main component of organic C in mangrove sediments**
- **Low abundances of lignin breakdown enzymes in mangrove sediments**
- **Accumulation of phenolic fragments and non-phenolic derivatives in subsurface sediments**

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

DOM transformation in mangrove sediments

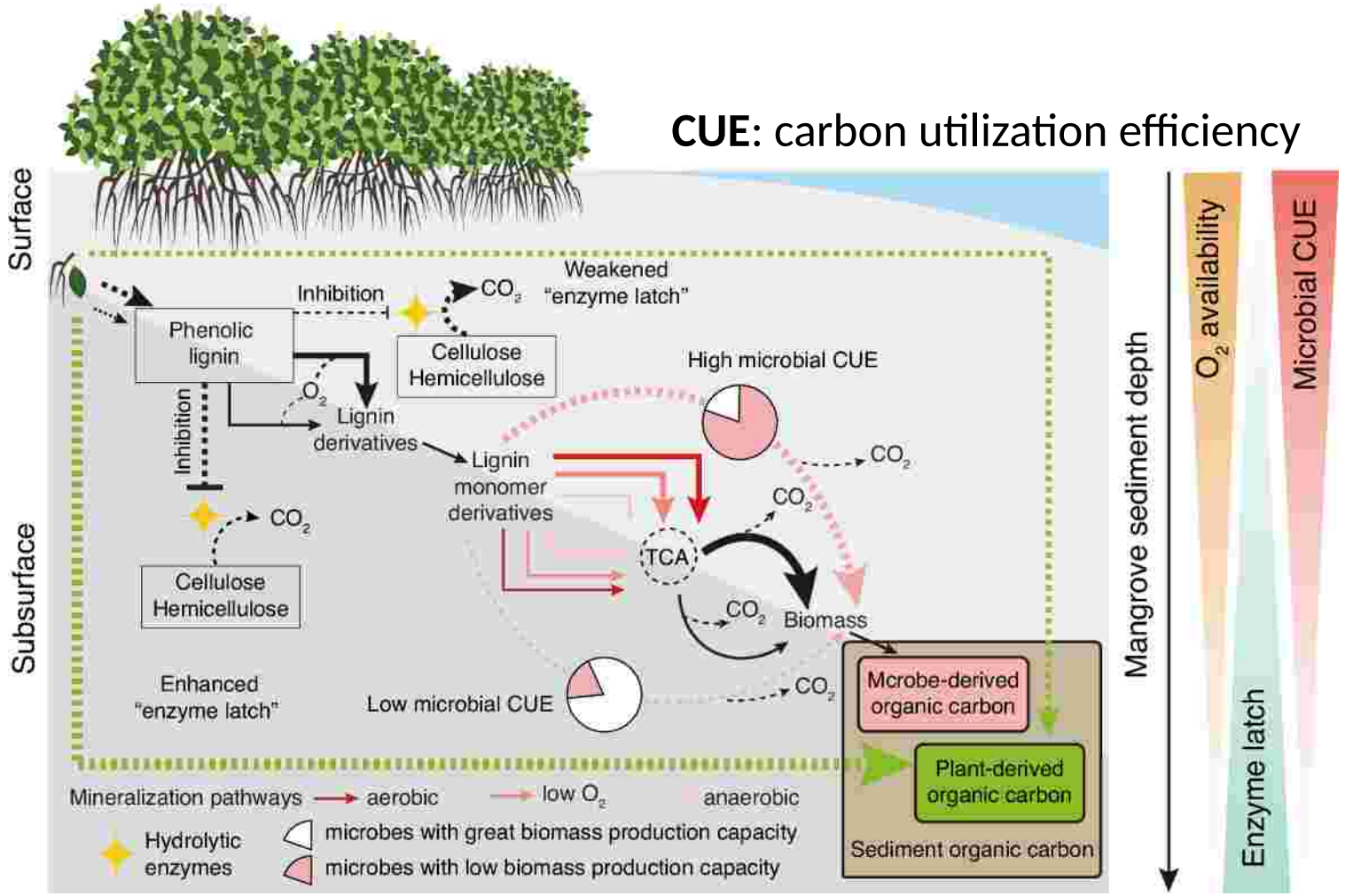


CRAM: carboxyl-rich alicyclic molecules

- Microbial communities exhibited widespread potentials for **DOM transformation**, primarily through key pathways
- **Interactions** between microbial communities and DOM played a crucial role in driving C sequestration in mangrove sediments

(Huang *et al*., unpublished)

Microbially-driven organic C storage with depths



CUE: carbon utilization efficiency

- **High microbial CUE potential** led to microbe-derived organic C in the surface sediments
- **Enhanced "enzymatic latch"** resulted in more plant-derived organic C storage in the subsurface sediments

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

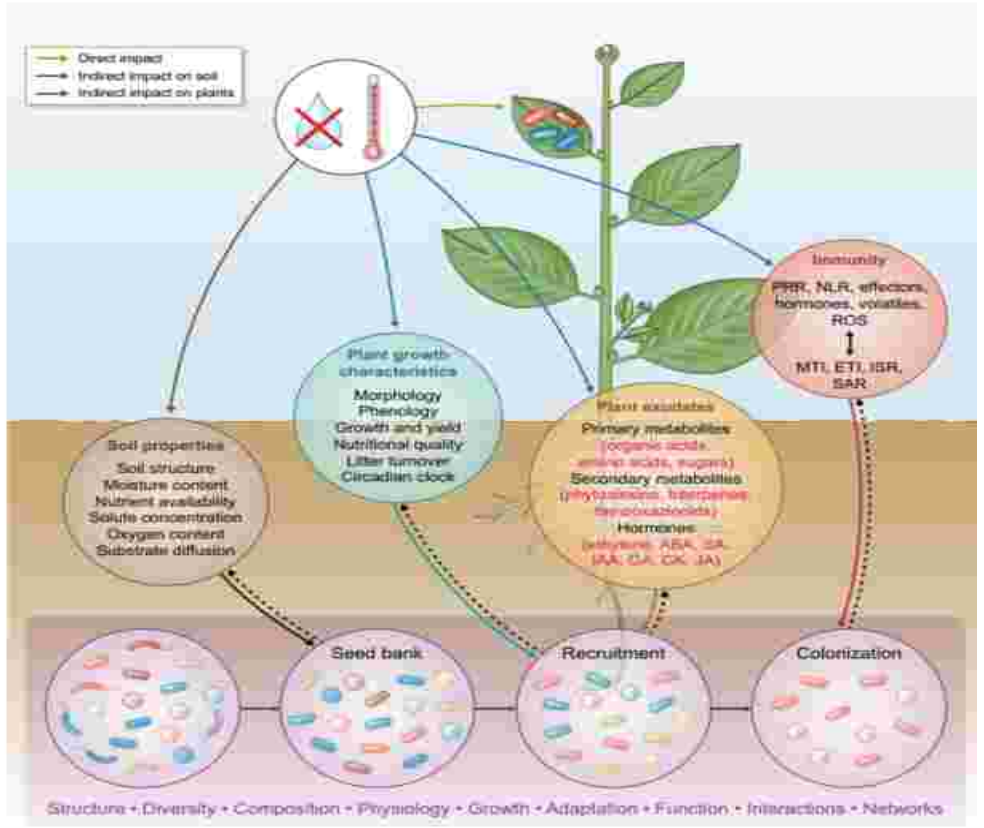
Microbial mechanisms of C sequestration

- Reducing CH_4 emissions
- Enhancing C storage
- Mediating by microbe-mangrove interactions

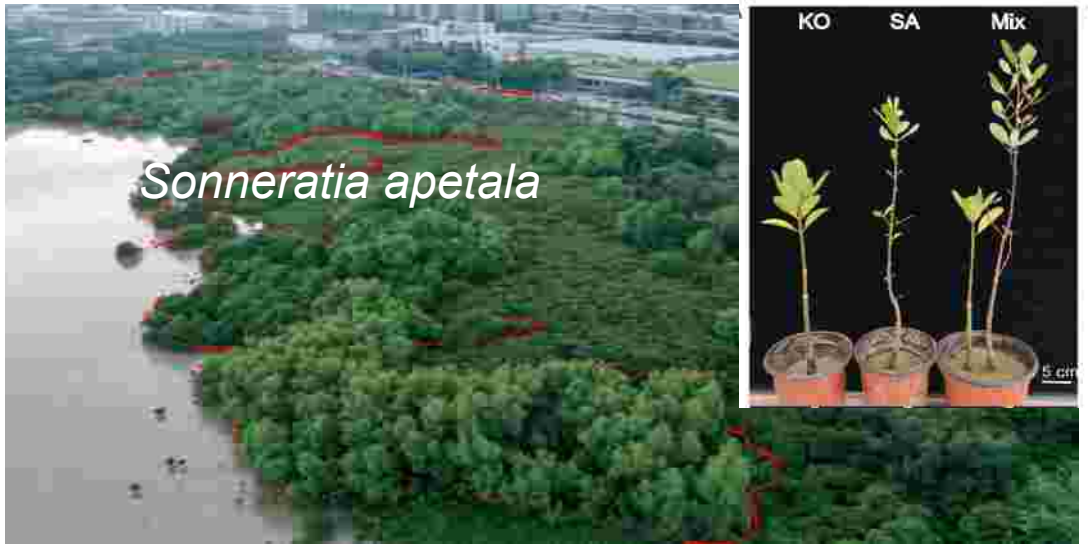
Microbe-plant interactions affect plant performance

How do plants and microbes interact in the mangrove rhizosphere ?

- By secreting key metabolites?
- By recuriting key microbes?



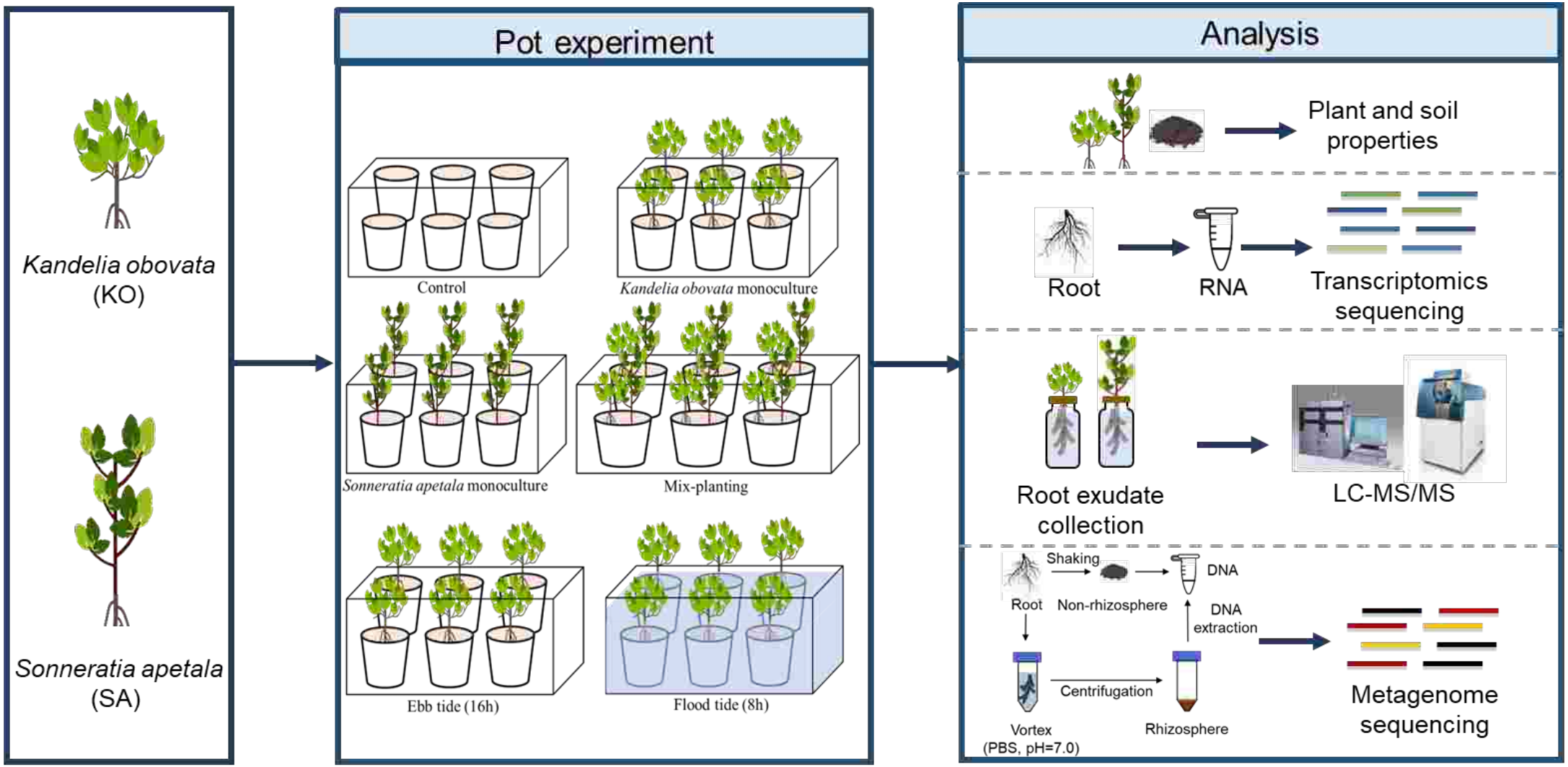
(Trivedi *et al*., 2022, *New Phytol*; Yue *et al*., 2023, *Microbiome*)



- The introduction of *Sonneratia apetala* (**SA**) shows inhibitory effects on the growth of native mangrove *Kandelia obovata* (**KO**)

(Nazaries *et al*., 2018, *Soil Biol Biochem* ; Yu *et al*., 2020, *Soil Biol Biochem*)

Experimental design and data analysis

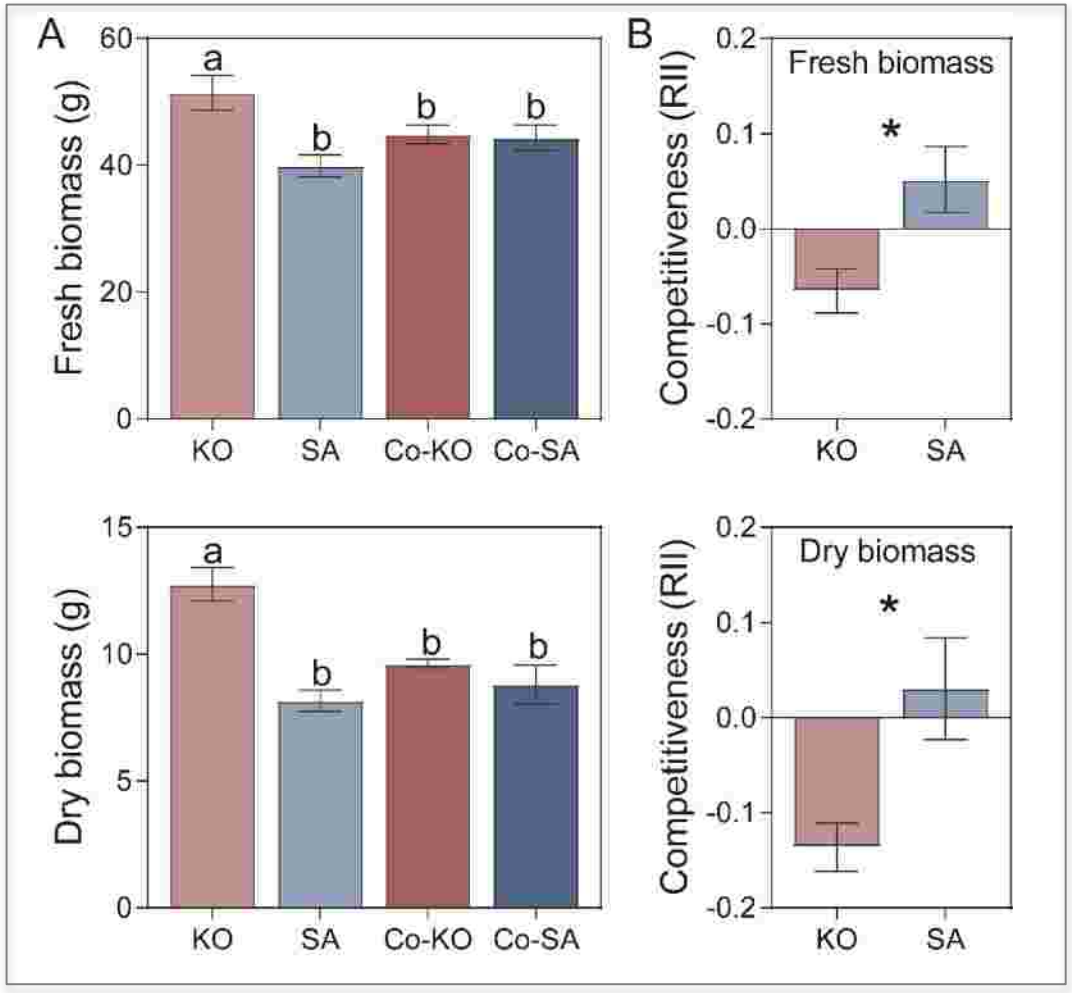


(Yu *et al.*, unpublished)

Low competitiveness of *K. obovata* led to inhibited growth under co-culture conditions

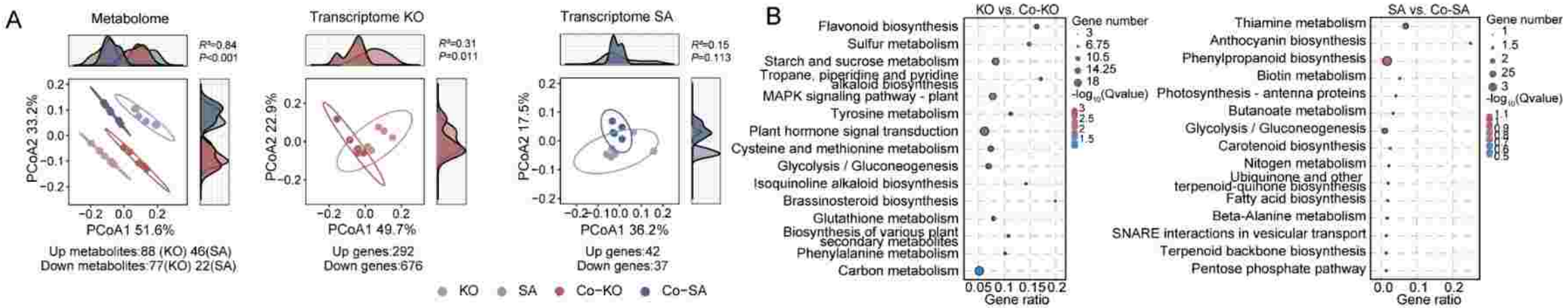
- ***K. obovata* growth was inhibited** in the co-culture
- *K. obovata* had **lower competitiveness** (RII value) than *S. apetala*

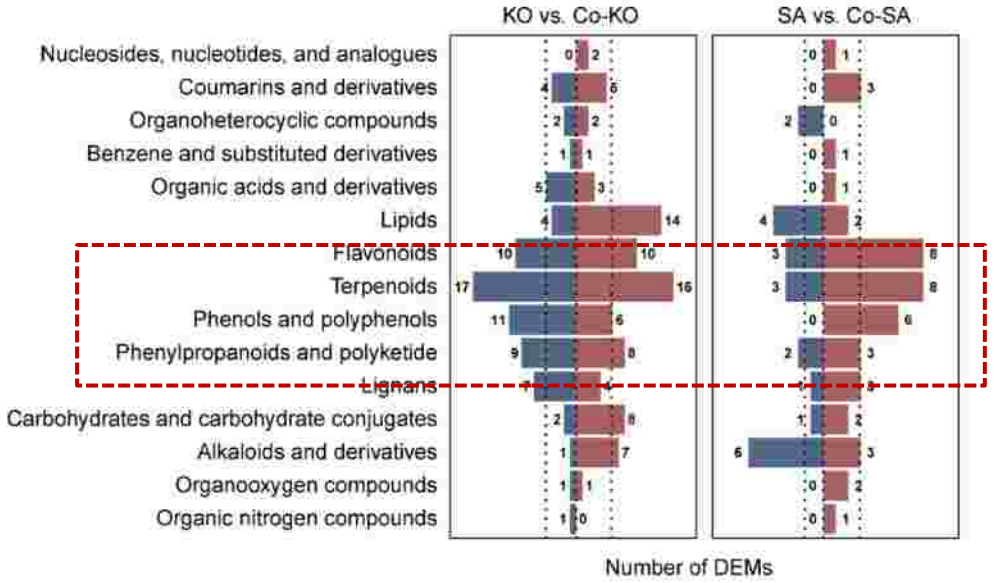




(Yu *et al*., unpublished)

Co-culture changed plant transcriptomes and metabolomes

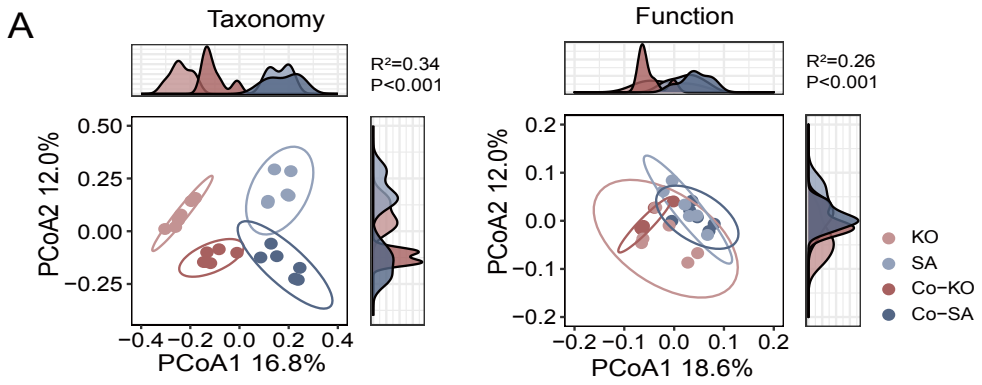


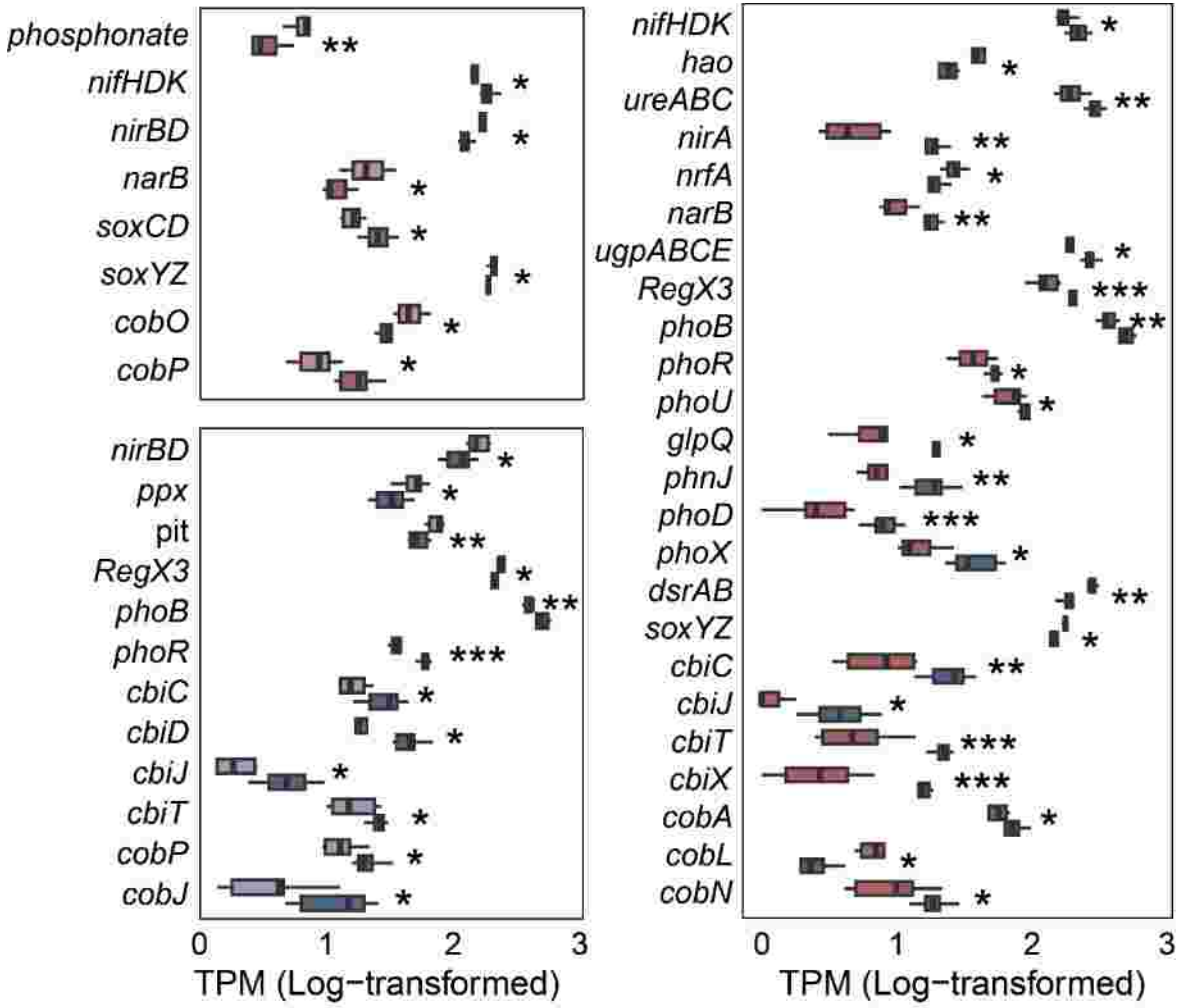


- Co-culture altered the **flavonoids biosynthesis**, sulfur metabolism, starch and sucrose metabolism, and plant hormone signal transduction of *K. obovata,* and changed related root exudates

(Yu *et al*., unpublished)

Co-culture changed microbiome functions

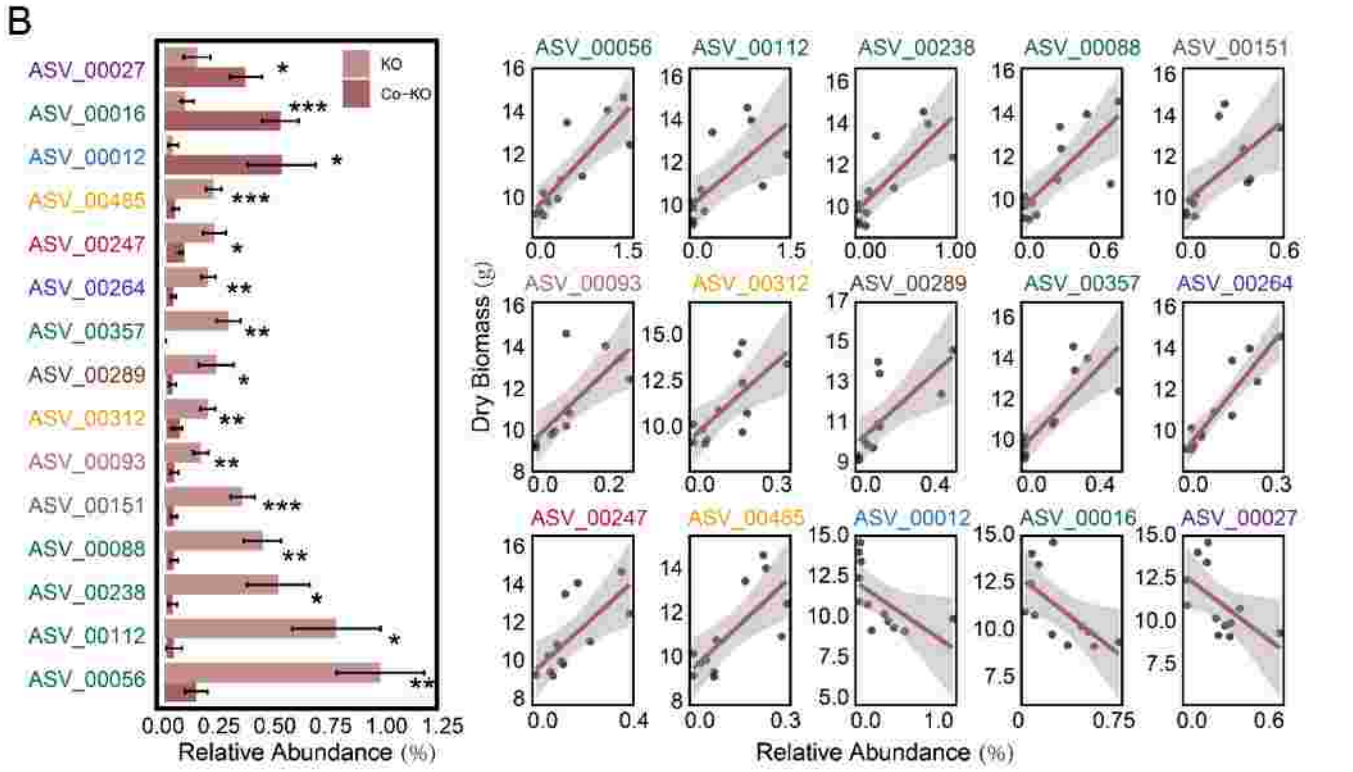


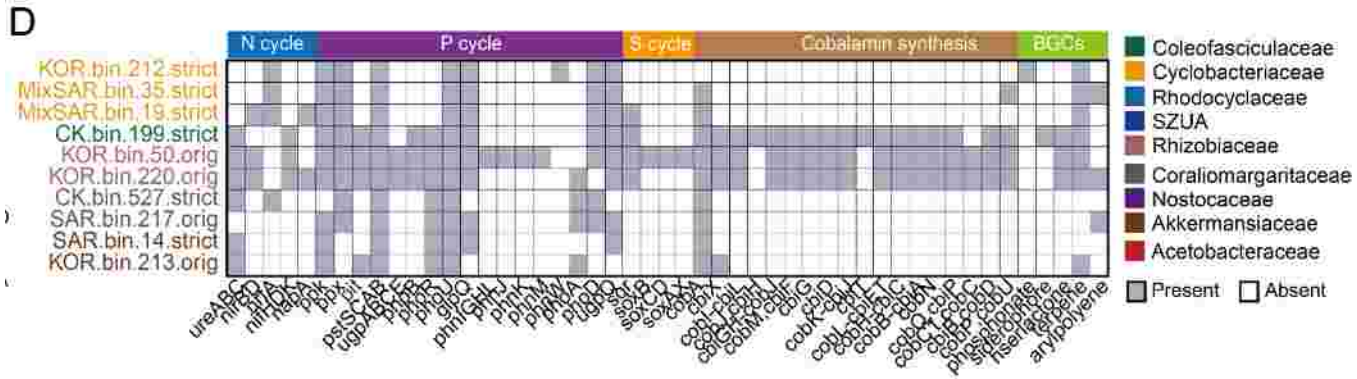


- SA showed significantly (P < 0.05) higher abundances of gene families involved in N_2 fixation, ureolysis, assimilatory nitrate reduction, P transporters, two-component systems, organic phosphoester hydrolysis and VB_{12} biosynthesis compared to KO
- Co-culture influenced the rhizosphere and non-rhizosphere microbiomes involved in N_2 fixation, P regulation, and $VB1_2$ biosynthesis, potentially impacting plant growth

(Yu *et al.*, unpublished)

Co-culture changed microbiome taxonomy

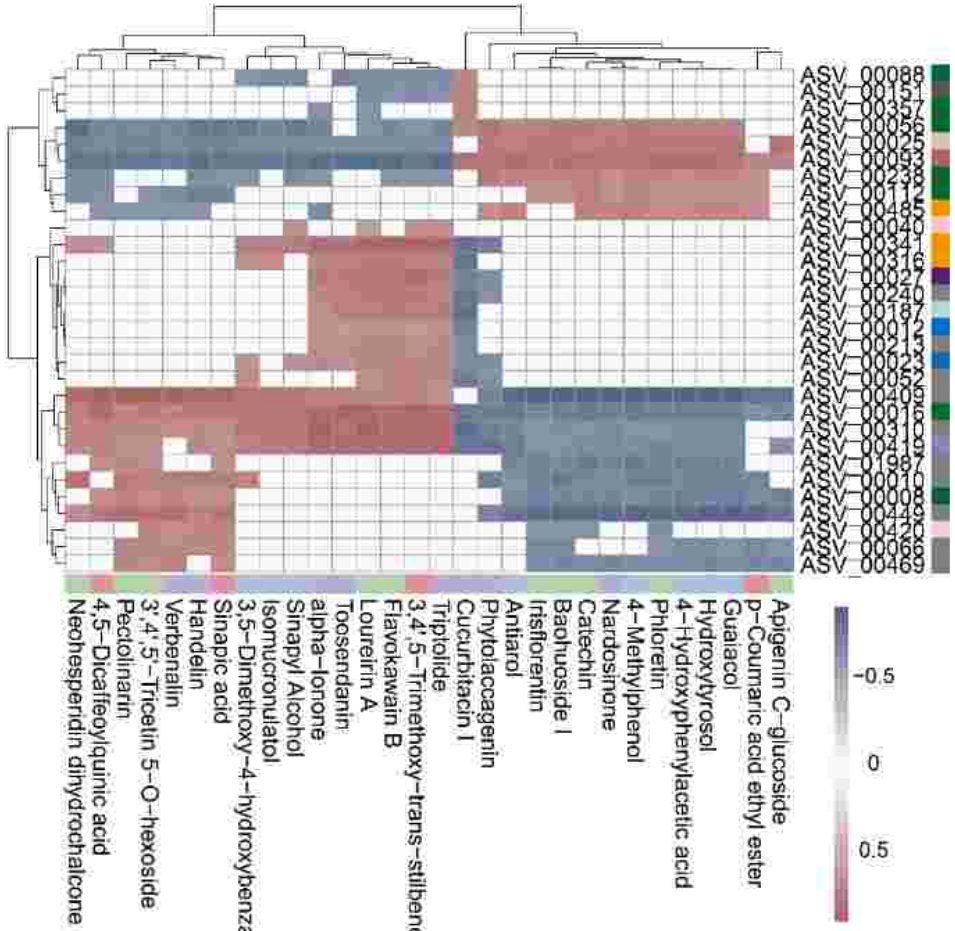




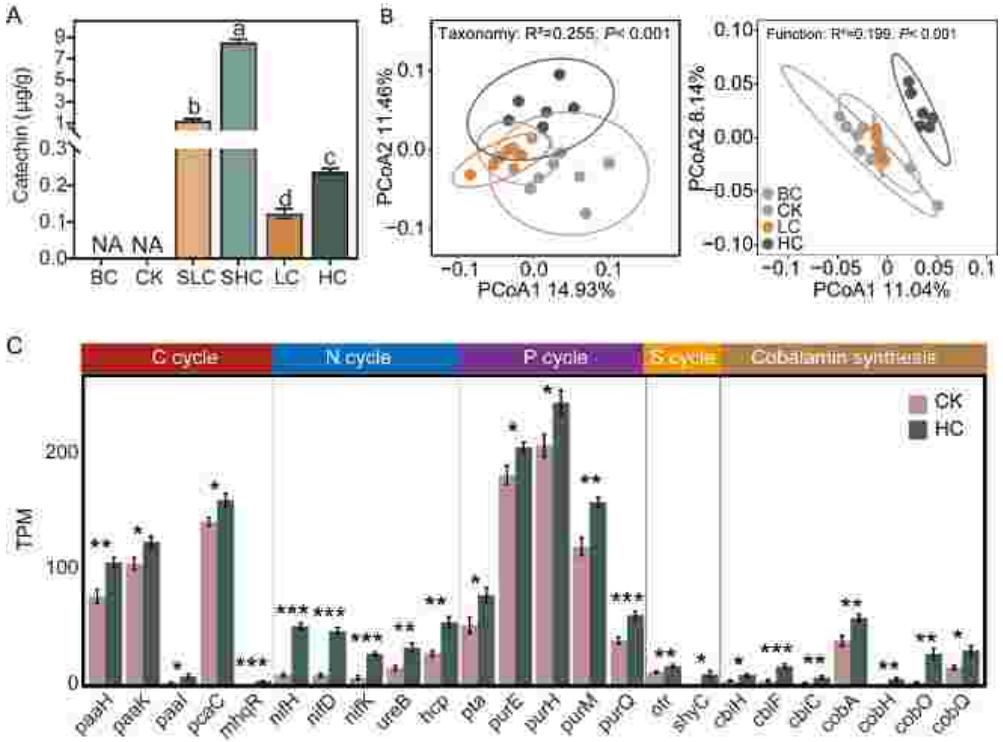
- Co-culture decreased the relative abundance of Cyclobacteriaceae, Coleofasciculaceae, Rhizobiaceae, Coraliomargaritaceae, Akkermansiaceae and SZUA−47 in the rhizosphere of *K. obovata,* which showed **positive correlations with plant biomass**
- MAGs harbored functional genes (e.g., **N_2 fixation**, **P regulation**) linked to plant growth promotion

(Yu *et al*., unpublished)

Flavonoids play important roles in mangrove-microbe interactions

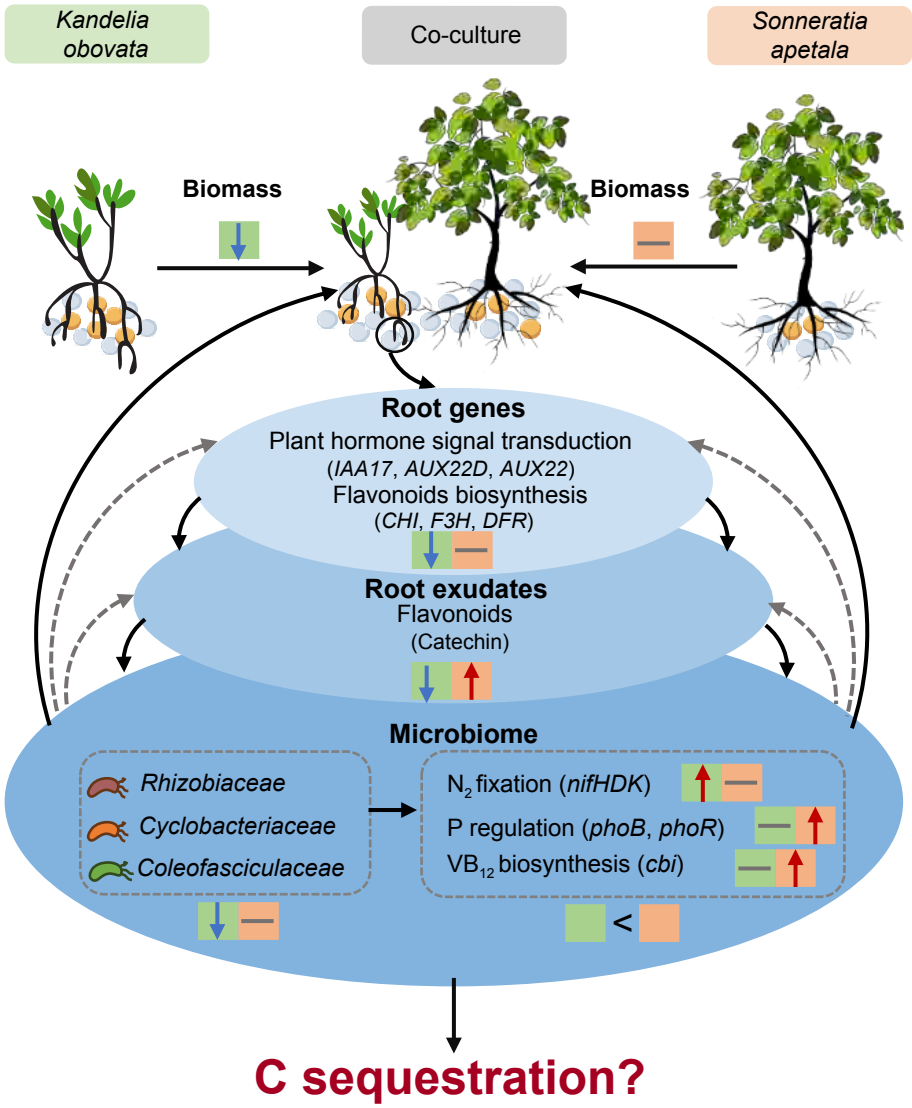


(Yu *et al*., unpublished)



- **Flavonoids** are pivotal in shaping the mangrove rhizosphere microbiome, likely by serving as C substrates for specialized taxa and modulating microbial functionality

Possible plant-microbe interaction mechanisms



- Flavonoids (e.g., catechin) act as key root exudates that modulate microbial functions and selectively enrich beneficial microorganisms
- The decreased relative abundance of beneficial microorganisms harboring functional genes involved in N_2 fixation, P regulation, and VB_{12} biosynthesis in *K. obovata* rhizosphere reduced its competitiveness and nutrient uptake

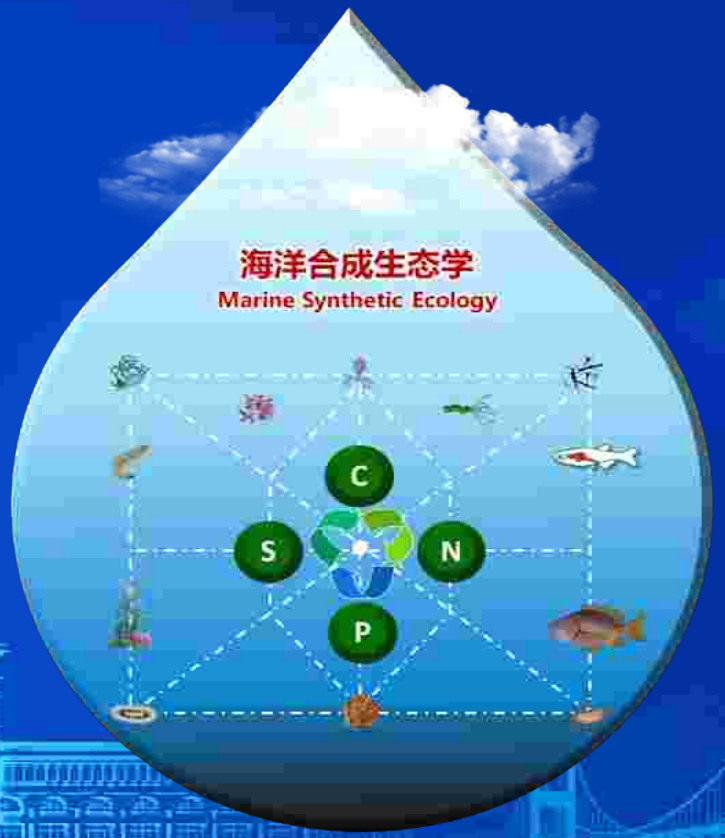
(Yu *et al.*, unpublished)

Summary

- The composition, structure and function of the microbiome in mangrove sediment show significant differences between the native and introduced species
- The native mangrove sediments had lower microbially-mediated methane emissions and higher functional potential of C fixation
- DOM transformation and lignin-degrading microbiomes are important for C sequestration in mangrove sediments
- The introduced mangrove inhibited the growth of native mangrove by altering plant gene expression, root exudation patterns, and modifying the plant-microbe interactions by exudates (e.g., flavonoids)
- How the plant-microbe interactions affect C sequestration needs further exploration

Thanks!

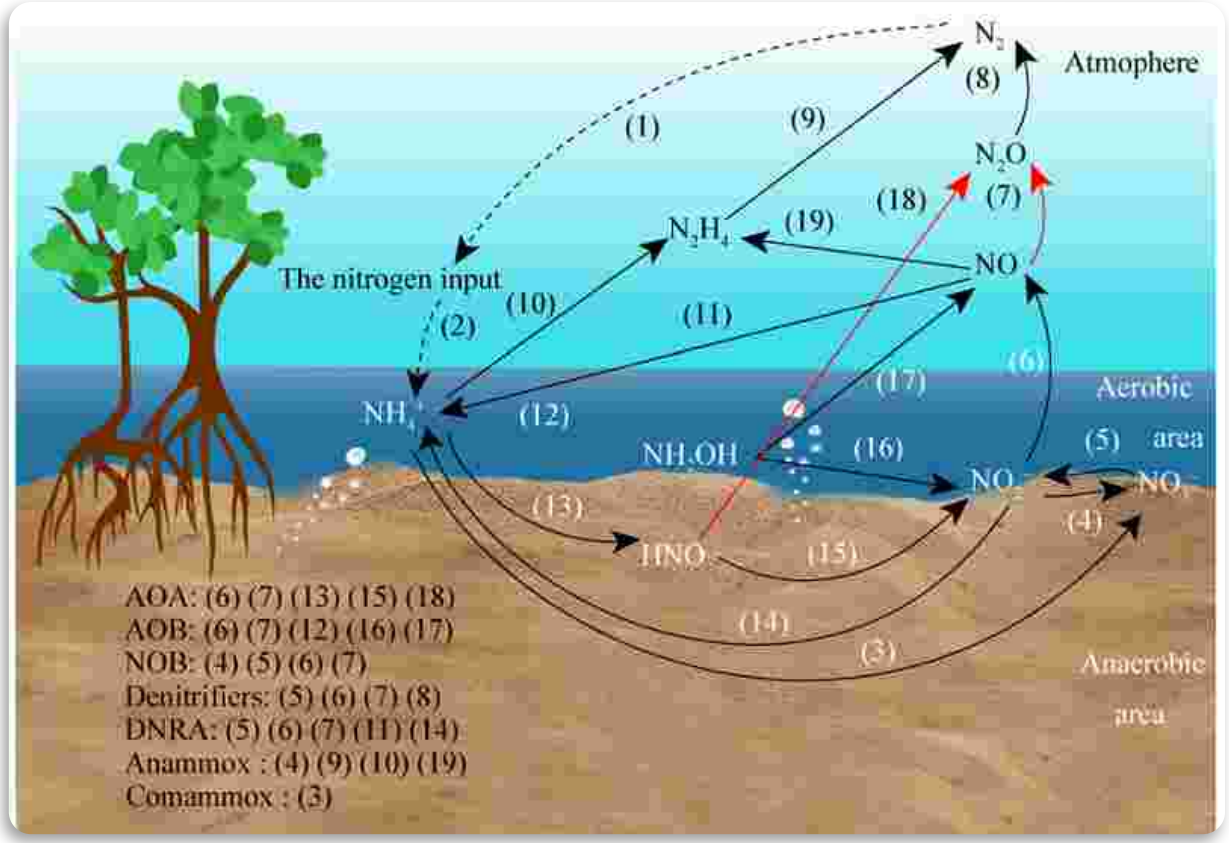




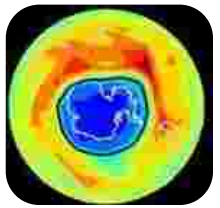
南方海洋科学与工程广东省实验室（珠海）
Southern Marine Science and Engineering Guangdong Laboratory(Zhuhai)

国家自然科学基金委员会
National Natural Science Foundation of China

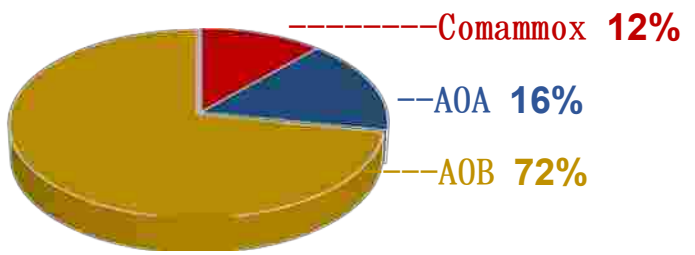
Microbially-driven N_2O production in coastal wetlands







The greenhouse effect of N_2O is 300 times of CO_2

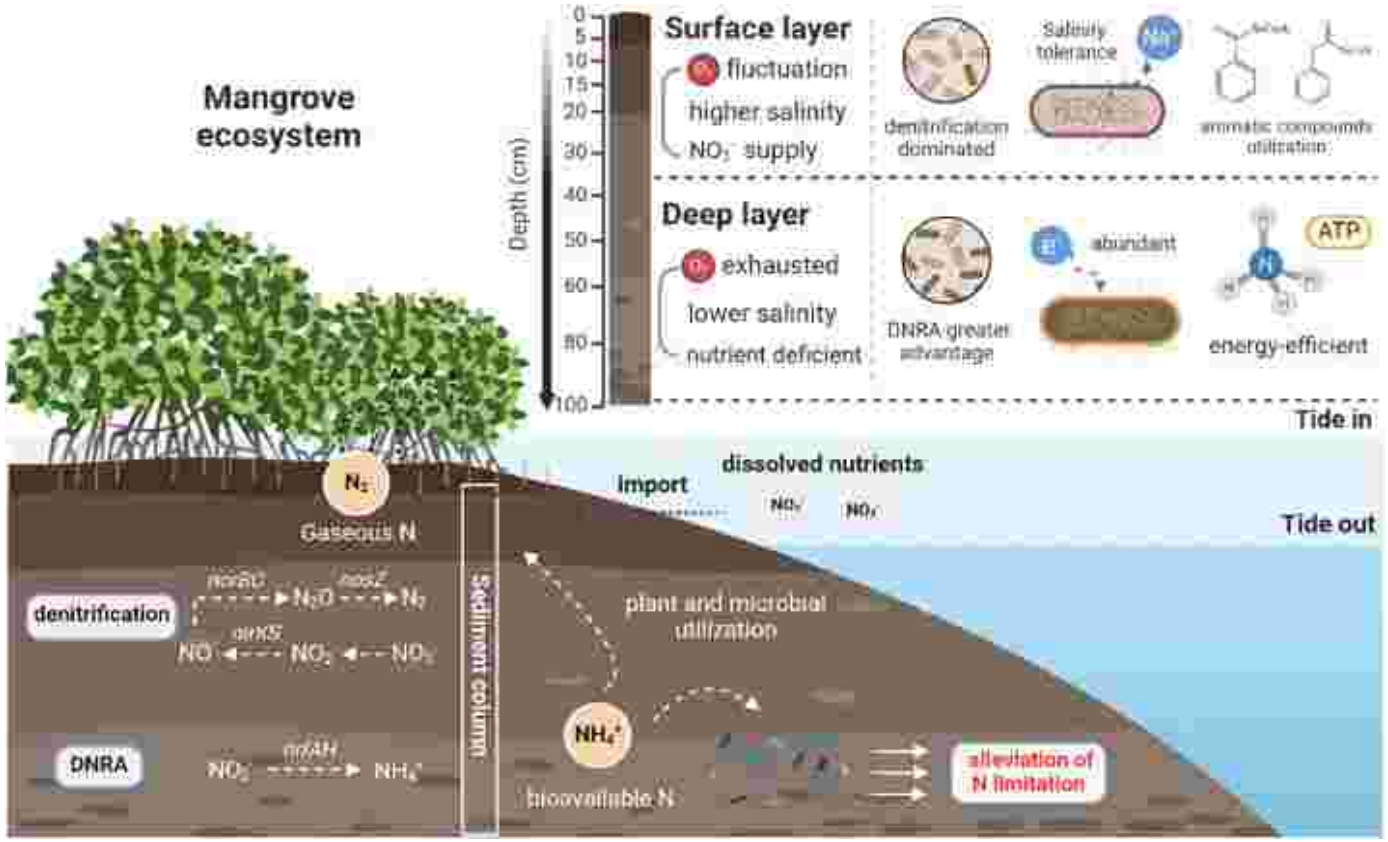


N_2O production

- **Nitrifiers and dentrifiers** mainly regulate the production of N_2O
- **Comammox bacteria** produce less N_2O than AOA and AOB

(Zhuang *et al*., 2019, *Microbiol China*; Jiang *et al*., 2023, *Glob Change Biol*)

The competition between denitrification and DNRA



- The high denitrification rates in surface sediments are crucial to **remove excess N**
- DNRA in deep sediments could conserve N and **reduce N_2O production**

(Fan *et al.*, 2025, *Water Res*)