读书报告

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Mangrove Sediment Microbiome: Adaptive Microbial Assemblages and Their Routed Biogeochemical Processes in Yunxiao Mangrove National Nature Reserve, China

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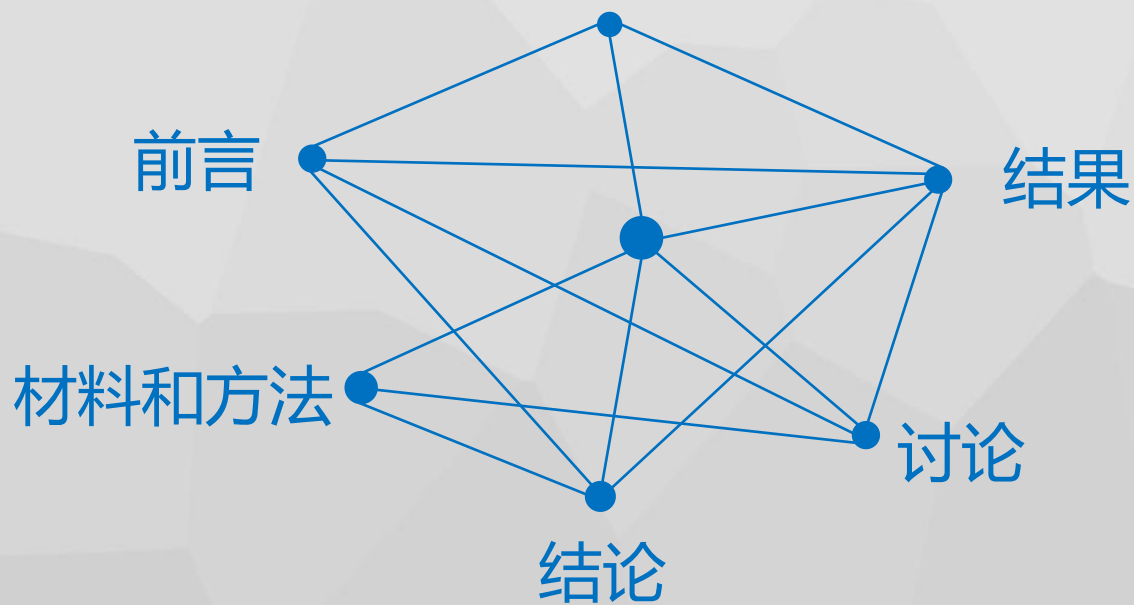
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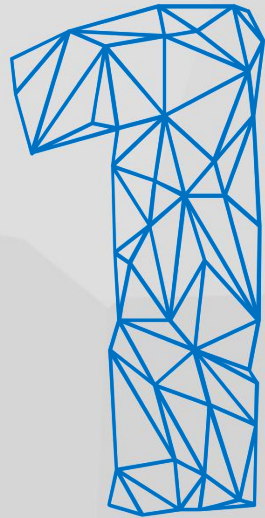
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前言
Introduction

研究背景

➤ Mangrove ecosystems are inter-tidal wetlands spreading along tropical and sub-tropical coastlines worldwide, and are famous for their unique geography and high productivity.

➤ Microbes play essential roles in maintaining mangrove ecosystems' high productivity and performance of ecological processes

➤ Thus, it is critical to unravel the microbial diversity and their metabolic potential for better understanding nutrient and biogeochemical cycling driven by microbes, and their roles in mangrove ecosystem functioning.

拟解决问题

01

Do sediment microbiomes at the YMNNR have a distinctive community structure from other typical mangroves worldwide? If so, how is the community structure associated with environmental characteristics?

02

How do mangrove microbial communities drive the biogeochemical cycles to match the habitat characteristics? Do these community-level metabolic pathways make a contribution to ecosystem-level functions?.
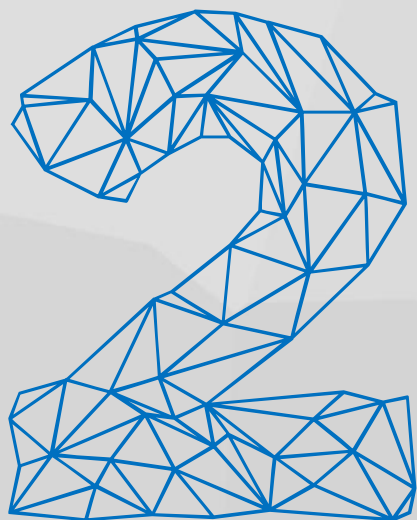
材料和方法

Research Method

材料和方法

Method & Tool 01

Sampling Sites and Sediment Collection

Yunxiao Mangrove National Nature Reserve
N 23° 55′51.31″,
E 117° 24′50.57″
5个采样点

Physicochemical Analysis of Selected Parameters

pH，Sal，Water content，Organic carbon，N，S，$NO2^-$，$NH4^+$

Method & Tool 02

DNA Extraction and 16S rRNA Gene Amplicon Sequencing

DNA Powersoil Total DNA Isolation Kit (MoBio Laboratories Inc., Carlsbad, CA,USA)

材料和方法

DNA Extraction and Metagenome Sequencing:

Powersediment Total DNA Isolation Kit

Method & Tool 03

Statistical Analysis of 16S rRNA Gene Amplicon Sequences

16S rRNA gene V3-V4 sequencing
OTU clustering <97%
16S datdbase: Silva、RDP、Greengene
Functional predictions: PICRUSt

Method & Tool 04

Statistical Analysis of Shotgun Metagenome Sequences

Sequences assembly: SOAP denovo v.2.21
Quality controlled: SoapAligner v.2.21
Functional predictions: NR、KEGG database

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结果与讨论

Research Procedure

The Composition of Mangrove Microbiomes Based on 16S rRNA Genes and Complete Metagenome

16S rRNA sequences

54 phyla,
Proteobacteria： 50.09%
Chloroflexi： 14.33%
Bacteroidetes： 8.69%
Nitrospirae： 4.64%
Acidobacteria： 4.49%

Smetagenome sequences

51 phyla
Proteobacteria： 60.78%
Chloroflexi： 4.00%
Bacteroidetes： 1.21%
Nitrospirae： 2.6%
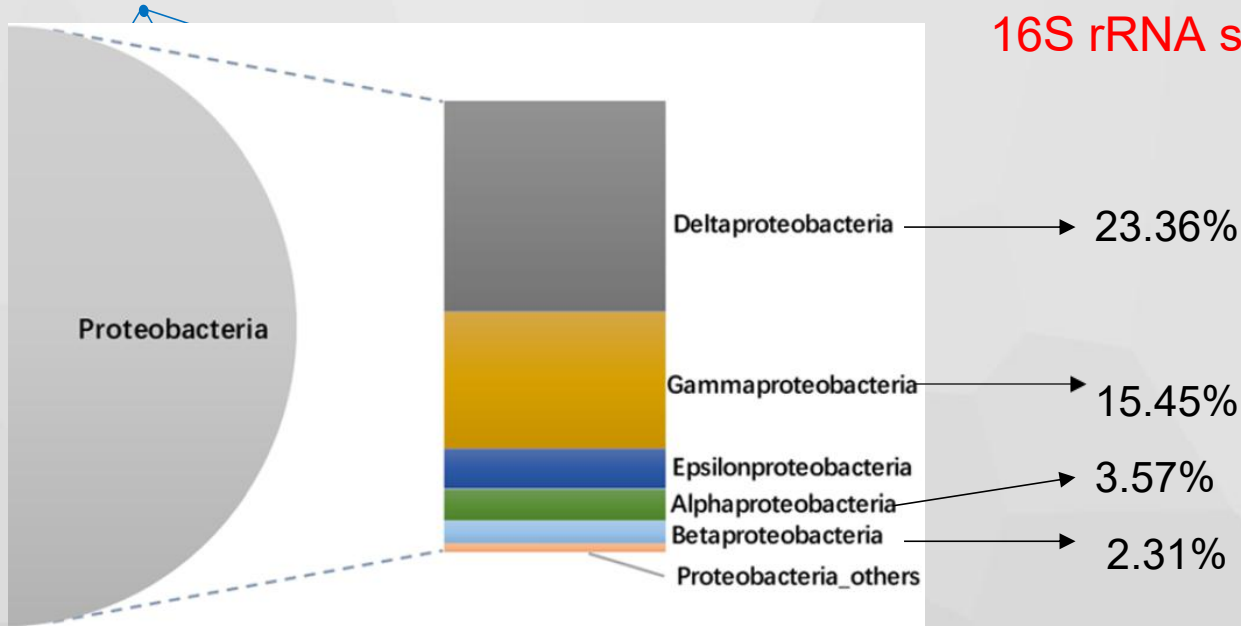*Acidobacteria*： 1.03%

the same highest abundance of the phyla

the different phyla

Latescibacteria: 1.79%,
Gemmatimonadetes:1.79%
Chlorobi :1.46%
Spirochaetae: 1.39%

Firmicutes: 2.43%
Cyanobacteria : 1.23%
Actinobacteria : 1.17%

16S rRNA sequences

Proteobacteria

Deltaproteobacteria → 23.36%

Gammaproteobacteria → 15.45%

Epsilonproteobacteria 3.57%
Alphaproteobacteria
Betaproteobacteria 2.31%
Proteobacteria_others

Smetagenome sequences

Proteobacteria

Deltaproteobacteria → 23.80%

Gammaproteobacteria → 18.55%

Betaproteobacteria → 6.67%

Alphaproteobacteria → 5.34%

Epsilonproteobacteria

Proteobacteria_others
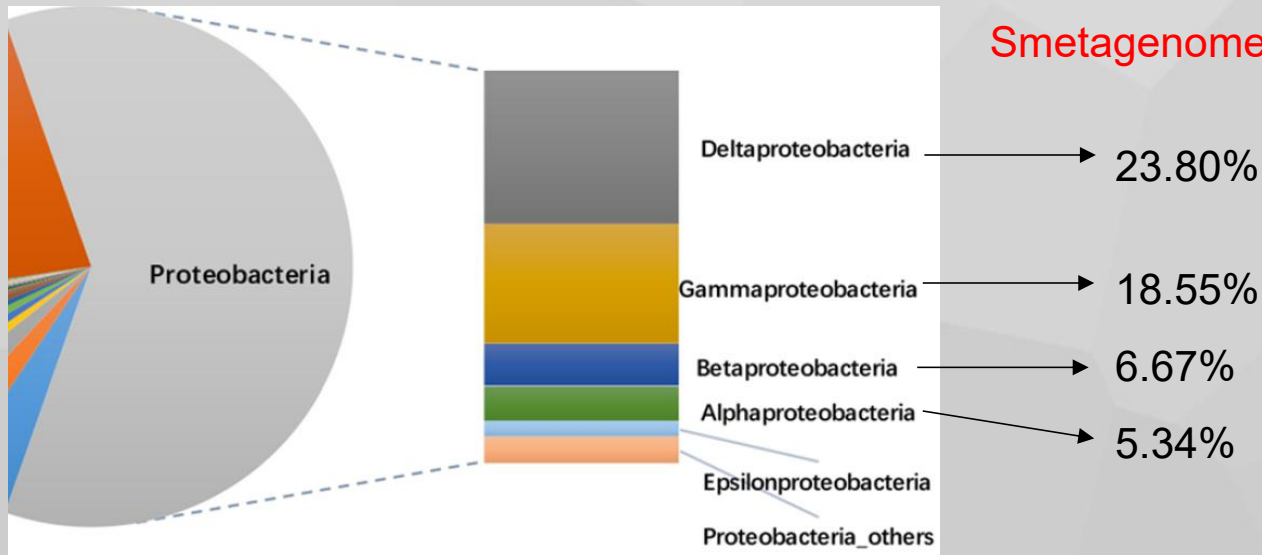
Class level
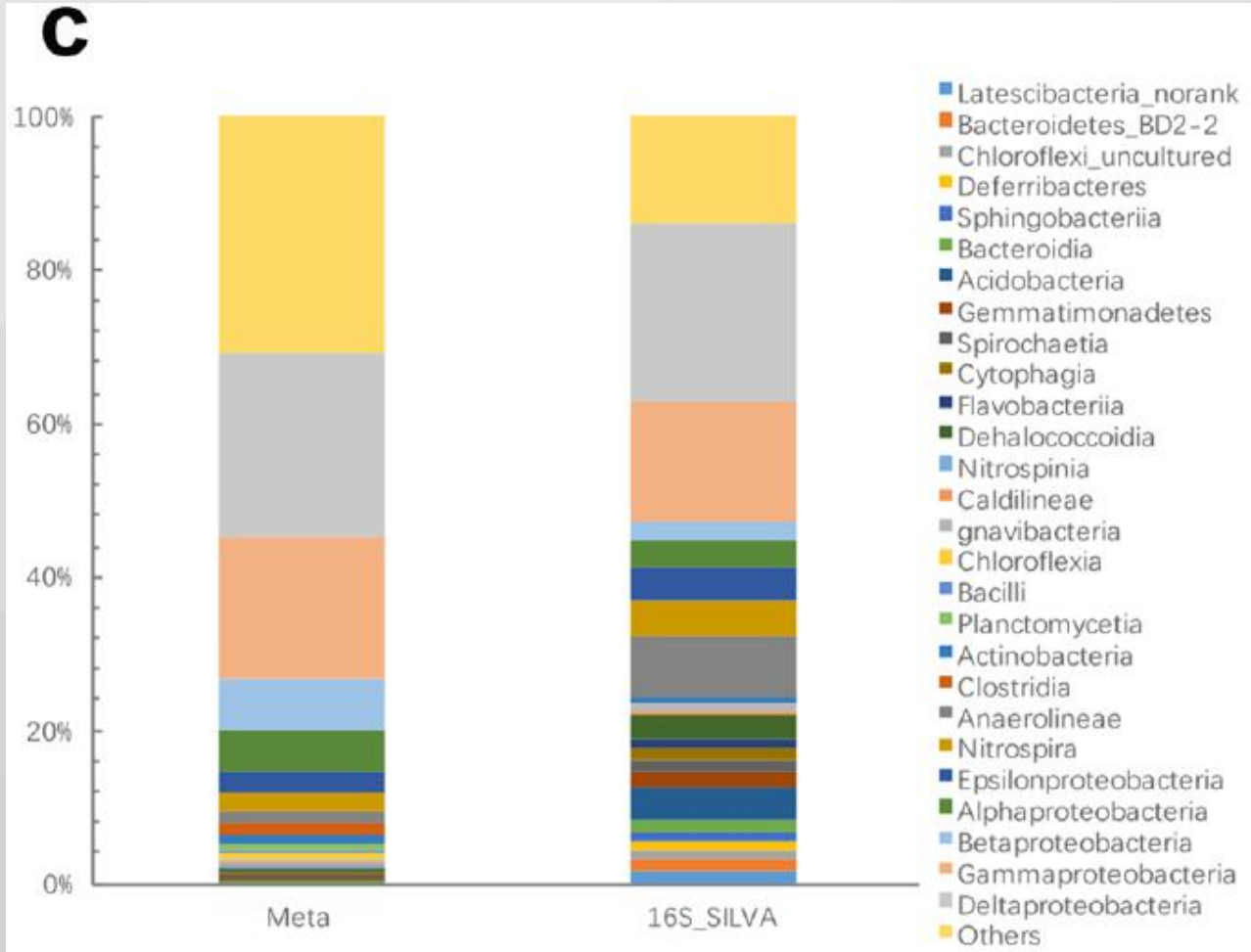
16S rRNA dataset

Anaerolineae

Nitrospira

Acidobacteria

Dehalococcoidia

Gemmatimonadetes

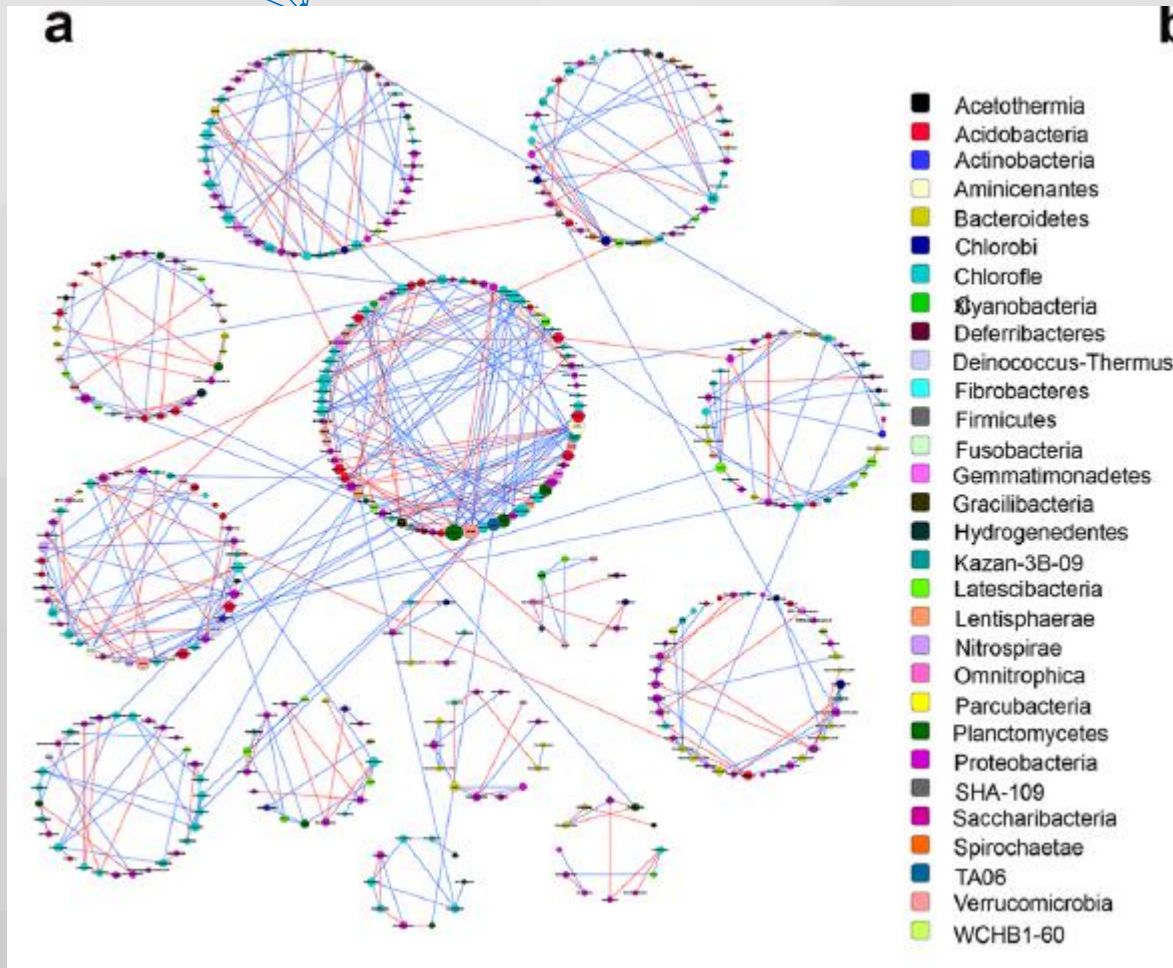Metagenome dataset:

Nitrospira
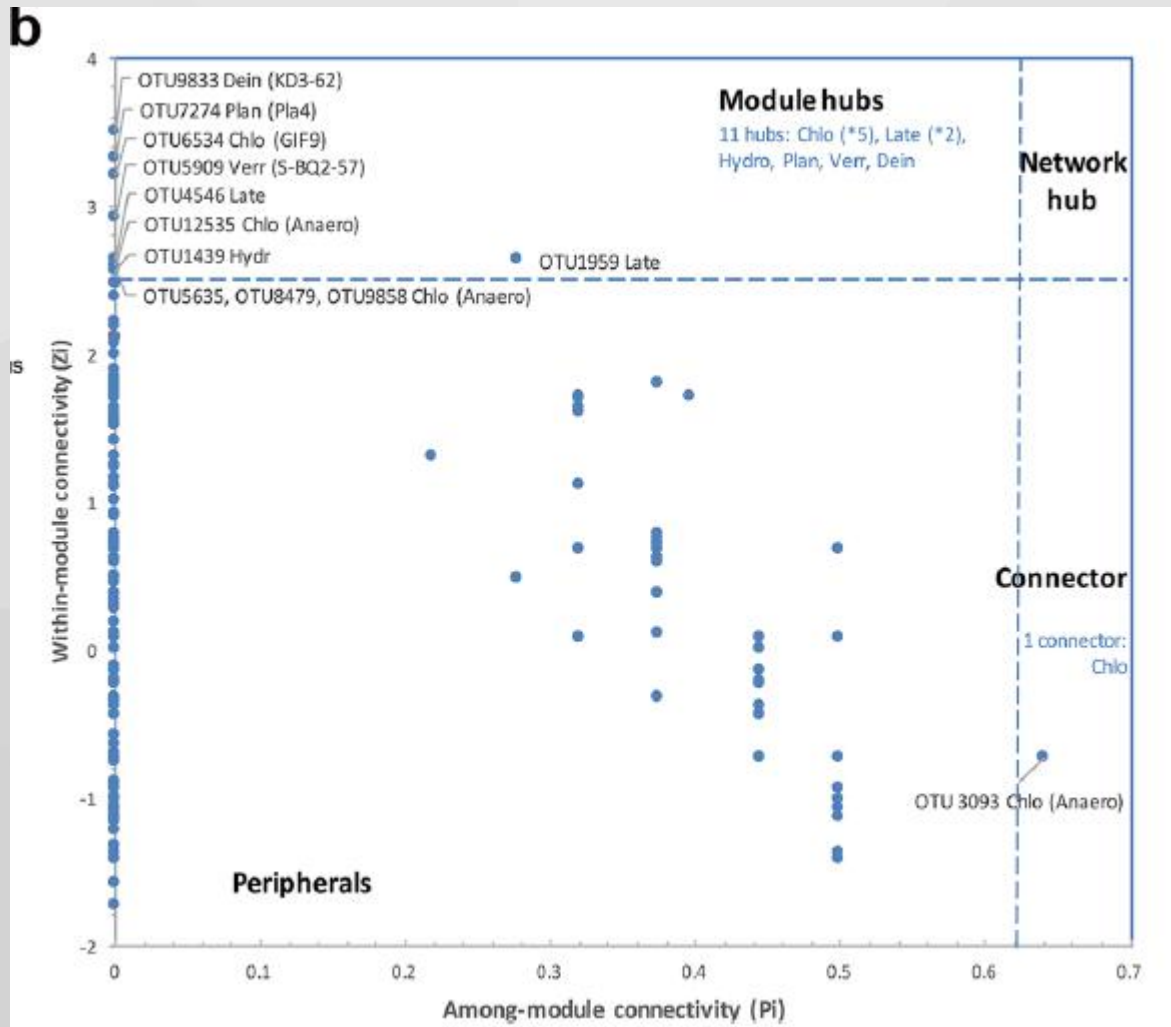
Anaerolineae

Clostridia

Actinobacteria

Planctomycetia

pMENs: explore interactions among different populations in microbial communities and assess the possible topological roles of each taxon in the network

Fig. 2 Phylogenetic molecular ecological networks based on in situ mangrove microbiomes and the topological roles of nodes. Red line, negative interaction; blue line, positive interaction

b

Within-module connectivity (Zi)

Among-module connectivity (Pi)

OTU9833 Dein (KD3-62)
OTU7274 Plan (Pla4)
OTU6534 Chlo (GIF9)
OTU5909 Verr (S-BQ2-57)
OTU4546 Late
OTU12535 Chlo (Anaero)
OTU1439 Hydr
OTU5635, OTU8479, OTU9858 Chlo (Anaero)

OTU1959 Late

Module hubs
11 hubs: Chlo (*5), Late (*2), Hydro, Plan, Verr, Dein

Network hub

Connector
1 connector: Chlo

OTU 3093 Chlo (Anaero)

Peripherals

11 module hubs : OTU1439;

OTU1959; OTU4546; OTU5635;

OTU5909; OTU6534; OTU7274

OTU8479; OTU9833; OTU9858;

OTU12535

1 connector: OTU3093 （Chloroflexi）

Chloroflexi: six

Latescibacteria:two

Others:

Hydrogenedentes, Verrucomicrobia,

Planctomycetes, Deinococcus-

Thermus.

Potential Metabolic Pathways of Carbon (Methane), Nitrogen, and Sulfur Cycling in Mangrove Sediment Microbiomes

Methane Metabolism

Pmetagenomes (predicted metagenomes based on 16S): 122 KOs annotated to the methane metabolic pathway

Smetagenomes: 100 KOs annotated to the methane metabolic pathway

甲烷代谢通常耦合C固定、N代谢、S代谢以及磷酸戊糖途径，检测到了formate-CO2-CO-acetylCOA-pyruvate代谢途径，*pmoA, pmoB, pmoC*基因被检测到也证实了甲烷氧化菌的存在。

Nitrogen Metabolism

40 and 43 KOs annotated to N metabolism in the Pmetagenomes and Smetagenomes, 参与N代谢的基因，其中参与谷氨酸代谢的合成酶、脱氢酶多次被检测到，另外还发现硝酸盐还原酶。并且关注了N转化的途径，注释到参与N固定、硝酸盐还原、硝化和反硝化的基因.
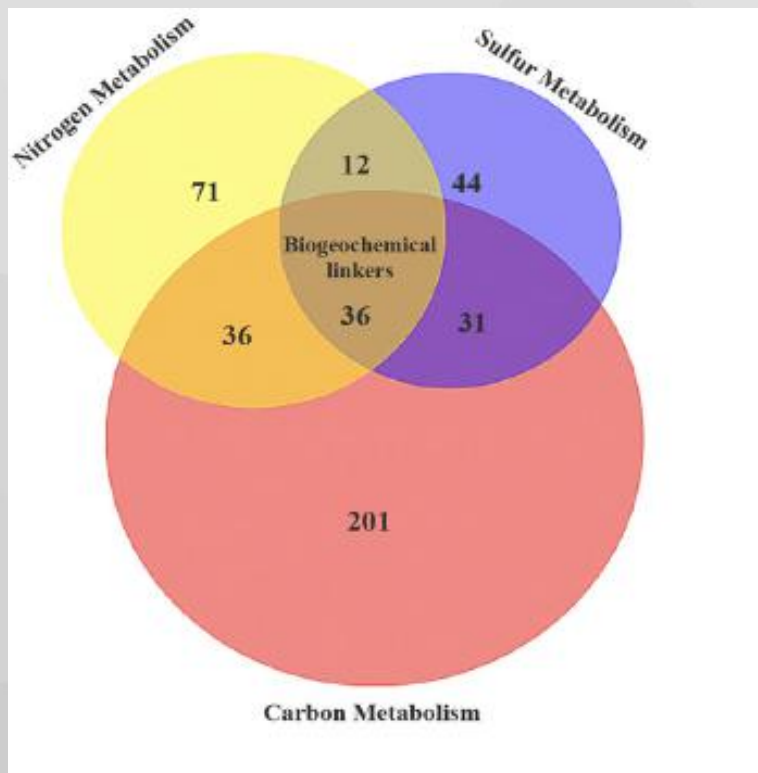
Sulfur Metabolism

43 and 52 KOs annotated to S metabolism (99 KOs in total) in the Pmetagenomes and Smetagenomes

通过对S转化通路的研究发现，编码半胱氨酸合成酶A的基因丰度较高。与S氧化途径相比，发现更多的基因是参与S还原过程，比如：sulfate—APS-to-sulfite途径多于APS-to-PAPS-to-sulfite途径.

Potential Biogeochemical Linkers Involved in the Coupling of Carbon, Nitrogen, and Sulfur Cycles in Mangrove Sediments

potential biogeochemical linkers

- *Deltaproteobacteria 14*
- *Gammaproteobacteria 6*
- *Epsilonproteobacteria 4*
- *Nitrospirae 2*
- *Nitrospinae 1*
- *Chloroflexi 1*
- *Verrucomicrobia 1*

Supplementary Table 2. Physicochemical characteristics of mangrove sediments in this study and others from Brazil, India and Red Sea.

Physicochemical parameters	China (Yunxiao)	Brazil	India	Red Sea
Sal(psu)	18	4.6	8-12	8.4-14.23
pH	7.27	6.3	7.3-7.7	9.34-9.43
WC[a](%)	52.49±0.41	49.18	\[c]	\
OC[b](g/kg)	21.79±1.35	63.5	1.5-7.2[d]	25.3-31.9
N(g/kg)	1.76±0.07	2.6-4.5	1.4-1.9[b]	\
S(g/kg)	4.27±1.09	1.4	\	1.8-2.0
NO_2-(ug/kg)	15.20±5.60	\	\	\
NH4+(mg/kg)	7.61±0.76	\	\	\

Note: [a]water content; [b]organic carbon; [c]not detected; [d] mg/L

To our knowledge, this is the first sediment microbiome study of mangrove ecosystems in this area, organic C-rich, S-rich, and N-limited.

These properties usually result in extensive and active microbial decomposition of organic C along with subsequent C metabolic processes in mangrove

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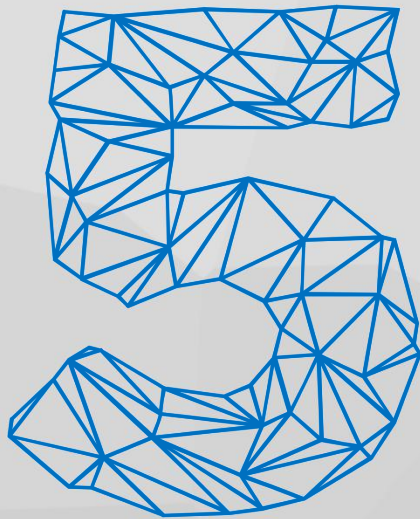
结论

Research Conclusion

1. 本研究揭示了与特定环境特征相适应的红树林微生物群落结构和代谢途径，对红树林生态系统功能具有重要的生态意义。

2. 在这种富含C、S、少N的红树林生境中，微生物组驱动元素循环促使红树林生态系统克服营养限制，维持其高是生产力的生态功能。

3. Syntrophobacter, Sulfurovum, Nitrospira, and Anaerolinea是红树林沉积物中连接C、N、S循环的关键类群，它们的活动可能促进红树林生态系统中元素流通中的有效循环。

4. 另外，本次研究发现的绿弯菌门中的厌氧绳菌纲在红树林生态系统中具有重要地位，它们不仅在微生物群落结构上占有优势，同时是参与物种间的互作作用的关键类群，也是生物地球化学循环的连接者。

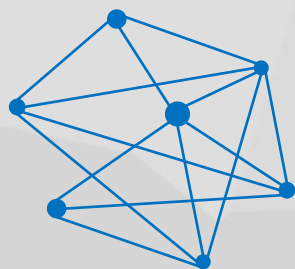5. 作者对微生物组和其代谢功能的详细描述可以有效帮助评估红树林沉积物中C、N的流通，对维持红树林高生产力具有重要意义。

1. 选题具有重要意义，对云霄红树林沉积物特定微生物组及其生物地球化学进程进行研究，通过两种方法对其微生物群落做了深入研究，突破了传统的分离培养方法的局限性，得到更为完整的微生物群落信息，而且预测了参与地球元素循环的微生物类群；

2. 通过宏基因组分析手段，对微生物群落参与的地球化学循环做了全面解析，深入探讨在红树林沉积物生态系统中微生物是通过哪些过程参与到地球化学循环中，对于揭示红树林生物地球化学循环，维持红树林生态系统稳定有很大的帮助；

3. 结果分析部分，我认为pMENs分析用的特别好。

敬请各位老师批评指正

THANKS

Bye