



Warm-wet transition restructures arid lake microbiomes and functional potential

Zhen Shen^{1,2}, Xingchen Li³, Zhijun Gong^{1,2*}, Yang Hu¹, Yongjiu Cai^{1,2},
Keqiang Shao^{1,2}, Guang Gao^{1,2}, Robbie M. Martin⁴, Xiangming Tang^{1,2*}

¹State Key Laboratory of Lake and Watershed Science for Water Security,
Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences

²University of Chinese Academy of Sciences

³School of Earth and Environment, Anhui University of Science & Technology

⁴Department of Microbiology, University of Tennessee, Knoxville



Shen Zhen, Li Xingchen, Gong Zhijun, Hu Yang, Cai Yongjiu, Shao Keqiang, Gao Guang, et al. 2026.

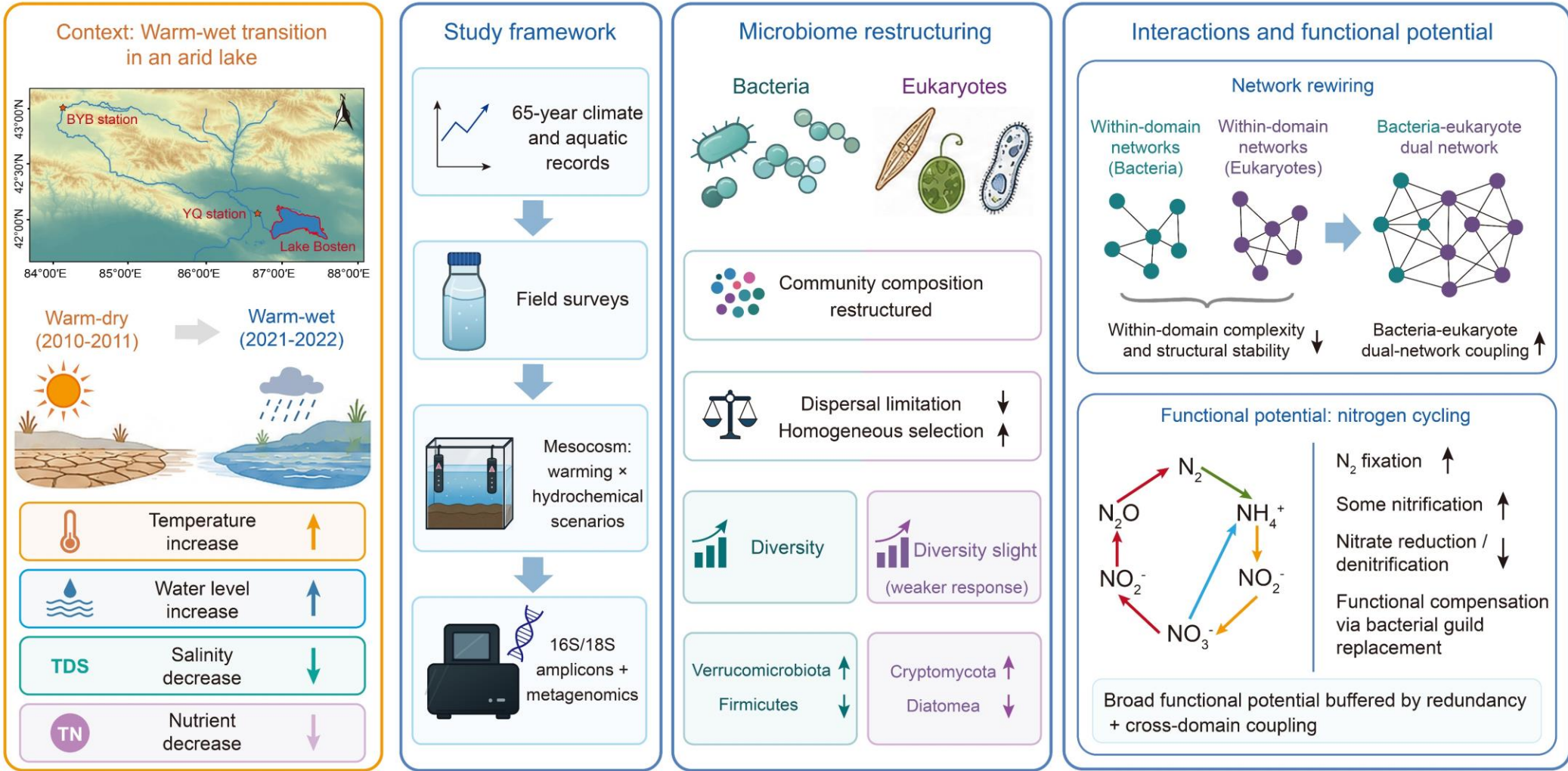
Warm-wet transition restructures arid lake microbiomes and functional potential.

iMetaOmics 3: e70119. <https://doi.org/10.1002/imo2.70119>



Abstract and Highlights

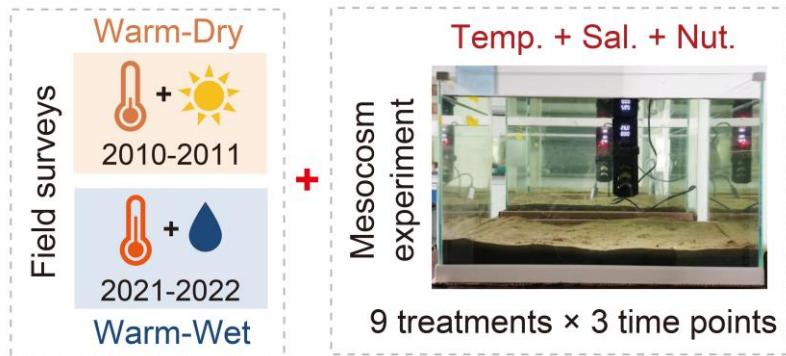
Warm-wet transition restructures arid lake microbiomes and their functional potential



Warm-wet hydroclimatic change rewires arid-lake microbiomes, weakens within-domain network stability, but preserves broad functional potential through cross-domain coupling and taxonomic compensation.

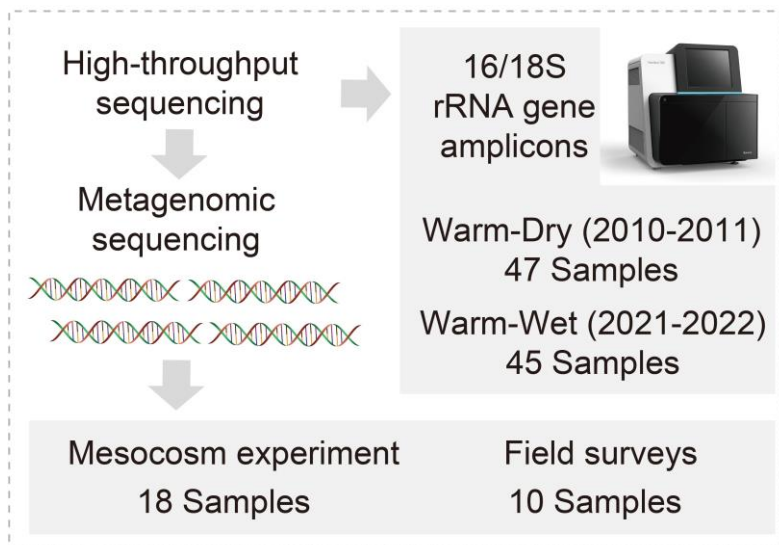
Study framework

Study



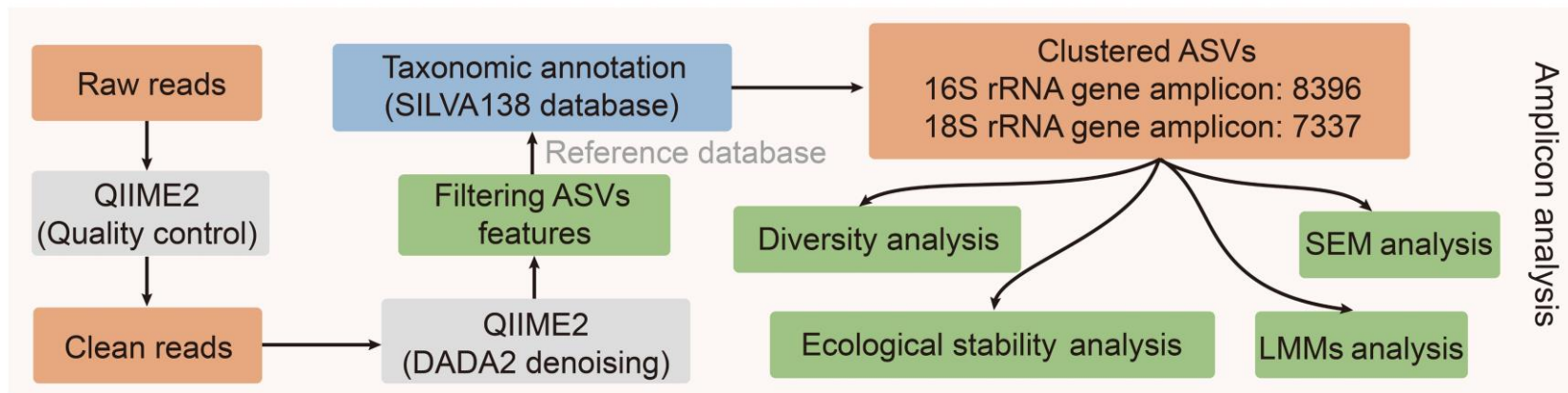
Cross-period field survey

Mesocosm scenario simulation

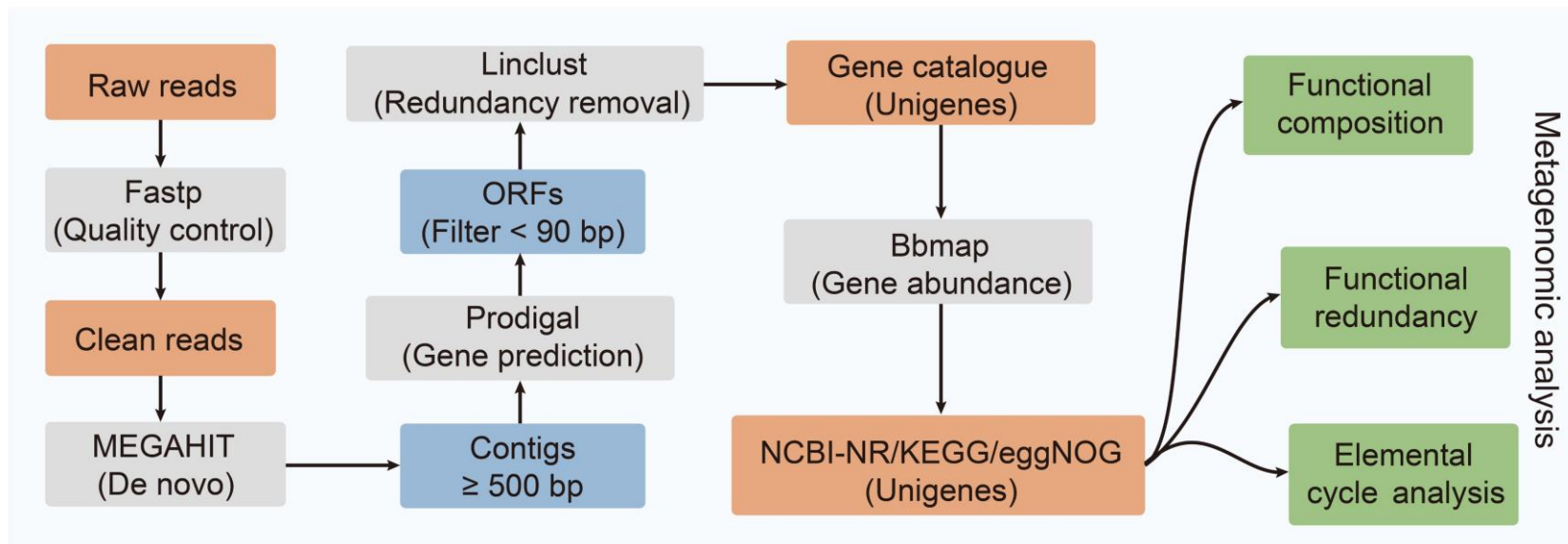


16S/18S + metagenomic sequencing

Bioinformatics



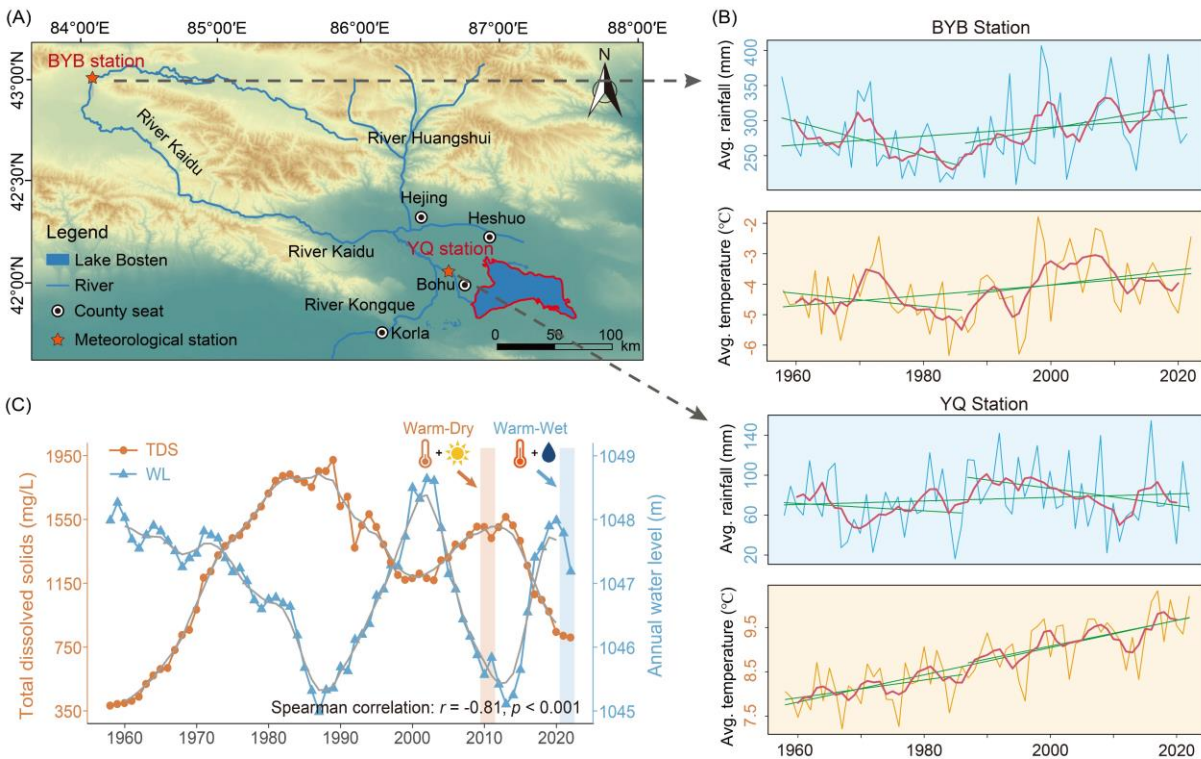
16S/18S analysis workflow



Metagenomic analysis workflow



Result 1: Environmental shifts and diversity responses



The Lake Bosten basin shifted from warm-dry to warm-wet.

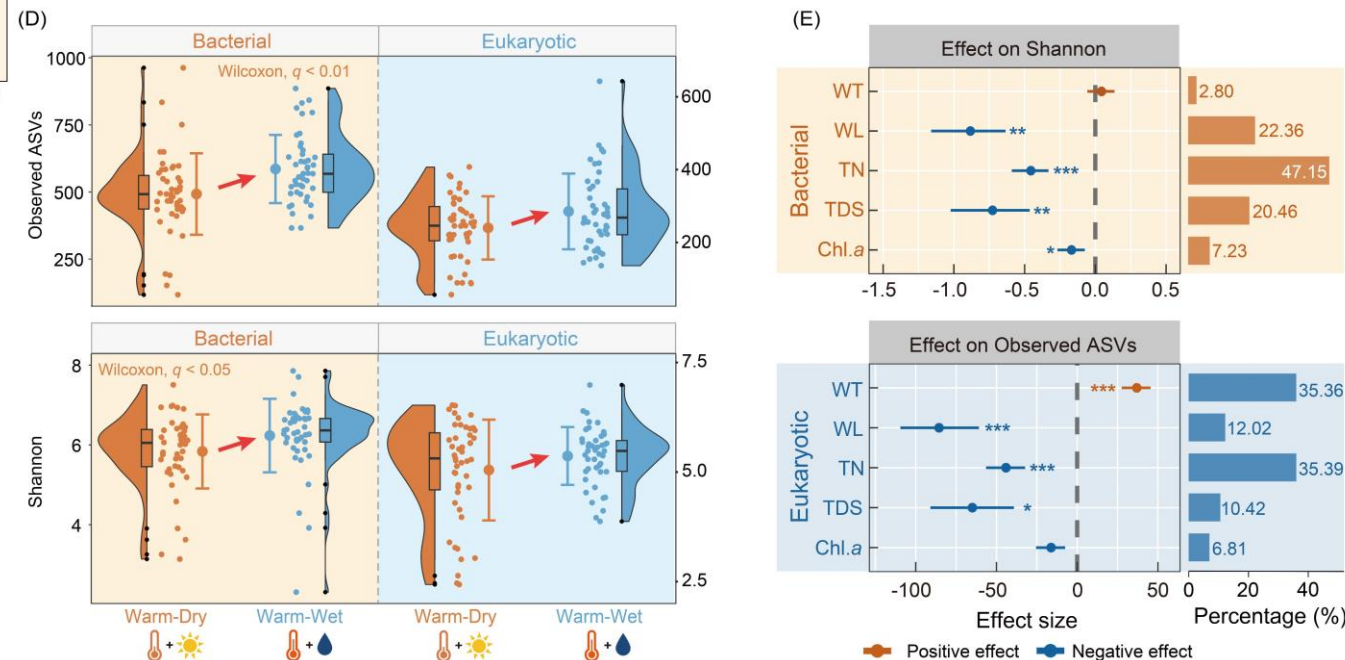
Warm-wet period: Water level $\uparrow$; TDS and TN $\downarrow$; WT and Chl.*a* $\uparrow$.

Bacterial Observed ASVs and Shannon index increased.

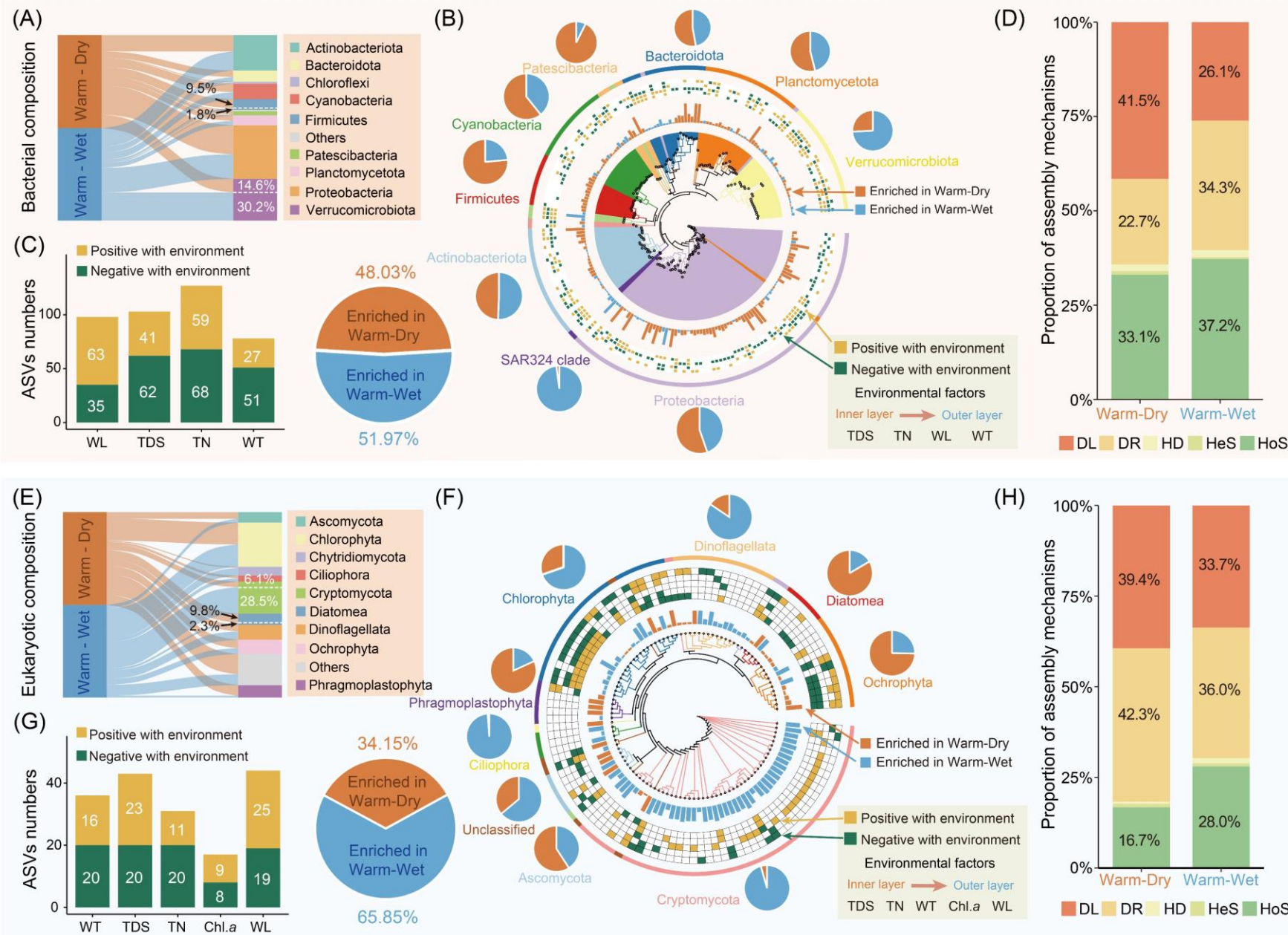
Mean eukaryotic diversity increased, but not significantly.

Bacterial diversity: mainly explained by TN, WL and TDS.

Eukaryotic diversity: jointly driven by TN, WT and WL.



Result 2: Community restructuring and assembly shift



Bacteria: Verrucomicrobiota

14.6% → 30.2%; Firmicutes 9.5% → 1.8%.

Eukaryotes: Cryptomycota 6.1%

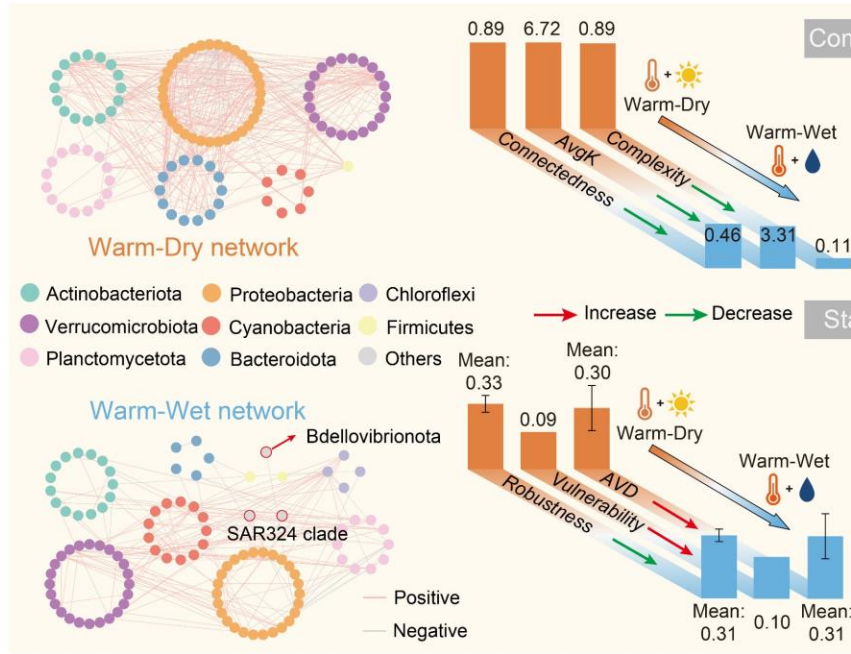
→ 28.5%; Diatomea 9.8% → 2.3%.

Homogeneous selection ↑; dispersal limitation ↓.

Result 3: Network rewiring

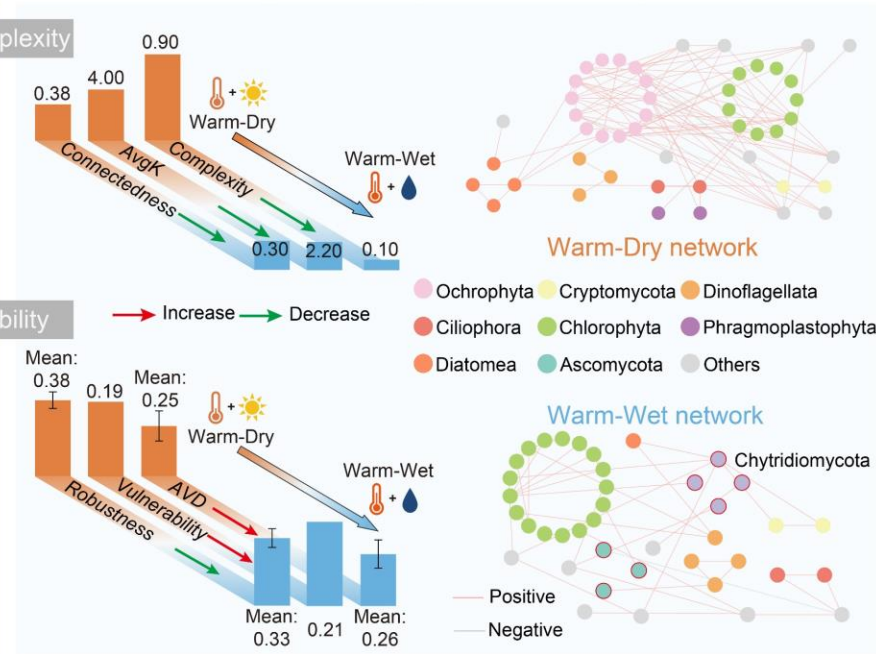
(A)

Bacterial network patterns in different periods



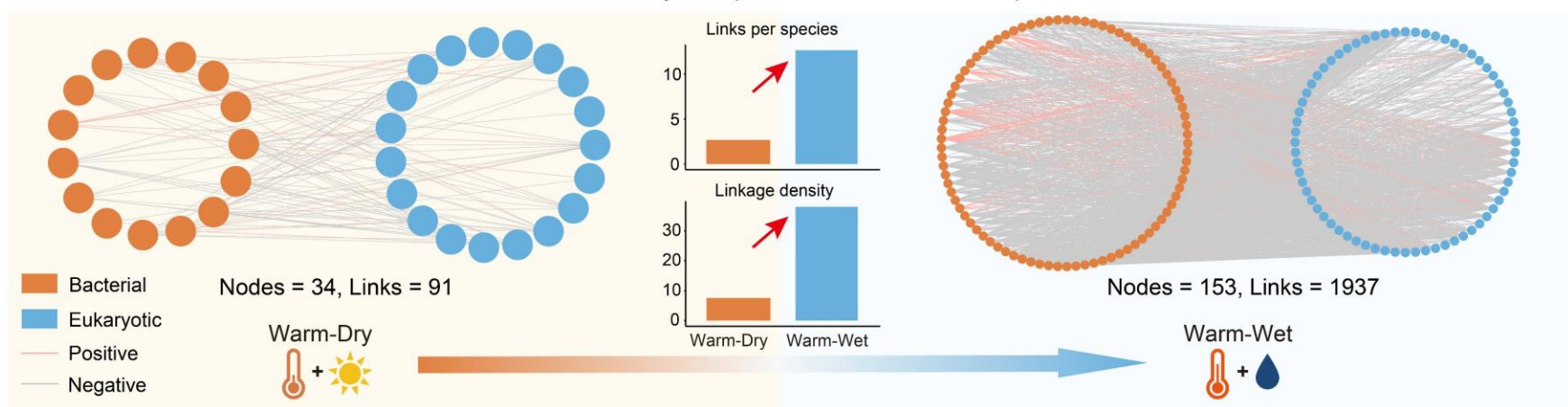
(B)

Eukaryotic network patterns in different periods



(C)

Bacterial-eukaryotic bipartite networks in different periods



Within-domain network complexity decreased.

Within-domain structural stability decreased.

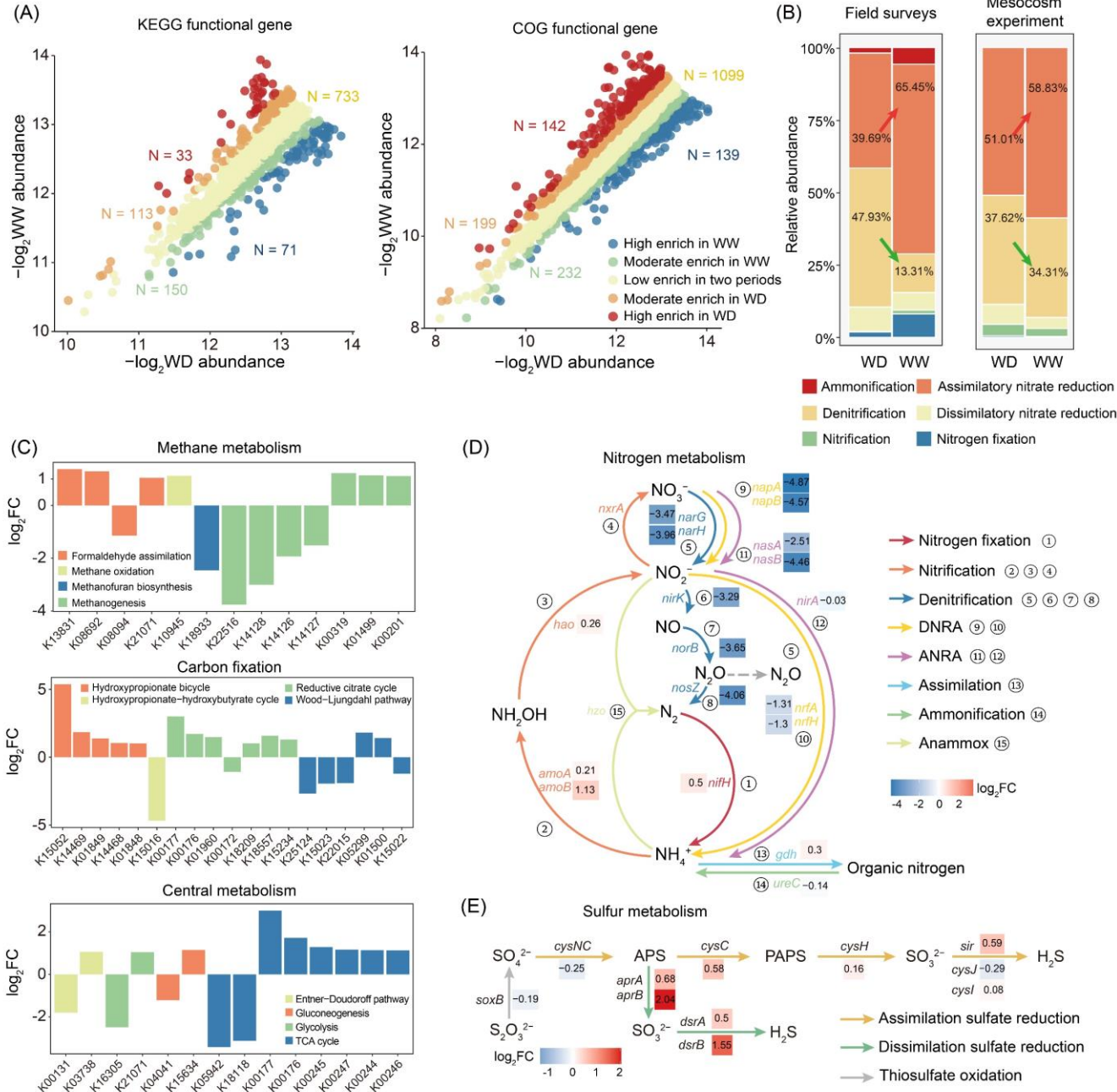
Bacteria-eukaryote interactions increased:

Nodes: 34 → 153

Links: 91 → 1937

Within-domain stability ↓; cross-domain coupling ↑.

Result 4: Functional buffering and pathway-specific redistribution



Broad KEGG/COG composition showed no significant period difference.

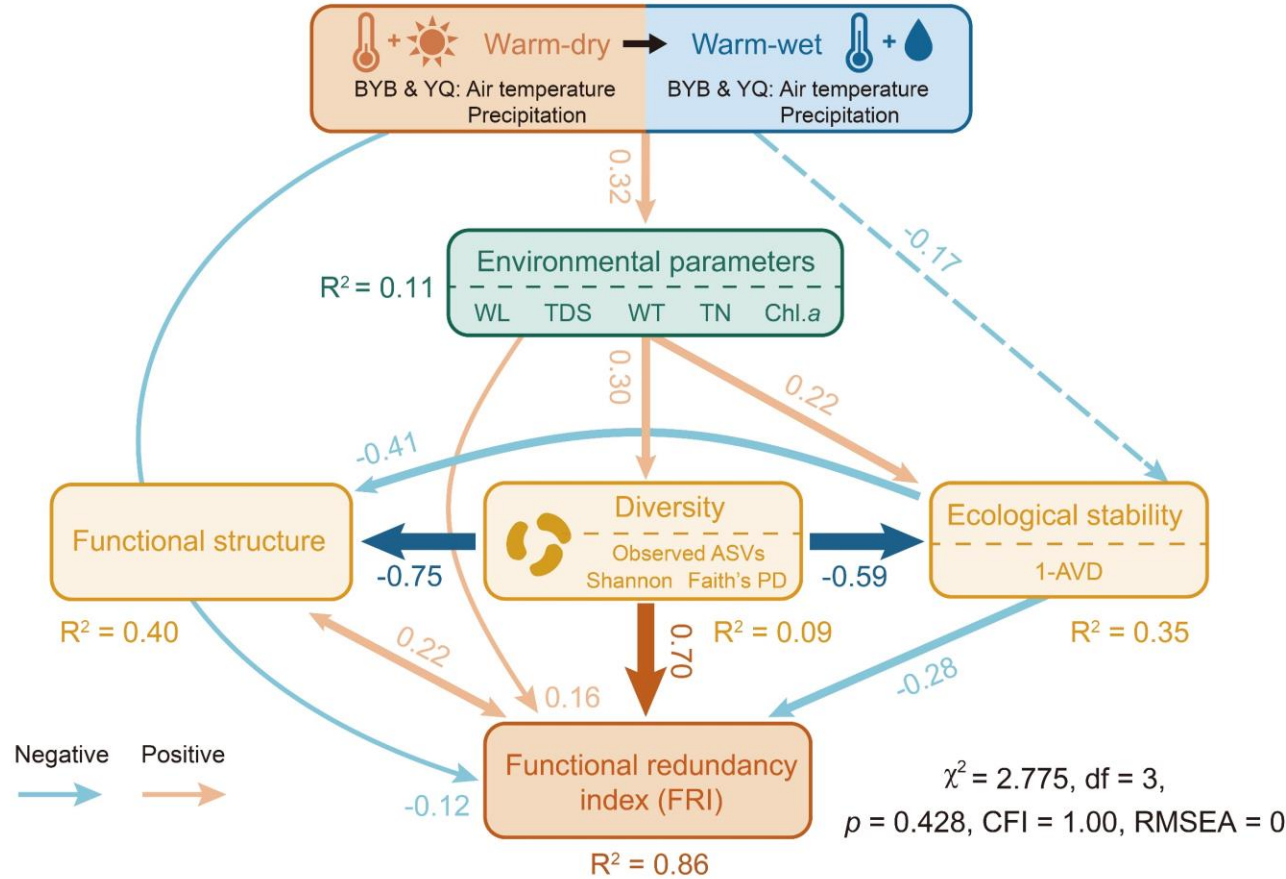
Assimilatory nitrate reduction: 39.7% → 65.5%; denitrification: 47.9% → 13.3%.

N fixation, nitrification or ammonification genes ↑; denitrification genes ↓.

No overall functional gain or loss, but selective pathway redistribution.

Result 5: Coupling among diversity, stability and functional traits

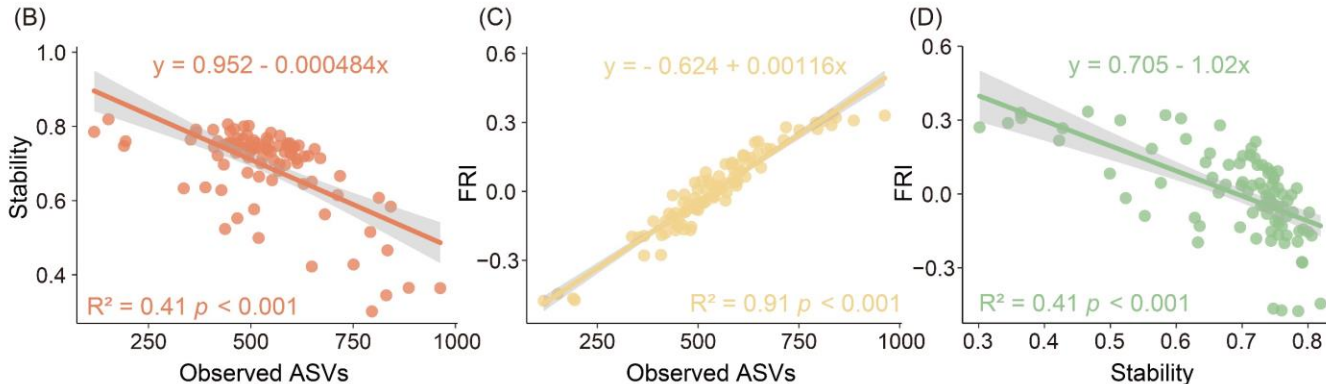
(A)



Climate transition was indirectly linked to microbial diversity through WL, TDS, WT, TN and Chl. *a*.

Diversity was negatively correlated with community compositional stability, but positively correlated with functional redundancy.

Warm-wet transition led to pronounced taxonomic restructuring and network rewiring, while functional redundancy, cross-domain coupling and functional-guild replacement buffered broad functional potential to some extent.





Conclusions

Warm-wet climate change restructures microbiomes, while functional potential remains buffered

Environmental

Warming and higher water level altered connectivity, dilution, salinity and nutrients.

Network

Within-domain complexity and stability declined, while bacteria-eukaryote coupling increased.

Community

Bacteria and eukaryotes were reorganized, with homogeneous selection ↑ and dispersal limitation ↓.

Functional

Functional redundancy and taxonomic replacement buffered broad functions, while elemental cycles were redistributed.



Warm-wet transition restructures arid-lake microbiome taxonomy and interactions, while functional redundancy, cross-domain coupling and functional-guild replacement buffer functional potential.

Shen Zhen, Li Xingchen, Gong Zhijun, Hu Yang, Cai Yongjiu, Shao Keqiang, Gao Guang, et al. 2026.

Warm-wet transition restructures arid lake microbiomes and functional potential.

iMetaOmics 3: e70119. <https://doi.org/10.1002/imo2.70119>



“***iMeta***” launched in 2022 by iMeta Science Society, **impact factor (IF) 44.4**, **ranking top 47/22643 in the world**. It aims to publish innovative and high-quality papers with broad and diverse audiences. Its scope is similar to *Cell*, *Nature* and *Science*. Its unique features include video abstract, bilingual publication, and social media with 800,000 followers. Indexed by [SCIE/ESI](#), [PubMed](#), [Google Scholar](#) etc.

“***iMetaOmics***” launched in 2024, indexed by [ESCI](#), [PubMed](#), [Google Scholar](#), with a **target IF>15**, and its scope is similar to *Nature Communications*, *Science Advances*, *Advanced Science*, *Nucleic Acids Research*, etc.

“***iMetaMed***” launched in 2025, with a target IF>15, similar to *Med*, *Cell Reports Medicine*, *eBioMedicine*, *eClinicalMedicine* etc.



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

Submission: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



[iMetaScience](#)



[iMetaScience](#)



office@imeta.science

imetaomics@imeta.science



[Promotion Video](#)

Update
2026/6/17