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Analysis of Soil Bacterial Community Characteristics in Typical Wetlands of Poyang Lake Based on High-Throughput Sequencing: A Postprint

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Abstract

High-throughput sequencing technology was employed to analyze the characteristics of soil bacterial communities in typical wetlands of Poyang Lake. Sequencing results revealed that the ranking of abundance and diversity of soil bacterial communities under different vegetation types was identical: Carex belt > Carex-Phalaris belt > Phragmites belt > mudflat belt > Artemisia selengensis belt. From the lake surface to the slope, soil bacterial community structures at spatially proximate locations exhibited greater similarity; the bacterial community structures of the Carex-Phalaris belt, Carex belt, and Phragmites belt were similar, while those of the mudflat belt and Artemisia selengensis belt showed relatively large differences. Proteobacteria (30.0%) was the phylum with the highest average relative abundance in wetland soils, followed by Acidobacteria (16.7%) and Chloroflexi (16.5%); the relative abundances of most phylum-level bacteria exhibited certain trends of variation from the lake surface to the slope. Nitrospira was the dominant genus-level bacterial community. Among soil chemical indicators, total phosphorus, ammonium nitrogen, and organic matter content showed relatively strong correlations with bacterial communities in the Poyang Lake wetland. These findings demonstrate that soil bacterial communities under different vegetation types in the Poyang Lake wetland exhibit structural differences, yet display regular patterns of variation from the lake surface to the slope.

Full Text

Preamble

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High-Throughput Sequencing Analysis of Bacterial Communities in Soils of a Typical Poyang Lake Wetland

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Abstract

High-throughput sequencing technology was employed to analyze the bacterial community characteristics in soils of a typical Poyang Lake wetland. Sequencing results revealed consistent trends in bacterial community richness and diversity across different vegetation types. Soils with similar spatial positions along the transect from lake surface to sloping field exhibited greater similarity in bacterial community structure. The bacterial community structures of the Carex and Phragmites zones were similar, while those of the mudflat and Artemisia zones showed substantial differences. Most phyla exhibited clear trends in relative abundance along the lake-to-upland gradient. Proteobacteria (30.0%) was the most abundant phylum across all soils, followed by Acidobacteria (16.7%) and Chloroflexi (16.5%). At the genus level, *Nitrospira* was the dominant taxon, with an average abundance of 10.2%. Among soil chemical parameters, total phosphorus (TP), ammonium nitrogen (NH -N), and soil organic carbon (SOC) showed the strongest correlations with bacterial community structure. These results demonstrate that bacterial communities in Poyang Lake wetland soils exhibit structural differences among vegetation types but follow regular patterns along the hydrological gradient from lake surface to sloping field.

Keywords: Poyang Lake wetland; high-throughput sequencing; bacterial diversity; bacterial community structure

1. Study Area Description

This study was conducted in a typical Poyang Lake wetland near the main branch of the Gan River estuary. The wetland topography gradually slopes from terrestrial areas toward the lake, with orientation aligned with water recession patterns. The highest elevation adjoins the Gan River levee, while areas near the lake are relatively flat and connect to the main lake body. The wetland experiences significant seasonal water level fluctuations. During the dry

season, falling water levels expose mudflats, Carex zones, Phragmites zones, and Artemisia zones distributed along the lake-to-upland transect. During the flood season, rising water submerges most of the flats except for portions of the Phragmites and Artemisia zones. Soil particle size increases from the lake margin toward the upland, with sandy soils becoming more prevalent at higher elevations. Elevations range from 11.2 m to 18.4 m above datum.

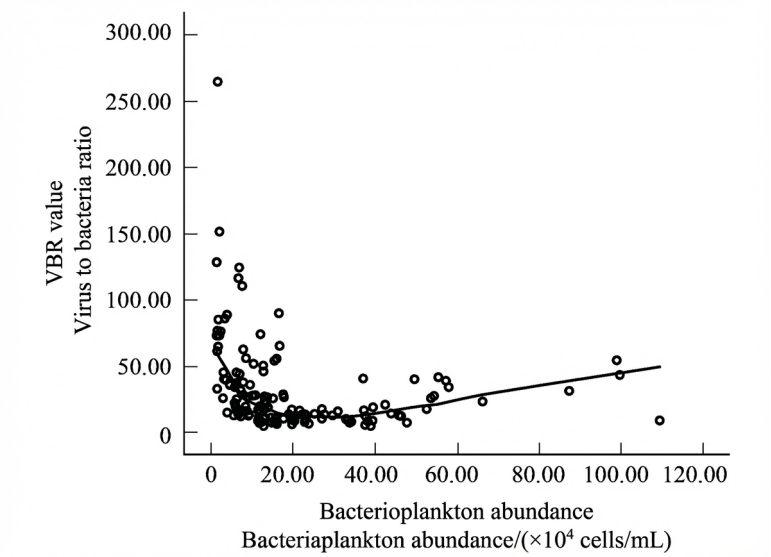

Figure 1: Figure 1

Sketch map of study area and sampling sites

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2. Soil Sampling and Physicochemical Analysis

Surface soils (0–10 cm depth) were collected from five vegetation zones (mudflat, Carex, Phragmites, Phalaris, and Artemisia) on November 15, 2014. Each sample was divided into two portions: one for chemical analysis and one for DNA extraction and sequencing. Soil chemical parameters measured included ammonium nitrogen (NH -N), nitrate nitrogen (NO -N), total nitrogen (TN), total phosphorus (TP), and soil organic carbon (SOC). NH -N and NO -N were extracted with potassium chloride solution and measured by spectrophotometry (HJ 632–2011 and HJ 634–2012, respectively). TN and TP were determined after concentrated sulfuric acid-perchloric acid digestion using the molybdenum-antimony anti-spectrophotometric method. SOC was measured by the potassium dichromate volumetric method (GB9834-88).

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3. Bacterial Community Analysis

Soil total DNA was extracted using the E.Z.N.A.® Soil DNA Kit (Omega Biotek, Norcross, GA, U.S.). Extracted genomic DNA was detected by 1% agarose gel electrophoresis. The V3–V4 hypervariable region of the 16S rRNA gene was amplified using primers 338F (5 -ACTCCTACGGGAGGCAGCA-3) and 806R (5 -GGACTACHVGGGTWTCTAAT-3). PCR amplification was performed under the following conditions: initial denaturation at 95°C for 2 min, followed by 25 cycles of denaturation at 95°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 30 s, with a final extension at 72°C for 5 min. Each sample was amplified in triplicate, and PCR products from the same sample were pooled. Amplicons were purified using the AxyPrepDNA Gel Extraction Kit (AXYGEN), quantified with the Quant-iT PicoGreen dsDNA Assay Kit (Promega) and a QuantiFluor fluorescence quantification system, then mixed in equimolar ratios before sequencing on the Illumina MiSeq PE300 platform at Shanghai Majorbio Bio-pharm Technology Co., Ltd.

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4. Bioinformatics Processing

Raw sequences were processed using Mothur (V.1.36.1). Sequences were filtered, chimeras removed, and optimized sequences obtained. Operational taxonomic units (OTUs) were clustered at 97% sequence similarity. The coverage index was calculated, and rarefaction curves were generated. Representative sequences were taxonomically classified using the RDP Classifier (http://rdp.cme.msu.edu/) against the Silva database (Release 119, http://www.arb-silva.de) with a Bayesian algorithm. Community composition was analyzed at each taxonomic level. Alpha diversity indices (Chao1 and Shannon) were calculated. Principal component analysis (PCA) was performed on OTU compositions, and redundancy analysis (RDA) was used to examine relationships between soil chemical parameters and bacterial community structure.

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5. Bacterial Community Abundance, Diversity, and Structural Differences

High-throughput sequencing of five soil samples yielded 134,223 high-quality sequences with an average length of 438.50 bp. Clustering at 97% similarity produced 2,072 OTUs. Coverage indices for all samples ranged from 99.04% to 99.65%, indicating deep sequencing that comprehensively captured the bacterial communities. The Chao1 richness estimator and Shannon diversity index showed identical trends across the five vegetation types: Phalaris soil > Carex soil > Phragmites soil > mudflat soil > Artemisia soil. This suggests that soils at intermediate positions along the hydrological gradient harbor higher bacterial

richness and diversity.

Bacterial richness and diversity in Poyang Lake wetland soils

Principal component analysis revealed that spatially adjacent soils had more similar bacterial community structures. The Carex (S2) and Phragmites (S3) zones showed the closest proximity in PCA ordination, indicating similar community composition, though their differences were greater than those within the Carex zone. The first and second principal axes explained 45.4% and 31.2% of the variance, respectively. Soils from the mudflat (S1) and Artemisia (S5) zones exhibited the greatest structural differences, while the Phragmites zone (S3) showed relatively smaller differences with Carex (S2) and Phalaris (S4) zones. Along the lake-to-upland transect, bacterial community structure showed regular variation, with spatial proximity predicting community similarity.

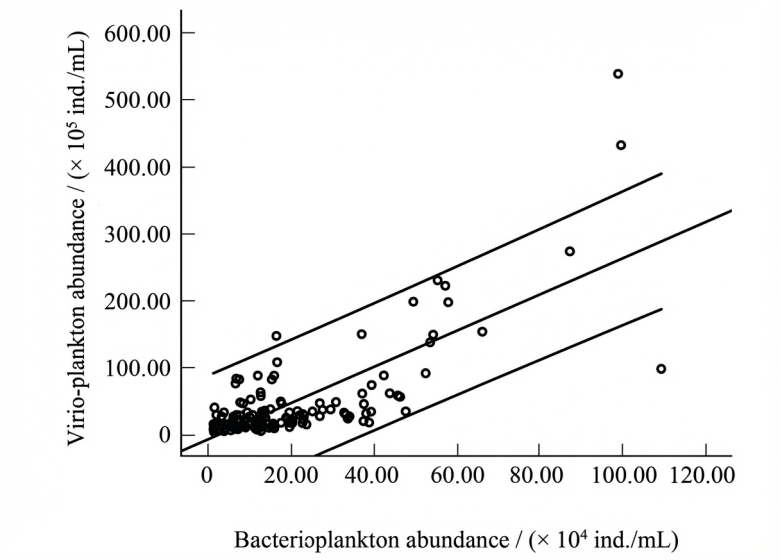

Figure 2: Figure 2

Principal component analysis of OTUs in sampling soils

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6. Bacterial Community Composition at Phylum and Genus Levels

At the phylum level, Proteobacteria (30.0%) dominated all soils, followed by Acidobacteria (16.7%), Chloroflexi (16.5%), Nitrospirae (10.2%), Firmicutes (7.5%), Actinobacteria (4.8%), Gemmatimonadetes (3.8%), and Chlorobi (1.8%). Proteobacteria was most abundant in Carex (S2), Phragmites (S3), and Phalaris (S4) soils, comprising 31.9%, 45.8%, and 35.5% respectively. In these soils, the

next most abundant phyla were Chloroflexi (16.1% in S2) and Firmicutes (15.3% in S3). In mudflat (S1) and Artemisia (S5) soils, Chloroflexi (24.9% in S1) and Acidobacteria (32.0% in S5) were the most abundant phyla, respectively.

Proteobacteria included Alphaproteobacteria (7.2%), Betaproteobacteria (8.9%), Deltaproteobacteria (10.5%), and Gammaproteobacteria (2.8%), with Epsilonproteobacteria present at only 0.1%. Most phyla showed distinct trends along the hydrological gradient: Proteobacteria abundance first increased then decreased; Acidobacteria and Chlorobi increased progressively; Nitrospirae and Firmicutes increased then decreased; Actinobacteria and Gemmatimonadetes showed no clear trend; Chloroflexi decreased then increased.

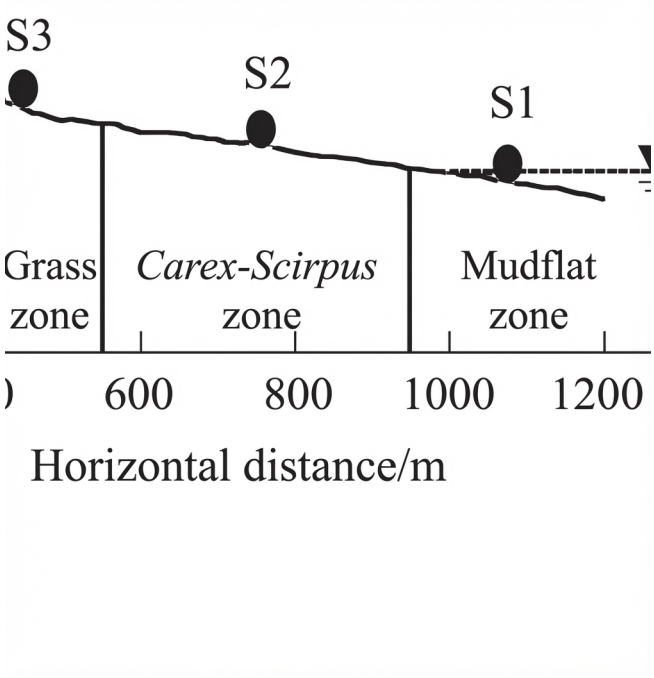

Figure 3: Figure 3

Relative abundances of bacterial phyla in Poyang Lake wetland soils

At the genus level, *Nitrospira* was the most abundant taxon (10.2% average), representing the entire Nitrospirae phylum. Other abundant genera included uncultured members of Anaerolineaceae (5.3%, within Chloroflexi), Acidobacteriaceae Subgroup 1 (4.6%, within Acidobacteria), and uncultured Nitrosomonadaceae (3.8%, within Proteobacteria). The dataset contained numerous unclassified or uncultured taxa, complicating ecological function interpretation. *Nitrospira* abundance was substantially higher than reported in other wetland soils, highlighting the importance of nitrogen cycling in Poyang Lake.

[FIGURE:4] Relative abundances of bacterial genera in Poyang Lake wetland soils

7. Relationships Between Bacterial Community and Soil Chemical Indicators

Soil chemical properties varied significantly among vegetation zones. SOC was highest in Phragmites soils (15.36 mg/kg) and lowest in mudflat soils (8.50 mg/kg). TN peaked in mudflat soils (0.50 mg/kg), while TP was highest in Carex soils (0.22 mg/kg). NH -N concentrations were greatest in mudflat soils (6.09 mg/kg), whereas NO -N was highest in Phragmites soils (4.40 mg/kg).

Chemical parameters in sampling soils

Redundancy analysis revealed that TP, NH -N, and SOC were the primary factors influencing bacterial community structure. The first and second RDA axes explained 62.8% and 30.0% of the variance, respectively, accounting for 92.8% of total variance in bacterial community composition. TP showed strong positive correlations with Acidobacteria and Actinobacteria, and negative correlations with Nitrospirae and Firmicutes. SOC was positively correlated with Proteobacteria, Gemmatimonadetes, and Chlorobi.

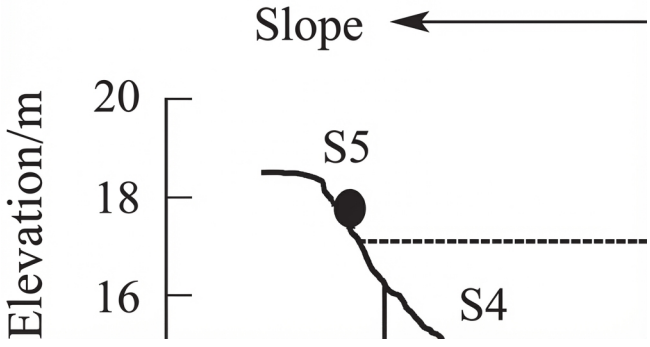

Figure 4: Figure 5

Redundancy analysis of bacterial phyla and chemical parameters in Poyang Lake wetland soils

8. Discussion

Species diversity is fundamental to ecosystem functioning. Bacterial richness and diversity enable wetlands to perform critical ecological functions including nutrient cycling, organic matter degradation, heavy metal transformation, and greenhouse gas emissions. In our study, bacterial richness and diversity followed a consistent pattern along the hydrological gradient, with intermediate positions (Carex, Phragmites, and Phalaris zones) supporting higher diversity than either permanently flooded (mudflat) or rarely flooded (Artemisia) zones. This pattern reflects the influence of seasonal water level fluctuations on soil microbial communities.

Hydrological conditions significantly shape wetland microbial communities. Soils experiencing alternating wet-dry cycles often harbor distinct bacterial assemblages compared to permanently inundated or permanently dry soils. In Poyang Lake, the mudflat zone remains flooded most of the year, the Artemisia zone is rarely flooded, while intermediate zones undergo seasonal wet-dry cycles. These hydrological differences, coupled with varying sedimentation rates and soil matrix properties, likely drive the observed community patterns. Additionally, vegetation-specific factors including root characteristics, root exudates, and rhizosphere redox conditions may influence bacterial communities.

The dominance of Proteobacteria across all soils aligns with findings from diverse wetlands worldwide, including the Ulansuhai Lake shoreline, Tibetan Plateau wetlands, Yellow River Delta, Hong Kong mangroves, and constructed treatment wetlands. Proteobacteria encompass metabolically versatile groups: Alphaproteobacteria include nitrogen-fixing symbionts, while Betaproteobacteria and Deltaproteobacteria participate in sulfur and organic matter cycling. The high relative abundance of Proteobacteria in soils with elevated SOC but moderate nitrogen content suggests their role in organic matter utilization and nitrogen fixation.

Acidobacteria, the second most abundant phylum, reached highest relative abundance in the rarely flooded Artemisia zone. This pattern is consistent with studies showing Acidobacteria prefer drier soils. The high abundance of Chloroflexi in mudflat soils may reflect their adaptation to phototrophic metabolism under low-nutrient conditions and frequent water level fluctuations. The exceptionally high abundance of Nitrospirae (particularly *Nitrospira*) in Poyang Lake soils, compared to typical wetland values (<1%), underscores the critical role of nitrogen cycling in this ecosystem.

9. Conclusion

High-throughput sequencing revealed distinct bacterial community structures among Poyang Lake wetland soils that vary systematically along the hydrological gradient from lake surface to sloping field. Key findings include:

1. Bacterial richness and diversity were highest in intermediate zones (Phalaris > Carex > Phragmites) and lowest in extreme hydrological conditions (mudflat and Artemisia zones).
2. Spatially adjacent soils shared more similar bacterial community structures, with Carex and Phragmites zones being most similar, and mudflat and Artemisia zones most distinct.
3. Proteobacteria (30.0%) was the dominant phylum, followed by Acidobacteria (16.7%) and Chloroflexi (16.5%). Most phyla exhibited clear abundance trends along the hydrological gradient.
4. *Nitrospira* was the most abundant genus (10.2%), indicating the importance of nitrogen cycling in this ecosystem.
5. Total phosphorus, ammonium nitrogen, and soil organic carbon were the primary chemical factors influencing bacterial community structure.

These results provide a scientific basis for understanding microbial-mediated ecosystem processes and inform wetland management strategies in Poyang Lake.

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Figures

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Figure 5: Figure 6

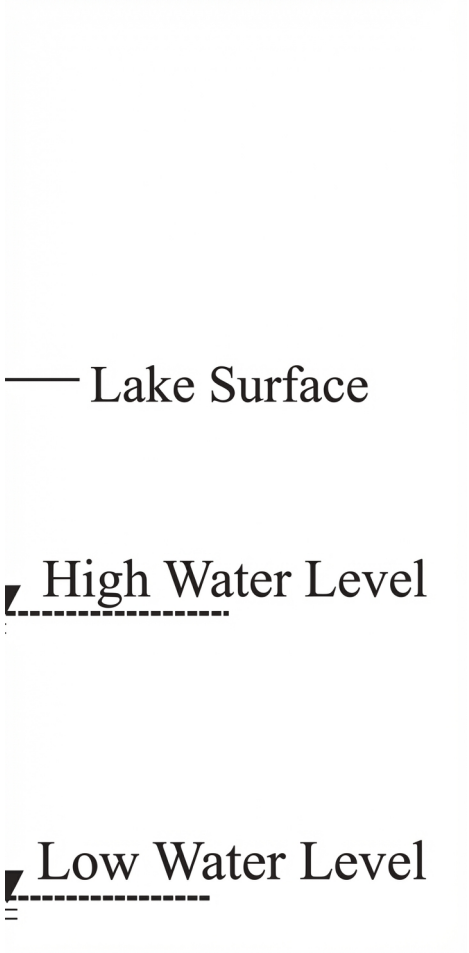
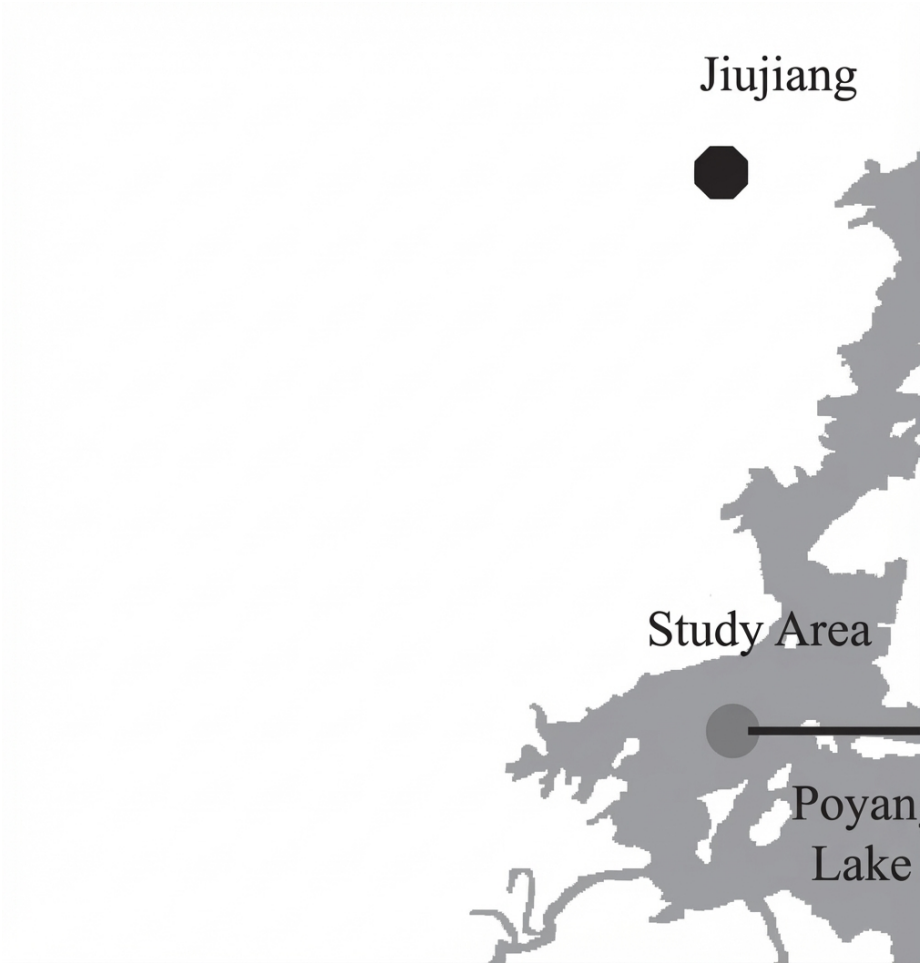


Figure 6: Figure 7



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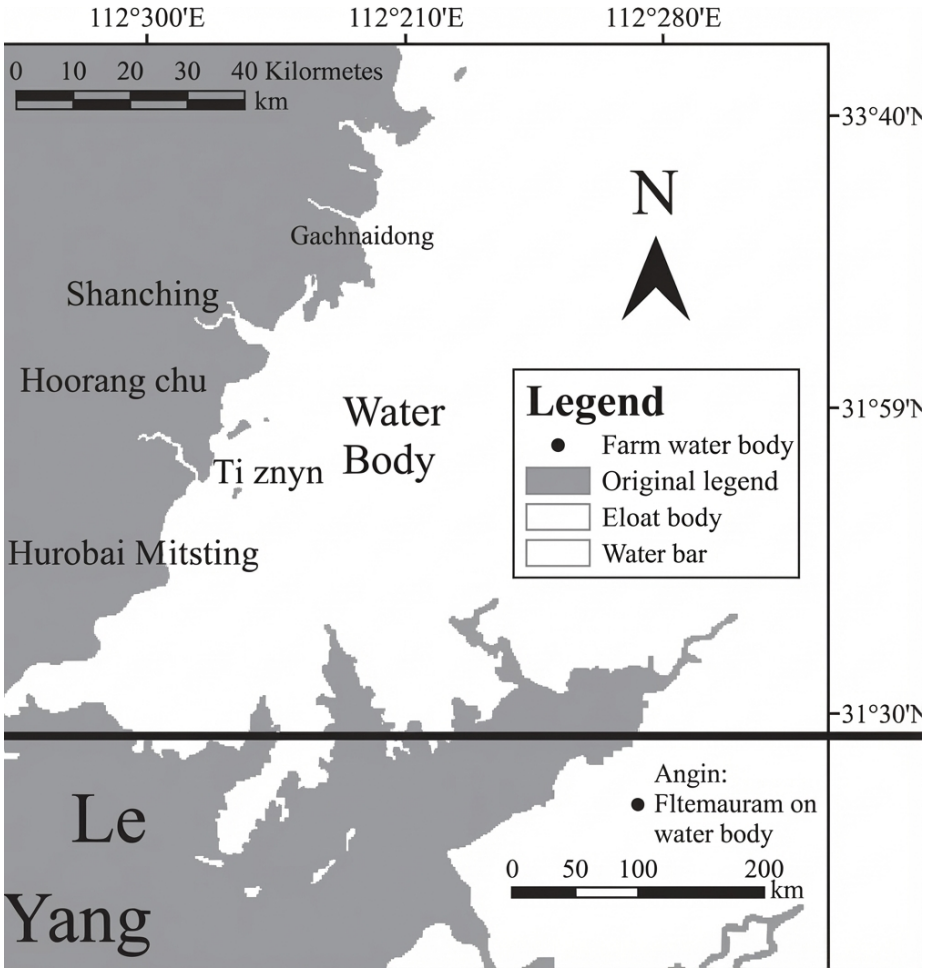

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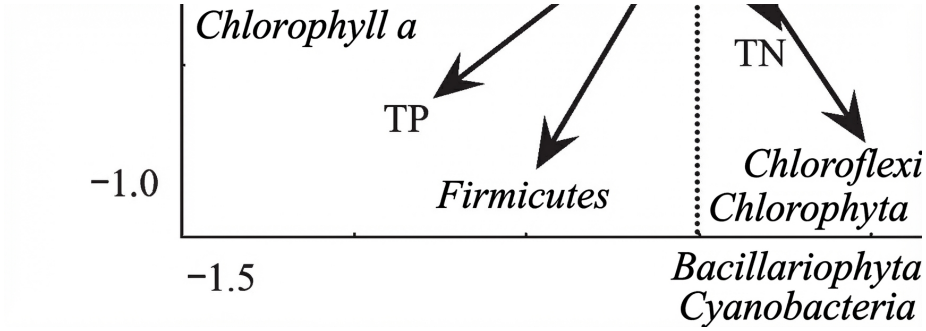

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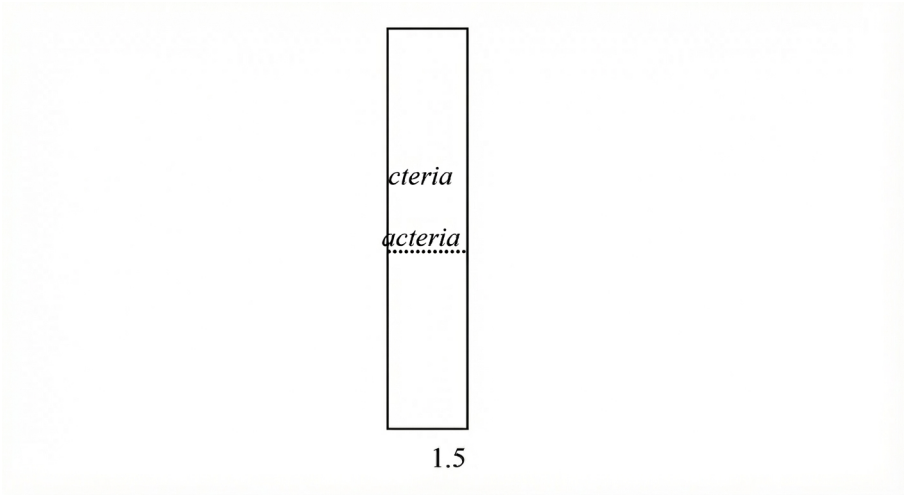

Figure 10: Figure 11