

# **Annual periodicity in planktonic bacterial and archaeal community composition of eutrophic Lake Taihu**

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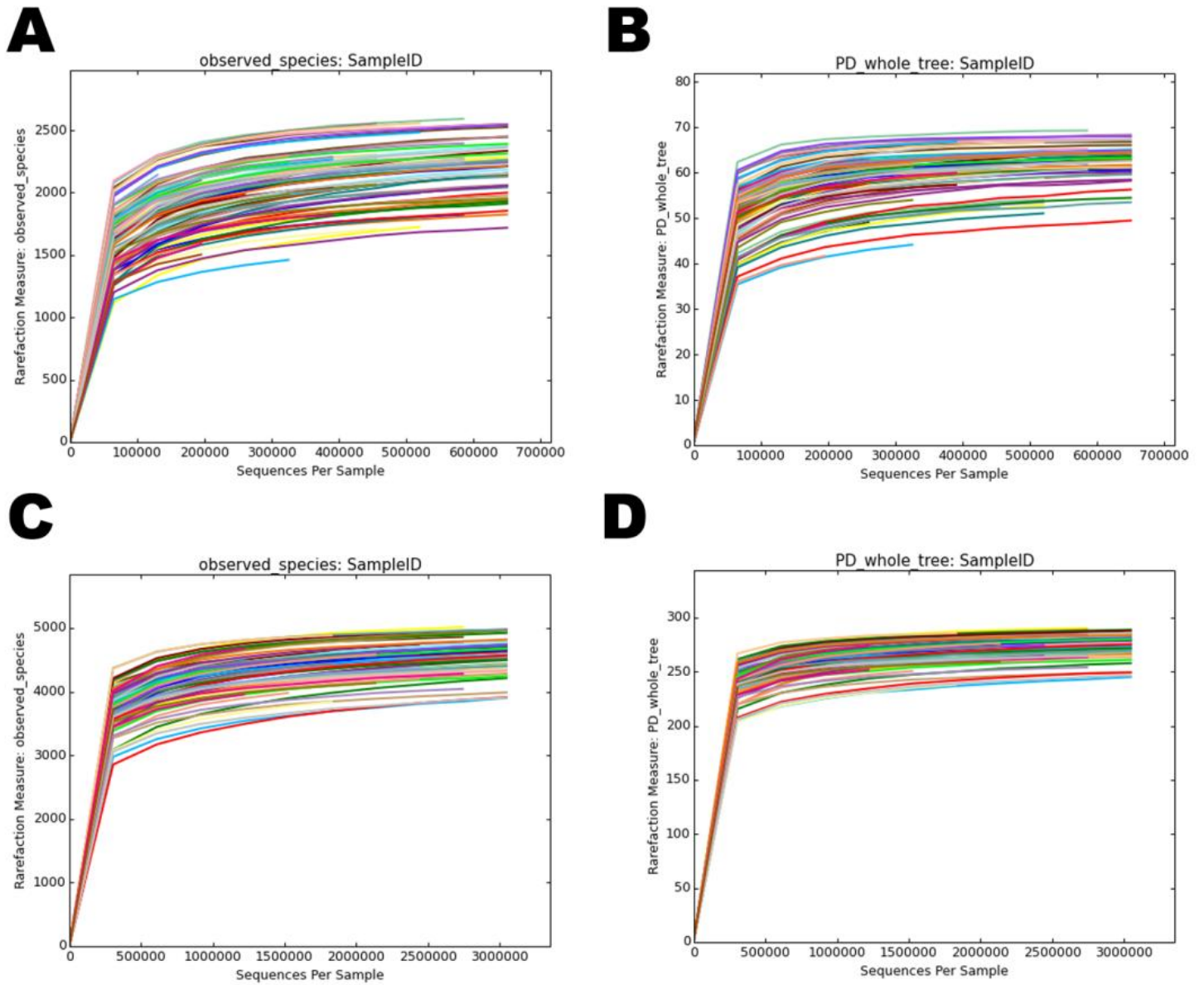
<sup>5</sup> Department of Biomedical Engineering, Peking University, Beijing, China

#These authors contributed equally to this work.

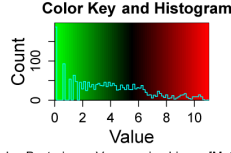
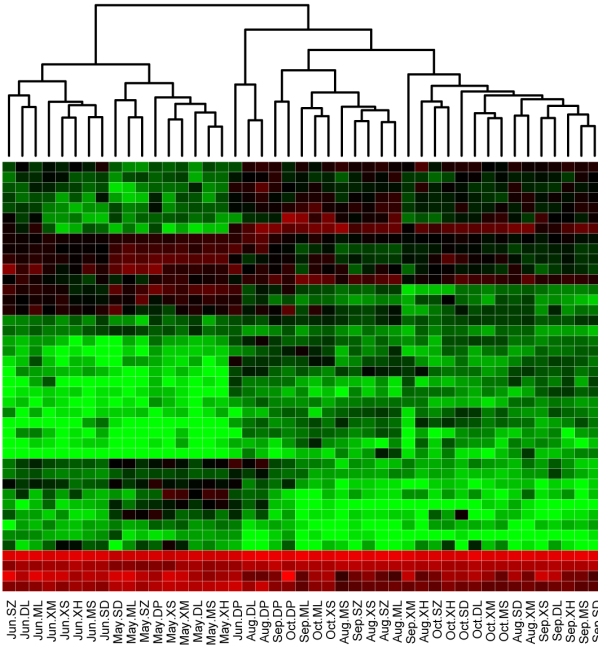
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**Figure S1.  $\alpha$ -diversity of archaeal community and bacterial community.**  $\alpha$ -diversity was evaluated by both “observed species” and “PD\_whole\_tree” metrics defined in QIIME. Each curve corresponds to a sample (totally 81 samples). (A) “observed species” within archaeal community; (B) “PD\_whole\_tree” metric of archaeal community; (C) “observed species” within bacterial community; (D) “PD\_whole\_tree” metric of bacterial community.







**B**

k\_Bacteria;p\_Verrucomicrobia;c\_[Methylacidiphilae];o\_Methylacidiphilales;f\_LD19;g\_

k\_Bacteria;p\_Proteobacteria;c\_Deltaproteobacteria;o\_MLZ46;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_MuWh-Lim;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Rubrivivax

k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Frankiaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_

k\_Bacteria;p\_Cyanobacteria;c\_Synechococcales;o\_Pseudonabaenales;f\_Pseudonabaenaceae;g\_Leptolyngbia

k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Microbacteriaceae;g\_CandidatusAquiluna

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Rhodocyclales;f\_Rhodocyclaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Polaromonas

k\_Bacteria;p\_Actinomycetes;c\_Planctomycetia;o\_Pirellulales;f\_Pirellulaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Alcaligenaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Rhodobacter

k\_Bacteria;p\_Bacteroidetes;c\_Flavobacteria;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Flavobacterium

k\_Bacteria;p\_Verrucomicrobia;c\_Opitutae;o\_Opitutales;f\_Opitutaceae;g\_

k\_Bacteria;p\_Bacteroidetes;c\_Cytophagia;o\_Cytophagales;f\_Cyclobacteriaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Hylemonella

k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Caulobacteriales;f\_Caulobacteraceae;g\_Phenylobacterium

k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Alteromonadales;f\_Chromatiaceae;g\_Rheinheimera

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Hydrogenophiales;f\_Hydrogenophiliaceae;g\_Thiobacillus

k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Xanthomonadales;f\_Xanthomonadaceae;g\_Dokdonella

k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Leptoneurales;f\_Leptoneuraceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_IS-44;f\_g\_

k\_Bacteria;p\_Cyanobacteria;c\_Oscillatoriothryoidales;o\_Chroococcales;f\_Chroococcaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhizobiales;f\_Hyphomicrobiaceae;g\_

k\_Bacteria;p\_Firmicutes;c\_Bacilli;o\_Bacillales;f\_Paenibacillaceae;g\_

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k\_Bacteria;p\_Verrucomicrobia;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Verrucomicrobiaceae;g\_Luteolibacter

k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Elin329;f\_g\_

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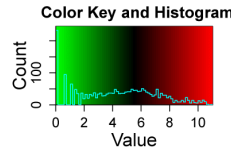
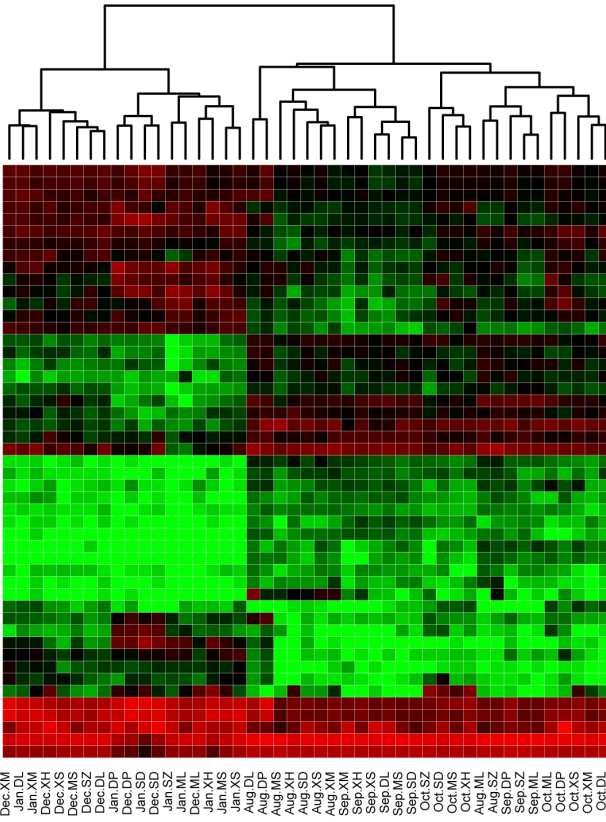
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k\_Bacteria;p\_Cyanobacteria;c\_Chloroplast;o\_Cryptophyta;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_



**C**

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_Polynucleobacter

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Oxalobacteraceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Polaromonas

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Rhodocyclales;f\_Rhodocyclaceae;g\_

k\_Bacteria;p\_Gammaproteobacteria;o\_Xanthomonadales;f\_Xanthomonadaceae;g\_

k\_Bacteria;p\_Bacteroidetes;c\_[Saprospirae];o\_[Saprospirales];f\_Saprospiraceae;g\_Aquiseitis

k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Microbacteriaceae;g\_

k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Microbacteriaceae;g\_

k\_Bacteria;p\_Bacteroidetes;c\_Flavobacteria;o\_Flavobacteriales;f\_Flavobacteriaceae;g\_Flavobacterium

k\_Bacteria;p\_Bacteroidetes;c\_Sphingobacteriia;o\_Sphingobacteriales;f\_Sphingobacteriaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rhodobacterales;f\_Rhodobacteraceae;g\_Rhodobacter

k\_Bacteria;p\_Proteobacteria;c\_TA18;o\_PHOS-HD29T;f\_g\_

k\_Bacteria;p\_Planctomycetes;c\_OM190;o\_CL500-15;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Rubrivivax

k\_Bacteria;p\_Proteobacteria;c\_Deltaproteobacteria;o\_MLZ46;f\_g\_

k\_Bacteria;p\_Planctomycetes;c\_Planctomycetia;o\_Planctomycetaceae;f\_Planctomycetes;g\_Planctomycetes

k\_Bacteria;p\_Chlorobci;OPB56;o\_f\_g\_

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k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Microbacteriaceae;g\_CandidatusAquiluna

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k\_Bacteria;p\_Proteobacteria;c\_Deltaproteobacteria;o\_Myxococcales;f\_Myxococcaceae;g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_IS-44;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Gammaproteobacteria;o\_Leptoneurales;f\_Leptoneuraceae;g\_

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k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Methylubium

k\_Bacteria;p\_Verrucomicrobia;c\_Verrucomicrobiae;o\_Verrucomicrobiales;f\_Verrucomicrobiaceae;g\_Luteolibacter

k\_Bacteria;p\_Cyanobacteria;c\_Chloroplast;o\_Haptophyceae;f\_g\_

k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_

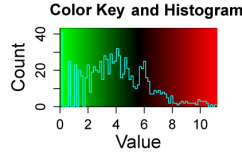
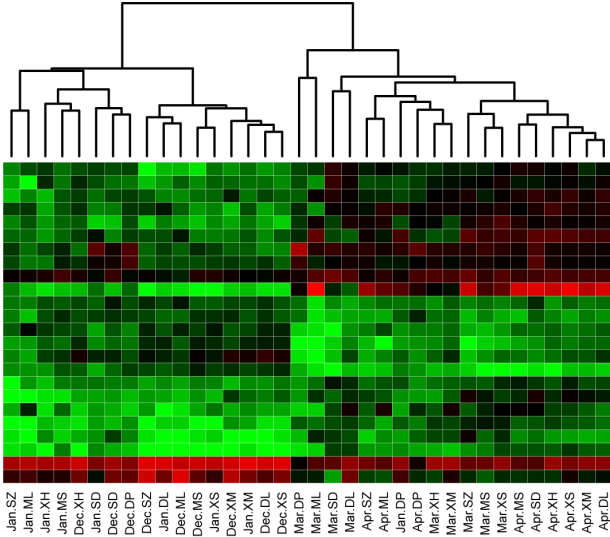
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k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_g\_

k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_g\_

Dec.XII  
Jan.XI  
Jan.XII  
Dec.XS  
Dec.MS  
Dec.SZ  
Dec.DL  
Jan.DP  
Dec.DP  
Dec.SD  
Jan.SZ  
Jan.ML  
Dec.ML  
Jan.XH  
Jan.MS  
Jan.DL  
Aug.DL  
Aug.DP  
Aug.XH  
Aug.SD  
Aug.MS  
Aug.XM  
Sep.XM  
Sep.XH  
Sep.XS  
Sep.DL  
Sep.MS  
Sep.SZ  
Oct.SZ  
Oct.SD  
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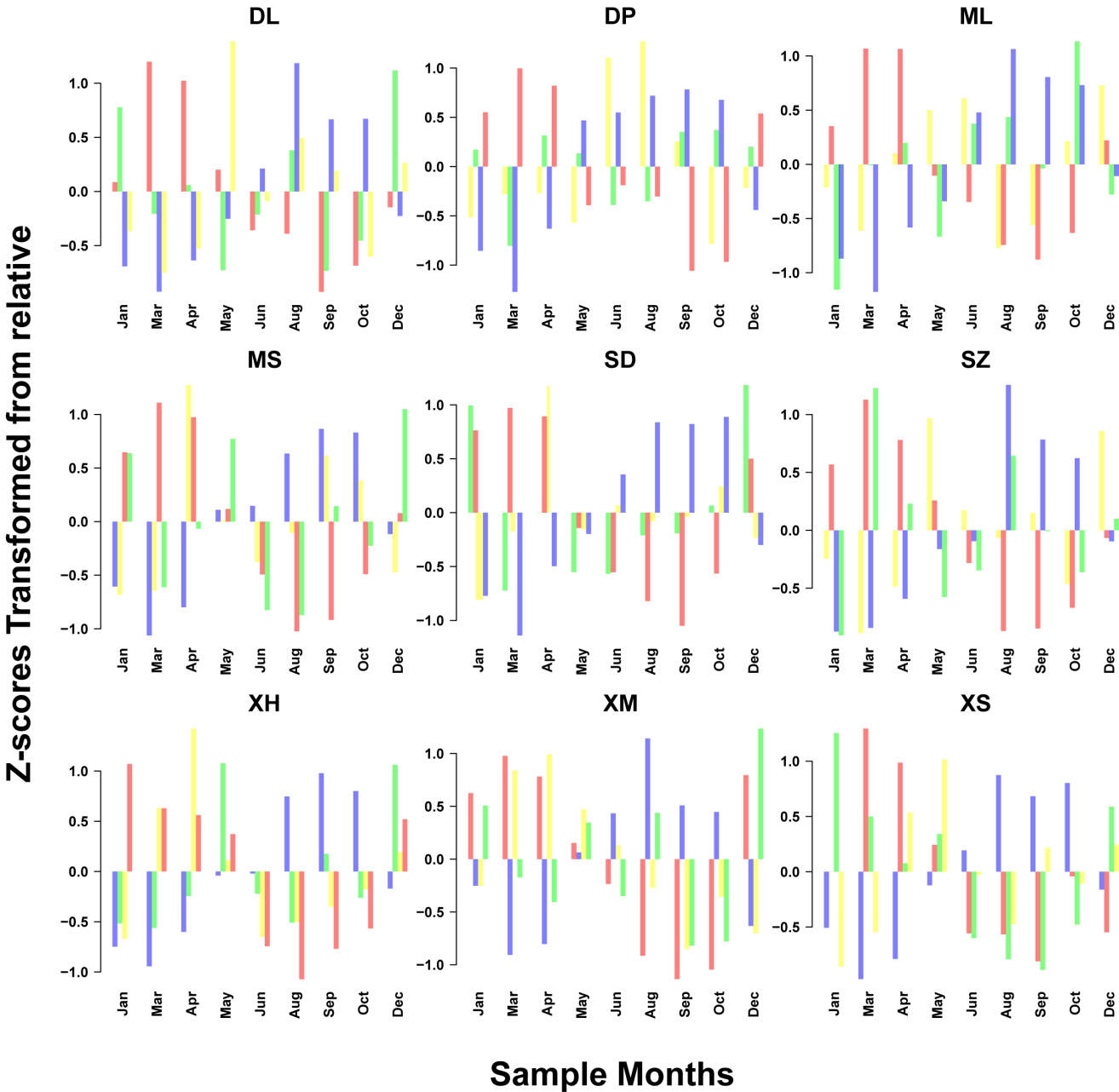


D

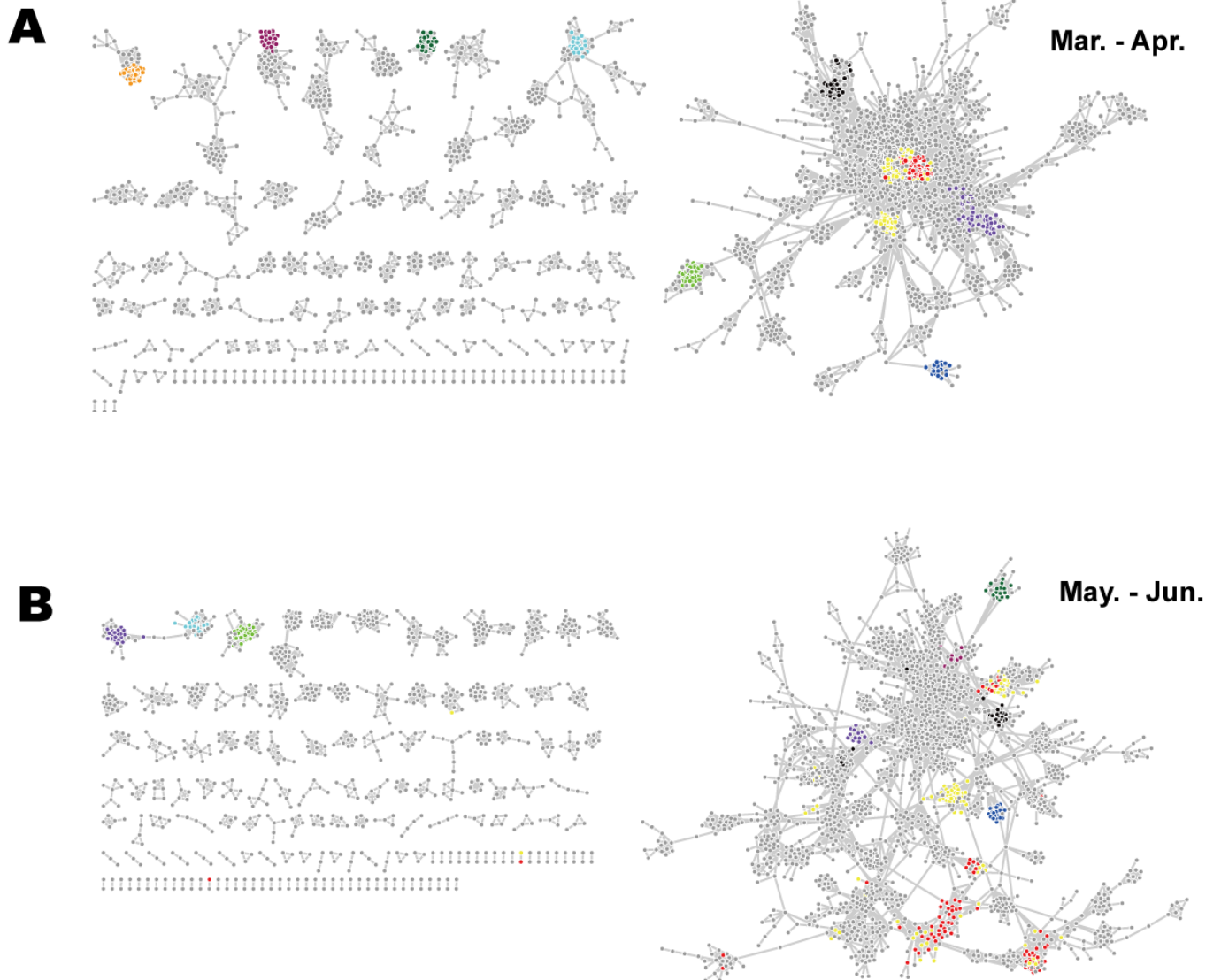
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- k\_Bacteria;p\_Gemmatimonadetes;c\_Gemmatimonadales;o\_Gemmatimonadales;f\_Gemmatimonadaceae;g\_Gemmatimonas
- k\_Bacteria;p\_Cyanobacteria;c\_Chloroplast\_o\_Chlorophyta;f\_Chlamydomonadaceae;g\_Haematococcus
- k\_Bacteria;p\_Actinobacteria;c\_Acidimicrobia;o\_Acidimicrobiales
- k\_Bacteria;p\_Cyanobacteria;c\_Synechococophycidae;o\_Pseudanabaenales;f\_Pseudanabaenaceae;g\_Leptolyngbya
- k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Limnochabans
- k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_Burkholderiales;f\_Comamonadaceae;g\_Comamonas
- k\_Bacteria;p\_Bacteroidetes;c\_[Saprospirae];o\_[Saprospirales];f\_[Chitinophagaceae];g\_
- k\_Bacteria;p\_Cyanobacteria;c\_Nostocophycidae;o\_Nostocales;f\_Nostocaceae;g\_
- k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Sphingomonadales;f\_Erythrobacteraceae;g\_
- k\_Bacteria;p\_Proteobacteria;c\_Betaproteobacteria;o\_SC-1-84;f\_g\_
- k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Frankiaceae;g\_
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- k\_Bacteria;p\_Actinobacteria;c\_Thermoleophilia;o\_Gaiellales;f\_g\_
- k\_Bacteria;p\_Actinobacteria;c\_Actinobacteria;o\_Actinomycetales;f\_Microbacteriaceae;g\_CandidatusAquiluna
- k\_Bacteria;p\_Verrucomicrobia;c\_Opitutae;o\_Opitutales;f\_Opitutaceae;g\_
- k\_Bacteria;p\_Planctomycetes;c\_Phycisphaerae;o\_Phycisphaerales;f\_g\_
- k\_Bacteria;p\_Proteobacteria;c\_Deltaproteobacteria;o\_MIZ46;f\_g\_
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- k\_Bacteria;p\_Verrucomicrobia;c\_[Spartobacteria];o\_[Chthoniobacteriales];f\_[Chthoniobacteraceae];g\_heteroC45\_4W
- k\_Bacteria;p\_Proteobacteria;c\_Alphaproteobacteria;o\_Rickettsiales;f\_Pelagibacteraceae;g\_
- k\_Bacteria;p\_Cyanobacteria;c\_Oscillatoriphyycidae;o\_Chroococcales;f\_Microcystaceae;g\_Microcystis

**Figure S3. Temporal variation of Z-scores of K-means clustering centers.** Relative abundance of bacterial genera at different sample sites was transformed into Z-scores respectively with similar method described in Materials and Methods. Unsupervised clustering was conducted using K-means algorithm. Average Z-scores of the genera of each cluster are demonstrated in 9 figures, corresponding to 9 different sample sites. Intuitively, we can see two clusters whose relative abundances vary in opposite ways are quite consistent across different sites.

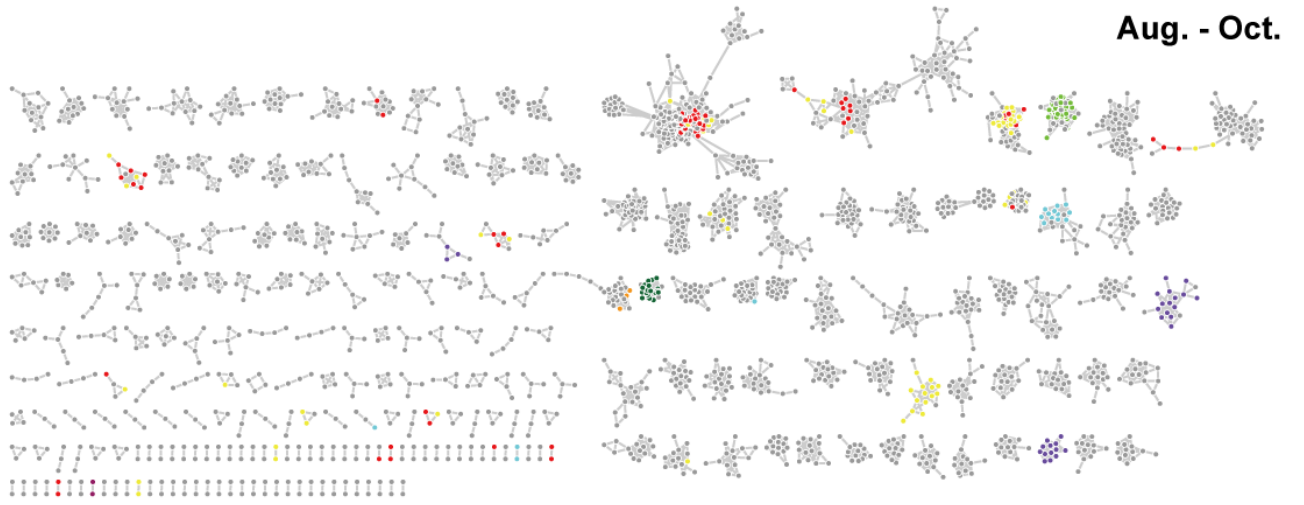
## K-means Clustering Centers of 9 Sample Sites



**Figure S4. Overview of the OTU co-occurrence networks of four stages.** We used MCODE to find network modules in Mar.-Apr. stage, as it had been reported to be the initiation period of harmful algal bloom in which temperature rose gradually. Top 10 modules ranked by ratio of edge number and node number were colored. OTUs within the modules were also colored in other three networks for tracing temporal variation of the modules.



**C**



**D**

