

Supplementary Materials

Article

Network analysis reveals seasonal patterns of bacterial community networks in Lake Taihu under aquaculture conditions

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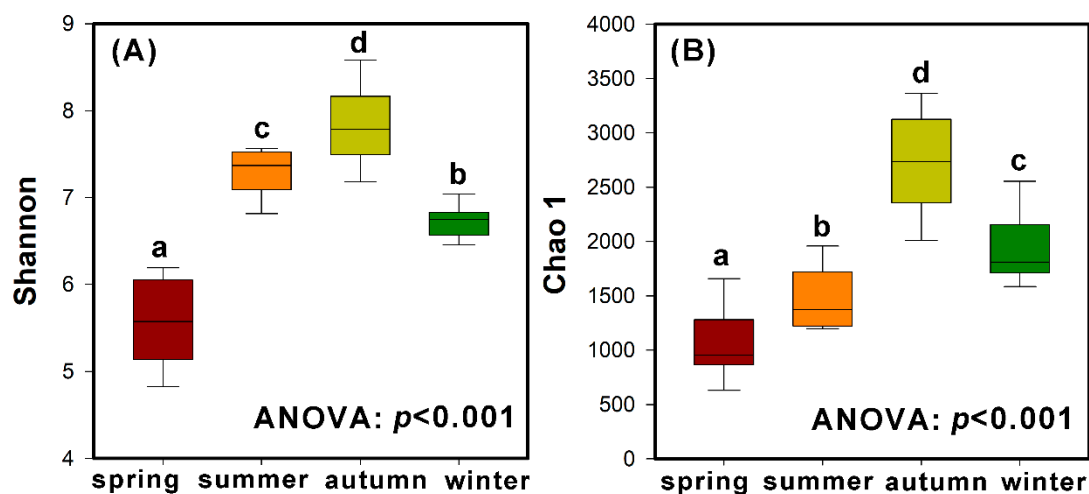


Figure S1. Diversity (A) and richness (B) of the bacterial communities across seasons. Different letters above columns show the remarkable differences based on one-way ANOVA with Duncan's comparisons ($p < 0.05$).

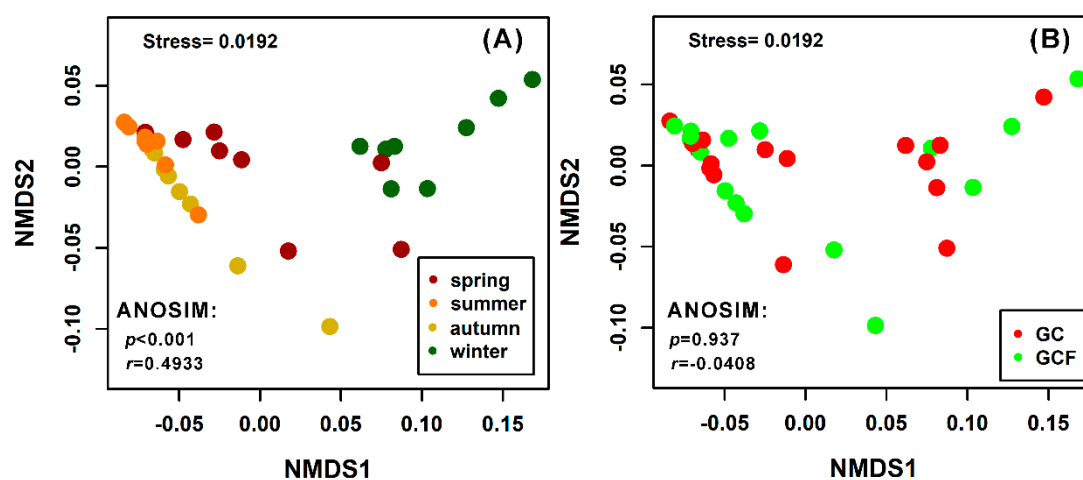


Figure S2. Non-metric multidimensional scaling analysis (NMDS) of bacterial community composition for each season (A) and each zone (B) based on the weighted UniFrac distance. Difference was tested based on 999 permutations using 'anosim' functions in R.

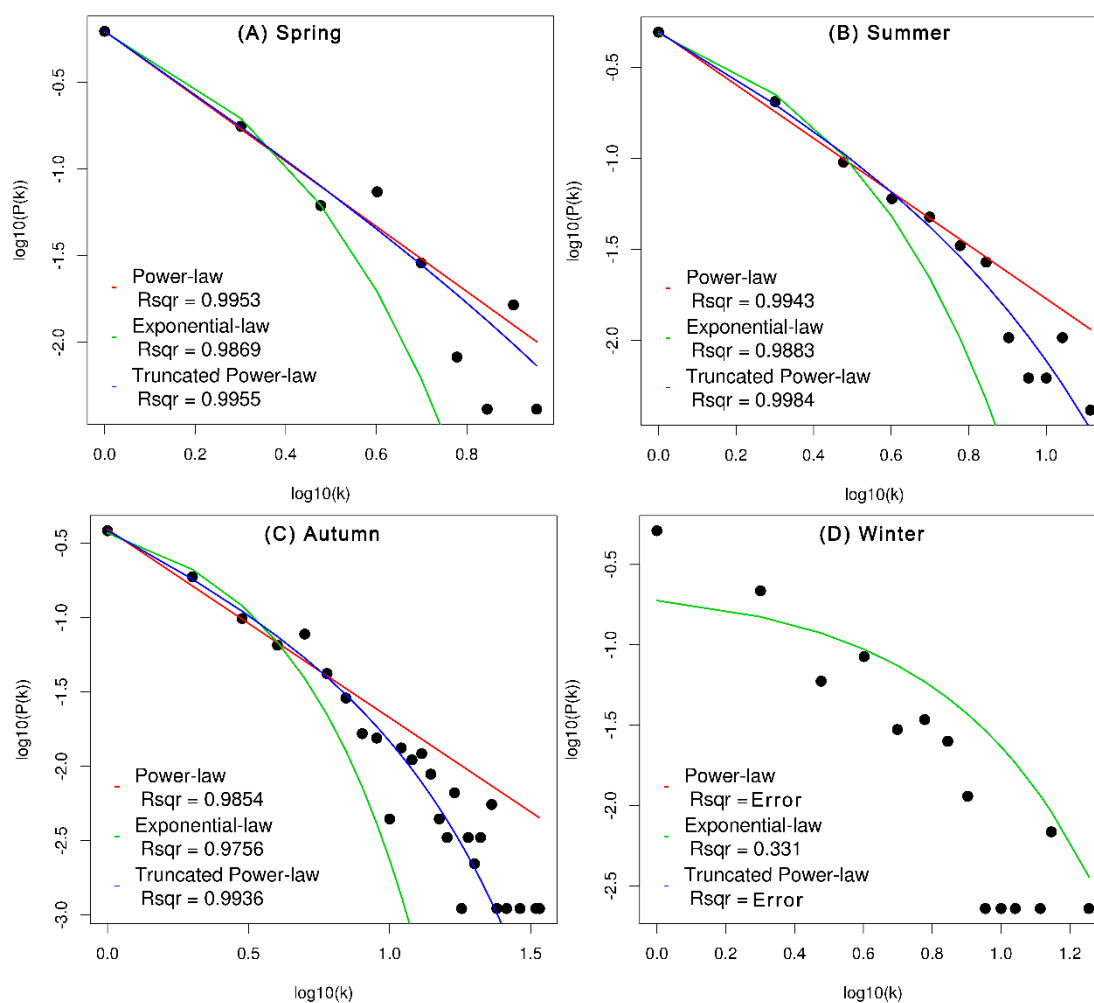


Figure S3. The OTU connectivity distributions of bacterial community networks in different seasons as fitted by power-law, exponential-law and truncated power-law models (A, spring; B, summer; C, autumn; D, winter). The x-axis is the node connectivity. The y-axis is the number of nodes under a given connectivity. The values on both axes are log transformed. R_{sqr} values represent the degree of fitting models (undetermined fitting value found are shown by 'Error').

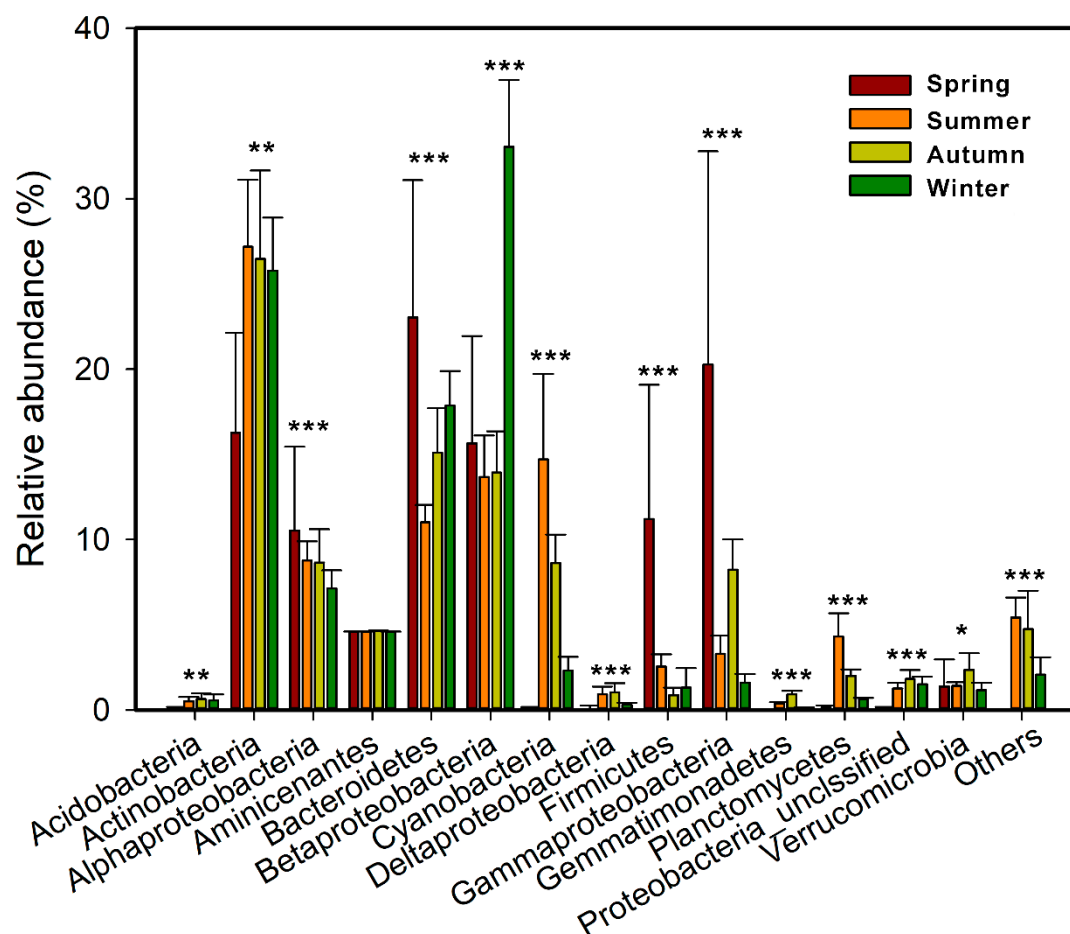


Figure S4. The relative abundance of dominant bacterial phyla/classes for each season. Phyla/classes with a relative abundance of $> 0.5\%$ are presented, whereas those with relative abundance $< 0.5\%$ were included in the 'others' group. The height of each bar denotes the average relative abundance of each phylum. Asterisks above bars represent significant differences from the Kruskal-Wallis H -test. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

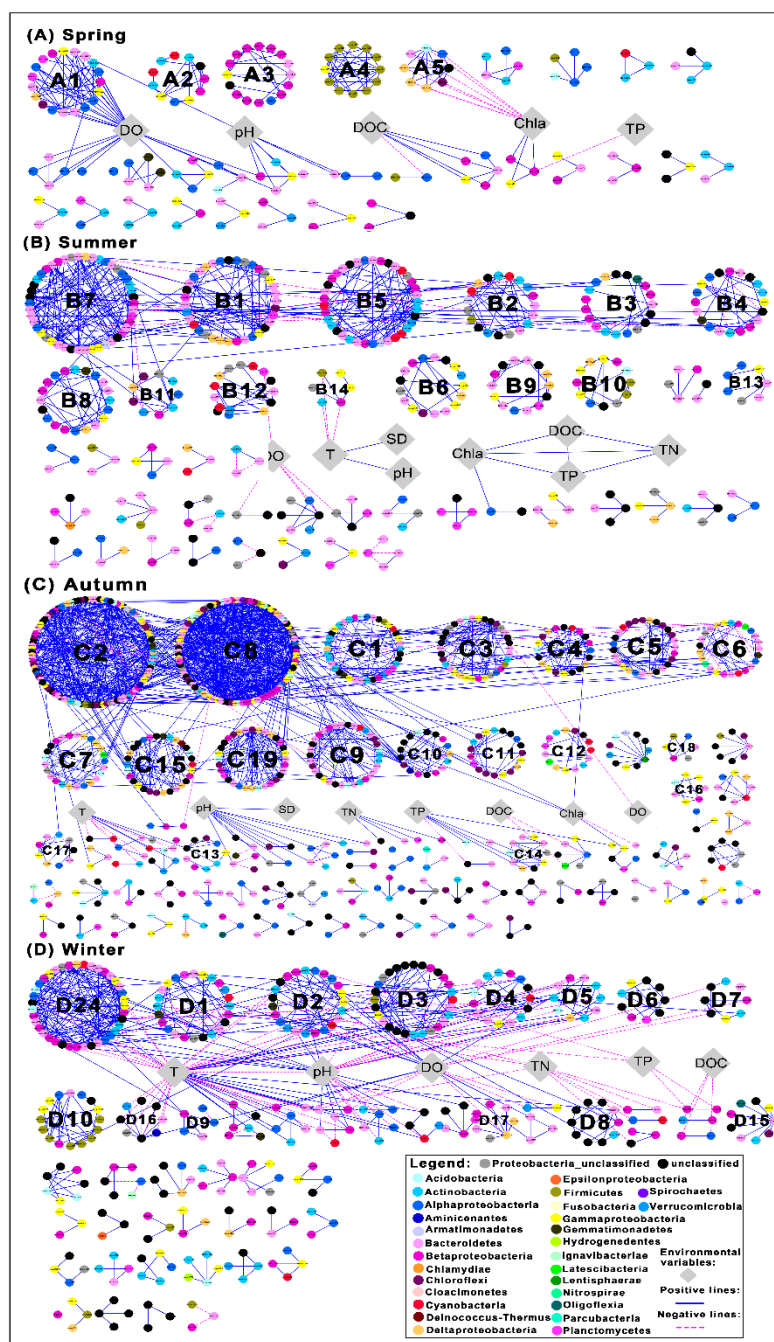


Figure S5. Species-environment network of bacterial communities in spring (A), summer (B), autumn (C) and winter (D). Only correlations between species that were statistically significant ($p < 0.001$) and strong ($r > 0.9$ or $r < -0.9$) are shown by solid blue lines (positive correlations) and dotted pink lines (negative correlations), respectively. Only correlations between environmental factors and species interactions that were significant ($p < 0.01$) are shown. Correlations between pairs of OTUs and OTUs uncorrelated to any environmental variables are not shown. Different bacterial phyla/subphyla are represented by different colors, and the number on each node represents the ID number of each OTU. T, water temperature; DO, dissolved oxygen; SD, Secchi depth; Chla, chlorophyll *a*; TN, total nitrogen; TP, total phosphorus; DOC, dissolved organic carbon.

Table S1. The percentage (%) of OTUs/nodes in the bacterial networks assigned to each phylum/class for each seasons.

Phylum/class	Percentage (%) of OTUs/nodes			
	Spring	Summer	Autumn	Winter
<i>Acidobacteria</i>	1.23	0.83	4.09	1.83
<i>Actinobacteria</i>	11.11	7.68	5.64	10.27
<i>Alphaproteobacteria</i>	15.23	10.37	6.52	10.05
<i>Aminicenantes</i>	--	--	0.44	0.23
<i>Armatimonadetes</i>	0.41	0.83	0.33	--
<i>Bacteroidetes</i>	19.75	23.65	19.23	15.75
<i>Betaproteobacteria</i>	22.22	10.37	9.83	18.04
<i>Chlamydiae</i>	--	0.21	--	--
<i>Chloroflexi</i>	0.82	1.04	6.74	0.23
<i>Cloacimonetes</i>	--	--	0.22	--
<i>Cyanobacteria</i>	2.06	3.94	1.99	2.74
<i>Deinococcus-Thermus</i>	--	--	0.22	--
<i>Deltaproteobacteria</i>	1.65	4.98	5.97	2.51
<i>Epsilonproteobacteria</i>	--	--	--	0.23
<i>Firmicutes</i>	5.76	2.28	1.10	2.97
<i>Fusobacteria</i>	--	--	0.11	--
<i>Gammaproteobacteria</i>	9.88	6.43	9.39	8.90
<i>Gemmatimonadetes</i>	0.82	0.41	0.66	0.68
<i>Hydrogenedentes</i>	--	--	--	0.23
<i>Ignavibacteriae</i>	--	--	0.55	0.23
<i>Latescibacteria</i>	--	--	0.44	--
<i>Lentisphaerae</i>	--	--	0.11	--
<i>Nitrospirae</i>	--	--	0.11	--
<i>Oligoflexia</i>	--	0.21	0.11	0.23
<i>Parcubacteria</i>	--	--	0.11	--
<i>Planctomycetes</i>	2.47	4.15	2.54	1.37
<i>Proteobacteria_unclassified</i>	0.41	6.64	3.09	1.83
<i>Spirochaetes</i>	--	--	0.22	--
<i>Verrucomicrobia</i>	1.65	2.70	1.88	2.51
Unclassified	4.53	13.28	18.34	19.18

Phyla/classes that were not found were shown as symbol '--'.

Table S2. The top 10 correlations of the species-species association network in the present study.

	OTU1	OTU2	Correlation	R value	Affiliated phylum/class of OTU1	Affiliated phylum/class of OTU2	Lowest taxonomic rank of OTU1	Lowest taxonomic rank of OTU2
Spring	denovo5147	denovo2394	pp	0.994	c__Betaproteobacteria	c__Betaproteobacteria	f__Alcaligenaceae	f__Comamonadaceae
	denovo7097	denovo3965	pp	0.994	p__Cyanobacteria	p__Actinobacteria	f__GpIIa	c__Actinobacteria
	denovo11316	denovo8326	pp	0.994	p__Unclassified	p__Actinobacteria	k__Bacteria	o__Acidimicrobiales
	denovo12335	denovo6254	pp	0.994	c__Alphaproteobacteria	p__Actinobacteria	g__Sandarakinorhabdus	g__Ilumatobacter
	denovo11448	denovo4829	pp	0.982	c__Betaproteobacteria	c__Betaproteobacteria	g__Undibacterium	g__Undibacterium
	denovo211	denovo103	pp	0.976	p__Firmicutes	p__Firmicutes	g__Leuconostoc	g__Lactococcus
	denovo555	denovo211	pp	0.976	p__Firmicutes	p__Firmicutes	g__Streptococcus	g__Leuconostoc
	denovo1806	denovo211	pp	0.976	p__Firmicutes	p__Firmicutes	g__Enterococcus	g__Leuconostoc
	denovo2757	denovo103	pp	0.976	p__Firmicutes	p__Firmicutes	g__Lactococcus	g__Lactococcus
	denovo2757	denovo555	pp	0.976	p__Firmicutes	p__Firmicutes	g__Lactococcus	g__Streptococcus
	denovo6043	denovo4553	pp	0.994	p__Cyanobacteria	p__Actinobacteria	f__GpIIa	f__Microbacteriaceae
	denovo11460	denovo2613	pp	0.994	c__Alphaproteobacteria	p__Bacteroidetes	c__Alphaproteobacteria	p__Bacteroidetes
Summer	denovo12748	denovo1296	pp	0.994	c__Deltaproteobacteria	p__Chloroflexi	o__Myxococcales	g__Litorilina
	denovo11333	denovo10543	np	-0.988	p__Bacteroidetes	p__Planctomycetes	f__Saprospiraceae	f__Planctomycetaceae
	denovo4866	denovo1741	pp	0.982	p__Bacteroidetes	p__Bacteroidetes	f__Chitinophagaceae	p__Bacteroidetes
	denovo5318	denovo5306	pp	0.982	p__Unclassified	c__Alphaproteobacteria	k__Bacteria	g__Rickettsia
	denovo9859	denovo6899	pp	0.982	c__Gammaproteobacteria	c__Deltaproteobacteria	c__Gammaproteobacteria	c__Deltaproteobacteria
	denovo919	denovo685	pp	0.976	c__Betaproteobacteria	p__Bacteroidetes	c__Betaproteobacteria	p__Bacteroidetes
	denovo2426	denovo919	pp	0.976	p__Bacteroidetes	c__Betaproteobacteria	p__Bacteroidetes	c__Betaproteobacteria
	denovo3768	denovo3343	pp	0.976	p__Planctomycetes	p__Planctomycetes	f__Planctomycetaceae	f__Planctomycetaceae
	denovo1304	denovo914	pp	0.994	p__Bacteroidetes	p__Unclassified	f__Prolixibacteraceae	k__Bacteria
	denovo2271	denovo914	pp	0.994	c__Betaproteobacteria	p__Unclassified	o__Burkholderiales	k__Bacteria
	denovo2296	denovo914	pp	0.994	c__Gammaproteobacteria	p__Unclassified	g__Poalibacter	k__Bacteria
	denovo2361	denovo742	pp	0.994	c__Betaproteobacteria	c__Betaproteobacteria	o__Methylophilales	c__Betaproteobacteria
Autumn	denovo2748	denovo635	pp	0.994	p__Unclassified	c__Gammaproteobacteria	k__Bacteria	g__Methylobacter
	denovo3384	denovo2823	pp	0.994	p__Unclassified	p__Bacteroidetes	k__Bacteria	p__Bacteroidetes
	denovo4530	denovo335	pp	0.994	p__Unclassified	p__Cyanobacteria	k__Bacteria	f__GpIIa
	denovo4929	denovo251	pp	0.994	p__Unclassified	p__Bacteroidetes	k__Bacteria	o__Cytophagales
	denovo5035	denovo1543	pp	0.994	p__Unclassified	c__Betaproteobacteria	k__Bacteria	c__Betaproteobacteria
	denovo5551	denovo242	pp	0.994	c__Gammaproteobacteria	c__Gammaproteobacteria	c__Gammaproteobacteria	g__Methylobacter
	denovo5210	denovo5015	pp	0.994	p__Unclassified	p__Cyanobacteria	k__Bacteria	f__GpIIa
Winter	denovo8283	denovo6695	pp	0.994	c__Betaproteobacteria	p__Bacteroidetes	g__Polynucleobacter	f__Chitinophagaceae
	denovo8659	denovo1748	pp	0.994	c__Gammaproteobacteria	c__Betaproteobacteria	c__Gammaproteobacteria	c__Betaproteobacteria

denovo8659	denovo4573	pp	0.994	<i>c__Gammaproteobacteria</i>	<i>c__Betaproteobacteria</i>	<i>c__Gammaproteobacteria</i>	<i>c__Betaproteobacteria</i>
denovo8659	denovo7022	pp	0.994	<i>c__Gammaproteobacteria</i>	<i>c__Betaproteobacteria</i>	<i>c__Gammaproteobacteria</i>	<i>c__Betaproteobacteria</i>
denovo9672	denovo716	pp	0.994	<i>p__Actinobacteria</i>	<i>p__Gemmatimonadetes</i>	<i>o__Actinomycetales</i>	<i>g__Gemmatimonas</i>
denovo12832	denovo11466	pp	0.994	<i>p__Actinobacteria</i>	<i>p__Unclassified</i>	<i>o__Actinomycetales</i>	<i>k__Bacteria</i>
denovo13130	denovo12472	pp	0.994	<i>c__Alphaproteobacteria</i>	<i>c__Gammaproteobacteria</i>	<i>f__Rhodobacteraceae</i>	<i>g__Pseudomonas</i>
denovo7051	denovo5210	pp	0.982	<i>p__Actinobacteria</i>	<i>p__Unclassified</i>	<i>g__Ilumatobacter</i>	<i>k__Bacteria</i>
denovo11947	denovo7809	pp	0.982	<i>p__Unclassified</i>	<i>c__Betaproteobacteria</i>	<i>k__Bacteria</i>	<i>f__Comamonadaceae</i>

pp: positive correlation, np: negative correlation.

Table S3. The number of positive/negative links between environmental variables and species interactions in species-environment association network of the different seasons.

	Spring		Summer		Autumn		Winter	
	positive links	negative links	positive links	negative links	positive links	negative links	positive links	negative links
T	--	--	2	3	4	6	16	33
pH	7	0	1	0	11	0	13	14
DO	24	0	0	5	0	1	11	8
SD	--	--	1	0	1	0	--	--
Chla	3	7	4	0	4	1	--	--
TN	--	--	3	0	4	0	0	9
TP	0	1	3	0	5	1	0	4
DOC	4	1	3	0	0	3	0	3
Total	38	9	17	8	29	12	40	71

T, water temperature; DO, dissolved oxygen; SD, Secchi depth; Chla, chlorophyll a; TN, total nitrogen; TP, total phosphorus; DOC, dissolved organic carbon. No relationship between environmental variables and species interactions was shown as symbol '--'.