

APPENDIX S1

Primer Sequences – Forward: (515F) GTGCCAGCMGCCGCGGTAA

Reverse: (806R) GGACTACHVGGGTWTCTAAT

Primers were designed to include the Lib-L adapters (A on forward, B on reverse), 12 bp Golay barcode on Forward Primer, and sequence linker (GT on forward, GG on Reverse). For more information see Fierer et al. (2008).

PCR Reaction Conditions –

Component	Stock Concentration	Final Concentration	µl per 50 µl rxn
10X Perfect Taq Plus PCR Buffer	10X	1X	5
5P solution (5X)	5X	1X	10
dNTP mix (50 mM, 10 mM each)	40 mM	200 µM	1
Forward Primer (10 µM)	10 µM	0.2 µM	1
Perfect Taq Plus DNA Polymerase	5 U/µl	1.25 U/rxn	0.25
Molecular Grade Water			<i>Add enough to make final vol 50 µl)</i>
<i>Added to each individual rxn</i>			
Reverse Primer (10 µM)	10 µM	0.2 µM	1
Template	~10 ng/µl	~10 ng	

PCR Thermal Cycler Conditions –

Temp	Time	Cycles
94°C	3 mi	
94°C	45 sec	\
50°C	30 sec	30
72°C	90 sec	/
72°C	10 min	
4°C	∞	

Table S1: Species-specific responses and taxonomic identity. Responses indicate significant increases (↑) or decreases (↓) in relative abundance in as tDOC supply rate increased. Responses are shown in regards to both the active and total communities. Clade refers to the phylogenetic group (phylum or subphylum) as inferred from best matches to the RDP taxonomy (Wang et al. 2007). Freshwater Tribe refers to the phylogenetic group as inferred from best matches to the Freshwater Bacterial Database (Newton et al. 2011). Some OTUs did not have best hits in the Freshwater Database. Known References are matches based on BLAST hits to known bacteria and are shown as a reference. Percent match and Genbank Accession are given for each.

OTU	Clade	Freshwater Tribe	Responses		Known Reference	% Match	Genbank Accession
			Total	Active			
Otu100	Actinobacteria	LiUU-11-47		↓	<i>Amycolatopsis niigatensis</i> strain LC11	87%	NR_041405
Otu049				↓	<i>Streptomyces scabrisporus</i> strain Cac02	93%	KF317986
Otu043		acSTL-A1	↑		<i>Actinobacterium</i> SCGC AAA028-009	100%	HQ663291
Otu041		Luna3	↑	↑	<i>Microbacterium</i> sp. LS-725	100%	KP162073
Otu053		acIII-A1	↑		<i>Actinobacterium</i> MS-B-44	100%	FJ460158
Otu028		acI-A	↓		<i>Actinobacterium</i> SCGC AAA278-F04	100%	HQ663546
Otu106		acI-C	↓		<i>Actinobacterium</i> SCGC AAA208-D13	96%	JF488148
Otu011		acI-B1	↓		<i>Rhodococcus</i> sp. SDB1	100%	HQ659580
Otu108		acI-C	↓		<i>Actinobacterium</i> SCGC AAA280-N08	95%	HQ663635
Otu030	Alphaproteobacteria	alfVI		↓	<i>Pseudorhodobacter</i> sp. 4-T-34	100%	KM978076
Otu034		alf-B2	↑		<i>Oligotropha carboxidovorans</i> strain ADB-19A	98%	KM210275
Otu101	Betaproteobacteria	betV-A1	↓	↓	<i>Thaueria</i> sp. NCCP-652	92%	AB920830
Otu085		betIII-A1		↓	Alcaligenaceae bacterium AKB-2008-KU8	99%	AM989122
Otu080		betI-A		↓	<i>Polaromonas</i> sp. M63	100%	KJ649715
Otu072		betIV	↑		<i>Methylophilus methylotrophus</i> strain HME9441	100%	KF911346
Otu110		betII	↓		<i>Polynucleobacter cosmopolitanus</i>	99%	AM110115
Otu097	Gammaproteobacteria	gamV		↓	<i>Dokdonella ginsengisoli</i> strain CP14	99%	KF378756
Otu008		gamI	↑		<i>Methylomonas</i> sp. R-45383	98%	AB683103
Otu098		gamIV-A		↓	<i>Pseudomonas putida</i> strain SKPF11	100%	KR492889
Otu031	Epsilonproteobacteria			↓	<i>Sulfuricum</i> sp. EW1	100%	KF494428
Otu022	Bacteroidetes	baclI	↓		<i>Flavobacterium</i> sp. THG-DN6.19	100%	KM035956
Otu020		bacVI	↑		<i>Bacteroidetes</i> sp. SCGC AAA027-P14	100%	HQ663214
Otu102	Cyanobacteria	Family_4.1		↓	<i>Tolypothrix</i> sp. Preslic8	100%	HG970654
Otu009		Family_4.1	↑		<i>Synechococcus</i> sp. LS143	100%	DQ519876
Otu004			↓		<i>Cyanobacterium</i> clone N400B	95%	GU940829
Otu005		Opiritaceae		↓	<i>Verrucomicrobia</i> bacterium SCGC AAA041-M18	99%	HQ663361
Otu047	Verrucomicrobia	verI-B	↓	↓	<i>Spartobacteria</i> bacterium NM5	89%	GU129926
Otu069		verI-A	↓	↓	<i>Verrucomicrobia</i> bacterium MS-B-100	92%	FJ460141
Otu083			↓	↓	<i>Verrucomicrobia</i> bacterium SCGC AAA204-G18	100%	JF488114

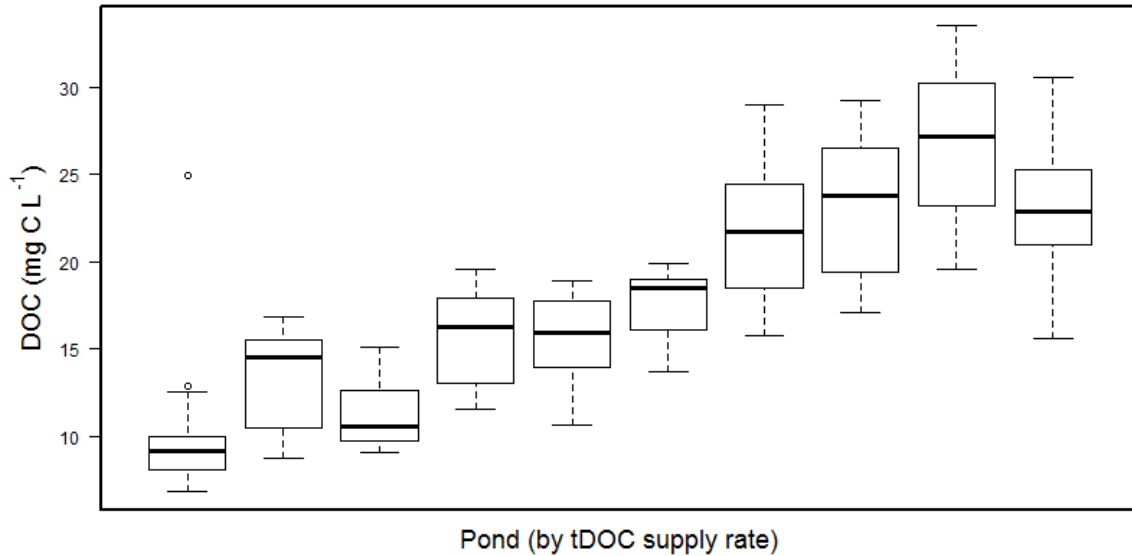


Figure S1: DOC concentrations across the tDOC supply rate gradient. DOC concentrations are given for each pond based on all time points between experimental day 60 and 100 which bounds the time points included in this study. Each pond is shown using a box-and-whisker plot across time points. The black line indicates the mean and the whiskers show the 95% confidence intervals. Ponds are ordered by supply rate along the x-axis.

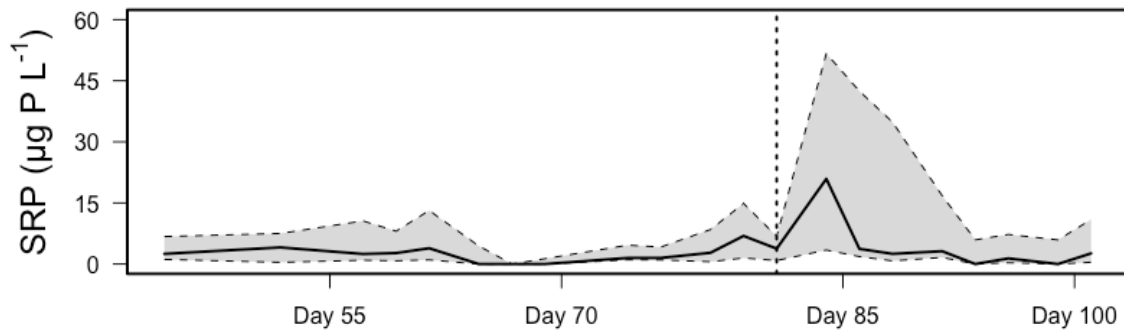
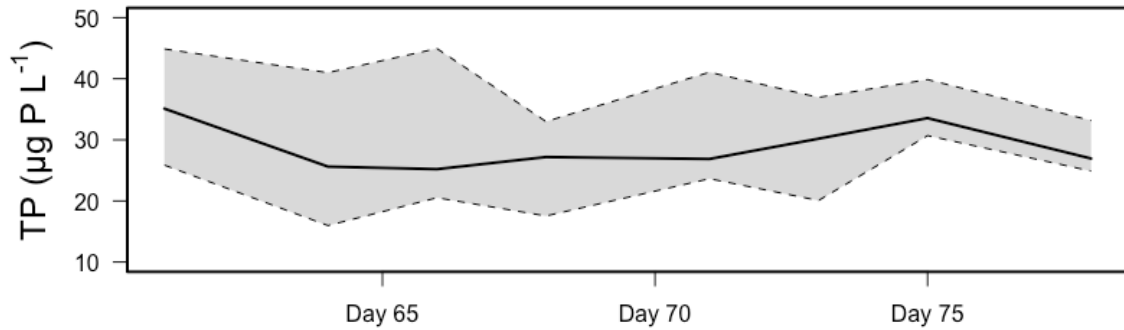


Figure S2: Soluble Reactive Phosphorus (SRP) concentration time series. SRP concentration is shown based on all ponds. The black line represents the average concentration across ponds. The gray region shows the bounds based on the minimum and maximum concentrations across ponds. The dashed vertical line indicates the day of the inorganic nutrient pulse.

3A:



3B:

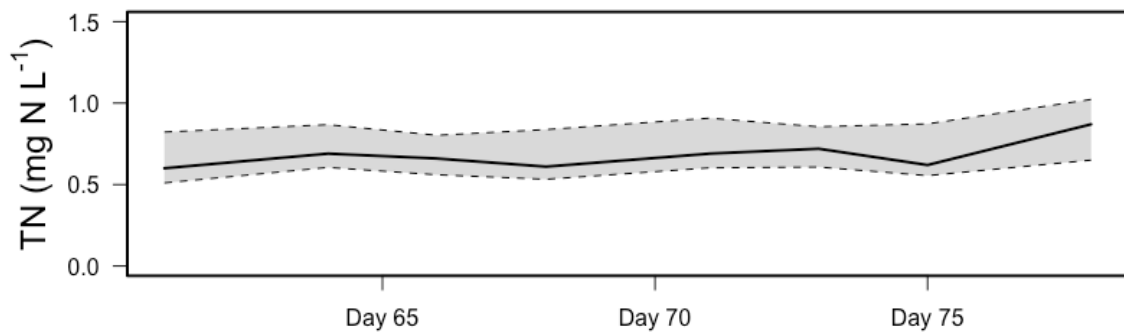


Figure S3A: Total phosphorus (TP) concentration time series. TP concentration is shown based on all ponds prior to the perturbation. Concentrations appear to be fairly constant. The blank line represents the average concentration across ponds. The gray region shows the bounds based on the minimum and maximum concentrations across ponds.

Figure S3B: Total phosphorus (TN) concentration time series. TN concentration is shown based on all ponds prior to the perturbation. Concentrations appear to be fairly constant. The blank line represents the average concentration across ponds. The gray region shows the bounds based on the minimum and maximum concentrations across ponds.

Literature cited

Fierer, N., M. Hamady, C. L. Lauber, and R. Knight. 2008. The influence of sex, handedness, and washing on the diversity of hand surface bacteria. *Proceedings of the National Academy of Sciences USA* 105:17994–17999.

Newton, R. J., S. E. Jones, A. Eiler, K. D. McMahon, and S. Bertilsson. 2011. A guide to the natural history of freshwater lake bacteria. *Microbiology and Molecular Biology Reviews* 75:14–49.

Wang, Q., G. M. Garrity, J. M. Tiedje, and J. R. Cole. 2007. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology* 73:5261–5267.