

Figure S1. Heatmap of OTUs (operational taxonomic units), representing soil cyanobacterial abundances in samples of the respective treatments. Varying shadings indicate nine categories, ranging from >120 sequences (black) to 0 sequences (white).

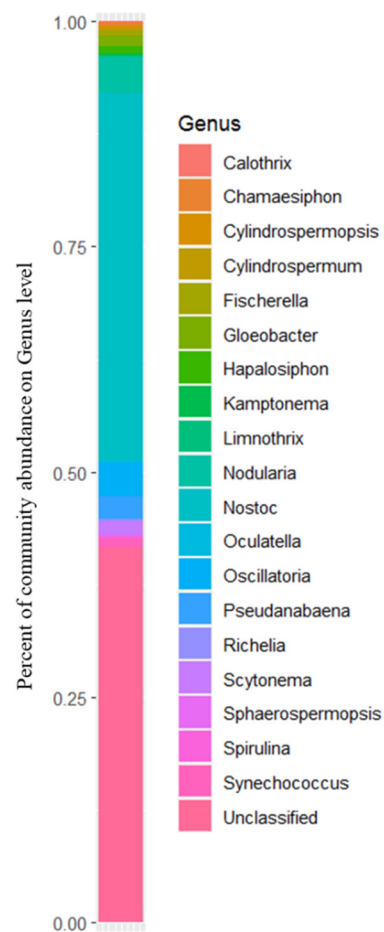


Figure S2. Soil cyanobacteria detected in the experimental site at genus level.

Table S1. Results of redundancy analysis suggesting the significance of each explanatory variable correlated to soil cyanobacterial community.

	<i>Df</i>	ChiSquare	<i>F</i>	<i>Pr (>F)</i>
N addition	1	0.05682	1.3998	0.081
P addition	1	0.06466	1.5593	0.045
Soil layer	1	0.17038	4.1974	0.001
pH	1	0.10741	2.6460	0.003
TC	1	0.05824	1.4347	0.097
TN	1	0.05117	1.2606	0.171
TP	1	0.05376	1.3244	0.147
NO ₃ ⁻ -N	1	0.04155	0.7873	0.774
NH ₄ ⁺ -N	1	0.05040	1.2425	0.171
P _{extra}	1	0.06236	1.5363	0.057
Residual	21	0.85243		

Notes: TC is total soil carbon determined by dry combustion. TN is total soil nitrogen. TP is total soil phosphorus. NO₃⁻-N is soil nitrate-N. NH₄⁺-N is soil ammonium-N. P_{extra} is soil extractable phosphorus. Significant correlations at the $\alpha = 0.050$ level are highlighted in bold.

Table S2. Abundance (Mean±SE) of each soil cyanobacterial genus in each treatment and soil layer.

Genus	Ctr	+N	+P	+NP	0–10cm	10–20cm
Calothrix	0.3 ± 0.3	0.9 ± 0.5	0.3 ± 0.2	0.4 ± 0.3	0.7 ± 0.3	0.2 ± 0.1
Chamaesiphon	1.0 ± 0.4	1.0 ± 0.9	1.0 ± 0.6	0.9 ± 0.6	1.8 ± 0.5	0.2 ± 0.1
Cylindrospermopsis	1.0 ± 0.9	0.0 ± 0.0	0.3 ± 0.2	1.5 ± 0.8	1.2 ± 0.6	0.2 ± 0.1
Cylindrospermum	0.0 ± 0.0	0.1 ± 0.1	0.0 ± 0.0	3.0 ± 2.0	0.7 ± 0.7	0.9 ± 0.8
Fischerella	0.9 ± 0.4	2.3 ± 1.2	0.8 ± 0.4	1.4 ± 0.7	2.1 ± 0.7	0.5 ± 0.2
Gloeobacter	3.6 ± 1.1	2.4 ± 0.8	4.8 ± 2.5	2.6 ± 0.9	1.7 ± 0.4	5.0 ± 1.3
Hapalosiphon	2.4 ± 0.7	2.1 ± 1.0	1.9 ± 0.6	2.9 ± 1.0	2.8 ± 0.5	1.9 ± 0.6
Kamptomena	1.5 ± 1.0	0.8 ± 0.4	0.0 ± 0.0	0.3 ± 0.3	1.0 ± 0.5	0.3 ± 0.2
Limnithrix	0.4 ± 0.3	0.4 ± 0.3	1.0 ± 0.5	0.9 ± 0.4	0.8 ± 0.3	0.5 ± 0.2
Nodularia	12.4 ± 3.8	3.6 ± 1.4	11.5 ± 3.7	15.8 ± 5.5	11.1 ± 3.1	10.5 ± 2.7
Nostoc	121.9 ± 32.0	149.3 ± 37.4	105.4 ± 10.5	76.5 ± 21.5	93.6 ± 9.1	132.9 ± 25.6
Oculatella	0.8 ± 0.5	0.6 ± 0.3	1.0 ± 0.6	0.3 ± 0.2	0.9 ± 0.4	0.4 ± 0.2
Oscillatoria	10.1 ± 2.4	11.4 ± 3.9	8.6 ± 2.4	11.6 ± 4.6	15.4 ± 2.7	5.5 ± 0.7
Pseudanabaena	4.5 ± 1.1	7.5 ± 2.4	2.1 ± 0.7	13.9 ± 4.3	6.9 ± 1.5	7.1 ± 2.5
Richelia	0.3 ± 0.3	0.3 ± 0.3	1.4 ± 0.7	0.1 ± 0.1	0.1 ± 0.1	0.9 ± 0.4
Scytonema	2.4 ± 1.0	4.8 ± 1.8	5.4 ± 2.0	4.9 ± 1.2	1.4 ± 0.5	7.3 ± 1.0
Sphaerospermopsis	0.6 ± 0.3	0.4 ± 0.3	1.0 ± 0.6	0.6 ± 0.3	0.8 ± 0.2	0.5 ± 0.3
Spirulina	0.5 ± 0.4	0.5 ± 0.4	0.4 ± 0.3	0.0 ± 0.0	0.4 ± 0.2	0.3 ± 0.2
Synechococcus	4.3 ± 1.4	2.3 ± 0.9	3.3 ± 0.9	2.1 ± 0.8	2.4 ± 0.7	3.5 ± 0.8
unclassified	145.3 ± 19.6	129.1 ± 20.3	97.4 ± 9.5	89.1 ± 10.8	129.4 ± 10.6	101.0 ± 12.8

Table S3. Effects of NP addition and soil layer on abundance of each soil cyanobacterial genus.

Genus	N Addition		P Addition		10–20 cm	
	Coefficient	<i>p</i>	Coefficient	<i>p</i>	coefficient	<i>p</i>
<i>Calothrix</i>	0.375	0.234	–0.250	0.428	–0.050	0.113
<i>Chamaesiphon</i>	–0.063	0.913	–0.063	0.913	–0.156	0.006
<i>Cylindrospermopsis</i>	0.125	0.836	0.375	0.535	–0.100	0.098
<i>Cylindrospermum</i>	1.563	0.127	1.438	0.161	0.019	0.855
<i>Fischerella</i>	1.000	0.118	–0.500	0.639	–0.214	0.002
<i>Gloeobacter</i>	–1.688	0.214	0.688	0.613	0.331	0.015
<i>Hapalosiphon</i>	0.375	0.655	0.125	0.882	–0.088	0.297
<i>Kamptonema</i>	–0.250	0.597	–1.000	0.035	–0.121	0.021
<i>Limnothrix</i>	–0.063	0.842	0.563	0.073	–0.024	0.481
<i>Nodularia</i>	–2.250	0.545	5.625	0.130	0.212	0.602
<i>Nostoc</i>	–0.750	0.977	–44.625	0.097	3.938	0.143
<i>Oculatella</i>	–0.438	0.295	–0.063	0.881	–0.041	0.337
<i>Oscillatoria</i>	2.125	0.460	–0.625	0.828	–0.978	0.001
<i>Pseudanabaena</i>	7.375	0.005	2.000	0.446	0.006	0.984
<i>Richelia</i>	–0.625	0.111	0.500	0.202	0.075	0.056
<i>Scytonema</i>	0.938	0.385	1.563	0.147	0.591	<0.001
<i>Sphaerospermopsis</i>	–0.313	0.440	0.313	0.440	–0.032	0.432
<i>Spirulina</i>	–0.188	0.471	–0.313	0.230	–0.038	0.192
<i>Synechococcus</i>	–1.563	0.066	–0.563	0.508	0.117	0.218
<i>unclassified</i>	–12.187	0.405	–43.937	0.003	–2.858	0.059

Notes: Significant values at the $\alpha = 0.050$ level are highlighted in bold.

Table S4. Effects of NP addition and soil layer on abundance of the 10 most abundant soil cyanobacterial genes.

Gene ID	N Addition		P Addition		Soil Depth	
	Coefficient	<i>p</i>	Coefficient	<i>p</i>	Coefficient	<i>p</i>
MGE465551	3.125	0.908	–49.500	0.047	4.675	0.084
MGE292404	–16.313	0.084	–16.438	0.082	1.356	0.151
MGE328949	–10.063	0.174	–12.688	0.086	–0.894	0.227
MGE860250	–2.250	0.466	5.625	0.068	–0.063	0.840
MGE221901	2.375	0.997	–0.838	0.600	–0.838	<0.001
MGE654199	5.625	0.096	–3.375	0.318	–0.713	0.035
MGE519988	–1.000	0.598	–3.000	0.114	–0.525	0.006
MGE176190	–0.250	0.904	–6.750	0.001	–0.613	0.003
MGE518492	–0.063	0.964	2.813	0.040	–0.106	0.438
MGE694158	0.313	0.773	–1.813	0.094	–0.081	0.453

Notes: Genes in the table are sorted according to their abundance in descending order. The most abundant gene (MEG465551) belongs to *Nostoc* genus. Please note that P addition significantly decreased two of these genes ($p < 0.050$) and tended to decrease another three ($p < 0.100$). Significant values at the $\alpha = 0.050$ level are highlighted in bold.

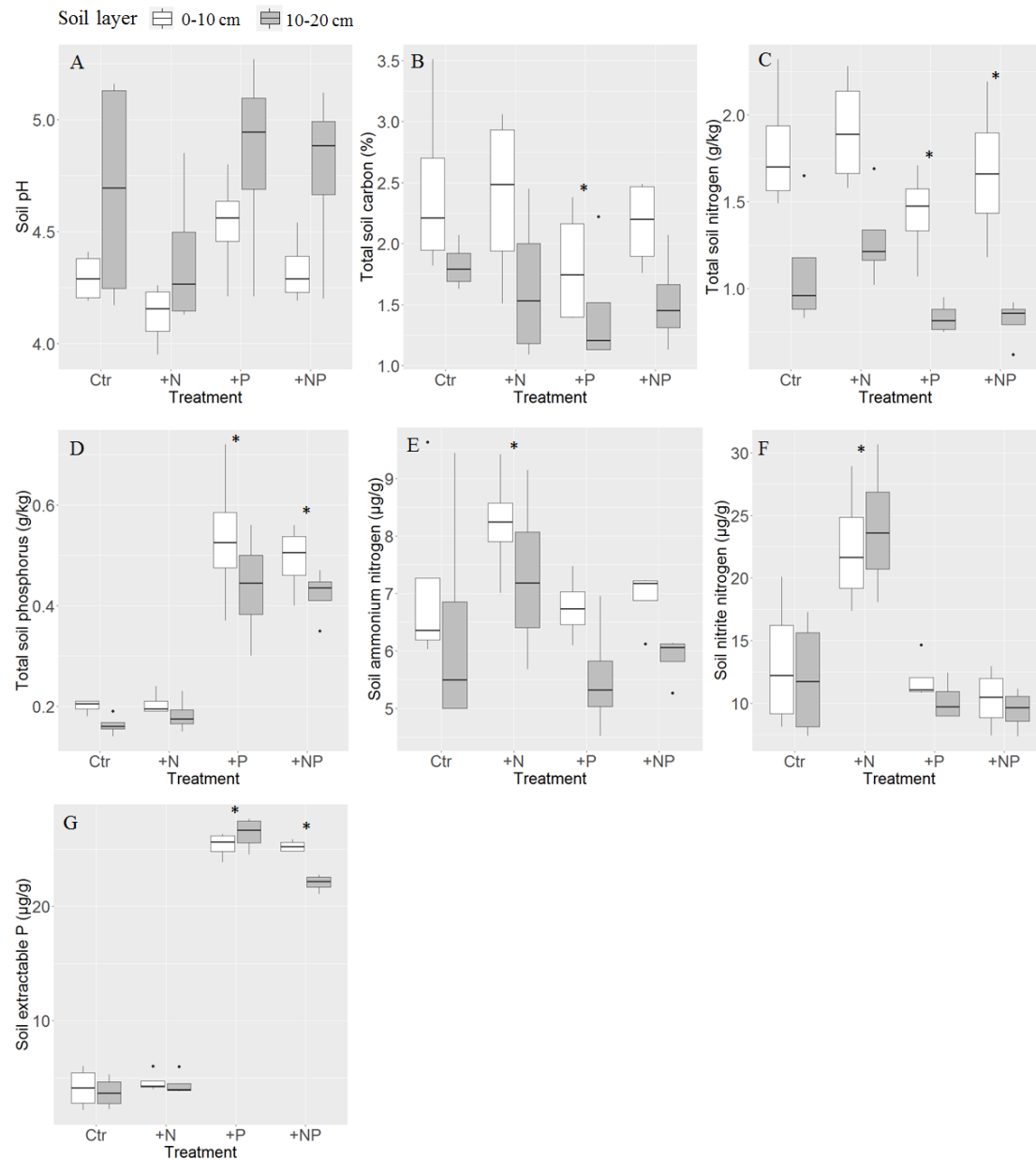


Figure S3. Effects of NP addition on (A) soil pH, (B) total soil carbon, and (C) total soil nitrogen, (D) total soil phosphorus, (E) soil ammonium nitrogen, (F) soil nitrite nitrogen and (G) soil extractable phosphorus. The * indicates there is a significant difference compared to the Ctr treatment at 0–20 cm soil layer ($p < 0.050$).

Table S5. Results of PerMANOVA examining the differences in soil cyanobacterial communities among treatments.

Pairs	F.Model	R^2	p
Ctr vs +N	0.836	0.056	0.543
Ctr vs +NP	1.409	0.091	0.176
Ctr vs +P	1.069	0.070	0.372
+N vs +NP	2.372	0.144	0.037
+N vs +P	1.311	0.085	0.212
+NP vs +P	1.832	0.115	0.076

Notes: Significant values at the $\alpha = 0.050$ level are highlighted in bold.