## Supporting Information:

# Nutrient-controlled niche differentiation of western Lake Erie cyanobacterial populations revealed via metatranscriptomic surveys 

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## Supplemental Tables

A
Latitude
Longitude
Temperature $\left[{ }^{\circ} \mathrm{C}\right]$
Dissolved Oxygen $\left[\mathrm{mg} \mathrm{L}^{-1}\right]$
Secchi depth [m]
DIN $[\mu \mathrm{M}]$
SRP $[\mu \mathrm{M}]$
Microcystis [cells $\mathrm{mL}^{-1}$ ]

## Fv/Fm

in vivo chlorophyll [RFU]
Extracted chlorophyll $\left[\mu \mathrm{g} \mathrm{L}^{-1}\right]$

Phycocyanin [RFU]
Microcystin $\left[\mu \mathrm{g} \mathrm{L}{ }^{-1}\right]$
Table S1 Physical, chemical, and community characterizing parameters measured at each station during September (A) and October (B) transects of the western basin of Lake Erie (Fig 1, Fig S8). Values in parenthesis are the standard deviation between two biological replicates. Values below detection limits are denoted with BD. For SRP, detection limit was $0.00254 \mu \mathrm{M}$.

| A | 9/12/2013 |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | L1 | L15 | L16 | L17 | L18 | L19 |
| Latitude | 41.705450 | 41.725032 | 41.710016 | 41.677711 | 41.692743 | 41.672816 |
| Longitude | -83.446490 | -83.406564 | -83.297111 | -83.235626 | -83.007609 | -82.897967 |
| Temperature [ ${ }^{\circ} \mathrm{C}$ ] | 23.4 | 23.6 | 23.1 | 23 | 23.2 | 23.3 |
| Dissolved Oxygen [ $\mathrm{mg} \mathrm{L}^{-1}$ ] | 5.19 | 6.87 | 6.62 | 6.86 | 7.60 | 7.17 |
| Secchi depth [m] | 0.4 | 0.4 | 0.5 | 0.6 | 1.7 | 1.9 |
| DIN $[\mu \mathrm{M}]$ | $\begin{aligned} & 27.33 \\ & (0.85) \end{aligned}$ | $\begin{aligned} & 10.83 \\ & (0.47) \end{aligned}$ | $\begin{gathered} 1.90 \\ (0.04) \end{gathered}$ | $\begin{gathered} 1.63 \\ (0.02) \end{gathered}$ | $\begin{gathered} 8.83 \\ (0.25) \end{gathered}$ | $\begin{gathered} 4.68 \\ (0.27) \end{gathered}$ |
| SRP $[\mu \mathrm{M}]$ | 1.11 (0.02) | 0.44 (0.06) | 0.28 (0.07) | 0.24 (0.03) | BD | 0.20 (0.07) |
| Microcystis [cells $\mathrm{mL}^{-1}$ ] | $\begin{aligned} & 29,967 \\ & (6,643) \end{aligned}$ | $\begin{aligned} & 51,633 \\ & (7,683) \end{aligned}$ | $\begin{aligned} & 51,317 \\ & (5,921) \end{aligned}$ | $\begin{gathered} 51,450 \\ (10,765) \end{gathered}$ | $\begin{aligned} & 29,433 \\ & (8,171) \end{aligned}$ | $\begin{aligned} & 15,900 \\ & (3,518) \end{aligned}$ |
| Fv/Fm | 0.30 (0.05) | 0.31 (0.04) | 0.27 (0.02) | 0.35 (0.06) | 0.46 (0.01) | 0.45 (0.01) |
| in vivo chlorophyll [RFU] | 0.87 (0.07) | 1.02 (0.05) | 0.77 (0.05) | 0.76 (0..08) | 0.43 (0.03) | 0.32 (0.04) |
| Extracted chlorophyll [ $\mu \mathrm{g} \mathrm{L}^{-1}$ ] | $\begin{aligned} & 20.01 \\ & (5.51) \end{aligned}$ | $\begin{aligned} & 36.45 \\ & (3.01) \end{aligned}$ | $\begin{aligned} & 21.86 \\ & (1.36) \end{aligned}$ | $\begin{aligned} & 23.04 \\ & (9.52) \end{aligned}$ | $\begin{aligned} & 10.32 \\ & (0.40) \end{aligned}$ | $\begin{gathered} 8.86 \\ (0.49) \end{gathered}$ |
| APA [ $\mathrm{nmol} \mathrm{mL}^{-1} \mathrm{hr}^{-1}$ ] | 0.22 (0.01) | 0.28 (0.00) | 0.32 (0.01) | 0.37 (0.01) | 0.81 (0.01) | 0.54 (0.01) |
| Fluoroprobe Bluegreen [ $\mu \mathrm{g} \mathrm{L}{ }^{-1}$ ] | $\begin{aligned} & 21.08 \\ & (2.10) \end{aligned}$ | $\begin{aligned} & 34.88 \\ & (6.12) \end{aligned}$ | $\begin{aligned} & 22.79 \\ & (0.66) \end{aligned}$ | $\begin{aligned} & 23.86 \\ & (1.08) \end{aligned}$ | $\begin{aligned} & 14.99 \\ & (0.73) \end{aligned}$ | 8.22 (0.51) |
| Phycocyanin [ RFU] | $\begin{aligned} & 17.20 \\ & (1.47) \end{aligned}$ | $\begin{aligned} & 26.97 \\ & (5.34) \end{aligned}$ | $\begin{aligned} & 20.83 \\ & (1.82) \end{aligned}$ | $\begin{aligned} & 18.53 \\ & (0.51) \end{aligned}$ | $\begin{aligned} & 15.03 \\ & (2.89) \end{aligned}$ | $\begin{aligned} & 10.77 \\ & (0.46) \end{aligned}$ |
| Microcystin $\left[\mu \mathrm{g} \mathrm{L}{ }^{-1}\right]$ | 2.31 (0.76) | 6.95 (0.19) | 3.87 (0.40) | 8.17 (0.69) | 0.33 (0.08) | 0.82 (0.07) |


| B | 10/8/2013 |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | LET7 | LET6 | LET5 | LET4 | LET3 | LET2 | LET1 |
| Latitude | 41.698889 | 41.739444 | 41.766667 | 41.725556 | 41.702778 | 41.670833 | 41.722778 |
| Longitude | -83.458889 | -83.375000 | -83.308611 | -83.110556 | -83.000556 | -82.849722 | -82.751389 |
| Temperature [ ${ }^{\circ} \mathrm{C}$ ] | 19.8 | 17.6 | 18.3 | 18.8 | 18.6 | 18.9 | 19.4 |
| Dissolved Oxygen [ $\mathrm{mg} \mathrm{L}^{-1}$ ] | 10.01 | 8.41 | 6.27 | 6.65 | 6.27 | 6.06 | 6.58 |
| Secchi depth [m] | NA | 0.75 | 1.1 | 1.8 | 2.8 | 1.8 | 1.2 |
| DIN $[\mu \mathrm{M}]$ | $\begin{aligned} & 50.14 \\ & (1.71) \end{aligned}$ | $\begin{gathered} 5.76 \\ (0.08) \end{gathered}$ | $\begin{gathered} 1.35 \\ (0.01) \end{gathered}$ | $\begin{gathered} 6.54 \\ (0.79) \end{gathered}$ | $\begin{aligned} & 14.74 \\ & (0.70) \end{aligned}$ | $\begin{gathered} 1.76 \\ (0.22 \end{gathered}$ | $\begin{gathered} 3.14 \\ (0.06) \end{gathered}$ |
| SRP $[\mu \mathrm{M}]$ | 1.61 (0.16) | 0.19 (0.02) | 0.06 (0.01) | BD | 0.05 (0.01) | 0.07 (0.00) | 0.25 (0.01) |
| Microcystis bioamass [ $\mu \mathrm{g} \mathrm{L}{ }^{-1}$ ] | 147 | 10,812 | 6,480 | 1,605 | 4,139 | 2,089 | 3,561 |
| Extracted chlorophyll [ $\mu \mathrm{g} \mathrm{L}^{-1}$ ] | $\begin{aligned} & 26.88 \\ & (0.86) \end{aligned}$ | $\begin{aligned} & 24.99 \\ & (1.95) \end{aligned}$ | $\begin{gathered} 6.85 \\ (0.55) \end{gathered}$ | $\begin{gathered} 4.59 \\ (0.58) \end{gathered}$ | $\begin{gathered} 3.43 \\ (0.23) \end{gathered}$ | $\begin{gathered} 5.26 \\ (0.36) \end{gathered}$ | $\begin{gathered} 6.97 \\ (0.21) \end{gathered}$ |
| Microcystin $\left[\mu \mathrm{g} \mathrm{L}{ }^{-1}\right]$ | 0.90 (0.21) | 1.51 (0.24) | 0.91 (0.26) | 0.74 (0.19) | 0.92 (0.09) | 0.78 (0.15) | 0.63 (0.24) |

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Table S2 Nutrient concentrations $[\mu \mathrm{M}]$ for each station of the September and October transects of the western basin of Lake Erie. Stations are ordered from west to east as in Figure 1. Values below detection limits are indicated with BD. Detection limits were $0.00697 \mu \mathrm{M}$ for urea, $0.00254 \mu \mathrm{M}$ DIP, and $0.00243 \mu \mathrm{M}$ for DOP. Values represent the average of duplicate samples with standard deviations in parenthesis.

|  | 9/12/2013 |  |  |  |  |  | 10/8/2013 |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | L1 | L15 | L16 | L17 | L18 | L19 | LET7 | LET6 | LET5 | LET4 | LET3 | LET2 | LET1 |
| $\mathrm{NO}_{\mathrm{x}}$ | $\begin{aligned} & 24.69 \\ & (0.81) \end{aligned}$ | $\begin{gathered} 9.53 \\ (0.42) \end{gathered}$ | $\begin{gathered} 0.21 \\ (0.02) \end{gathered}$ | $\begin{gathered} 0.11 \\ (0.01) \end{gathered}$ | $\begin{gathered} 7.11 \\ (0.27) \end{gathered}$ | $\begin{gathered} 3.08 \\ (0.24) \end{gathered}$ | $\begin{aligned} & 40.70 \\ & (1.29) \end{aligned}$ | $\begin{gathered} 4.91 \\ (0.08) \end{gathered}$ | $\begin{gathered} 0.38 \\ (0.01) \end{gathered}$ | $\begin{gathered} 5.48 \\ (0.12) \end{gathered}$ | $\begin{aligned} & 12.50 \\ & (0.12) \end{aligned}$ | $\begin{gathered} 0.28 \\ (0.02) \end{gathered}$ | $\begin{gathered} 0.84 \\ (0.01) \end{gathered}$ |
| $\mathrm{NH}_{4}$ | $\begin{gathered} 2.64 \\ (0.04) \end{gathered}$ | $\begin{gathered} 1.29 \\ (0.05) \end{gathered}$ | $\begin{gathered} 1.69 \\ (0.02) \end{gathered}$ | $\begin{gathered} 1.52 \\ (0.01) \end{gathered}$ | $\begin{gathered} 1.72 \\ (0.03) \end{gathered}$ | $\begin{gathered} 1.60 \\ (0.04) \end{gathered}$ | $\begin{gathered} 9.44 \\ (0.42) \end{gathered}$ | $\begin{gathered} 0.85 \\ (0.00) \end{gathered}$ | $\begin{gathered} 0.97 \\ (0.03) \end{gathered}$ | $\begin{gathered} 1.06 \\ (0.08) \end{gathered}$ | $\begin{gathered} 2.25 \\ (0.82) \end{gathered}$ | $\begin{gathered} 1.48 \\ (0.24) \end{gathered}$ | $\begin{gathered} 2.30 \\ (0.07) \end{gathered}$ |
| Urea | $\begin{gathered} 1.60 \\ (0.03) \end{gathered}$ | $\begin{gathered} 0.62 \\ (0.01) \end{gathered}$ | $\begin{gathered} 1.98 \\ (0.19) \end{gathered}$ | $\begin{gathered} 0.18 \\ (0.01) \end{gathered}$ | $\begin{gathered} 0.20 \\ (0.04) \end{gathered}$ | $\begin{gathered} 0.08 \\ (0.01) \end{gathered}$ | $\begin{gathered} 3.61 \\ (0.04) \end{gathered}$ | $\begin{gathered} 0.21 \\ (0.01) \end{gathered}$ | BD | $\begin{gathered} 1.27 \\ (0.01) \end{gathered}$ | $\begin{gathered} 4.53 \\ (0.26) \end{gathered}$ | BD | $\begin{gathered} 0.46 \\ (0.09) \end{gathered}$ |
| TN | $\begin{aligned} & 53.79 \\ & (4.58) \end{aligned}$ | $\begin{aligned} & 46.83 \\ & (0.44) \end{aligned}$ | $\begin{aligned} & 45.76 \\ & (0.66) \end{aligned}$ | $\begin{aligned} & 42.57 \\ & (0.95) \end{aligned}$ | $\begin{aligned} & 36.47 \\ & (0.23) \end{aligned}$ | $\begin{aligned} & 25.10 \\ & (1.83) \end{aligned}$ | $\begin{aligned} & 60.88 \\ & (0.13) \end{aligned}$ | $\begin{aligned} & 52.37 \\ & (4.92) \end{aligned}$ | $\begin{aligned} & 27.80 \\ & (0.46) \end{aligned}$ | $\begin{aligned} & 48.44 \\ & (0.54) \end{aligned}$ | $\begin{aligned} & 39.18 \\ & (0.01) \end{aligned}$ | $\begin{aligned} & 23.57 \\ & (0.36) \end{aligned}$ | $\begin{aligned} & 23.99 \\ & (1.78) \end{aligned}$ |
| TDN | $\begin{aligned} & 44.61 \\ & (4.26) \end{aligned}$ | $\begin{aligned} & 31.39 \\ & (0.19) \end{aligned}$ | $\begin{aligned} & 28.64 \\ & (1.06) \end{aligned}$ | $\begin{aligned} & 20.02 \\ & (0.20) \end{aligned}$ | $\begin{aligned} & 17.72 \\ & (0.39) \end{aligned}$ | $\begin{aligned} & 11.17 \\ & (0.14) \end{aligned}$ | $\begin{aligned} & 32.52 \\ & (1.99) \end{aligned}$ | $\begin{aligned} & 34.44 \\ & (0.93) \end{aligned}$ | $\begin{aligned} & 13.33 \\ & (0.99) \end{aligned}$ | $\begin{aligned} & 16.31 \\ & (0.06) \end{aligned}$ | $\begin{aligned} & 29.64 \\ & (0.36) \end{aligned}$ | $\begin{aligned} & 10.87 \\ & (0.68) \end{aligned}$ | $\begin{aligned} & 16.32 \\ & (1.05) \end{aligned}$ |
| DON | $\begin{aligned} & 19.92 \\ & (5.07) \end{aligned}$ | $\begin{aligned} & 21.86 \\ & (0.23) \end{aligned}$ | $\begin{aligned} & 28.43 \\ & (1.04) \end{aligned}$ | $\begin{aligned} & 19.91 \\ & (0.21) \end{aligned}$ | $\begin{aligned} & 10.61 \\ & (0.12) \end{aligned}$ | $\begin{gathered} 8.09 \\ (0.37) \end{gathered}$ | BD | $\begin{aligned} & 29.53 \\ & (0.84) \end{aligned}$ | $\begin{aligned} & 12.94 \\ & (1.00) \end{aligned}$ | $\begin{aligned} & 10.83 \\ & (0.93) \end{aligned}$ | $\begin{aligned} & 17.15 \\ & (0.23) \end{aligned}$ | $\begin{aligned} & 10.59 \\ & (0.66) \end{aligned}$ | $\begin{aligned} & 15.48 \\ & (1.05) \end{aligned}$ |
| PN | $\begin{gathered} 9.18 \\ (0.32) \end{gathered}$ | $\begin{aligned} & 15.44 \\ & (0.25) \end{aligned}$ | $\begin{aligned} & 17.12 \\ & (1.72) \end{aligned}$ | $\begin{aligned} & 22.55 \\ & (1.15) \end{aligned}$ | $\begin{aligned} & 18.75 \\ & (0.16) \end{aligned}$ | $\begin{aligned} & 13.93 \\ & (1.96) \end{aligned}$ | $\begin{aligned} & 28.36 \\ & (1.86) \end{aligned}$ | $\begin{aligned} & 17.93 \\ & (5.84) \end{aligned}$ | $\begin{aligned} & 14.48 \\ & (0.53) \end{aligned}$ | $\begin{aligned} & 32.13 \\ & (0.60) \end{aligned}$ | $\begin{gathered} 9.54 \\ (0.34) \end{gathered}$ | $\begin{aligned} & 12.70 \\ & (1.04) \end{aligned}$ | $\begin{gathered} 7.68 \\ (2.84) \end{gathered}$ |
| SRP | $\begin{gathered} 1.11 \\ (0.02) \end{gathered}$ | $\begin{gathered} 0.44 \\ (0.06) \end{gathered}$ | $\begin{gathered} 0.28 \\ (0.07) \end{gathered}$ | $\begin{gathered} 0.24 \\ (0.03) \end{gathered}$ | BD | $\begin{gathered} 0.20 \\ (0.07) \end{gathered}$ | $\begin{gathered} 1.61 \\ (0.16) \end{gathered}$ | $\begin{gathered} 0.19 \\ (0.02) \end{gathered}$ | $\begin{gathered} 0.06 \\ (0.01) \end{gathered}$ | BD | $\begin{gathered} 0.05 \\ (0.01) \end{gathered}$ | $\begin{gathered} 0.07 \\ (0.00) \end{gathered}$ | $\begin{gathered} 0.25 \\ (0.01) \end{gathered}$ |
| TP | $\begin{gathered} 6.22 \\ (0.06) \end{gathered}$ | $\begin{gathered} 6.47 \\ (0.21) \end{gathered}$ | $\begin{gathered} 3.58 \\ (0.04) \end{gathered}$ | $\begin{gathered} 4.60 \\ (0.15) \end{gathered}$ | $\begin{gathered} 1.54 \\ (0.19) \end{gathered}$ | $\begin{gathered} 1.27 \\ (0.06) \end{gathered}$ | $\begin{aligned} & 10.11 \\ & (0.32) \end{aligned}$ | $\begin{gathered} 4.44 \\ (0.22) \end{gathered}$ | $\begin{gathered} 1.85 \\ (0.08) \end{gathered}$ | $\begin{gathered} 2.34 \\ (0.59) \end{gathered}$ | $\begin{gathered} 2.10 \\ (0.05) \end{gathered}$ | $\begin{gathered} 1.98 \\ (0.07) \end{gathered}$ | $\begin{gathered} 3.43 \\ (0.12) \end{gathered}$ |
| TDP | $\begin{gathered} 0.65 \\ (0.03) \end{gathered}$ | $\begin{gathered} 1.28 \\ (0.63) \end{gathered}$ | $\begin{gathered} 0.49 \\ (0.05) \end{gathered}$ | $\begin{gathered} 0.26 \\ (0.03) \end{gathered}$ | $\begin{gathered} 0.24 \\ (0.09) \end{gathered}$ | $\begin{gathered} 0.17 \\ (0.05) \end{gathered}$ | $\begin{gathered} 1.72 \\ (0.22) \end{gathered}$ | $\begin{gathered} 1.19 \\ (0.28) \end{gathered}$ | $\begin{gathered} 0.41 \\ (0.04) \end{gathered}$ | $\begin{gathered} 0.53 \\ (0.37) \end{gathered}$ | $\begin{gathered} 0.98 \\ (0.23) \end{gathered}$ | $\begin{gathered} 0.52 \\ (0.08) \end{gathered}$ | $\begin{gathered} 0.33 \\ (0.09) \end{gathered}$ |
| DOP | BD | $\begin{gathered} 0.84 \\ (0.57) \end{gathered}$ | $\begin{gathered} 0.22 \\ (0.12) \end{gathered}$ | $\begin{gathered} 0.03 \\ (0.06) \end{gathered}$ | $\begin{gathered} 0.27 \\ (0.12) \end{gathered}$ | BD | $\begin{gathered} 0.11 \\ (0.37) \end{gathered}$ | $\begin{gathered} 1.00 \\ (0.29) \end{gathered}$ | $\begin{gathered} 0.34 \\ (0.04) \end{gathered}$ | $\begin{gathered} 0.53 \\ (0.37) \end{gathered}$ | $\begin{gathered} 0.94 \\ (0.23) \end{gathered}$ | $\begin{gathered} 0.45 \\ (0.08) \end{gathered}$ | $\begin{gathered} 0.08 \\ (0.10) \end{gathered}$ |
| PP | $\begin{gathered} 5.57 \\ (0.03) \end{gathered}$ | $\begin{gathered} 5.19 \\ (0.84) \end{gathered}$ | $\begin{gathered} 3.09 \\ (0.09) \end{gathered}$ | $\begin{gathered} 4.33 \\ (0.13) \end{gathered}$ | $\begin{gathered} 1.29 \\ (.010) \end{gathered}$ | $\begin{gathered} 1.10 \\ (0.01) \end{gathered}$ | $\begin{gathered} 8.39 \\ (0.54) \end{gathered}$ | $\begin{gathered} 3.25 \\ (0.50) \end{gathered}$ | $\begin{gathered} 1.44 \\ (0.11) \end{gathered}$ | $\begin{gathered} 1.81 \\ (0.96) \end{gathered}$ | $\begin{gathered} 1.11 \\ (0.28) \end{gathered}$ | $\begin{gathered} 1.47 \\ (0.01) \end{gathered}$ | $\begin{gathered} 3.09 \\ (0.21) \end{gathered}$ |


| Station or |  |  |  |  |  |
| :--- | :---: | :---: | :---: | :---: | :---: |
| Treatment | Number of <br> reads | Aligned 0 <br> times | Aligned exactly <br> $\mathbf{1}$ time | Aligned $>\mathbf{1}$ <br> time | Overall alignment <br> rate |
| LET1 | $27,903,522$ | $24,945,541$ | $1,659,152$ | $1,298,829$ | $10.60 \%$ |
|  | $27,536,041$ | $24,284,725$ | $1,444,752$ | $1,806,564$ | $11.81 \%$ |
| LET2 | $36,997,191$ | $26,746,690$ | $4,204,127$ | $6,046,374$ | $27.71 \%$ |
|  | $29,833,053$ | $22,659,861$ | $2,156,750$ | $5,016,442$ | $24.04 \%$ |
| LET3 | $28,864,110$ | $23,924,801$ | $2,316,711$ | $2,622,598$ | $17.11 \%$ |
|  | $28,650,471$ | $23,552,927$ | $2,043,243$ | $3,054,301$ | $17.79 \%$ |
| LET4 | $35,597,296$ | $21,792,004$ | $4,869,108$ | $8,936,184$ | $38.78 \%$ |
|  | $27,014,116$ | $19,210,720$ | $3,625,526$ | $4,177,870$ | $28.89 \%$ |
| LET5 | $25,556,343$ | $17,968,910$ | $4,150,242$ | $3,437,191$ | $29.69 \%$ |
|  | $25,153,667$ | $18,465,371$ | $3,093,990$ | $3,594,306$ | $26.59 \%$ |
| LET6 | $31,451,508$ | $20,254,955$ | $4,011,289$ | $7,185,264$ | $35.60 \%$ |
|  | $33,128,987$ | $32,764,260$ | 191,220 | 173,507 | $1.10 \%$ |
| LET7 | $38,595,755$ | $37,911,204$ | 156,426 | 528,125 | $1.77 \%$ |
|  | $33,928,689$ | $32,938,676$ | 113,686 | 876,327 | $2.92 \%$ |
| +P | $25,734,772$ | $21,133,075$ | $3,170,522$ | $1,431,175$ | $17.88 \%$ |
|  | $30,634,245$ | $24,635,004$ | $3,748,488$ | $2,250,753$ | $19.58 \%$ |
| +NH4 | $36,319,164$ | $29,604,594$ | $4,557,190$ | $2,157,380$ | $18.49 \%$ |
|  | $32,820,933$ | $26,160,377$ | $4,705,489$ | $1,955,067$ | $20.29 \%$ |
| +Urea | $36,497,773$ | $28,856,115$ | $4,602,858$ | $3,038,800$ | $20.94 \%$ |
| Control | $28,528,820$ | $22,765,343$ | $3,605,361$ | $2,158,116$ | $20.20 \%$ |
|  | $33,983,026$ | $27,619,927$ | $4,156,741$ | $2,206,358$ | $18.72 \%$ |
| Initial | $37,595,286$ | $30,176,832$ | $4,697,085$ | $2,721,369$ | $19.73 \%$ |
|  | $32,420,679$ | $25,081,626$ | $4,671,776$ | $2,667,277$ | $22.67 \%$ |
|  | $32,000,000$ | $24,144,624$ | $5,275,028$ | $2,580,348$ | $24.55 \%$ |
|  |  |  |  |  |  |

## Station or

LET1

LET2

LET3

LET4

LET5

LET6

LET7
$+P$
$+\mathrm{NH} 4$
+Urea

Initial

Table S3 Transcriptomic sequencing results. Alignment results are the number of reads aligning to the Microcystis aeruginosa NIES-843 genome using Bowtie2 within RSEM. Each station or treatment has two biological replicates.

Table S4 Transcriptomic sequencing results. Alignment results are the number of reads aligning to the Anabaena sp. PCC7108 genome using Bowtie 2 within RSEM. Each station or treatment has two biological replicates.

| Treatment <br> or Station | Number of <br> Reads | Aligned $\mathbf{0}$ <br> times | Aligned exactly <br> $\mathbf{1}$ time | Aligned $>\mathbf{1}$ <br> time | Overall alignment <br> rate |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Initial (L16) | $32,420,679$ | $32,301,184$ | 47,013 | 72,482 | $0.37 \%$ |
|  | $31,858,827$ | $31,722,341$ | 60,070 | 76,416 | $0.43 \%$ |
| +P | $25,734,772$ | $25,686,336$ | 8,500 | 39,936 | $0.19 \%$ |
|  | $30,634,245$ | $30,595,894$ | 10,372 | 27,979 | $0.13 \%$ |
| +NH4 | $36,319,164$ | $36,281,206$ | 11,106 | 26,852 | $0.10 \%$ |
|  | $32,820,933$ | $32,768,476$ | 19,206 | 33,251 | $0.16 \%$ |
| +Urea | $36,497,773$ | $36,461,942$ | 11,309 | 24,522 | $0.10 \%$ |
|  | $28,528,820$ | $28,503,313$ | 9,030 | 16,477 | $0.09 \%$ |
| Control | $33,983,026$ | $33,948,716$ | 13,789 | 20,521 | $0.10 \%$ |
|  | $37,595,286$ | $37,547,609$ | 14,757 | 32,920 | $0.13 \%$ |
| LET1 | $27,903,522$ | $27,886,920$ | 5,456 | 11,146 | $0.06 \%$ |
|  | $27,536,041$ | $27,512,968$ | 7,029 | 16,044 | $0.08 \%$ |
| LET2 | $36,997,191$ | $36,979,812$ | 3,135 | 14,244 | $0.05 \%$ |
|  | $29,833,053$ | $29,819,785$ | 2,927 | 10,341 | $0.04 \%$ |
| LET3 | $28,864,110$ | $28,855,616$ | 819 | 7,675 | $0.03 \%$ |
|  | $28,650,471$ | $28,637,702$ | 912 | 11,857 | $0.04 \%$ |
| LET4 | $35,597,296$ | $35,588,672$ | 1,235 | 7,389 | $0.02 \%$ |
|  | $27,014,116$ | $26,996,707$ | 1,388 | 16,021 | $0.06 \%$ |
| LET5 | $25,556,343$ | $25,544,824$ | 1,902 | 9,617 | $0.05 \%$ |
|  | $25,153,667$ | $25,124,403$ | 2,410 | 26,854 | $0.12 \%$ |
| LET6 | $31,451,508$ | $31,439,930$ | 1,088 | 10,490 | $0.04 \%$ |
|  | $33,128,987$ | $32,941,384$ | 122,110 | 65,493 | $0.57 \%$ |
| LET7 | $38,595,755$ | $38,438,228$ | 105,090 | 52,437 | $0.41 \%$ |
|  | $33,928,689$ | $33,756,246$ | 116,697 | 55,746 | $0.51 \%$ |


| Treatment <br> or Station | Number of <br> Reads | Aligned 0 <br> times | Aligned exactly <br> 1 time | Aligned >1 <br> time | Overall alignment <br> rate |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Initial (L16) | $32,420,679$ | $32,383,565$ | 16,153 | 20,961 | $0.11 \%$ |
|  | $31,858,827$ | $31,827,593$ | 18,704 | 12,530 | $0.10 \%$ |
| +P | $25,734,772$ | $25,682,548$ | 16,632 | 35,592 | $0.20 \%$ |
|  | $30,634,245$ | $30,596,304$ | 18,071 | 19,870 | $0.12 \%$ |
| +NH4 | $36,319,164$ | $36,278,491$ | 22,331 | 18,342 | $0.11 \%$ |
|  | $32,820,933$ | $32,779,619$ | 21,632 | 19,682 | $0.13 \%$ |
| +Urea | $36,497,773$ | $36,461,668$ | 21,926 | 14,179 | $0.10 \%$ |
|  | $28,528,820$ | $28,500,991$ | 17,992 | 9,837 | $0.10 \%$ |
| Control | $33,983,026$ | $33,952,384$ | 20,332 | 10,310 | $0.09 \%$ |
|  | $37,595,286$ | $37,549,421$ | 24,755 | 21,110 | $0.12 \%$ |
| LET1 | $27,903,522$ | $27,888,104$ | 10,243 | 5,175 | $0.06 \%$ |
|  | $27,536,041$ | $27,518,397$ | 8,300 | 9,344 | $0.06 \%$ |
| LET2 | $36,997,191$ | $36,960,342$ | 27,142 | 9,707 | $0.10 \%$ |
|  | $29,833,053$ | $29,811,914$ | 14,688 | 6,451 | $0.07 \%$ |
| LET3 | $28,864,110$ | $28,842,315$ | 17,098 | 4,697 | $0.08 \%$ |
|  | $28,650,471$ | $28,627,157$ | 14,574 | 8,740 | $0.08 \%$ |
| LET4 | $35,597,296$ | $35,553,217$ | 40,135 | 3,944 | $0.12 \%$ |
|  | $27,014,116$ | $26,973,973$ | 28,119 | 12,024 | $0.15 \%$ |
| LET5 | $25,556,343$ | $25,516,138$ | 31,521 | 8,684 | $0.16 \%$ |
|  | $25,153,667$ | $25,106,056$ | 22,813 | 24,798 | $0.19 \%$ |
| LET6 | $31,451,508$ | $31,416,940$ | 24,518 | 10,050 | $0.11 \%$ |
|  | $33,128,987$ | $32,222,541$ | 875,006 | 31,440 | $2.74 \%$ |
| LET7 | $38,595,755$ | $37,906,634$ | 664,944 | 24,177 | $1.79 \%$ |
|  | $33,928,689$ | $33,363,190$ | 542,576 | 22,923 | $1.67 \%$ |

Table S5 Transcriptomic sequencing results. Alignment results are the number of reads aligning to the Planktothrix agardhii NIVA-CYA 15 genome using Bowtie2 within RSEM. Each station or treatment has two biological replicates.


|  | Initial <br> (Station L16) | Control | $+\mathbf{P}$ | $+\mathbf{N H}_{4}$ | +Urea |
| :--- | ---: | ---: | ---: | ---: | ---: |
|  | $0.21(0.02)$ | $0.19(0.06)$ | $0.23(0.05)$ | $0.14(0.02)$ | $0.16(0.06)$ |
| $\mathrm{NO}_{x}$ | $1.69(0.02)$ | $1.25(0.19)$ | $1.42(0.40)$ | $1.23(0.10)$ | $1.11(0.10)$ |
| $\mathrm{NH}_{4}$ | $1.98(0.19)$ | $0.36(0.09)$ | $0.11(0.03)$ | $0.30(0.14)$ | $0.28(0.04)$ |
| Urea | $45.76(0.66)$ | $40.07(1.38)$ | $38.92(2.14)$ | $46.38(3.65)$ | $42.33(5.54)$ |
| TN | $28.64(1.06)$ | $19.14(2.43)$ | $20.98(0.47)$ | $21.79(1.36)$ | $19.13(1.66)$ |
| TDN | $28.43(1.04)$ | $18.95(2.44)$ | $20.75(0.49)$ | $21.65(1.35)$ | $18.97(1.62)$ |
| DON | $17.12(1.72)$ | $20.94(2.78)$ | $17.94(2.17)$ | $24.59(3.46)$ | $23.21(4.69)$ |
| PN | $0.28(0.07)$ | $0.22(0.07)$ | $0.25(0.03)$ | $0.17(0.09)$ | $0.19(0.01)$ |
| SRP | $3.58(0.04)$ | $5.17(0.99)$ | $4.98(0.51)$ | $3.56(0.37)$ | $5.16(1.18)$ |
| TP | $0.49(0.05)$ | $0.75(0.64)$ | $0.30(0.24)$ | $0.46(0.28)$ | $0.38(0.17)$ |
| TDP | $0.22(0.12)$ | $0.57(0.65)$ | $B D$ | $0.29(0.31)$ | BD |
| DOP | $3.09(0.09)$ | $4.42(0.78)$ | $4.68(0.45)$ | $3.10(0.37)$ | $4.78(1.19)$ |
| PP |  |  |  |  |  |

Table S6 Nutrient concentrations $[\mu \mathrm{M}]$ for each treatment for the nutrient amendment experiment. Values in parentheses represent the standard deviation between biological replicates $(\mathrm{n}=2)$. Values below detection limits are denoted with BD. For DOP, detection limit was $0.00243 \mu \mathrm{M}$.

| Category | +P | +NH4 | +Urea |
| :--- | ---: | ---: | ---: |
| Amino acid biosynthesis | 6 | 2 | 4 |
| Biosynthesis of cofactors, prosthetic groups, and carriers | 6 | 8 | 7 |
| Cell envelope | 5 | 9 | 3 |
| Cellular processes | 3 | 6 | 12 |
| Central intermediary metabolism | 4 | 2 | 1 |
| Energy metabolism | 32 | 7 | 14 |
| Fatty acid, phospholipid and sterol metabolism | 8 | 2 | 2 |
| Photosynthesis and respiration | 53 | 42 | 29 |
| Purines, pyrimidines, nucleosides, and nucleotides | 12 | 4 | 3 |
| Regulatory functions | 35 | 12 | 9 |
| DNA replication, restriction, modification, recombination, and repair | 16 | 5 | 6 |
| Transcription | 6 | 7 | 6 |
| Translation | 22 | 38 | 53 |
| Transport and binding proteins | 51 | 18 | 12 |
| Unknown | 150 | 52 | 54 |
| RNA | 0 | 0 | 0 |
| Other categories | 489 | 179 | 158 |
| Hypothetical | 377 | 167 | 131 |

## Supplemental Figures

Figure S1 Composite of MODIS Cyanobacterial Index images from the NOAA Experimental Lake Erie Harmful Algal Bloom Bulletin (http://www.glerl.noaa.gov/res/Centers/HABS/lake_erie_hab/lake_erie_hab.html) for 2013. Grey indicates cloud cover or missing data. Black represents no cyanobacteria detected. Colored pixels indicate the presence of cyanobacteria. Cooler colors (blue and purple) indicate low concentrations and warmer colors (red, orange, and yellow) indicate high concentrations.


56 57


Figure S2 A) The number of significant differentially expressed genes for Microcystis at each station relative to station LET7 and B) relative to the control after 48 hr . incubation. Blue denotes increases in transcript abundance and yellow denotes decrease in transcript abundance. Stations are ordered from west to east as appearing in Figure 1.

Figure S3 Heat map of genes involved in nitrogen transport and metabolism and their significant differential expression at each station relative to LET7 and under each treatment relative to the control for Microcystis. Values are the $\log _{2}$ fold change in gene expression. Blue colors correspond to a decrease in transcript abundance while red colors correspond to an increase in transcript abundance. White denotes no difference from the reference condition.

| Log 2 Fold Change |  |  |  |
| :---: | :---: | :---: | :---: |
| -3.09 | 0 |  |  |



| Gene Symbol | MAE Number | Product |
| :---: | :---: | :---: |
|  | 25850 | amino acid ABC -transporter permease protein |
|  | 26840 | amino-acid ABC-transporter ATP-binding protein |
|  | 26850 | amino-acid ABC-transporter permease protein |
|  | 27820 | amino acid adenvlation |
| amt1 | 40020 | ammonium tranport protein |
| amt1 | 40010 | ammonium/methylammonium permease |
| cphB | 29150 | cvanophycinase |
| cphB | 27450 | cyanophycinase |
| cphA | 27460 | cvanophycin svnthetase |
| cyns | 10370 | cvanate hydratase |
| adhA | 8260 | glutamate dehvdrogenase (NADP+) |
| glnA | 9050 | glutamate-ammonia ligase |
| 9 ln A | 19270 | glutamate-ammonia ligase |
| alnB | 57460 | nitrogen regulatory protein P-II |
| glsF | 29110 | ferredoxin-dependent glutamate synthase |
| altB | 7560 | NADH-dependent glutamate synthase large subunit |
| altD | 14900 | NADH-dependent glutamate synthase small subunit |
| nadB | 36480 | L-aspartate oxidase |
| narB | 53960 | ferredoxin-nitrate reductase |
| natC | 300 | amino acid transport system permease protein |
| nirA | 18410 | ferredoxin-nitrite reductase |
| nrtA | 14800 | ABC transporter nitrate-binding protein |
| nrtB | 14790 | nitrate/nitrite transport svstem permease protein |
| nitC | 14780 | nitrate/nitrite transport svstem ATP-bindina protein |
| $n t c A$ | 1830 | global nitrogen requlatory protein Ycf28 |
| pipX | 55930 | Pll interaction protein X |
| speA | 46810 | arginine decarboxvlase |
| ureE | 41100 | urease accessory protein E |
| ureG | 24230 | urease accessory protein G |
| urtA | 6220 | ABC-type urea transport system substrate-binding protein |
| urtC | 6200 | urea transport system permease protein |

Figure S4 Heat map of genes involved in phosphorus transport and metabolism and their significant differential expression at each station relative to LET7 and under each treatment relative to the control for Microcystis. Values are the $\log _{2}$ fold change in gene expression. Blue colors correspond to a decrease in transcript abundance while red colors correspond to an increase in transcript abundance. White denotes no difference from the reference condition.

| Log $_{2}$ Fold Change |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| -3.74 |  |  | 0 |  | 6.87 |
|  |  |  |  |  |  |
|  |  |  | Gene Symbol | MAE Number | Product |
|  |  |  | ppk1 | 1300 | polyphosphate kinase |
|  |  |  | pstC | 9270 | phosphate transport system permease protein |
|  |  |  |  | 16640 | alkaline phosphatase |
|  |  |  | pstA | 18290 | phosphate transport system permease protein |
|  |  |  | pstS | 18310 | phosphate-binding periplasmic protein |
|  |  |  | pstB2 | 18340 | phosphate transport ATP-binding protein |
|  |  |  | pstB | 18350 | phosphate transport ATP-binding protein |
|  |  |  | pstA | 18360 | phosphate transport system permease protein |
|  |  |  | pstC | 18370 | phosphate ABC transporter permease |
|  |  |  | pstS | 18380 | phosphate-binding periplasmic protein |
|  |  |  | sphX | 18390 | phosphate transport svstem substrate-binding protein |
|  |  |  | phoX | 30190 | alkaline phosphatase |
|  |  |  | phoH | 43330 | phoH like protein |
|  |  |  | phnZ | 52210 | metal dependent phosphohydrolase HD region |
|  |  |  | phoU | 52660 | phosphate transport system requlatory protein |
|  |  |  | ppx | 53740 | exopolyphosphatase |

Figure S5 Heat map of transposase genes and their significant differential expression at each station relative to LET7 for Microcystis．Values are the $\log _{2}$ fold change in gene expression．Blue colors correspond to a decrease in transcript abundance while red colors correspond to an increase in transcript abundance．White denotes no difference from the reference condition．


MAE Number Transposase Family

山山山山
MAE Number Transposase Family


 | $\square$ |  | $\square$ |
| :--- | :--- | :--- |
|  | 34110 |  |
| 34130 |  |  |

IS605
IS605
IS605

IS605
IS605
IS605

ISL3

ISL3／204／100／1096／1165
IS605
IS605
IS605
IS605
IS605
IS605
IS605
｜S605
IS605
IS605
IS66
IS605
IS605
IS605
IS605
IS605
IS605
｜SL3／204／100／1096／1165
IS605
IS110
IS605
IS605



| 36260 |  |  |  |
| :--- | :--- | :--- | :--- |
|  |  |  |  |
| 36520 |  |  |  |

IS605
IS605
IS605
IS605

|  |  |  |
| :--- | :--- | :--- |
|  |  |  |
|  |  |  |

S605
S605

$$
\begin{aligned}
& \text { IS605 } \\
& \text { IS605 }
\end{aligned}
$$

IS605

## IS605

IS605
S605

## IS605

## S605

IS605

$+1$






ISL3
ISL3
｜S605
ISL3
IS605
is605

## IS605

IS605
IS605
IS605

## IS605

IS605
IS605
IS605
IS605
IS605

## IS605

IS605
IS605
ISL3
IS605
IS605
ISL3
IS605
IS605
IS605

78 79

Figure S6 Cyanobacterial abundance during the October transect of the western basin of Lake Erie for the three genera discussed. Stations are ordered from west to east as appearing in Figure 1.


80

81

Figure S7 The number of significant differentially expressed genes in Planktothrix agaradhii NIVA-CYA 15 relative to station LET7 (A), relative to the control (B), and relative to the initial (C). Blue denotes an increase in transcript abundance and yellow denotes a decrease in transcript abundance. Stations are ordered from west to east as appearing in Figure 1.


86 87

Figure S8 The number of significant differentially expressed genes in Anabaena sp. PCC7108 relative to station LET7 (A), relative to the control (B), and relative to the initial (C). Blue denotes an increase in transcript abundance and yellow denotes a decrease in transcript abundance. Stations are ordered from west to east as appearing in Figure 1.


Figure S9 Heat map of transposase genes and their significant differential expression relative to the control for Microcystis. Values are the $\log _{2}$ fold change in gene expression. Blue colors correspond to a decrease in transcript abundance while red colors correspond to an increase in transcript abundance. White denotes no difference from the reference condition.


Figure S10 Heat map of genes involved in DNA replication, restriction, modification, recombination, and repair and their significant differential expression at each station relative to LET7 and under each treatment relative to the control for Microcystis. Values are the $\log _{2}$ fold change in gene expression. Blue colors correspond to a decrease in transcript abundance while red colors correspond to an increase in transcript abundance. White denotes no difference from the reference condition.

## $\log _{2}$ Fold Change

| -1.0782 | 0 | 1.6716 |
| :--- | :--- | :--- |



MAE Number
Product
2360
2480
4450
8090
10280
13000
13870
14620
18110
19880
20800
21630
25180
28300
28520
33690
33970
38670
39060
42270
46790
52930
53850
56630
59890

SNF2 helicase homolog DNA replication and repair protein RecF DNA gvrase subunit A sinale-strand-DNA-specific exonuclease hollidav iunction DNA helicase RuvA putative helicase probable DNA methyltransferase DNA polymerase beta domain DNA polymerase I mutator MutT homolog transcription-repair coupling factor DNA mismatch repair protein formamidopyrimidine-DNA alycosylase DNA repair protein RecN DNA repair protein RecO putative modulator of DNA avrase excinuclease $A B C$ subunit $A$ DNA polymerase III beta subunit single-stranded DNA-bindina protein DNA mismatch repair protein MutL recombination protein RecR hollidav iunction DNA helicase RuvB chromosome partitioning protein DNA topoisomerase I DNA gyrase subunit A

Figure S12 The number of significant differentially expressed transposase genes from Harke, M. J., \& Gobler, C. J. (2013). Global transcriptional responses of the toxic cyanobacterium, Microcystis aeruginosa, to nitrogen stress, phosphorus stress, and growth on organic matter. PLoS ONE, 8(7), e69834. doi: 10.1371/journal.pone. 0069834.
$\square$ Increase $\square$ Decrease


Figure S11 Community analysis via Metaphlan displaying the average \% abundance across two biological replicates for the nutrient enrichment experiments.


