Supplementary material for:

**Microbial communities mediating algal detritus turnover under anaerobic conditions**

Jessica M. Morrison\*1, Chelsea L. Murphy\*1, Kristina Baker1, Richard Zamor2, Steve Nikolai2, Shawn Wilder3, Mostafa S. Elshahed1, Noha H. Youssef1

1Department of Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK, USA

2Grand River Dam Authority (GRDA), Vinita, OK, USA

3Department of Integrative Biology, Oklahoma State University, Stillwater, OK, USA

Running Title: Degradation of algal biomass by anaerobes

Table S1. Number of high-quality sequences, and observed OTU0.03 and OTU0.1 obtained in this study. Datasets are grouped by the inoculum source then by algae type used then by week of enrichment. Species richness estimates (Chao and ACE) and Good’s coverage are also shown for each dataset.

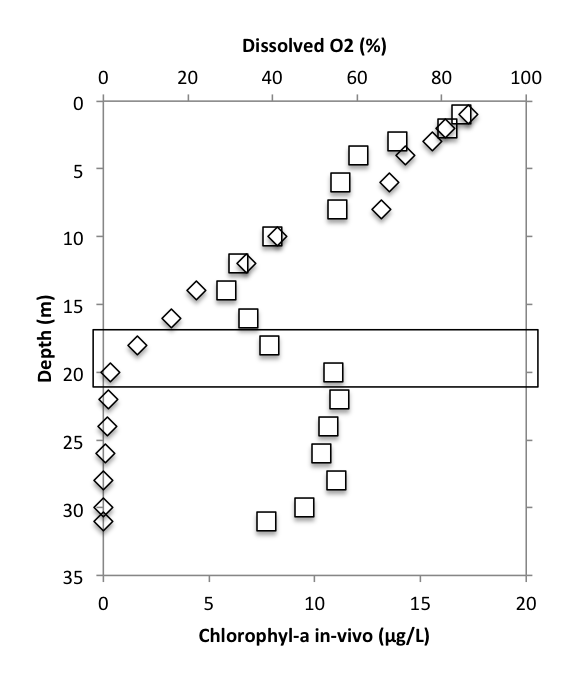
|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Enrichment Source | Algae type | Week of enrichment | # of sequences | 0.03 | | | | 0.1 | | | |
| Coverage | OTUs | Chao | ACE | Coverage | OTUs | Chao | ACE |
| ZDT | None | 0 | 17,310 | 0.898 | 3337 | 6449 | 8674 | 0.982 | 876 | 1346 | 1525 |
| Chara | 7 | 54,440 | 0.99 | 1167 | 2155 | 3031 | 0.998 | 427 | 589 | 566 |
| 10 | 29,906 | 0.987 | 888 | 1531 | 2030 | 0.996 | 365 | 508 | 478 |
| 16 | 39,294 | 0.986 | 1114 | 2323 | 3079 | 0.996 | 433 | 625 | 739 |
| Chlorella | 7 | 16,398 | 0.987 | 506 | 892 | 1091 | 0.994 | 259 | 381 | 464 |
| 10 | 39,740 | 0.989 | 873 | 1691 | 2305 | 0.997 | 373 | 528 | 612 |
| 16 | 50,640 | 0.988 | 1282 | 2560 | 3474 | 0.997 | 454 | 631 | 704 |
| Kelp | 7 | 15,701 | 0.962 | 943 | 2045 | 4004 | 0.988 | 407 | 672 | 904 |
| 10 | 16,459 | 0.957 | 1133 | 2442 | 4358 | 0.989 | 433 | 697 | 874 |
| 16 | 18,341 | 0.969 | 846 | 2171 | 3810 | 0.991 | 357 | 536 | 735 |
| WWT | None | 0 | 16,348 | 0.977 | 792 | 1423 | 1770 | 0.995 | 215 | 358 | 479 |
| Chara | 7 | 17,216 | 0.981 | 735 | 1240 | 1588 | 0.995 | 315 | 424 | 412 |
| 10 | 82,226 | 0.991 | 1606 | 2945 | 3799 | 0.998 | 497 | 704 | 759 |
| 16 | 39,150 | 0.987 | 1187 | 1997 | 2650 | 0.997 | 416 | 586 | 669 |
| Chlorella | 7 | 9,827 | 0.971 | 645 | 1076 | 1372 | 0.990 | 293 | 425 | 468 |
| 10 | 28,353 | 0.987 | 928 | 1468 | 1721 | 0.996 | 363 | 547 | 549 |
| 16 | 52,042 | 0.991 | 1090 | 1887 | 2214 | 0.998 | 407 | 528 | 515 |
| Kelp | 7 | 50,137 | 0.99 | 645 | 1959 | 2780 | 0.998 | 313 | 474 | 612 |
| 10 | 42,544 | 0.989 | 854 | 1820 | 2718 | 0.997 | 267 | 429 | 585 |
| 16 | 52,653 | 0.994 | 620 | 1312 | 1837 | 0.998 | 206 | 359 | 458 |
| GL | None | 0 | 12,320 | 0.974 | 527 | 1120 | 1729 | 0.991 | 249 | 397 | 512 |
| Chara | 4 | 33,765 | 0.996 | 263 | 657 | 1114 | 0.998 | 118 | 228 | 315 |
| 8 | 17,584 | 0.993 | 244 | 563 | 776 | 0.997 | 114 | 261 | 346 |
| 13 | 6,945 | 0.989 | 154 | 379 | 396 | 0.997 | 71 | 106 | 98 |
| Chlorella | 4 | 14,464 | 0.993 | 209 | 365 | 506 | 0.996 | 119 | 214 | 316 |
| 8 | 23,447 | 0.995 | 244 | 458 | 553 | 0.998 | 125 | 208 | 241 |
| 13 | 28,407 | 0.995 | 307 | 518 | 812 | 0.998 | 153 | 213 | 222 |
| Kelp | 4 | 132 | 0.788 | 39 | 228 | 329 | 0.848 | 33 | 81 | 140 |
| 8 | 3,971 | 0.968 | 366 | 459 | 488 | 0.987 | 202 | 230 | 241 |
| 13 | 18,027 | 0.983 | 655 | 1127 | 1375 | 0.994 | 306 | 463 | 526 |

Table S2. Detailed bacterial and archaeal community composition in the 9 microcosms studied as compared to the source inoculum (T0). Datasets are grouped by the inoculum source then by algae type used then by week of enrichment. Values are percentages of total sequences affiliated with Bacteria or Archaea. The number of sequences affiliated with Archaea in all GL enrichments and inmost of the WWT enrichments were either completely absent or were <50 sequences total and so archaeal community composition is not reported in these datasets.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Inoculum source | Phyla | T0 | Chara | | | Chlorella | | | Kelp | | |
| T7 | T10 | T16 | T7 | T10 | T16 | T7 | T10 | T16 |
| ZDT | **Archaeal phyla/classes** | | | | | | | | | | |
| Methanobacteria | 0.478 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Methanococci | 0.957 | 0 | 0 | 0 | 79.660 | 0 | 3.090 | 1.720 | 0.850 | 0 |
| Methanomicrobia | 7.177 | 78.470 | 69.880 | 31.940 | 13.560 | 61.700 | 42.270 | 12.070 | 21.370 | 16.360 |
| Thermoplasmata | 8.612 | 9.030 | 8.430 | 18.750 | 3.390 | 2.130 | 6.190 | 8.620 | 8.550 | 7.270 |
| Other Euryarchaeota | 10.048 | 0 | 0 | 0.690 | 0 | 4.260 | 11.340 | 3.450 | 3.420 | 0 |
| Bathyarchaeota | 12.440 | 8.330 | 13.250 | 40.280 | 0 | 8.510 | 21.650 | 3.450 | 0.850 | 3.640 |
| Thaumarchaeota | 54.060 | 4.170 | 7.230 | 8.330 | 3.390 | 21.280 | 14.430 | 67.240 | 63.250 | 72.730 |
| Unclassified Archaea | 6.220 | 0 | 0 | 0 | 0 | 2.130 | 1.040 | 3.450 | 1.710 | 0 |
| **Bacterial phyla/classes** | | | | | | | | | | |
| Acidobacteria | 1.524 | 0.037 | 0.073 | 0.118 | 0.019 | 0.031 | 0.039 | 0.105 | 0.311 | 0.052 |
| Actinobacteria | 10.795 | 0.133 | 0.209 | 0.145 | 0.224 | 0.597 | 0.661 | 2.445 | 3.872 | 3.741 |
| BD1-5 | 0.006 | 0.023 | 0.007 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Bacteroidetes | 17.321 | 30.565 | 29.523 | 39.186 | 12.659 | 10.133 | 17.345 | 5.822 | 1.768 | 1.094 |
| Caldiserica | 0 | 0 | 0 | 0 | 0 | 0.005 | 0.047 | 0 | 0 | 0 |
| Candidate\_division\_BRC1 | 0 | 0.023 | 0.017 | 0.018 | 0.025 | 0.010 | 0.008 | 0 | 0 | 0 |
| Candidate\_division\_JS1 | 0.095 | 0.002 | 0 | 0 | 0 | 0.005 | 0.008 | 0.013 | 0.006 | 0 |
| Candidate\_division\_OD1 | 0.006 | 0.002 | 0 | 0 | 0 | 0 | 0 | 0.007 | 0 | 0 |
| Candidate\_division\_OP11 | 0 | 0 | 0 | 0.003 | 0 | 0.003 | 0.004 | 0 | 0 | 0 |
| Candidate\_division\_OP3 | 0.019 | 0 | 0 | 0 | 0 | 0 | 0.002 | 0.007 | 0.026 | 0 |
| Candidate\_division\_OP8 | 0.341 | 0.006 | 0.007 | 0.008 | 0.019 | 0.039 | 0.327 | 0.079 | 0.142 | 0.040 |
| Candidate\_division\_SR1 | 0.196 | 0.002 | 0 | 0 | 0 | 0 | 0 | 0.033 | 0 | 0.011 |
| Candidate\_division\_TM7 | 0.013 | 0.004 | 0 | 0.005 | 0 | 0 | 0 | 0 | 0 | 0 |
| Chlorobi | 0.171 | 0.054 | 0.056 | 0.179 | 0.043 | 0.036 | 0.114 | 0.007 | 0.019 | 0.017 |
| Chloroflexi | 6.292 | 0.239 | 0.689 | 0.886 | 0.286 | 0.929 | 2.098 | 0.361 | 0.699 | 0.350 |
| Cyanobacteria | 0.329 | 0.056 | 0.049 | 0.039 | 7.816 | 6.560 | 4.204 | 3.160 | 4.008 | 2.785 |
| Deferribacteres | 0.341 | 0 | 0 | 0 | 0.006 | 0.003 | 0.004 | 0.013 | 0.045 | 0.011 |
| Deinococcus-Thermus | 0.032 | 0.010 | 0 | 0.011 | 0 | 0.003 | 0 | 0 | 0.006 | 0.006 |
| Elusimicrobia | 0 | 0.027 | 0.014 | 0.008 | 0.360 | 0.093 | 0.093 | 0.007 | 0 | 0 |
| Fibrobacteres | 0 | 0.039 | 0.007 | 0.003 | 0 | 0 | 0 | 0 | 0 | 0 |
| Firmicutes | 8.069 | 18.009 | 20.769 | 22.485 | 43.155 | 54.223 | 43.288 | 74.103 | 68.383 | 63.468 |
| Fusobacteria | 0.006 | 0.035 | 0.014 | 0.008 | 0.068 | 0.023 | 0.002 | 0.079 | 0 | 0 |
| Gemmatimonadetes | 0.095 | 0.013 | 0.007 | 0.011 | 0 | 0 | 0.008 | 0.020 | 0.013 | 0.011 |
| Hyd24-12 | 0.525 | 0 | 0 | 0 | 0.006 | 0.010 | 0 | 0.013 | 0.013 | 0.006 |
| Lentisphaerae | 0.108 | 0.142 | 0.330 | 0.181 | 0.137 | 0.085 | 0.233 | 0.013 | 0 | 0.017 |
| Nitrospirae | 0.038 | 0 | 0 | 0 | 0.012 | 0 | 0.002 | 0.052 | 0.013 | 0.006 |
| Planctomycetes | 2.416 | 0.177 | 0.184 | 0.134 | 0.130 | 0.090 | 0.172 | 0.157 | 0.220 | 0.235 |
| Alphaproteobacteria | 11.155 | 1.016 | 0.410 | 0.273 | 4.141 | 2.488 | 1.581 | 1.036 | 1.800 | 0.951 |
| Betaproteobacteria | 1.322 | 0.296 | 0.177 | 0.134 | 0.019 | 0.013 | 0.018 | 0.426 | 0.227 | 0.155 |
| Deltaproteobacteria | 6.672 | 14.904 | 20.456 | 11.157 | 21.394 | 15.610 | 18.114 | 2.249 | 2.357 | 2.876 |
| Epsilonproteobacteria | 0.386 | 1.684 | 1.495 | 0.507 | 1.136 | 2.441 | 0.690 | 0.118 | 0.097 | 0.097 |
| Gammaproteobacteria | 12.332 | 17.234 | 12.061 | 8.675 | 0.168 | 0.159 | 0.191 | 1.541 | 1.891 | 0.991 |
| Other Proteobacteria | 1.549 | 0.296 | 0.563 | 0.305 | 0.453 | 0.818 | 1.138 | 0.072 | 0.110 | 0.052 |
| SHA-109 | 0.006 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Spirochaetae | 2.397 | 8.986 | 7.877 | 8.134 | 4.470 | 2.868 | 5.984 | 6.058 | 11.415 | 20.358 |
| Synergistetes | 0.076 | 0.472 | 0.417 | 0.302 | 0.317 | 0.412 | 0.513 | 0.052 | 0.058 | 0.023 |
| TM6 | 0.013 | 0 | 0 | 0.005 | 0.068 | 0.286 | 0.146 | 0 | 0.013 | 0 |
| Tenericutes | 0.841 | 0.566 | 0.254 | 0.368 | 0.596 | 0.365 | 0.438 | 0.538 | 0.544 | 0.183 |
| Thermotogae | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.007 | 0.006 | 0 |
| Verrucomicrobia | 0.247 | 0.040 | 0.045 | 0.055 | 0 | 0.008 | 0.004 | 0.039 | 0.065 | 0.940 |
| WCHB1-60 | 0.006 | 0 | 0 | 0 | 0 | 0.005 | 0.002 | 0.007 | 0.013 | 0.011 |
| Unclassified | 14.260 | 4.907 | 4.246 | 6.625 | 2.223 | 1.608 | 2.490 | 1.364 | 1.858 | 1.501 |
|  |  |  |  |  |  |  |  |  |  |  |  |
| WWT | **Archaeal phyla/classes** | | | | | | | | | | |
| Methanomicrobia | 0 | 0 | 99.664 | 98.806 | 0 | 0 | 0 | 0 | 0 | 0 |
| Thaumarchaeota | 0 | 0 | 0.336 | 0.597 | 0 | 0 | 0 | 0 | 0 | 0 |
| Bathyarchaeota | 0 | 0 | 0 | 0.597 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Bacterial phyla/classes** | | | | | | | | | | |
| Acidobacteria | 0.107 | 0.165 | 0.144 | 0.181 | 0.270 | 0.300 | 0.148 | 0.098 | 0.078 | 0.015 |
| Actinobacteria | 0.181 | 0.412 | 0.238 | 0.299 | 0.301 | 0.218 | 0.270 | 0.167 | 0.603 | 1.604 |
| Aquificae | 0 | 0 | 0 | 0 | 0 | 0 | 0.002 | 0 | 0 | 0 |
| Armatimonadetes | 0 | 0 | 0 | 0 | 0 | 0.011 | 0.019 | 0 | 0 | 0 |
| BD1-5 | 0.008 | 0.059 | 0.536 | 0.115 | 0.603 | 0.029 | 0.002 | 0.006 | 0.007 | 0 |
| Bacteroidetes | 43.485 | 17.761 | 33.054 | 39.128 | 33.590 | 26.415 | 33.460 | 5.729 | 4.742 | 1.680 |
| Caldiserica | 0.008 | 0.006 | 0.009 | 0.024 | 0 | 0.014 | 0.021 | 0 | 0 | 0 |
| Candidate\_division\_BRC1 | 0.049 | 0.012 | 0.008 | 0.030 | 0 | 0.018 | 0.021 | 0 | 0 | 0 |
| Candidate\_division\_OD1 | 0 | 0 | 0 | 0 | 0 | 0 | 0.002 | 0 | 0 | 0 |
| Candidate\_division\_OP3 | 0.008 | 0 | 0 | 0 | 0 | 0.004 | 0.014 | 0.002 | 0 | 0 |
| Candidate\_division\_OP9 | 0 | 0 | 0 | 0 | 0 | 0.007 | 0 | 0 | 0 | 0 |
| Candidate\_division\_SR1 | 0 | 0 | 0.028 | 0.012 | 0.021 | 0 | 0 | 0 | 0 | 0 |
| Candidate\_division\_TM7 | 0 | 0.006 | 0.003 | 0 | 0 | 0.004 | 0 | 0 | 0 | 0 |
| Chlamydiae | 0 | 0 | 0.001 | 0.006 | 0 | 0 | 0 | 0 | 0 | 0 |
| Chlorobi | 1.214 | 0.318 | 0.789 | 1.556 | 0.301 | 0.868 | 1.345 | 0.018 | 0.005 | 0.002 |
| Chloroflexi | 0.312 | 0.300 | 0.247 | 0.522 | 0.229 | 0.500 | 0.655 | 0.002 | 0.007 | 0.002 |
| Cyanobacteria | 0.304 | 15.184 | 0.030 | 0.100 | 0.042 | 13.084 | 4.629 | 0.207 | 0.243 | 0.091 |
| Deferribacteres | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.005 | 0.002 |
| Deinococcus-Thermus | 0 | 0 | 0.004 | 0.006 | 0.021 | 0 | 0 | 0.002 | 0 | 0.002 |
| Elusimicrobia | 0.107 | 0.271 | 0.129 | 0.066 | 0.083 | 0.214 | 0.288 | 0.046 | 0.026 | 0.006 |
| Fibrobacteres | 0 | 0 | 0.015 | 0.012 | 0.021 | 0 | 0 | 0.002 | 0.005 | 0.002 |
| Firmicutes | 9.608 | 9.260 | 10.911 | 13.096 | 12.384 | 11.462 | 7.879 | 20.142 | 28.622 | 68.106 |
| Fusobacteria | 0 | 0.035 | 0.016 | 0.012 | 0.042 | 0.007 | 0.008 | 0.419 | 0.482 | 0.088 |
| Gemmatimonadetes | 0 | 0 | 0.001 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Lentisphaerae | 1.748 | 0.665 | 0.771 | 0.501 | 0.758 | 0.593 | 1.415 | 0.026 | 0.019 | 0.013 |
| Planctomycetes | 0.041 | 0.159 | 0.044 | 0.039 | 0.042 | 0.125 | 0.247 | 0 | 0 | 0.006 |
| Alphaproteobacteria | 0.139 | 0.482 | 0.279 | 0.383 | 0.281 | 0.357 | 0.369 | 0.789 | 0.411 | 0.095 |
| Betaproteobacteria | 0.788 | 1.565 | 1.271 | 0.661 | 1.932 | 1.065 | 0.527 | 6.483 | 5.777 | 2.420 |
| Deltaproteobacteria | 10.535 | 33.527 | 25.414 | 9.199 | 30.556 | 12.387 | 4.808 | 0.514 | 0.553 | 0.181 |
| Epsilonproteobacteria | 3.307 | 2.865 | 2.795 | 3.867 | 3.158 | 3.724 | 1.689 | 39.258 | 37.155 | 11.075 |
| Gammaproteobacteria | 0.673 | 2.077 | 1.141 | 0.947 | 2.016 | 0.829 | 0.396 | 25.192 | 20.510 | 14.443 |
| other Proteobacteria | 0.246 | 0.141 | 0.228 | 0.042 | 0.052 | 1.762 | 0.976 | 0.032 | 0.021 | 0.011 |
| SHA-109 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.002 | 0 |
| Spirochaetae | 14.990 | 6.554 | 11.841 | 19.077 | 5.330 | 13.846 | 28.463 | 0.054 | 0.026 | 0.015 |
| Synergistetes | 2.117 | 2.577 | 4.304 | 3.818 | 3.626 | 4.392 | 3.761 | 0.287 | 0.213 | 0.027 |
| TM6 | 0.016 | 0 | 0.005 | 0.003 | 0 | 0.007 | 0 | 0 | 0 | 0 |
| Tenericutes | 0.090 | 0.094 | 0.054 | 0.247 | 0.094 | 0.082 | 0.101 | 0.006 | 0.005 | 0 |
| Thermotogae | 0.131 | 0.018 | 0.049 | 0.178 | 0 | 0.025 | 0.492 | 0 | 0 | 0 |
| Verrucomicrobia | 1.173 | 0.471 | 0.177 | 0.247 | 0.208 | 0.590 | 0.857 | 0.150 | 0.116 | 0.032 |
| unclassified | 8.615 | 5.018 | 5.465 | 5.625 | 4.042 | 7.059 | 7.137 | 0.369 | 0.366 | 0.082 |
|  |  |  |  |  |  |  |  |  |  |  |  |
| GL | **Bacterial phyla/classes** | T0 | Chara | | | Chlorella | | | Kelp | | |
| T4 | T8 | T13 | T4 | T8 | T13 | T4 | T8 | T13 |
| Acidobacteria | 0.146 | 0.003 | 0 | 0 | 0.016 | 0.009 | 0.046 | 0 | 0.881 | 0.338 |
| Actinobacteria | 1.696 | 0.074 | 0.014 | 0.063 | 0.275 | 0.176 | 0.127 | 0.758 | 1.712 | 0.782 |
| Aquificae | 0 | 0.003 | 0 | 0.006 | 0 | 0.005 | 0 | 0 | 0 | 0.011 |
| BD1-5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.011 |
| Bacteroidetes | 0.804 | 7.304 | 12.498 | 13.583 | 7.731 | 10.226 | 10.693 | 6.061 | 3.979 | 1.093 |
| Candidate\_division\_BRC1 | 0 | 0 | 0 | 0.006 | 0 | 0 | 0 | 0 | 0.176 | 0.039 |
| Candidate\_division\_OP10 | 0.041 | 0 | 0 | 0.046 | 0 | 0.009 | 0 | 0 | 0.050 | 0.078 |
| Candidate\_division\_OP8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.006 |
| Candidate\_division\_SR1 | 0.024 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Candidate\_division\_TM6 | 0.024 | 0 | 0 | 0.006 | 0 | 0 | 0 | 0 | 0.025 | 0.044 |
| Candidate\_division\_TM7 | 0 | 0.003 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Candidate\_division\_WS3 | 0.041 | 0 | 0 | 0 | 0 | 0.005 | 0.004 | 0 | 0.227 | 0.100 |
| Chlamydiae | 0.032 | 0 | 0 | 0 | 0 | 0.005 | 0.004 | 0 | 0.025 | 0.033 |
| Chlorobi | 0.081 | 0 | 0 | 0 | 0 | 0.005 | 0.039 | 0 | 0.025 | 0.044 |
| Chloroflexi | 0.260 | 0.012 | 0.043 | 0.006 | 0.024 | 0.036 | 0.039 | 0 | 0.680 | 0.233 |
| Cyanobacteria | 5.008 | 0.113 | 0.187 | 0.108 | 0 | 0 | 2.260 | 19.700 | 35.030 | 22.910 |
| Deferribacteres | 0.008 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.050 | 0.055 |
| Deinococcus-Thermus | 0.057 | 0.003 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Fibrobacteres | 0.008 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Firmicutes | 0.390 | 14.789 | 20.778 | 19.015 | 21.834 | 11.871 | 9.781 | 25.758 | 20.927 | 60.568 |
| Fusobacteria | 0.008 | 0 | 0 | 0 | 0.016 | 0 | 0.028 | 0 | 0 | 0.006 |
| Gemmatimonadetes | 0.073 | 0 | 0 | 0 | 0 | 0.005 | 0.004 | 0 | 0.025 | 0.128 |
| Lentisphaerae | 0.008 | 0 | 0 | 0 | 0.008 | 0 | 0 | 0 | 0.076 | 0.033 |
| NPL-UPA2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.006 |
| Nitrospirae | 0.008 | 0 | 0 | 0 | 0.008 | 0 | 0 | 0 | 0 | 0.055 |
| OPS8 | 0.008 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Planctomycetes | 0.528 | 0.027 | 0.014 | 0.023 | 0.146 | 0.072 | 0.063 | 3.788 | 3.274 | 2.008 |
| Alphaproteobacteria | 1.384 | 0.113 | 0.173 | 0.119 | 0.307 | 0.135 | 0.137 | 2.273 | 4.533 | 2.291 |
| Betaproteobacteria | 1.230 | 0.053 | 0.029 | 0.040 | 0.202 | 0.068 | 0.115 | 2.273 | 5.011 | 2.779 |
| Deltaproteobacteria | 0.436 | 6.481 | 6.911 | 8.458 | 14.734 | 18.956 | 22.254 | 16.667 | 2.367 | 1.032 |
| Epsilonproteobacteria | 0.094 | 0.003 | 0.029 | 0.011 | 0 | 0 | 0.011 | 4.545 | 0.252 | 0.006 |
| Gammaproteobacteria | 91.823 | 71.014 | 59.294 | 58.472 | 54.569 | 56.792 | 53.979 | 17.424 | 19.214 | 4.627 |
| Other Proteobacteria | 0 | 0.003 | 0 | 0 | 0 | 0 | 0 | 0 | 0.025 | 0 |
| Spirochaetes | 0.106 | 0 | 0.029 | 0.023 | 0.081 | 1.582 | 2.007 | 0 | 0.176 | 0.011 |
| Synergistetes | 0.016 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.076 | 0.006 |
| Thermodesulfobacteria | 0.008 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Verrucomicrobia | 0.390 | 0.003 | 0 | 0.017 | 0.040 | 0.045 | 0.141 | 0.758 | 1.184 | 0.671 |
| WCHB1-60 | 0.016 | 0 | 0 | 0 | 0.008 | 0 | 0 | 0 | 0 | 0 |
| Unclassified | 0 | 0.012 | 0 | 0.017 | 0 | 0 | 0 | 0 | 0 | 0 |
|  |  |  |  |  |  |  |  |  |  |  |  |

**Supplementary figures:**

**Figure S1**. Chlorophyll-a levels and oxygen concentration along depth in Grand Lake sites used as inoculum source in this study. Chlorophyll A concentration is shown as 🞎 on the primary X-axis, while average dissolved O2 is shown as ◇ on the secondary X-axis. Boxed region depicts the depth at which the samples were obtained for this study.



**Figure S2.** Change in sulfate concentration with enrichment time in ZDT (A), WWT (B), and GL (C) enrichments on Chara (△), Chlorella (□), and Kelp (◇).

