**Supporting Information**

**Supporting Tables**

**Table A.** Summary of Results Obtained with the MAGC Approach in Comparison to the WGPB Approach for Metatranscriptomes from the Two Oceanic Regions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Organism | Category | WGPB [1,2] | | MAGC (This study) | | |
| Average per sample ± sd | Total | Average per sample ± sd | Total | Reads total as percent of reads identified by WGPB |
| **North Pacific Subtropical Gyre** | | | | | | |
| All | Reads | 4.1±1.0 E+06 | 0.12 E+09a | 22.6±9.5 E+03 | 0.68 E+06 | 0.55 |
| *Prochlorococcus* | Reads | 96±37 E+03 | 2.9 E+06 | 10.6±4.7 E+03 | 0.32 E+06 | 11.0 |
| Transcript-OTUs |  | 2.8 E+03 |  | 791b |  |
| Genes |  | 2.8 E+03 |  | 54c |  |
| SAR11 | Reads | 26±8 E+03 | 0.77 E+06 | 104±53 | 3.1 E+03 | 0.40 |
| Transcript-OTUs |  | 2.8 E+03 |  | 49b |  |
| Genes |  | 2.8 E+03 |  | 4c |  |
| **California Current System** | | | | | | |
| All | Reads | 0.77±0.24 E+06 | 1.0 E+07q | 2.9±1.4 E+03 | 3.8 E+04 | 0.38 |
| *Synechococcus* | Reads | 10.5±4.6 E+03 | 0.14 E+06 | 500±200 | 6.5 E+03 | 4.70 |
| Transcript-OTUs |  | 4.0 E+03 |  | 98b |  |
| Genes |  | 4.0 E+03 |  | 37c |  |
| SAR11 | Reads | 13.5±3.2 E+03 | 0.18 E+06 | 110±38 | 1.4 E+03 | 0.82 |
| Transcript-OTUs |  | 1.8 E+03 |  | 83b |  |
| Genes |  | 1.8 E+03 |  | 3c |  |
| *Ostreococcus* | *rbcL* reads | 0.97±0.65 E+03 | 12.6 E+03 | 170±88 | 2.2 E+03 | 17.6 |

Nucleotide sequences (reads) detected in this study in all samples, average per sample and as percent of reads detected by WGPB are shown.

a The total read number includes reads for ribosomal RNA

b Number of transcripts detected as described in the Methods.

c Number of genes with detected transcription (for example, *psaA, psbA, coxA*).

**Table B.** Genes with Similar Transcriptional Patterns among *Prochlorococcus* OTUs during the 72-h Study in the NPSG.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Annotation** | **KEGG Pathway** | **OTU-transcripts detected** |
| *amt* | ammonium transporter | Membrane transport | 16 |
| *coxA* | cytochrome c oxidase subunit I | Energy metabolism (oxidative phosphorylation) | 15 |
| *coxB* | cytochrome c oxidase subunit II | Energy metabolism (oxidative phosphorylation) | 7 |
| *fur* | Fur family transcriptional regulator; Ferric uptake regulator | Transcription factors | 9 |
| *glnA* | glutamine synthetase, type I | Amino acid metabolism | 2 |
| *kaiC* | circadian clock protein KaiC | [Circadian clock] | 8 |
| *sodN* | nickel-containing superoxide dismutase (NiSOD) | [Oxidative stress response] | 2 |
| *phrB* | similar to DNA photolyase | Replication and repair | 5 |
| *pip* | proline iminopeptidase | Amino acid metabolism | 10 |
| *pmm1148* | possible EF-1 guanine nucleotide exchange domain | Nucleotide metabolism | 9 |
| *pmm1359* | predicted membrane protein PMM1359 | Membrane transport | 9 |
| *psaB* | photosystem I P700 chlorophyll a apoprotein A10 | Energy metabolism (photosynthesis) | 28 |
| *psbA* | photosystem II PsbA protein (D1) | Energy metabolism (photosynthesis) | 15 |
| *ptox* | plastoquinol terminal oxidase | Energy metabolism | 5 |
| *rbcL* | RuBisCO, large chain | Carbon metabolism (carbon fixation) | 3 |
| *urtA* | urea substrate binding transporter protein | Membrane transport | 13 |
| **SUM** | **16** |  | **161** |

For each gene, number of reads identified using MAGC for all samples and as a percent relative to the number of reads identified by WGPB [2], correlation (the Pearson correlation coefficient) between results obtained by the two approaches and number of transcript-OTUs identified in all samples are shown. In the KEGG pathway column, the square brackets indicate pathways/metabolisms/processes that do not have KEGG assignment.

**Table C.** Genes with Similar Transcriptional Patterns among *Synechococcus* OTUs during the 48-h Study in the CCS.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Annotation** | **KEGG Pathway** | **OTU-transcripts detected** |
| *amt* | ammonium transporter | Membrane transport | 3 |
| *cpaB2* | phycocyanin, beta subunit | Energy metabolism (photosynthesis) | 2 |
| *dxs* | 1-deoxy-D-xylulose-5-phosphate synthase | Carbohydrate and lipid metabolism | 7 |
| *glnA* | glutamine synthetase, type I | Amino acid metabolism | 4 |
| *idiA* | iron ABC transporter, substrate binding protein | Membrane transport | 6 |
| *isiB* | flavodoxin | Energy metabolism (photosynthesis) | 3 |
| *kaiC* | circadian clock protein KaiC | [Circadian clock] | 7 |
| *phoH* | phosphate starvation-inducible protein | [Phosphorus stress response] | 3 |
| *pmm1148* | possible EF-1 guanine nucleotide exchange domain | Nucleotide metabolism | 2 |
| *pyk* | pyruvate kinase | Carbon metabolism (glycolysis) | 5 |
| *sodC* | copper/zinc superoxide dismutase | [Oxidative stress response] | 3 |
| **SUM** | **11** |  | **55** |

For each gene, number of reads identified using MAGC for all samples and as a percent relative to the number of reads identified by WGPB [1], correlation (the Pearson correlation coefficient) between results obtained by the two approaches and number of transcript-OTUs identified in all samples are shown. In the KEGG pathway column, the square brackets indicate pathways/metabolisms/processes that do not have KEGG assignment.

**Table D. Phosphate Concentrations and Primary Production during the NPSG Cruise.** Concentrations of phosphate were obtained from Robidart *et al.* [3], and primary production rates were obtained from Bombar *et al.* [4]. Primary production had a significant positive relationship with phosphate concentrations over the course of the NPSG cruise (r=0.38, n=5).

|  |  |  |
| --- | --- | --- |
| Date | Phosphate (μmol) | Primary production (nmol C L-1 day-1) |
| 9/10/11 | 0.017 | 229 |
| 9/11/11 | 0.127 | 237 |
| 9/13/11 | 0.099 | 135 |
| 9/16/11 | 0.143 | 330 |
| 9/18/11 | 0.118 | 400 |

**References**

1. Ottesen EA, Young CR, Eppley JM, Ryan JP, Chavez FP, Scholin CA, et al. Pattern and synchrony of gene expression among sympatric marine microbial populations. Proc Natl Acad Sci U S A. 2013;110(6): E488-E97.
2. Ottesen EA, Young CR, Gifford SM, Eppley JM, Marin R, Schuster SC, et al. Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. Science. 2014;345(6193): 207-12.
3. Robidart JC, Church MJ, Ryan JP, Ascani F, Wilson ST, Bombar D, et al. Ecogenomic sensor reveals controls on N2-fixing microorganisms in the North Pacific Ocean. ISME J. 2014;8(6): 1175-85.
4. Bombar D, Taylor CD, Wilson ST, Robidart JC, Rabines A, Turk-Kubo KA, et al. Measurements of nitrogen fixation in the oligotrophic North Pacific Subtropical Gyre using a free-drifting submersible incubation device. J Plankton Res. 2015;37: 727-739.